

Table S1. Significance of differences in abundance of molecular components detected by MSI between tissue regions shown as the Cohen's d effect size

MSI molecular component (m/z)	Tumor vs. normal Thyroid	Metastasis vs. normal LN	Tumor vs. Metastasis	normal Thyroid vs. normal LN
699,45	0,0815	-0,1035	-0,0432	-0,1983
699,62	0,0813	-0,0716	-0,0572	-0,1888
699,87	0,0829	-0,0759	-0,0774	-0,1956
700,18	0,0793	-0,0953	-0,0550	-0,1962
700,38	0,2165	-0,1918	-0,0929	-0,4692
701,31	0,2080	-0,1220	-0,0245	-0,3727
701,40	0,1381	-0,0416	-0,0059	-0,1791
702,33	0,3390	-0,1606	-0,1017	-0,5219
702,40	0,3466	-0,1297	-0,0143	-0,4405
703,39	0,3448	-0,2031	0,2273	-0,3192
704,39	0,1593	-0,0749	-0,0195	-0,2352
705,40	0,1180	-0,1518	-0,0240	-0,2673
706,39	0,0608	-0,1279	-0,1090	-0,2524
707,39	0,0492	-0,0905	-0,0863	-0,2381
708,33	0,1246	-0,1515	-0,0475	-0,2520
708,38	0,1201	-0,1254	-0,0074	-0,2115
709,34	0,2006	-0,2151	0,1508	-0,2382
710,36	0,0036	-0,1223	0,0180	-0,1144
711,42	0,0611	-0,1327	-0,1036	-0,2426
712,40	0,0948	-0,1627	-0,1037	-0,3247
713,42	0,0564	-0,1332	-0,0660	-0,2384
714,42	-0,0059	-0,1201	-0,0450	-0,1362
715,42	0,1163	-0,0422	0,2150	0,0588
716,33	0,1342	-0,1510	0,1212	-0,1639
716,44	0,1750	-0,1487	0,1933	-0,1312
717,42	0,1179	-0,1081	-0,0452	-0,2387
718,38	0,0355	-0,1314	-0,0451	-0,2238
718,41	0,0397	-0,1664	-0,0464	-0,2613
719,41	0,0345	-0,1297	-0,0951	-0,2315
720,41	0,0545	-0,1221	-0,0558	-0,2191
721,42	0,0477	-0,1155	-0,0752	-0,2304
722,39	0,0810	-0,1465	-0,1206	-0,2849
723,37	0,0398	-0,1051	-0,1036	-0,2219
723,46	0,0095	-0,0697	-0,1955	-0,2308
724,36	0,1066	-0,1139	-0,0720	-0,2953
724,41	0,1256	-0,1521	-0,1735	-0,3799
725,42	0,1114	-0,1160	-0,0545	-0,3051
726,40	0,0561	-0,1052	-0,1396	-0,2539
727,42	0,1561	-0,2089	-0,1305	-0,4145
728,42	0,0562	-0,1110	-0,1390	-0,2760
729,43	0,0239	-0,1085	-0,1424	-0,2571
730,38	0,4047	-0,1993	-0,1106	-0,5885
731,40	0,3290	-0,1219	-0,1329	-0,4828
731,43	0,3881	-0,1562	-0,1915	-0,5865
731,72	0,1202	-0,0916	-0,3370	-0,5063
732,41	0,1836	-0,1570	-0,1104	-0,4079
733,18	0,0682	-0,0731	-0,0892	-0,2213
733,42	0,0650	-0,1152	-0,0777	-0,2154
733,42	0,0845	-0,1559	-0,0877	-0,2934
734,43	0,0709	-0,1794	-0,1350	-0,3325
735,31	0,0284	-0,0930	-0,0230	-0,1813
735,42	0,0210	-0,1745	-0,0922	-0,2906
735,60	0,0504	-0,1675	-0,2318	-0,3748
736,33	0,0378	-0,1314	0,0068	-0,1656
736,42	0,0181	-0,1129	-0,0636	-0,1952
737,42	0,0201	-0,1354	0,0017	-0,1495
737,79	0,1935	-0,1404	-0,2372	-0,4801
738,39	0,1255	-0,1975	-0,0363	-0,3134
739,38	0,0634	-0,1142	-0,0490	-0,2109
739,44	0,0728	-0,0875	-0,0890	-0,2504
740,40	0,0700	-0,1439	-0,1096	-0,2789
741,43	0,0783	-0,1357	-0,1196	-0,3100
742,38	0,0395	-0,1182	-0,0829	-0,2327
742,45	0,0299	-0,0726	-0,0910	-0,1658
743,46	0,0998	-0,0899	-0,1160	-0,2778
744,41	0,1806	-0,1674	-0,1070	-0,3980
745,44	0,0766	-0,1286	-0,0472	-0,2409
746,34	0,1086	-0,1545	-0,0686	-0,2869
746,42	0,1425	-0,1580	-0,0737	-0,3185
747,52	0,0779	-0,2189	-0,2119	-0,4525
748,42	0,0197	-0,1133	-0,1107	-0,2411
749,42	0,0646	-0,1240	-0,1125	-0,2733
750,42	0,0318	-0,1605	-0,0654	-0,2207
751,42	0,0455	-0,1058	-0,1021	-0,2141
752,40	0,1067	-0,1096	-0,1300	-0,3140

753,42	0,1116	-0,1156	-0,1034	-0,3066
754,42	0,0701	-0,1200	-0,0988	-0,2697
755,40	0,0493	-0,1097	-0,0888	-0,2450
755,53	0,1278	-0,0903	-0,1267	-0,3133
756,45	0,0527	-0,1467	-0,1445	-0,3155
757,43	0,0209	-0,0803	-0,0881	-0,1771
757,44	0,0389	-0,1255	-0,1235	-0,2775
758,41	0,1587	-0,2032	-0,1742	-0,4530
759,39	0,0465	-0,1745	-0,0777	-0,2536
759,45	0,0325	-0,1831	-0,1034	-0,2914
760,42	0,0534	-0,1712	-0,1346	-0,3605
761,41	0,0004	-0,1170	-0,1639	-0,2589
762,40	-0,0075	-0,1076	-0,1572	-0,2324
763,51	0,0270	-0,1942	-0,2424	-0,3708
764,41	0,0269	-0,1775	-0,0774	-0,2213
764,45	0,0450	-0,1841	-0,1549	-0,3084
765,44	0,0514	-0,1486	-0,0845	-0,2575
766,42	0,0560	-0,1977	-0,1224	-0,3261
767,42	-0,0016	-0,1869	-0,0914	-0,2324
768,35	0,0632	-0,1592	-0,0772	-0,2817
768,43	0,0622	-0,1293	-0,0775	-0,2446
769,31	0,0729	-0,1501	-0,0742	-0,3172
769,44	0,1085	-0,1431	-0,1092	-0,3260
770,42	0,0143	-0,1020	-0,0955	-0,2040
771,42	0,1148	-0,2638	-0,0509	-0,4290
772,43	-0,0621	-0,1480	-0,2379	-0,3032
773,43	-0,0386	-0,0725	-0,1458	-0,1488
774,42	0,0530	-0,1327	-0,0732	-0,2496
775,37	0,1975	-0,1061	-0,0596	-0,3288
775,49	0,7752	-0,2314	-0,1030	-0,8789
776,36	0,0889	-0,1021	-0,0721	-0,2661
776,50	0,5543	-0,1339	-0,1210	-0,7043
777,14	0,0820	-0,1057	-0,0196	-0,1983
777,44	0,1422	-0,1803	-0,0930	-0,3868
778,15	0,0751	-0,1124	-0,0500	-0,2438
778,42	0,0846	-0,1081	-0,1485	-0,2964
779,42	0,0444	-0,1332	-0,1435	-0,2906
780,37	0,0754	-0,1127	-0,1349	-0,2647
780,44	0,0692	-0,0960	-0,1687	-0,2864
781,44	0,2393	-0,2529	-0,1356	-0,4583
782,43	0,1064	-0,1689	-0,1495	-0,3417
783,44	0,0301	-0,1584	-0,0954	-0,2500
784,44	-0,0517	-0,1351	-0,2188	-0,2856
785,40	0,0787	-0,2391	-0,1756	-0,4004
786,41	-0,0425	-0,1314	-0,1597	-0,2297
787,43	-0,0361	-0,1216	-0,1022	-0,1776
788,47	0,1461	0,3597	1,3579	1,3705
788,99	0,1080	0,3228	0,6114	0,5823
789,47	0,0972	0,1801	0,5726	0,6936
790,41	0,0961	-0,1046	0,0239	-0,1633
790,46	0,0935	-0,0555	0,0866	-0,0670
791,43	0,0627	-0,1227	-0,1024	-0,2664
792,42	0,0253	-0,1122	-0,1129	-0,2268
793,46	-0,0292	-0,1356	-0,1827	-0,2776
794,41	-0,0289	-0,0820	-0,1614	-0,2488
795,41	0,2489	-0,2954	-0,1028	-0,5070
795,60	0,0809	-0,0402	-0,1403	-0,2502
796,42	0,1708	-0,1700	-0,1480	-0,4296
797,44	0,0951	-0,0775	-0,1525	-0,2866
798,41	0,0683	-0,1156	-0,1098	-0,2695
798,49	0,1076	-0,1080	-0,0951	-0,2867
799,47	0,0312	-0,1132	-0,1019	-0,2649
800,44	0,0225	-0,1017	-0,0350	-0,1419
800,46	0,0344	-0,1187	-0,0662	-0,2114
801,47	0,0300	-0,1009	-0,0409	-0,1700
802,46	0,0278	-0,0766	0,0431	-0,0618
802,46	0,0283	-0,0697	0,0632	-0,0322
803,39	0,0280	-0,0805	-0,0576	-0,1687
803,46	0,0228	-0,0939	-0,0521	-0,1612
804,47	-0,0293	-0,0640	-0,1081	-0,1452
805,44	0,1614	-0,1937	-0,0768	-0,3594
806,45	0,0445	-0,1486	-0,1009	-0,2410
807,43	0,0744	-0,1459	-0,1593	-0,3216
808,43	-0,0521	-0,1217	-0,1421	-0,1953
808,71	0,0639	-0,1753	-0,2301	-0,3880
809,47	0,0995	-0,1665	-0,1663	-0,3548
810,46	0,0293	-0,0062	0,0012	-0,0346
811,44	0,0623	-0,0713	-0,0083	-0,1341
812,46	0,0358	-0,0372	-0,0218	-0,0851
813,43	0,0258	-0,0513	-0,0589	-0,1202
813,46	0,0425	-0,0756	-0,1043	-0,1969
814,44	-0,0071	-0,0548	-0,0840	-0,1100

814,45	0,0096	-0,1014	-0,1086	-0,1754
815,42	-0,0245	-0,0628	0,0278	-0,0012
816,44	0,1764	-0,0545	0,9515	0,6926
817,35	-0,0701	0,0358	0,0329	0,1260
817,44	-0,0688	0,1106	0,4104	0,5181
818,43	-0,1011	-0,0493	-0,0246	0,0200
819,43	-0,0453	-0,1191	-0,1151	-0,1892
820,42	-0,0219	-0,1043	-0,0631	-0,1262
820,48	0,0356	-0,1543	-0,1279	-0,3287
821,22	0,0356	-0,1213	-0,0789	-0,2501
821,42	-0,0325	-0,1186	-0,0763	-0,1666
821,83	0,0556	-0,1189	-0,1455	-0,2653
822,17	0,0381	-0,0929	-0,1835	-0,2553
822,42	0,0219	-0,1195	-0,1065	-0,2255
822,48	0,0232	-0,0864	-0,1139	-0,2144
823,11	0,0402	-0,0555	-0,1081	-0,2013
823,41	0,0220	-0,1127	-0,1844	-0,2959
823,44	0,0094	-0,1025	-0,1501	-0,2394
824,47	0,1479	-0,1200	0,0543	-0,2183
824,70	0,2108	-0,1667	-0,0822	-0,4528
825,12	0,1000	-0,1629	0,0248	-0,2311
825,37	0,0910	-0,1126	-0,0782	-0,2752
825,50	0,1432	-0,1278	-0,0266	-0,2686
826,45	0,0433	-0,0507	-0,0183	-0,1431
826,47	0,0527	-0,0680	-0,0747	-0,2131
827,39	0,0553	-0,0644	-0,1463	-0,2290
827,51	0,0835	-0,0466	-0,1309	-0,2268
828,40	0,0621	-0,0716	-0,1049	-0,2010
828,48	0,0626	-0,0932	-0,0998	-0,2150
829,46	0,0003	-0,1138	-0,1159	-0,1924
830,47	-0,0701	-0,0520	-0,0803	-0,0742
831,48	0,1209	-0,1907	0,3736	0,0634
832,38	-0,0540	-0,0248	-0,0780	-0,0305
832,49	-0,0541	-0,0423	0,1138	0,1307
833,07	0,0453	-0,0682	-0,1257	-0,2202
833,36	-0,0103	-0,0774	-0,0797	-0,1476
833,48	-0,0340	-0,0990	-0,0544	-0,0981
834,41	-0,0364	-0,0993	-0,1069	-0,1472
834,44	-0,0178	-0,1308	-0,1263	-0,2100
835,42	0,0030	-0,1322	-0,0479	-0,1493
835,44	0,0020	-0,1293	-0,0718	-0,1689
836,43	0,0178	-0,5228	-0,2127	-0,5291
837,29	0,0221	-0,0504	-0,1828	-0,1991
837,43	-0,0339	-0,3176	-0,2748	-0,4303
837,60	0,0295	0,0717	-0,1823	-0,1379
838,44	0,3979	-0,1542	-0,1371	-0,5859
839,08	0,0466	-0,1040	-0,0388	-0,1656
839,21	0,0539	0,0502	-0,0214	-0,0375
839,36	0,0865	0,1356	0,0720	0,1050
839,51	0,1536	0,0921	0,0864	0,0131
839,89	0,0817	-0,0366	-0,0887	-0,1907
840,16	0,0682	-0,0925	-0,0762	-0,2017
840,34	-0,0171	0,0154	-0,1170	-0,0840
840,48	-0,0111	-0,2952	-0,0585	-0,2962
840,82	0,0587	-0,0813	-0,1859	-0,3197
841,09	0,0633	-0,1053	-0,0988	-0,2252
841,32	0,0197	-0,1406	-0,2059	-0,3279
841,51	-0,0758	-0,1795	-0,3506	-0,3841
842,10	0,0496	-0,0604	-0,1373	-0,2385
842,44	0,0144	0,0266	-0,0992	-0,0231
842,57	0,0858	-0,0557	0,1272	-0,0399
843,46	0,0423	-0,0447	0,0693	-0,0404
843,48	0,0340	-0,0095	0,0280	-0,0189
843,59	0,0680	-0,0911	0,1687	-0,0276
844,48	-0,0249	-0,0357	-0,0824	-0,0885
844,57	0,0125	-0,0531	-0,0022	-0,0714
845,50	-0,0022	-0,0587	-0,1557	-0,1931
846,48	0,0220	-0,0799	-0,1881	-0,2238
847,47	0,0150	-0,0640	-0,1358	-0,1725
848,48	-0,0267	-0,0499	-0,1112	-0,1089
849,45	-0,0569	-0,1055	-0,0045	-0,0506
850,49	-0,4469	0,1139	0,7425	1,0388
850,51	-0,3535	0,1100	0,8027	1,0659
850,80	0,0380	-0,0818	-0,0292	-0,1209
851,44	-0,1222	-0,0055	0,0823	0,1146
851,51	-0,2510	0,0586	0,3369	0,5909
852,42	0,1104	-0,4221	-0,1666	-0,4801
852,42	0,1100	-0,4216	-0,1679	-0,4807
852,69	0,0327	-0,0590	-0,1848	-0,2672
853,43	0,0435	-0,2194	-0,0797	-0,2910
854,43	-0,0204	-0,1164	-0,1502	-0,2476
855,05	0,0775	-0,1830	-0,0277	-0,1979

855,40	-0,0279	-0,0631	-0,0749	-0,1292
855,45	-0,0785	-0,0423	-0,0818	-0,0363
856,07	0,0618	-0,0739	-0,0475	-0,1668
856,34	0,0403	-0,0614	-0,0099	-0,1068
856,49	0,0638	-0,0896	0,0887	-0,0815
856,57	0,1174	-0,1341	0,1587	-0,1030
857,52	0,0265	-0,0761	-0,1097	-0,2226
857,54	0,0236	-0,0627	-0,0362	-0,1190
858,46	-0,0760	-0,1647	-0,1804	-0,2477
859,42	-0,0724	-0,0367	-0,2064	-0,1474
859,49	-0,0666	-0,0624	-0,2137	-0,1822
860,43	0,0226	-0,0497	-0,1247	-0,1833
860,49	0,0246	-0,0667	-0,1696	-0,2445
861,13	0,1379	-0,2797	0,2972	-0,1282
861,44	0,1470	-0,2887	0,2632	-0,1866
862,13	0,1106	-0,2223	0,2166	-0,1217
862,45	-0,0266	-0,0680	-0,0404	-0,1191
862,51	-0,0331	-0,0576	-0,0667	-0,1303
863,06	0,0731	-0,0700	-0,0099	-0,1658
863,13	0,0719	-0,0705	-0,0261	-0,1772
863,49	-0,0453	-0,0426	-0,0902	-0,1469
864,46	0,0156	-0,0795	-0,0731	-0,1518
864,56	0,0737	-0,2327	0,1501	-0,1547
865,41	0,0196	-0,0576	-0,0866	-0,1307
865,53	0,0038	-0,0559	-0,1366	-0,1774
866,49	0,0171	-0,0910	-0,1286	-0,2125
867,45	0,0128	-0,0575	-0,1482	-0,1809
868,45	0,1371	-0,4451	-0,1730	-0,5515
869,34	0,0335	-0,1157	-0,1993	-0,2646
869,46	0,0122	-0,3322	-0,2671	-0,4320
870,48	-0,0170	-0,1247	-0,2713	-0,2595
870,55	0,1162	-0,1366	0,0544	-0,1852
871,51	-0,0300	-0,0349	-0,1427	-0,1317
872,41	-0,0947	-0,0651	-0,1826	-0,1134
872,49	-0,0891	-0,0316	-0,0580	0,0059
873,46	-0,0443	-0,0553	-0,1645	-0,1024
874,42	0,1094	-0,2403	-0,0532	-0,3610
875,43	0,0659	-0,1079	-0,0642	-0,1825
876,46	-0,0088	-0,1912	0,1031	-0,1300
877,07	0,0758	-0,1225	-0,0811	-0,2171
877,46	0,0201	-0,1574	-0,0348	-0,1374
878,07	0,0436	-0,1016	-0,0885	-0,1417
878,43	0,0484	-0,0986	-0,0917	-0,1599
878,53	0,0729	-0,0872	-0,0348	-0,1516
879,05	0,0385	-0,0199	-0,1497	-0,1476
879,42	-0,0091	-0,0600	-0,1548	-0,1615
879,51	0,0391	-0,0747	-0,1491	-0,2070
880,39	-0,0004	-0,1363	-0,1293	-0,2460
880,50	0,1177	-0,1602	-0,0361	-0,3051
881,40	-0,0187	-0,1032	-0,0898	-0,1664
881,48	-0,0175	-0,1107	-0,1461	-0,2038
882,44	0,0081	-0,1447	-0,1145	-0,2631
882,50	0,0169	-0,1242	-0,1147	-0,2443
883,41	-0,0057	-0,1217	-0,0964	-0,2157
883,49	-0,0025	-0,0940	-0,1273	-0,1738
884,46	-0,0123	-0,0571	-0,1178	-0,1523
884,48	-0,0002	-0,0656	-0,1447	-0,1870
885,47	-0,0519	-0,0417	-0,1869	-0,1851
886,43	0,1808	-0,3710	0,0253	-0,4421
887,44	-0,0338	-0,0880	-0,2907	-0,3105
888,46	-0,0695	-0,0994	-0,2014	-0,1956
889,45	-0,0384	-0,0923	-0,1806	-0,2007
890,43	-0,0169	-0,1795	-0,2068	-0,3129
891,43	-0,0667	-0,1605	-0,2187	-0,2569
892,39	-0,0503	-0,0904	-0,1533	-0,1825
892,50	0,0252	-0,2004	-0,0674	-0,2132
893,01	0,0749	-0,0333	-0,1489	-0,2431
893,40	-0,0423	-0,0836	-0,1188	-0,1594
893,50	-0,0419	-0,1074	-0,1775	-0,2048
894,39	-0,0379	-0,0969	-0,0847	-0,1361
894,49	-0,0790	-0,0811	-0,1153	-0,1049
895,45	-0,0568	-0,0566	-0,1310	-0,1033
895,46	-0,0388	-0,0894	-0,1498	-0,1800
896,43	-0,0166	-0,1599	-0,1761	-0,2582
897,44	-0,0263	-0,1288	-0,1539	-0,2682
897,47	-0,0542	-0,0886	-0,0784	-0,1404
898,50	0,0245	-0,4530	-0,1766	-0,5155
899,50	-0,0241	-0,2161	-0,2400	-0,3786
900,39	0,0262	-0,0304	-0,1281	-0,1457
900,51	0,0228	0,0650	0,0015	0,0316
900,98	0,1747	-0,0958	-0,1948	-0,3955
901,51	0,0258	0,1690	0,1725	0,3447

902,49	-0,0145	0,0636	-0,0180	0,0585
903,47	-0,0082	-0,0602	-0,1310	-0,1493
904,48	0,0170	-0,0764	-0,0466	-0,1367
905,28	-0,0042	0,0328	0,0357	0,0652
905,48	-0,0248	-0,0279	0,0094	0,0016
906,23	0,0215	-0,0375	-0,0544	-0,1054
906,46	-0,0084	-0,0478	-0,1042	-0,1303
907,46	-0,0737	-0,0632	-0,1822	-0,1542
908,48	0,1894	-0,2987	0,0702	-0,3819
909,40	-0,0115	-0,1035	-0,1263	-0,1960
909,50	0,0096	-0,1064	-0,1428	-0,2002
910,49	-0,0400	-0,0728	-0,1562	-0,1814
911,49	-0,0863	-0,1109	-0,1589	-0,2114
912,49	0,1392	-0,1460	-0,0555	-0,3028
913,10	0,1190	-0,0803	-0,0759	-0,2705
913,43	0,1159	-0,1520	-0,0459	-0,2805
913,54	0,1229	-0,1488	-0,0604	-0,2889
914,49	0,0157	-0,1144	-0,0812	-0,1859
915,51	0,0393	-0,1044	-0,0564	-0,1696
916,58	-0,0140	-0,0840	-0,1635	-0,1910
917,53	0,0404	-0,1055	-0,1316	-0,2472
918,44	0,0210	-0,0970	-0,1077	-0,1913
918,48	0,0195	-0,0987	-0,1361	-0,2115
919,50	-0,0381	-0,1026	-0,1287	-0,1499
920,49	0,1134	-0,1403	-0,1114	-0,3085
921,50	0,0240	-0,0849	-0,1033	-0,2099
922,51	0,0289	-0,0863	-0,1058	-0,2114
923,52	0,0257	-0,0155	-0,0888	-0,1153
924,38	0,0567	-0,0845	-0,0807	-0,2088
924,50	0,0451	-0,0665	-0,1289	-0,2048
925,48	0,0137	-0,0628	-0,1639	-0,2100
926,49	-0,0120	-0,0580	-0,0946	-0,1483
927,51	0,1144	-0,0805	0,0293	-0,1526
928,43	0,1373	-0,1668	-0,1208	-0,3780
928,50	0,1164	-0,1423	-0,0272	-0,2578
929,40	0,0340	-0,0783	-0,1072	-0,1979
929,51	0,0300	-0,0420	-0,0674	-0,1324
930,48	0,0960	-0,0889	-0,0816	-0,2308
931,48	0,1083	-0,1170	-0,1976	-0,3513
932,51	0,1181	-0,0791	-0,1403	-0,2969
933,47	0,0892	-0,0781	-0,1435	-0,2878
934,48	0,4764	-0,1744	-0,2645	-0,7769
934,51	0,4745	-0,1202	-0,1263	-0,6459
935,54	0,2748	-0,0832	-0,1756	-0,4409
936,52	0,3284	0,0874	-0,0805	-0,3339
937,53	0,3068	0,0048	-0,1252	-0,4130
938,52	0,1350	-0,0245	-0,1520	-0,2778
939,49	0,0402	-0,0393	-0,1329	-0,2038
940,50	0,0985	-0,1552	0,0963	-0,1560
941,50	0,0413	-0,1116	-0,0092	-0,1634
942,46	0,0263	-0,0656	-0,0858	-0,1494
942,52	0,0364	-0,0649	-0,1108	-0,1905
943,54	-0,0619	0,1921	0,2371	0,4611
944,52	-0,3336	0,2905	1,8795	1,5031
944,74	-0,3401	0,3363	1,8634	1,5094
945,52	-0,4594	0,4006	1,9134	1,6405
946,51	-0,2512	0,4563	1,2590	1,6734
946,52	-0,2511	0,4357	1,3300	1,7088
947,49	-0,0558	0,0492	0,0811	0,1613
947,52	-0,0499	0,0567	0,1111	0,1869
948,50	0,0010	-0,0807	-0,0661	-0,1421
949,48	-0,0019	-0,0660	-0,0181	-0,0718
950,47	0,1218	-0,1645	-0,0113	-0,2535
951,51	0,1136	-0,0493	-0,0372	-0,1828
952,37	0,0545	-0,0627	-0,1189	-0,1996
952,51	0,0494	-0,0795	-0,0717	-0,1866
953,44	0,0500	-0,0614	-0,0900	-0,1962
953,46	0,0318	-0,0279	-0,0835	-0,1337
953,61	0,0565	-0,0413	-0,1068	-0,1933
954,50	0,0718	-0,0781	-0,0670	-0,2266
955,53	0,0985	0,0332	-0,0322	-0,1039
956,41	0,0394	-0,0431	-0,0988	-0,1481
956,54	0,0368	0,0357	-0,0831	-0,0812
957,43	-0,0002	0,0381	-0,0692	-0,0292
957,55	0,0718	0,2808	0,1596	0,3552
958,42	-0,0003	-0,0447	-0,0021	-0,0506
958,56	0,1495	0,1622	0,0891	0,0649
959,44	0,0275	-0,0108	-0,0564	-0,0867
959,56	0,0242	0,1398	-0,0552	0,0267
960,45	0,0384	-0,0446	-0,0950	-0,1603
960,56	0,0554	-0,0734	-0,0490	-0,1679
961,50	0,1136	-0,0896	-0,1415	-0,2979

962,44	0,0656	-0,0560	-0,0497	-0,1680
962,53	0,0785	-0,0712	-0,0931	-0,2220
963,51	0,1258	-0,0556	-0,1729	-0,3257
964,42	0,0845	-0,0606	-0,1168	-0,2343
964,53	0,0771	-0,0933	-0,1088	-0,2306
965,45	-0,0238	-0,0531	-0,1055	-0,1036
965,55	-0,0178	-0,0227	-0,0808	-0,0691
966,50	0,1406	0,4377	0,6435	0,8894
967,51	0,0373	0,3705	0,2851	0,5538
967,95	0,0417	0,0679	-0,2421	-0,2086
968,10	0,0280	-0,0505	-0,3125	-0,3469
968,52	-0,0112	0,0716	-0,0166	0,0636
969,06	0,0602	-0,0548	-0,2405	-0,3495
969,52	0,0030	-0,0444	-0,0437	-0,0898
970,52	0,0470	-0,0301	-0,1064	-0,1484
971,54	0,1365	0,2397	0,0735	0,1530
972,45	0,1095	-0,0380	-0,0248	-0,1811
972,55	0,1166	0,1091	-0,0073	-0,0305
973,53	0,0743	0,0621	-0,0277	-0,0450
974,49	0,0950	-0,0687	-0,0996	-0,2398
975,45	-0,0391	-0,0100	-0,1706	-0,0952
975,55	-0,0204	0,1258	0,0179	0,1334
976,46	0,2265	-0,0271	0,3028	0,0555
976,70	0,0552	-0,0453	-0,0817	-0,1783
977,48	0,0396	0,1584	0,0127	0,1307
978,46	-0,0113	0,0507	-0,0885	-0,0146
978,54	-0,0084	0,0165	-0,0937	-0,0650
979,52	-0,0097	0,0042	-0,1032	-0,0804
980,50	0,1257	-0,1269	0,0373	-0,2153
981,44	0,0559	-0,0514	-0,0481	-0,1342
981,54	0,0476	-0,0278	-0,0661	-0,1224
982,51	0,0752	0,1022	0,1001	0,0992
983,53	0,0259	0,0318	0,0185	0,0222
984,09	0,0817	-0,0776	-0,1840	-0,3165
984,52	0,0016	0,0079	-0,0383	-0,0306
985,56	0,1113	0,4407	0,1635	0,4910
986,48	0,0557	0,1341	-0,0124	0,0530
986,56	0,0717	0,2749	0,0191	0,1993
987,54	0,0646	0,0244	-0,0397	-0,0799
988,52	0,1385	0,1232	0,1155	0,0652
989,54	0,0309	0,0493	0,0271	0,0340
990,45	0,0500	-0,0388	-0,0736	-0,1624
990,57	0,0538	-0,0488	-0,0485	-0,1394
991,43	0,0226	-0,0627	-0,0726	-0,1482
991,55	0,0310	-0,0381	-0,0125	-0,0860
992,44	0,0184	-0,0625	-0,0520	-0,1632
992,56	0,0471	-0,0541	-0,0789	-0,1704
993,47	0,0616	-0,0228	-0,0840	-0,1549
993,56	0,0798	-0,0072	-0,0847	-0,1700
994,47	0,0570	-0,0719	-0,0499	-0,1661
994,58	0,0511	-0,0433	-0,0753	-0,1587
995,54	0,0278	-0,0288	-0,1200	-0,1608
996,53	0,0484	-0,0581	-0,1386	-0,2171
997,46	0,1274	-0,0549	-0,0677	-0,2266
997,52	0,1266	-0,0345	-0,0242	-0,1761
998,42	0,0954	-0,0209	-0,0279	-0,1442
998,55	0,1289	-0,0125	-0,0542	-0,1853
999,43	0,0437	-0,0386	-0,0761	-0,1353
999,57	0,0862	-0,0689	-0,0477	-0,2055
999,91	0,0657	-0,1167	-0,2543	-0,3672
1000,06	0,0710	-0,1028	-0,2602	-0,3947
1000,54	0,0993	-0,0727	-0,1150	-0,2659
1001,00	0,0610	-0,1020	-0,3072	-0,4257
1001,47	0,0294	-0,0576	-0,1294	-0,1945
1001,58	0,0531	-0,0415	-0,1396	-0,2109
1002,54	0,1188	-0,0787	-0,0784	-0,2446
1003,53	0,0559	-0,0485	-0,1095	-0,1981
1004,53	0,1177	-0,0412	-0,0234	-0,1761
1005,48	0,0627	-0,0398	-0,0449	-0,1339
1005,61	0,0568	-0,0550	-0,0622	-0,1615
1006,47	0,0517	-0,0541	-0,0777	-0,1695
1006,56	0,0476	-0,0464	-0,0994	-0,1740
1007,60	-0,0097	-0,0679	-0,1110	-0,1533
1008,58	-0,0166	-0,0448	-0,1825	-0,1916
1009,56	-0,0036	-0,0130	-0,2381	-0,2172
1011,71	0,2778	-0,1964	0,1174	-0,3419
1012,59	0,0084	-0,0238	-0,1401	-0,1582
1012,72	0,0616	-0,0100	-0,0889	-0,1493
1013,50	0,0106	-0,0636	-0,0419	-0,1266
1013,68	-0,0104	-0,0366	-0,0639	-0,1004
1014,59	0,0819	-0,0681	-0,0433	-0,1780
1015,60	0,0876	-0,0595	-0,0611	-0,1865

1016,51	0,0810	-0,0854	-0,0045	-0,1742
1016,60	0,0671	-0,0652	-0,0697	-0,1957
1017,60	0,0438	0,0010	-0,1317	-0,1531
1018,25	0,0596	-0,0044	0,0084	-0,0527
1018,53	0,2489	-0,0970	-0,0247	-0,3458
1019,24	0,0367	-0,0196	-0,0384	-0,0923
1019,53	0,1357	-0,0806	-0,0640	-0,2699
1020,55	0,0883	-0,0892	-0,0814	-0,2430
1021,55	0,0637	-0,0732	-0,0475	-0,1743
1022,55	0,0587	-0,0618	-0,0956	-0,1789
1023,56	0,0203	-0,0445	-0,1143	-0,1545
1024,53	0,0255	-0,0715	-0,1668	-0,2193
1025,45	-0,0225	-0,0416	-0,1198	-0,1171
1025,58	0,0751	-0,0894	-0,0519	-0,1839
1026,47	0,0416	-0,0654	-0,0508	-0,1683
1026,59	0,0942	-0,0932	-0,0544	-0,2218
1027,48	-0,0034	-0,0546	-0,0579	-0,1125
1027,57	-0,0140	-0,0073	-0,1196	-0,0834
1028,57	0,0604	0,0584	-0,0237	-0,0283
1029,56	0,0085	0,0047	-0,0616	-0,0559
1030,55	0,0121	-0,0498	-0,0559	-0,1114
1031,51	-0,0385	-0,0296	-0,0525	-0,0303
1031,54	-0,0281	-0,0313	-0,0648	-0,0485
1032,57	0,1430	0,5242	1,5902	1,3873
1033,58	-0,0269	0,5603	1,0647	1,3847
1034,59	-0,0735	0,2889	0,2804	0,6172
1035,55	-0,0602	-0,0428	-0,0019	0,0240
1036,55	-0,0197	-0,0496	-0,0431	-0,0831
1037,56	-0,0323	-0,0722	-0,0842	-0,1140
1038,54	-0,0278	-0,0775	-0,0787	-0,1050
1039,56	0,0733	-0,0148	0,0181	-0,0720
1040,54	0,0468	-0,0156	-0,0353	-0,0903
1041,49	-0,0049	-0,0238	-0,0650	-0,0971
1041,58	0,0033	-0,0362	-0,0865	-0,1302
1042,57	0,1285	-0,0493	-0,1346	-0,2829
1043,55	0,0567	-0,0642	-0,0575	-0,1641
1044,55	-0,0479	-0,0303	-0,1279	-0,1073
1045,55	0,1357	-0,0945	-0,0338	-0,2453
1046,54	0,1159	-0,0746	-0,0269	-0,1977
1047,57	0,0264	-0,0510	-0,1011	-0,1519
1048,56	0,0779	-0,0686	-0,0532	-0,1772
1049,55	0,0792	-0,0797	-0,0297	-0,1804
1049,62	0,1167	-0,0984	-0,0765	-0,2783
1050,59	0,0854	-0,0475	-0,1101	-0,2062
1051,57	0,0461	-0,0419	-0,1275	-0,1988
1052,55	0,0662	-0,0624	-0,0588	-0,1263
1053,57	0,0131	-0,0452	-0,1412	-0,1742
1054,57	0,1340	0,1100	0,0975	-0,0628
1055,60	0,0890	0,1006	0,0129	-0,0169
1056,58	0,0979	-0,0425	0,0075	-0,1087
1057,58	0,1271	-0,0132	-0,1025	-0,2061
1058,56	0,0986	-0,0611	-0,0359	-0,1472
1059,57	0,0435	-0,0624	-0,1113	-0,1905
1060,56	0,1191	-0,1239	-0,0327	-0,2195
1061,58	0,1297	-0,0688	-0,1017	-0,2641
1062,56	0,1027	-0,0733	-0,0923	-0,2266
1063,56	0,1147	-0,0480	-0,1271	-0,2556
1064,60	0,0894	-0,1219	-0,1116	-0,2797
1065,60	0,0368	-0,0809	-0,1137	-0,1961
1066,07	0,0887	-0,0922	0,0396	-0,1506
1066,17	0,1117	-0,0766	-0,0529	-0,2281
1066,58	0,0895	-0,1181	0,0081	-0,1872
1067,13	0,0756	-0,1037	-0,1207	-0,2724
1067,46	0,0621	-0,0732	-0,0846	-0,2017
1067,59	0,1072	-0,0966	-0,0010	-0,1880
1068,60	0,0671	-0,0531	-0,1448	-0,2139
1069,59	0,0280	-0,0422	-0,1127	-0,1750
1070,79	0,0456	0,1262	0,0810	0,1242
1071,57	0,0357	0,0235	0,0278	0,0109
1071,89	0,0089	0,0553	-0,0148	0,0304
1072,61	0,0667	0,0590	0,0864	0,0562
1073,59	0,0182	0,0590	-0,0731	-0,0254
1074,58	0,0083	-0,0259	-0,0992	-0,1021
1075,62	0,5482	-0,2786	0,0525	-0,5766
1075,84	0,2599	-0,0499	-0,1300	-0,3894
1076,46	0,1584	-0,0717	-0,0800	-0,3190
1076,62	0,5567	-0,1524	-0,1123	-0,6204
1077,60	0,3391	-0,1056	-0,2191	-0,6056
1078,59	0,0304	-0,0653	-0,1855	-0,2690
1079,58	0,0421	-0,0725	-0,1786	-0,2421
1080,39	0,0576	-0,0735	-0,1722	-0,2721
1080,60	0,0268	-0,0661	-0,1335	-0,2200

1081,26	0,0628	-0,0800	-0,1961	-0,2905
1081,60	0,0359	-0,0801	-0,1161	-0,2010
1082,04	0,0751	-0,0744	-0,0949	-0,2154
1082,17	0,0706	-0,0651	-0,1313	-0,2294
1082,27	0,0793	-0,0851	-0,1703	-0,2773
1082,57	0,0417	-0,1002	-0,1432	-0,2350
1083,58	0,0422	-0,0635	-0,1512	-0,2264
1084,61	0,0459	-0,0946	-0,1118	-0,2300
1085,58	0,0003	-0,0251	-0,1488	-0,1536
1086,59	-0,0155	-0,0346	-0,1701	-0,1849
1087,57	0,0802	-0,1156	-0,1696	-0,3023
1088,55	0,1476	-0,1112	-0,0462	-0,2630
1089,57	0,0266	-0,0666	-0,1516	-0,1973
1090,61	0,0616	-0,0773	-0,1258	-0,2278
1091,20	0,0546	-0,0693	-0,1072	-0,2256
1091,59	0,0126	-0,0399	-0,1373	-0,1650
1092,56	0,0127	-0,0120	-0,1639	-0,1261
1093,55	-0,0239	0,0230	-0,2242	-0,1169
1094,57	0,0644	-0,1472	-0,1473	-0,2952
1095,56	0,1750	-0,3357	0,0751	-0,3847
1096,56	-0,0435	-0,0146	-0,3315	-0,2551
1097,20	0,0393	-0,0383	-0,2414	-0,2761
1097,56	0,0753	-0,0386	-0,3119	-0,3452
1098,52	0,1036	-0,0675	-0,2502	-0,3441
1098,55	0,0735	-0,0477	-0,1758	-0,2411
1099,54	0,0317	-0,0325	-0,1311	-0,1647
1100,57	-0,0265	0,0252	-0,0711	-0,0172
1101,31	0,0164	-0,0502	-0,2243	-0,2419
1101,50	-0,0332	-0,0149	-0,1505	-0,1123
1101,65	-0,0187	0,0011	-0,0664	-0,0410
1102,30	0,0501	-0,0482	-0,2130	-0,2614
1102,57	-0,0103	-0,0356	-0,1187	-0,1274
1103,56	-0,0472	-0,0612	-0,1428	-0,1291
1104,56	0,1231	-0,2299	-0,1762	-0,3977
1105,56	-0,0343	-0,5015	-0,0870	-0,4233
1106,56	-0,0943	-0,3499	-0,2389	-0,4154
1107,57	-0,1454	-0,2131	-0,3657	-0,3621
1108,57	-0,0841	-0,0694	-0,2382	-0,2068
1109,57	-0,0314	-0,0431	-0,2234	-0,1943
1110,55	0,4909	-0,1929	-0,2841	-0,5864
1111,54	0,6559	-0,2424	-0,0336	-0,8111
1111,57	0,6486	-0,2674	0,1637	-0,7188
1112,53	0,4268	-0,0588	-0,3688	-0,6777
1112,58	0,4196	-0,0449	-0,2547	-0,5684
1113,16	0,0364	-0,0410	-0,2023	-0,2444
1113,58	0,1824	0,0041	-0,3013	-0,4022
1114,56	0,0235	-0,0468	-0,1380	-0,2162
1115,58	-0,0425	0,0001	-0,1629	-0,1078
1116,53	0,0839	-0,1103	-0,0323	-0,2130
1117,54	0,1237	-0,1813	0,0893	-0,2168
1118,56	0,0164	-0,0162	-0,1356	-0,1416
1119,57	-0,0090	-0,0198	-0,1443	-0,1312
1120,57	0,0301	-0,1052	-0,1410	-0,1232
1121,57	0,0220	-0,0855	-0,1418	-0,1656
1122,59	0,0601	-0,0957	-0,0754	-0,1123
1123,42	0,0565	-0,0460	-0,0754	-0,1652
1123,59	0,0536	-0,0709	-0,0863	-0,1046
1124,54	0,0469	-0,0523	-0,0476	-0,0738
1125,53	0,0598	-0,0613	-0,0597	-0,0752
1125,55	0,0598	-0,0621	-0,0685	-0,0767
1126,55	0,0538	-0,0845	-0,0369	-0,0793
1127,55	0,0985	-0,3430	0,1802	-0,1313
1128,56	0,0423	-0,0694	-0,1324	-0,0984
1129,56	0,0479	-0,0322	-0,0870	-0,0686
1130,57	0,0441	-0,0520	-0,0793	-0,0737
1131,56	0,0510	-0,0478	-0,0619	-0,0758
1132,54	0,0872	-0,0370	-0,0264	-0,1157
1133,56	0,0876	-0,0444	-0,0755	-0,1702
1134,57	0,0119	0,0063	-0,1331	-0,1067
1135,58	-0,0141	-0,0218	-0,0864	-0,0813
1136,57	0,0326	0,0133	-0,1615	-0,1515
1137,57	0,0359	0,0123	-0,1168	-0,1450
1138,55	0,3402	-0,5510	0,2909	-0,5464
1139,56	0,1380	-0,1812	-0,1394	-0,3977
1140,56	0,3043	-0,0996	-0,2489	-0,5296
1141,58	0,1879	-0,0618	-0,1657	-0,3836
1142,57	0,0482	-0,0677	-0,0937	-0,1956
1143,57	-0,1389	-0,0860	-0,2230	-0,1223
1144,58	-0,0805	-0,1187	-0,0960	-0,1036
1145,52	-0,0152	-0,0317	-0,1029	-0,0983
1145,63	-0,0358	-0,0226	-0,1136	-0,0737
1146,58	-0,0212	-0,0329	-0,0707	-0,0758

1147,51	0,0081	-0,0145	-0,0944	-0,1024
1147,61	-0,0082	-0,0178	-0,0757	-0,0872
1148,52	0,0260	-0,0281	-0,0675	-0,1042
1148,62	0,0354	-0,0066	-0,0606	-0,0957
1149,57	0,1779	-0,1434	0,0758	-0,2356
1150,58	-0,0097	-0,0427	-0,0983	-0,1084
1151,58	-0,2362	-0,1370	-0,2822	-0,1525
1152,61	-0,1777	-0,1013	-0,1984	-0,1179
1153,61	-0,0966	-0,0470	-0,1542	-0,0829
1154,59	0,1752	-0,0848	0,0281	-0,2271
1155,60	0,1291	-0,0300	-0,0332	-0,1859
1156,60	0,0411	0,0168	-0,0555	-0,0756
1157,52	0,0331	-0,0384	-0,0463	-0,1126
1157,66	0,0322	-0,0195	-0,0400	-0,0856
1158,62	-0,0047	0,0220	-0,0813	-0,0399
1159,63	-0,0584	0,0237	-0,1132	-0,0201
1160,58	0,1553	-0,0894	0,0301	-0,2045
1161,62	0,1037	-0,0750	-0,0322	-0,1931
1162,64	0,0222	-0,0189	-0,1173	-0,1336
1163,48	-0,0223	0,1585	0,0274	0,1921
1163,60	0,0248	0,0664	0,0487	0,0751
1164,58	-0,0783	0,0759	-0,0568	0,0971
1164,58	-0,0660	0,0580	-0,0194	0,1015
1165,59	0,1955	-0,1194	0,1154	-0,1989
1166,59	0,0660	-0,0241	-0,0837	-0,1597
1167,53	0,0115	-0,0399	-0,0692	-0,1111
1167,63	-0,0027	-0,0137	-0,0751	-0,0758
1168,67	0,0684	-0,0206	-0,0457	-0,1253
1169,49	0,0330	-0,0025	-0,0894	-0,1204
1169,65	0,0201	-0,0029	-0,0595	-0,0712
1170,53	0,0587	-0,0124	-0,0580	-0,1242
1170,68	0,0863	-0,0114	0,0511	-0,0465
1171,54	0,0803	-0,0310	0,0177	-0,0933
1171,68	0,0973	0,0041	0,0518	-0,0509
1172,64	0,0314	-0,0420	-0,0030	-0,0746
1173,59	0,0928	-0,0900	0,0327	-0,1456
1174,52	0,0168	-0,0224	-0,0611	-0,0981
1174,63	-0,0064	-0,0136	-0,0594	-0,0776
1175,61	0,0235	-0,0082	-0,0545	-0,0874
1176,60	0,1459	-0,0788	-0,0215	-0,2307
1177,53	0,0518	-0,0521	-0,0568	-0,1558
1177,68	0,0837	-0,0314	-0,0644	-0,1742
1178,59	0,0204	-0,0158	-0,0785	-0,1170
1179,62	0,0292	-0,0162	-0,0797	-0,1102
1180,64	0,0200	-0,0259	-0,0065	-0,0499
1181,63	-0,0489	-0,0013	-0,0477	0,0064
1182,61	0,1924	-0,1668	0,1398	-0,2187
1183,60	0,0757	-0,0671	0,0810	-0,0646
1184,32	-0,0567	0,2464	0,1996	0,4930
1184,57	0,0754	0,0880	0,1037	0,1069
1185,39	-0,0785	0,2518	0,0305	0,3514
1185,62	0,0036	0,0809	-0,0347	0,0413
1186,41	-0,0738	0,0672	-0,0904	0,0505
1186,62	-0,0399	0,0344	-0,0628	0,0105
1187,52	0,0237	-0,0093	-0,0800	-0,1008
1187,66	0,0334	-0,0158	-0,0070	-0,0545
1188,54	0,0158	-0,0346	-0,0141	-0,0642
1188,67	0,0186	0,0453	0,0022	0,0241
1189,63	0,0205	-0,0250	0,0144	-0,0291
1190,64	-0,0089	-0,0244	0,0126	-0,0030
1191,63	-0,0044	-0,0086	-0,0201	-0,0215
1192,64	-0,0228	-0,0033	-0,0462	-0,0200
1193,55	-0,0242	0,1057	0,0284	0,1428
1193,64	-0,0335	0,0826	-0,0104	0,1001
1194,55	-0,0587	0,0350	0,0278	0,1198
1194,68	-0,1754	0,0793	0,1406	0,3860
1195,47	-0,0816	-0,0049	0,0115	0,0899
1195,56	-0,1271	-0,0063	0,0388	0,1590
1195,68	-0,2339	0,0286	0,0916	0,3743
1196,57	-0,1453	0,0066	-0,0384	0,1130
1196,67	-0,1982	0,0459	-0,0245	0,2137
1197,63	-0,2492	-0,0044	0,0390	0,2671
1198,49	-0,0766	0,2019	0,0005	0,2626
1198,71	-0,2391	0,4708	1,6244	1,4980
1198,91	-0,0898	0,4203	0,6751	0,8185
1199,52	-0,1290	0,3017	0,0649	0,4724
1199,71	-0,3057	0,5562	1,5465	1,5762
1200,71	-0,3067	0,6668	1,0295	1,6220
1200,71	-0,3494	0,6603	1,2017	1,6971
1201,63	-0,1061	0,2024	0,1520	0,4304
1201,70	-0,1828	0,2413	0,3817	0,8100
1202,65	-0,0408	0,0776	0,0380	0,1392

1203,65	0,0106	0,0334	0,0141	0,0313
1204,64	0,0243	0,0146	-0,0244	-0,0370
1205,63	0,0066	0,0397	-0,0490	-0,0132
1206,33	0,0240	0,0132	-0,0712	-0,0770
1206,50	0,0033	-0,0059	-0,0227	-0,0313
1206,65	0,0442	-0,0331	0,0388	-0,0400
1207,62	0,0366	-0,0217	-0,0127	-0,0684
1208,65	0,0599	-0,0520	-0,0075	-0,1092
1209,63	0,0108	0,0114	-0,0358	-0,0325
1210,56	-0,0193	0,0157	-0,0424	-0,0072
1210,68	0,0083	0,0511	0,0020	0,0363
1211,38	0,0038	0,0304	-0,0289	-0,0028
1211,53	0,0187	0,0550	-0,0529	-0,0122
1211,68	0,0682	0,0332	0,0635	0,0091
1212,38	0,0091	0,0570	-0,1019	-0,0412
1212,65	-0,0178	0,0654	-0,0096	0,0653
1213,64	-0,0626	-0,0639	-0,0332	-0,0235
1214,58	0,0706	-0,1222	-0,0950	-0,2607
1214,63	0,0810	-0,1481	0,0347	-0,1819
1215,49	-0,0092	-0,0151	-0,0621	-0,0696
1215,64	-0,0322	-0,0495	-0,0464	-0,0555
1216,65	-0,0988	0,0749	-0,0511	0,1224
1217,43	0,0005	0,0588	-0,0394	0,0189
1217,64	-0,0488	-0,0150	-0,0133	0,0181
1218,65	-0,0961	0,0005	-0,0787	0,0204
1219,40	-0,0142	0,0596	-0,1081	-0,0281
1219,67	-0,1100	0,0888	-0,0629	0,1347
1220,49	-0,0248	0,1184	-0,0635	0,0743
1220,68	0,1128	0,4890	0,4863	0,9058
1221,67	-0,0031	0,4209	0,3595	0,7276
1221,67	0,0043	0,4343	0,4315	0,8170
1222,63	-0,0279	0,1373	0,0173	0,1806
1222,66	-0,0568	0,2100	0,1089	0,3660
1223,64	0,0045	0,0546	-0,0931	-0,0341
1224,65	-0,0026	-0,0222	-0,0634	-0,0786
1225,65	0,0810	-0,0320	-0,0372	-0,1417
1226,66	0,1343	-0,0364	-0,0228	-0,1895
1227,64	0,0493	-0,0096	-0,0598	-0,1153
1228,67	0,0329	0,0213	-0,0182	-0,0291
1229,56	0,1272	0,0076	-0,0327	-0,1452
1229,69	0,1716	-0,0196	0,0017	-0,1868
1230,65	0,1271	-0,0229	-0,0226	-0,1680
1231,63	0,0502	0,0362	-0,0436	-0,0531
1232,59	0,0011	0,0665	-0,0507	0,0118
1232,67	0,0159	0,0593	-0,0440	-0,0053
1233,63	-0,0353	0,0826	-0,0796	0,0353
1234,66	-0,1531	0,0877	-0,1593	0,0842
1235,61	0,1636	-0,3487	0,3763	-0,1464
1236,62	-0,1169	0,0599	-0,0451	0,1317
1237,62	-0,1612	0,1189	-0,1616	0,1320
1238,63	-0,0553	0,0558	-0,0980	0,0228
1239,61	-0,0127	0,0073	-0,0864	-0,0582
1240,45	0,1435	-0,0382	-0,0924	-0,2549
1240,52	0,0556	-0,0299	-0,0267	-0,1195
1240,64	0,0316	-0,0011	-0,0561	-0,0819
1241,53	0,0623	-0,0161	-0,0267	-0,1113
1241,68	0,0631	0,0311	-0,0558	-0,0735
1242,52	0,0591	0,0097	-0,0253	-0,0734
1242,68	0,0635	0,0946	0,0059	0,0346
1243,53	0,1190	-0,0099	0,0387	-0,0843
1243,65	0,1123	-0,0390	0,1328	0,0210
1244,62	0,0623	0,0499	-0,0663	-0,0754
1244,65	0,0408	0,0680	0,0386	0,0533
1245,51	0,0190	0,0284	-0,0566	-0,0365
1245,66	0,0674	0,0479	0,0083	-0,0198
1246,65	0,0160	0,0310	-0,0620	-0,0452
1247,65	0,0393	0,0141	-0,0533	-0,0699
1248,64	0,0516	0,0202	-0,0427	-0,0725
1249,65	0,0175	0,0178	-0,0615	-0,0564
1250,65	0,0684	-0,0263	0,0455	-0,0524
1251,64	0,1131	-0,0313	0,0439	-0,1026
1252,58	0,0394	-0,0084	-0,0155	-0,0612
1252,69	0,0408	-0,0061	-0,0164	-0,0625
1253,62	0,0207	0,0294	-0,0512	-0,0410
1253,67	0,0256	0,0334	-0,0807	-0,0613
1254,55	0,0482	0,0172	-0,0004	-0,0323
1254,70	0,0654	0,0337	0,0802	0,0340
1255,57	0,0144	0,0154	-0,0081	-0,0072
1255,71	-0,0223	0,0708	0,0084	0,0957
1256,58	-0,0212	0,0517	-0,0934	-0,0033
1256,70	-0,0553	0,1098	-0,0916	0,0721
1257,63	0,1352	-0,0949	0,0951	-0,1328

1258,64	0,0433	0,0146	-0,0072	-0,0359
1259,66	0,0054	0,0133	-0,0226	-0,0139
1260,61	0,0019	0,0542	-0,0267	0,0209
1260,67	0,0098	0,0296	-0,0321	-0,0111
1261,65	0,0114	0,0071	-0,0228	-0,0258
1262,64	0,1018	-0,0091	-0,1004	-0,1772
1262,65	0,0224	0,0349	-0,0235	-0,0077
1263,68	0,0227	0,0096	-0,0306	-0,0409
1264,63	0,0058	0,0349	-0,1242	-0,0925
1265,53	-0,0294	0,0429	-0,1654	-0,0880
1265,67	-0,0383	0,0572	-0,1284	-0,0354
1266,64	-0,0515	0,1175	-0,2609	-0,0591
1267,66	0,0958	-0,2978	0,2214	-0,1692
1268,67	-0,1064	-0,0328	-0,1194	-0,0350
1269,68	-0,0949	0,1544	-0,1781	0,0731
1270,69	-0,0280	0,0893	-0,0872	0,0294
1271,68	0,2487	-0,0018	-0,1154	-0,3117
1271,69	0,2636	-0,0020	-0,1189	-0,3273
1271,86	0,3314	-0,0593	-0,0045	-0,3432
1272,42	0,1764	0,0325	-0,1709	-0,2016
1272,69	0,1694	0,0335	-0,1532	-0,2071
1272,87	0,2816	-0,0098	-0,0884	-0,3010
1273,26	0,0988	0,0140	-0,1170	-0,1215
1273,53	0,1570	0,0338	-0,1507	-0,1878
1273,71	0,4169	0,0456	-0,1922	-0,4377
1274,00	0,2678	0,0201	-0,0935	-0,3354
1274,72	0,5077	0,0570	0,5654	-0,0706
1275,72	0,3145	0,0838	0,3953	0,0420
1276,54	0,1017	0,0560	-0,1338	-0,1528
1276,72	0,2506	0,0696	0,1008	-0,0283
1277,57	0,0675	0,0223	-0,1034	-0,1310
1277,73	0,0982	0,0371	-0,0793	-0,1277
1278,57	0,0431	-0,0338	-0,0168	-0,0944
1278,73	0,0250	0,0133	-0,0762	-0,0839
1279,49	0,0990	-0,0024	-0,1277	-0,2040
1279,58	0,0375	0,0061	-0,0686	-0,0945
1279,73	0,0314	-0,0035	-0,0798	-0,1087
1280,66	0,0426	-0,0007	-0,0848	-0,1259
1281,67	0,0358	0,0358	-0,0986	-0,0849
1282,70	0,0382	-0,0166	-0,0256	-0,0764
1283,57	0,0313	-0,0924	0,0847	-0,0472
1283,68	0,0130	-0,0376	0,0094	-0,0380
1284,68	-0,0093	0,0141	-0,0320	-0,0034
1285,60	-0,0694	0,0235	-0,0623	0,0321
1285,71	-0,0829	0,0194	-0,0371	0,0645
1286,67	0,0811	-0,1913	0,3167	0,0618
1287,67	0,0793	-0,2272	0,3235	0,0113
1288,71	-0,0085	-0,0968	0,1275	0,0239
1289,68	0,0740	-0,0528	0,0475	-0,0789
1290,70	0,0224	-0,0010	-0,0219	-0,0406
1291,62	-0,0351	0,0325	-0,0642	0,0075
1291,73	-0,0474	0,0325	-0,1022	-0,0093
1292,49	0,0210	-0,0210	-0,0509	-0,0870
1292,67	-0,0442	0,0115	-0,1268	-0,0525
1293,49	0,0488	0,0163	-0,1229	-0,1265
1293,71	0,1156	-0,0189	-0,1201	-0,2200
1294,57	0,0635	0,0209	-0,0983	-0,1336
1294,71	0,0842	0,0273	-0,1057	-0,1549
1295,62	0,0423	0,0223	-0,1276	-0,0959
1295,64	0,0248	0,0219	-0,0662	-0,0452
1295,66	0,0325	0,0234	-0,0993	-0,0671
1296,65	0,0316	0,0166	-0,0067	-0,0150
1296,73	0,0678	0,0025	-0,0031	-0,0569
1297,63	0,1967	-0,2037	0,3093	-0,0939
1298,63	0,0583	0,0106	0,0572	0,0027
1299,62	-0,0973	-0,0415	0,0114	0,0632
1299,65	-0,1041	-0,0304	-0,0114	0,0570
1300,57	-0,0620	0,0424	-0,0996	0,0158
1300,69	-0,0834	0,0420	-0,0847	0,0487
1301,67	-0,0602	-0,0251	0,0108	0,0446
1302,66	-0,0791	-0,0422	-0,0128	0,0116
1303,60	0,2238	-0,2182	0,2198	-0,2261
1304,62	0,0210	0,0135	-0,0708	-0,0636
1305,65	-0,0553	0,0306	-0,1006	-0,0164
1306,61	0,0097	0,0482	-0,0666	-0,0269
1306,70	0,0253	0,0530	-0,0478	-0,0217
1307,68	-0,0077	0,0839	-0,0850	0,0075
1308,63	0,0127	0,0214	0,0220	0,0267
1308,72	0,0160	0,0176	0,0193	0,0172
1309,67	0,0464	-0,0074	-0,0015	-0,0544
1310,64	0,0196	0,0389	-0,0296	-0,0101
1310,68	0,0393	0,0518	-0,0620	-0,0468

1311,67	0,0195	0,0332	-0,0387	-0,0241
1312,69	-0,0283	0,0756	-0,0729	0,0377
1313,66	-0,0506	0,0882	-0,0997	0,0482
1314,66	0,2701	-0,1072	0,4079	0,0060
1315,66	0,1496	0,0603	0,2019	0,1042
1316,67	0,0387	0,0885	0,0642	0,1017
1317,68	-0,0120	0,0936	-0,0256	0,0803
1318,64	-0,0264	0,1080	-0,0749	0,0526
1318,67	-0,0209	0,1148	-0,0957	0,0331
1319,67	-0,0705	0,1386	-0,1263	0,0884
1320,65	0,0622	-0,2180	0,2361	-0,0605
1321,65	-0,0228	0,0304	-0,0540	0,0051
1322,67	-0,0856	0,0840	-0,1347	0,0401
1323,67	-0,1773	0,0286	-0,1076	0,0991
1324,63	-0,2310	0,1341	-0,0219	0,3416
1325,56	-0,1252	0,4013	0,3073	0,8319
1325,57	-0,1498	0,3887	0,2704	0,8029
1325,73	0,1154	0,5781	1,3040	1,5039
1326,58	-0,0924	0,3265	0,1552	0,5753
1326,73	0,0009	0,6525	1,0276	1,4619
1327,59	-0,0744	0,2114	0,0299	0,3161
1327,74	-0,0865	0,4786	0,3553	0,9630
1328,71	-0,0946	0,2856	0,0875	0,4619
1329,64	-0,0755	0,0990	0,0375	0,2106
1329,72	-0,0753	0,1458	0,0261	0,2542
1330,45	0,0198	0,0530	0,0283	0,0638
1330,70	-0,0532	0,1342	0,0469	0,2315
1331,42	0,0328	0,0380	0,0122	0,0169
1331,67	-0,0403	0,1397	0,0395	0,2139
1331,72	-0,0126	0,1326	0,0225	0,1607
1332,72	-0,0209	0,1049	-0,0048	0,1197
1333,33	0,0508	0,0033	-0,0167	-0,0699
1333,72	-0,0251	0,0735	-0,0303	0,0631
1334,69	-0,0589	0,0882	-0,0285	0,1201
1335,69	-0,0684	0,1738	-0,0837	0,1440
1336,70	-0,0245	0,1231	0,0051	0,1428
1337,67	0,2368	-0,1904	0,3479	-0,0866
1338,69	0,0795	0,0075	0,1026	0,0186
1339,70	-0,0673	0,1090	-0,0156	0,1613
1340,66	-0,0236	0,0857	-0,0561	0,0546
1341,66	-0,0665	0,1545	-0,0548	0,1615
1342,67	0,0389	0,0027	0,0955	0,0586
1343,67	0,1015	0,0264	0,0194	-0,0486
1344,69	0,0375	0,0500	-0,0568	-0,0438
1345,69	-0,0310	0,0317	-0,0496	0,0153
1346,67	-0,0254	0,0670	-0,0462	0,0312
1347,71	0,0450	0,2826	0,1668	0,3876
1348,71	-0,0431	0,3471	0,0753	0,4623
1349,69	0,0893	-0,1098	0,3084	0,1128
1350,69	-0,0970	0,0128	0,0678	0,1777
1351,71	-0,1526	0,0890	-0,0705	0,1706
1352,71	-0,0899	0,0610	-0,0389	0,1115
1353,21	0,0156	0,0429	-0,1016	-0,0766
1353,66	-0,0485	0,0319	0,0034	0,0835
1353,75	-0,0411	0,0562	-0,0285	0,0699
1354,22	0,0055	0,0215	-0,0667	-0,0506
1354,37	0,0088	0,0417	-0,0882	-0,0456
1354,66	-0,0424	0,0624	-0,0114	0,0959
1354,71	-0,0423	0,0643	0,0059	0,1126
1355,65	-0,0803	0,0507	-0,0541	0,0780
1355,75	-0,0773	0,0889	-0,0440	0,1215
1356,72	-0,1620	0,0399	-0,1578	0,0519
1357,73	-0,1515	0,0299	-0,1303	0,0583
1358,71	-0,0403	0,0539	-0,0790	0,0205
1359,35	0,0888	0,0322	-0,1160	-0,1562
1359,70	-0,0225	0,0654	-0,0671	0,0222
1360,73	-0,0359	0,1325	-0,1491	0,0172
1361,64	0,3279	-0,0264	0,0111	-0,3352
1361,67	0,3941	-0,0703	0,0413	-0,4018
1361,80	0,4923	-0,2745	0,2484	-0,4976
1362,67	0,3787	0,0727	-0,0525	-0,3792
1362,81	0,4720	-0,0088	0,0297	-0,4749
1363,10	0,3133	0,0180	-0,0708	-0,3385
1363,70	0,3417	0,0783	0,1034	-0,2264
1363,82	0,4544	0,1154	-0,0321	-0,4203
1364,72	0,1143	0,1706	0,0012	0,0428
1365,73	0,0034	0,0971	-0,0251	0,0790
1366,69	0,0502	0,0220	0,0324	0,0083
1367,69	-0,0058	-0,0143	0,0487	0,0432
1368,68	-0,0033	0,0015	0,0214	0,0250
1369,67	0,0062	0,0530	-0,0043	0,0376
1369,77	0,0075	0,0672	-0,0166	0,0379

1370,75	-0,0224	0,0402	-0,0172	0,0449
1371,28	0,0102	-0,0259	-0,1255	-0,1317
1371,72	0,0307	-0,0179	0,0292	-0,0217
1372,22	0,0001	-0,0088	-0,1099	-0,1014
1372,71	0,0012	-0,0183	0,0147	-0,0042
1373,72	-0,0047	0,0071	-0,0080	0,0040
1374,65	0,0264	0,0186	-0,0088	-0,0178
1374,74	0,0360	0,0290	-0,0048	-0,0158
1375,66	0,0051	0,0205	-0,0018	0,0125
1375,76	-0,0018	0,0458	-0,0287	0,0207
1376,72	-0,0240	0,0839	-0,0370	0,0740
1377,68	0,0648	0,1537	0,1991	0,2576
1378,68	0,0140	0,1346	0,1237	0,2232
1379,71	-0,0405	0,0902	-0,0009	0,1228
1380,72	0,2194	-0,0032	0,0326	-0,1965
1380,85	0,3551	-0,0234	0,0265	-0,3511
1381,66	0,0549	0,0256	-0,0262	-0,0580
1381,81	0,2496	0,0125	-0,0192	-0,2533
1382,63	0,0172	0,0047	-0,0117	-0,0237
1382,76	0,0479	0,0561	-0,0232	-0,0180
1383,65	0,2195	0,0592	-0,0303	-0,1978
1383,77	0,2354	0,0775	-0,0354	-0,2103
1384,72	0,5124	-0,0609	0,0707	-0,5135
1384,85	0,5213	-0,1093	0,1173	-0,5208
1385,76	0,4932	-0,0743	0,0856	-0,4900
1386,75	0,1846	-0,0056	0,0014	-0,1872
1387,75	0,0285	0,0450	-0,0222	-0,0036
1388,73	0,0439	0,0621	-0,0224	-0,0060
1389,75	0,0152	-0,0001	0,0396	0,0208
1390,75	0,0049	0,0209	0,0090	0,0211
1391,76	-0,0111	0,0219	-0,0112	0,0210
1392,72	-0,0102	0,0678	-0,0488	0,0267
1393,73	0,0039	0,0138	0,0089	0,0164
1394,72	-0,0266	0,0216	-0,0439	0,0073
1395,74	0,0106	-0,0201	-0,0152	-0,0417
1396,73	0,0286	-0,0250	0,0225	-0,0311
1397,73	-0,0232	0,0384	-0,0481	0,0164
1397,74	-0,0290	0,0433	-0,0569	0,0195
1398,77	0,0044	0,1028	0,0461	0,1271
1399,64	0,0196	0,0705	0,0109	0,0614
1399,77	0,0307	0,1292	0,0406	0,1280
1400,67	-0,0163	0,0850	-0,0167	0,0850
1400,80	0,0000	0,0564	0,0094	0,0660
1401,70	0,0955	-0,0399	0,0580	-0,0802
1402,71	0,0072	0,0033	-0,0296	-0,0310
1403,67	-0,0301	0,0153	-0,0250	0,0214
1403,80	-0,0067	0,0560	-0,0341	0,0304
1404,63	-0,0312	-0,0283	-0,0048	-0,0036
1404,78	-0,0396	0,0373	-0,0527	0,0258
1405,76	-0,0610	0,0452	-0,1037	0,0046
1406,74	0,4147	-0,2775	0,0636	-0,5513
1407,74	0,2738	-0,1677	-0,1133	-0,4570
1408,74	0,0477	-0,0242	-0,0695	-0,1344
1409,74	-0,0432	0,0381	-0,0618	0,0186
1410,73	-0,0452	0,1088	-0,0458	0,1056
1411,73	-0,0588	0,0337	0,0035	0,0941
1412,75	-0,0249	0,0476	0,0778	0,1361
1413,66	-0,0112	-0,0083	0,0145	0,0173
1413,77	-0,0098	0,0070	0,0885	0,0931
1414,69	-0,0302	0,0172	-0,0244	0,0239
1414,78	-0,0408	0,0172	0,0117	0,0692
1415,75	-0,0110	-0,0258	0,0258	0,0095
1416,75	-0,0059	-0,0043	-0,0099	-0,0066
1417,77	0,0106	-0,0145	-0,0071	-0,0299
1418,75	0,0481	-0,0151	0,0325	-0,0327
1419,75	0,0431	-0,0379	0,0366	-0,0456
1420,73	-0,0157	0,0125	-0,0381	-0,0051
1421,75	-0,0340	0,0275	-0,0543	0,0116
1422,74	0,0189	0,0153	-0,0020	-0,0056
1423,74	0,1061	-0,0214	0,0525	-0,0791
1424,72	0,0145	0,0173	-0,0012	0,0002
1425,68	-0,0339	0,0750	-0,0660	0,0386
1425,75	-0,0274	0,0780	-0,0569	0,0458
1426,77	-0,0398	0,0481	-0,0440	0,0398
1427,75	-0,0633	0,0994	-0,0550	0,1016
1428,72	0,1311	-0,0542	0,2503	0,0449
1429,73	0,0258	0,0728	0,1207	0,1509
1430,74	0,3289	0,0352	0,0254	-0,2897
1431,74	0,1557	-0,1748	-0,0567	-0,3480
1432,75	-0,0829	-0,0936	-0,1524	-0,1455
1433,75	-0,1199	0,0143	-0,1167	0,0236
1434,74	-0,0800	0,0408	-0,0480	0,0731

1435,76	-0,0385	0,0255	-0,0335	0,0315
1436,77	-0,0064	0,0085	0,0080	0,0216
1437,77	-0,0069	0,0469	-0,0408	0,0118
1438,76	0,0062	0,0394	0,0016	0,0310
1439,69	-0,0240	0,0062	0,0044	0,0354
1440,10	0,0174	0,0029	-0,0428	-0,0519
1440,97	-0,0107	0,0257	-0,0485	-0,0094
1441,74	0,0314	-0,0384	0,0428	-0,0263
1442,21	-0,0109	0,0544	-0,1370	-0,0618
1442,77	0,0314	-0,0266	0,0418	-0,0193
1443,77	-0,0813	0,0235	-0,0558	0,0501
1444,78	-0,0264	0,0256	0,0062	0,0555
1445,76	-0,0065	0,0469	0,0046	0,0520
1446,76	0,0145	0,0106	0,0358	0,0248
1447,76	0,0314	-0,0200	0,0311	-0,0214
1448,76	0,0199	0,0575	-0,0437	-0,0022
1449,47	-0,0051	0,0212	-0,0734	-0,0350
1449,75	0,0260	0,0650	-0,0433	-0,0069
1450,33	0,0356	0,0167	-0,0776	-0,0840
1450,49	0,0150	0,0174	-0,0763	-0,0661
1450,73	0,0129	0,0508	0,0046	0,0371
1451,31	0,0543	0,0398	-0,1067	-0,1036
1451,75	-0,0184	0,0599	-0,0310	0,0469
1452,71	-0,0158	0,0697	-0,0445	0,0389
1453,74	-0,1849	-0,0564	-0,0881	0,0457
1453,80	-0,1651	-0,0900	-0,0526	0,0438
1454,68	-0,1704	0,0524	-0,1149	0,1100
1454,88	-0,2179	0,0143	-0,1517	0,0853
1455,40	-0,0404	0,0945	-0,1398	0,0029
1456,23	-0,2109	0,1299	-0,1468	0,1985
1457,24	-0,0158	0,0618	-0,1072	-0,0177
1457,72	-0,1042	0,0645	0,0012	0,1758
1458,72	-0,1237	0,0701	-0,0235	0,1686
1459,67	-0,0622	-0,1223	0,0764	-0,0061
1460,17	0,0361	-0,0166	-0,0206	-0,0637
1460,45	0,0525	-0,0086	-0,0347	-0,0865
1460,68	-0,1865	0,0260	-0,1751	0,0483
1461,24	0,0060	0,0151	-0,0731	-0,0704
1461,72	-0,1722	0,0502	-0,1971	0,0361
1462,41	0,0107	0,0505	-0,0937	-0,0548
1462,71	-0,1329	0,0829	-0,1501	0,0727
1463,33	0,0090	0,0619	-0,1171	-0,0528
1463,68	-0,0943	0,1330	-0,1445	0,0910
1463,71	-0,1245	0,1351	-0,1343	0,1305
1464,75	0,1412	-0,0347	-0,1850	-0,1669
1465,00	0,2636	-0,0067	-0,1825	-0,2898
1465,68	0,5365	-0,1958	0,1036	-0,5539
1466,20	0,5610	0,0073	-0,2263	-0,5991
1466,68	0,5221	-0,0114	-0,1026	-0,5383
1467,01	0,3351	0,0928	-0,1693	-0,3766
1467,37	0,5248	0,1076	-0,2713	-0,5917
1467,68	0,5142	0,0770	-0,2070	-0,5391
1468,34	0,3495	0,1557	-0,2120	-0,3793
1468,71	0,3323	0,1553	-0,1625	-0,3269
1469,64	0,1125	0,1953	-0,2011	-0,0747
1469,71	0,0278	0,1378	-0,1099	0,0064
1470,37	0,0550	0,1494	-0,0936	0,0066
1470,71	-0,0456	0,1258	-0,0615	0,1071
1470,71	-0,0236	0,1529	-0,0886	0,0928
1471,44	0,0499	0,0833	-0,0447	-0,0045
1471,71	-0,0524	0,0412	0,0262	0,1226
1472,40	0,0583	0,0427	-0,0358	-0,0557
1472,75	-0,0436	0,0510	0,0009	0,0942
1473,25	0,0794	0,0287	-0,0498	-0,0961
1473,90	-0,0233	0,0363	-0,0179	0,0392
1474,73	-0,0820	0,0774	-0,0447	0,1148
1475,76	-0,1394	0,1731	-0,0806	0,2236
1476,75	-0,1747	0,1718	-0,0836	0,2560
1477,74	-0,4820	-0,6733	-0,0307	-0,1428
1478,06	-0,4205	-0,4933	-0,1579	-0,1293
1478,75	-0,5950	-0,4950	-0,2131	-0,0919
1479,11	-0,1065	0,0113	-0,2017	-0,0908
1479,75	-0,5594	-0,2564	-0,3158	-0,0022
1480,76	-0,3445	-0,0325	-0,1906	0,1271
1481,73	-0,1843	0,1019	-0,1137	0,1781
1482,74	-0,1405	0,1407	-0,0637	0,2123
1483,73	-0,1100	0,1301	-0,0606	0,1786
1484,67	-0,0580	0,1201	-0,0871	0,0850
1484,76	-0,0682	0,1384	-0,0721	0,1299
1485,75	-0,0731	0,0532	-0,0327	0,0926
1486,76	0,2481	0,0233	-0,0448	-0,2632
1487,73	0,2439	-0,0794	0,1095	-0,2144

1488,72	0,1430	0,0161	0,0806	-0,0574
1489,68	0,0061	0,0785	-0,0051	0,0692
1489,85	-0,0237	0,3160	0,0577	0,4213
1490,69	-0,0228	0,1197	-0,0095	0,1318
1490,84	-0,0550	0,2837	0,0475	0,4165
1491,71	-0,0847	0,1732	-0,0193	0,2478
1491,84	-0,0638	0,3495	0,0655	0,5020
1492,78	-0,1609	0,2940	-0,0309	0,4428
1493,74	0,1383	-0,1103	0,2493	0,0085
1494,73	0,0527	0,0729	0,1768	0,1841
1495,75	-0,0328	-0,0009	0,2382	0,2620
1496,75	-0,1016	0,1436	0,0402	0,2773
1497,75	-0,1091	0,1186	-0,0079	0,2110
1498,74	-0,1271	0,1007	-0,0101	0,2143
1499,74	-0,1251	-0,1378	0,0645	0,0468
1500,74	-0,1583	-0,0754	0,0091	0,0734
1501,74	-0,0815	0,0085	0,0551	0,1409
1502,74	0,0025	0,0379	0,0471	0,0820
1503,76	-0,0059	0,1863	0,0423	0,2263
1504,75	-0,0621	0,2152	0,0242	0,2984
1505,79	-0,0770	0,4240	0,2199	0,7526
1505,84	-0,0594	0,4195	0,2267	0,7661
1506,71	-0,1240	0,2927	0,0693	0,4837
1506,84	-0,1204	0,4280	0,1903	0,7586
1507,80	-0,1258	0,2497	0,0208	0,4116
1508,70	0,1984	-0,0716	0,3083	0,1443
1509,71	0,0515	-0,0479	0,2110	0,2110
1510,70	0,1247	-0,1582	0,2803	0,0197
1511,75	0,0672	-0,1592	0,2754	0,0726
1512,76	-0,0494	-0,0695	0,1767	0,1751
1513,77	-0,1231	0,0675	0,0598	0,2571
1514,75	-0,1935	0,0912	-0,0203	0,2592
1515,73	-0,0354	-0,1425	0,2088	0,0819
1516,71	-0,1694	0,0329	0,0496	0,2430
1516,74	-0,1753	0,0346	0,0481	0,2492
1517,75	-0,2016	0,0914	-0,0228	0,2657
1518,75	-0,1490	0,1050	-0,0430	0,2152
1519,77	-0,0985	0,2903	-0,0377	0,3501
1520,77	-0,0865	0,2717	0,0061	0,3470
1521,76	-0,1109	0,1903	-0,0300	0,2564
1522,75	-0,0960	0,0937	-0,0112	0,1707
1523,75	-0,0647	0,1060	-0,0209	0,1395
1524,71	-0,0405	0,1039	-0,0256	0,1132
1525,73	-0,0737	0,1043	-0,0318	0,1535
1526,74	-0,1121	0,1424	-0,0131	0,2364
1527,70	-0,1575	0,1309	-0,0004	0,2896
1527,80	-0,1521	0,2256	-0,0086	0,3687
1528,74	-0,2618	0,2513	-0,1304	0,3859
1529,70	0,1909	0,1333	0,6591	0,3992
1530,70	0,2515	0,0594	0,7182	0,3645
1531,70	0,0606	0,1699	0,3200	0,3582
1532,67	-0,0949	-0,0197	0,2081	0,2939
1532,70	-0,0936	-0,0242	0,2193	0,3007
1533,68	-0,0501	-0,2149	0,3699	0,2224
1534,68	-0,0665	0,0221	0,0832	0,1699
1535,69	-0,1043	0,0341	0,0389	0,1872
1536,72	-0,1243	0,0776	-0,0155	0,1801
1537,71	-0,1123	0,0577	0,0169	0,1770
1538,73	-0,1111	0,0485	0,0197	0,1774
1539,74	-0,0776	0,0726	0,0035	0,1454
1540,69	-0,0785	0,0215	0,0346	0,1320
1540,78	-0,0738	0,0433	0,0301	0,1451
1541,69	-0,0792	0,0665	0,0019	0,1435
1541,78	-0,0761	0,1073	0,0053	0,1796
1542,76	-0,1198	0,2062	0,0721	0,4060
1543,75	-0,1622	0,2366	-0,0120	0,3868
1544,76	-0,1824	0,0679	-0,0427	0,2056
1545,75	-0,2225	0,0413	-0,1007	0,1564
1546,76	-0,1932	-0,4009	0,2016	-0,0206
1546,76	-0,1932	-0,4006	0,2007	-0,0211
1547,33	-0,0247	0,0189	-0,0797	-0,0480
1547,77	-0,2536	-0,1586	0,0153	0,0878
1548,33	-0,0313	0,0361	-0,0995	-0,0857
1548,77	-0,1715	-0,0504	-0,1073	0,0156
1549,38	-0,0066	0,0349	-0,0867	-0,0409
1549,61	-0,0130	0,0369	-0,0547	-0,0054
1549,77	-0,1168	0,0432	-0,1162	0,0529
1550,65	-0,0704	0,0372	-0,0468	0,0615
1550,79	-0,2237	0,0333	-0,1022	0,1584
1551,72	-0,1167	0,1022	0,1194	0,3137
1552,72	-0,0641	0,1001	0,1579	0,3171
1553,73	-0,1969	0,0574	0,0017	0,2565

1554,33	-0,0153	-0,0153	-0,0107	-0,0061
1554,64	-0,1986	-0,0009	-0,0266	0,1629
1554,78	-0,2861	0,0351	-0,0536	0,2606
1555,33	-0,0123	0,0249	-0,0557	-0,0099
1555,74	-0,2198	0,0701	-0,0729	0,2152
1556,67	-0,1183	0,0647	-0,0871	0,1033
1556,79	-0,1582	0,1011	-0,0750	0,1867
1557,75	-0,1067	0,0613	-0,0532	0,1196
1558,73	-0,0919	0,0896	-0,0318	0,1503
1559,75	-0,1131	0,0699	-0,0384	0,1444
1560,76	-0,1276	0,0486	-0,0357	0,1393
1561,77	-0,5409	-0,1424	-0,1109	0,1997
1562,77	-0,2248	-0,2563	0,2637	0,1220
1563,75	-0,3377	-0,0941	0,0665	0,2071
1563,78	-0,3404	-0,0872	0,0543	0,2089
1564,78	-0,3664	-0,0259	-0,0172	0,2616
1565,77	-0,2633	0,0582	-0,0648	0,2503
1565,79	-0,2613	0,0628	-0,0697	0,2492
1566,78	-0,2282	0,0343	-0,0431	0,2190
1567,76	-0,1759	0,0703	-0,0537	0,1903
1568,49	-0,0531	0,0202	-0,0384	0,0367
1568,76	-0,1954	-0,0276	0,0316	0,1905
1569,36	-0,0306	-0,0124	-0,0138	0,0003
1569,54	-0,0489	0,0014	-0,0229	0,0259
1569,76	-0,2015	-0,0436	0,0736	0,2295
1570,49	-0,0938	0,0182	-0,0290	0,0822
1570,73	-0,2114	0,0563	-0,0002	0,2544
1570,87	-0,2831	0,0503	0,0987	0,4157
1571,33	-0,0098	0,0348	-0,0740	-0,0188
1571,77	-0,1975	0,0811	0,0147	0,2770
1571,84	-0,2524	0,0686	0,0820	0,3781
1572,70	-0,1079	0,0730	-0,0108	0,1643
1572,85	-0,1731	0,0606	0,0295	0,2511
1573,68	-0,0457	0,0812	0,0059	0,1222
1573,84	-0,1140	0,0637	0,0167	0,1897
1574,77	-0,1036	0,1110	0,0234	0,2308
1575,77	-0,1661	0,1289	-0,0416	0,2575
1576,71	-0,0154	0,0514	0,3730	0,3690
1576,77	0,0012	0,0390	0,4008	0,3705
1577,77	-0,0614	0,0831	0,4214	0,4160
1578,78	-0,1170	0,1486	0,1592	0,3976
1579,77	-0,1565	0,2065	-0,0840	0,2845
1580,75	0,1022	-0,2311	0,2537	-0,0813
1581,76	-0,0984	0,0630	-0,0828	0,0848
1582,77	-0,1698	0,0637	-0,0934	0,1426
1583,77	-0,2394	0,0581	-0,1167	0,1835
1584,77	-0,2913	0,0932	-0,1054	0,2761
1585,75	-0,0390	-0,2652	0,3782	0,0971
1586,75	-0,1801	-0,0029	0,0888	0,2267
1587,76	-0,2144	0,0714	-0,0529	0,2244
1588,76	-0,1954	0,1239	-0,1089	0,2159
1589,74	-0,2716	0,2136	-0,0950	0,3903
1589,83	-0,3200	0,2477	-0,0745	0,5024
1590,71	-0,1967	0,1290	-0,0566	0,2667
1590,83	-0,3065	0,1941	-0,0553	0,4500
1591,73	-0,1645	0,0747	-0,0225	0,2164
1591,86	-0,2170	0,0927	-0,0260	0,2769
1592,71	-0,1510	0,0356	-0,0027	0,1762
1592,84	-0,2250	0,0043	0,0168	0,2390
1593,80	-0,1722	0,0162	-0,0124	0,1721
1593,81	-0,1833	0,0137	-0,0071	0,1856
1594,80	-0,1410	0,0380	-0,0117	0,1676
1595,75	-0,1084	0,0588	-0,0169	0,1480
1595,83	-0,1102	0,0407	0,0081	0,1553
1596,81	-0,1156	0,0427	0,0098	0,1652
1597,83	-0,1015	0,0480	0,0002	0,1454
1598,80	-0,0929	0,0781	0,0307	0,1931
1599,82	-0,0963	0,0956	0,0574	0,2378
1600,80	-0,0367	0,0087	0,1381	0,1642
1601,81	-0,1544	0,0445	0,0129	0,2063
1602,79	0,0499	-0,0665	0,1910	0,0516
1603,79	-0,1210	0,0316	0,0133	0,1573
1604,81	-0,1542	0,0597	-0,0703	0,1430
1605,82	-0,1382	0,0473	-0,0470	0,1364
1606,81	-0,1563	0,0417	0,0032	0,2058
1607,78	0,0864	-0,0790	0,2259	0,0286
1608,76	-0,0754	0,0465	0,0467	0,1566
1608,80	-0,0731	0,0534	0,0417	0,1571
1609,80	-0,1270	0,0588	-0,0073	0,1780
1610,81	-0,1144	0,1178	-0,0513	0,1763
1611,79	-0,1307	0,1261	-0,0260	0,2253
1612,82	-0,0533	0,0791	0,0544	0,1776

1613,82	-0,0774	0,0694	0,0471	0,1803
1614,78	-0,1079	0,1071	-0,0009	0,2030
1614,83	-0,1082	0,1161	-0,0163	0,2008
1615,82	-0,0891	0,0556	0,0657	0,1916
1616,80	-0,1334	0,0746	0,0181	0,2215
1617,77	-0,1240	0,0697	-0,0204	0,1710
1617,90	-0,0796	0,0652	-0,0181	0,1231
1618,77	-0,1738	0,0755	-0,0653	0,1838
1618,89	-0,1302	0,0852	-0,0595	0,1564
1619,77	0,1037	-0,1435	0,2236	-0,0362
1620,78	0,0201	-0,1069	0,1551	0,0021
1621,79	-0,1910	-0,0308	0,0369	0,1878
1622,80	-0,1928	0,0327	-0,0122	0,2104
1623,78	-0,1537	0,0361	-0,0071	0,1846
1624,81	-0,1781	0,0379	-0,0233	0,1894
1625,80	-0,2093	0,0734	-0,0623	0,2169
1626,78	-0,0991	0,0425	0,0228	0,1574
1627,78	-0,0117	0,0735	0,0388	0,1161
1628,78	-0,0477	0,1903	0,0191	0,2383
1629,82	0,4496	-0,0530	0,0810	-0,4461
1630,83	0,4181	-0,0147	-0,0416	-0,4352
1631,83	0,3302	0,0175	-0,0474	-0,3415
1632,90	0,0770	0,0701	-0,0507	-0,0524
1633,85	-0,0472	0,0988	-0,0453	0,1047
1634,86	-0,0762	0,0563	0,0259	0,1548
1635,83	-0,0780	0,0644	0,0316	0,1635
1636,84	-0,0914	0,1091	0,0362	0,2259
1637,83	-0,0269	0,0646	0,1054	0,1725
1638,83	-0,1166	0,1133	0,0045	0,2303
1639,85	0,0332	-0,1270	0,2816	0,1357
1640,88	-0,0734	-0,1180	0,2378	0,1851
1641,83	0,0523	-0,1191	0,2336	0,0512
1642,81	0,0421	-0,0289	0,1343	0,0424
1643,81	-0,0440	0,0304	0,0403	0,1076
1644,83	-0,0498	0,0585	0,0190	0,1151
1645,77	-0,0585	0,0390	0,0205	0,1096
1645,85	-0,0699	0,0509	0,0098	0,1232
1646,82	-0,0554	0,0397	0,0197	0,1075
1647,86	-0,1062	0,0649	-0,0133	0,1539
1648,83	-0,0337	0,0672	0,0175	0,1129
1649,82	-0,0430	0,0598	0,0101	0,1068
1650,83	-0,0392	0,0941	-0,0074	0,1194
1651,77	-0,0352	0,0299	-0,0074	0,0577
1651,86	-0,0342	0,0224	-0,0063	0,0500
1652,84	-0,0965	0,0882	-0,1082	0,0859
1653,83	-0,1015	0,0975	-0,0740	0,1264
1654,84	-0,1801	0,1334	-0,1244	0,1903
1655,80	0,1921	-0,1752	0,3464	-0,0443
1656,82	0,0284	0,0545	0,1351	0,1773
1657,82	-0,1287	0,1722	-0,0002	0,3087
1658,82	-0,1332	0,1289	-0,0177	0,2482
1659,81	-0,1161	0,0802	-0,0259	0,1709
1660,83	-0,0931	0,0804	-0,0183	0,1531
1661,85	-0,0685	0,0305	0,0209	0,1140
1662,84	-0,0555	0,0703	0,0071	0,1213
1663,75	-0,0590	0,0360	0,0154	0,1102
1663,86	-0,0569	0,0491	0,0163	0,1155
1664,81	-0,0891	0,0469	-0,0066	0,1241
1665,82	-0,1033	0,0570	-0,0260	0,1316
1666,83	-0,0834	0,0023	0,0321	0,1159
1667,82	-0,1123	0,0430	-0,0572	0,0988
1668,80	-0,1472	0,0263	-0,0726	0,1012
1669,85	-0,2115	0,0844	-0,1547	0,1552
1670,79	0,1841	-0,1246	0,2367	-0,0942
1671,81	-0,1007	-0,0280	0,0325	0,0960
1672,81	-0,1746	0,0259	-0,0116	0,1840
1673,84	-0,1705	0,0651	-0,0420	0,1910
1674,85	-0,1259	0,0911	-0,0408	0,1733
1675,83	-0,1070	0,0377	0,0070	0,1405
1676,84	-0,0848	0,0880	-0,0128	0,1546
1677,82	-0,0558	0,0443	0,0204	0,1161
1678,85	-0,0837	0,0515	0,0032	0,1360
1679,83	-0,1008	0,0873	-0,0404	0,1463
1680,76	-0,0772	0,0473	-0,0199	0,1029
1680,89	-0,1008	0,0494	-0,0069	0,1422
1681,83	-0,0979	0,0648	-0,0035	0,1539
1682,78	-0,0909	0,0418	-0,0112	0,1196
1682,91	-0,0675	0,0491	0,0200	0,1317
1683,85	-0,0382	0,0176	0,0725	0,1222
1684,84	-0,0515	0,0208	0,0612	0,1360
1685,84	-0,0710	0,0737	0,0163	0,1550
1686,83	0,0164	0,0117	0,0990	0,0818

1687,84	-0,0527	0,0623	0,0178	0,1264
1688,84	-0,0703	0,0574	-0,0199	0,1050
1689,86	-0,0993	0,0727	-0,1036	0,0793
1690,83	-0,0237	0,0220	0,0255	0,0628
1691,85	0,0828	-0,0201	0,1052	-0,0078
1692,39	0,0930	-0,0163	-0,0097	-0,1164
1692,85	0,0469	0,0792	0,1160	0,1262
1693,47	0,0344	0,0133	-0,0643	-0,0823
1693,85	-0,0751	0,1177	0,0053	0,1948
1694,85	-0,1755	0,1006	-0,0512	0,2257
1695,83	-0,1861	0,1188	-0,0960	0,2127
1696,84	-0,0902	0,0546	-0,0130	0,1291
1697,84	-0,0631	0,0547	0,0134	0,1268
1698,83	-0,0649	0,0688	0,0063	0,1324
1699,86	-0,0898	0,0369	0,0221	0,1454
1700,85	-0,0853	0,0662	-0,0378	0,1174
1701,72	-0,0479	0,0444	-0,0071	0,0820
1701,89	-0,0975	0,0693	-0,0360	0,1294
1702,73	-0,0869	0,0234	-0,0359	0,0750
1702,89	-0,1229	0,0111	-0,0470	0,0905
1703,76	-0,1525	0,0596	-0,0890	0,1271
1703,85	-0,1622	0,0577	-0,0945	0,1308
1704,86	-0,1756	0,0631	-0,0738	0,1665
1705,86	-0,2405	0,0894	-0,1102	0,2208
1706,75	0,1884	-0,1167	0,4144	0,0384
1707,78	0,0100	0,0144	0,2370	0,1754
1708,77	-0,1566	0,0755	0,0189	0,2319
1709,54	-0,2257	0,0638	-0,2203	0,0823
1709,80	-0,2533	0,0710	-0,1594	0,1692
1710,56	-0,2239	0,0584	-0,2063	0,0786
1710,83	-0,2804	0,1191	-0,2110	0,1951
1711,83	-0,1999	0,0844	-0,1185	0,1673
1712,82	-0,1476	0,0720	-0,0692	0,1510
1713,82	-0,0804	0,0378	-0,0050	0,1126
1714,83	-0,0715	0,0974	0,0208	0,1845
1715,73	-0,0667	0,0645	-0,0019	0,1219
1715,86	-0,0811	0,0581	0,0376	0,1974
1716,83	-0,0387	0,0601	0,0319	0,1164
1717,69	-0,0144	0,0375	-0,0032	0,0440
1717,85	-0,0437	0,0638	-0,0078	0,0946
1718,88	0,0035	0,0275	0,0290	0,0478
1719,49	0,1338	-0,0050	0,0043	-0,1223
1719,85	0,0482	0,0204	0,0360	0,0074
1720,84	0,1155	0,0377	0,0324	-0,0523
1721,83	0,0765	0,0506	0,0128	-0,0128
1722,85	0,0310	0,0455	0,0198	0,0295
1723,76	-0,0093	-0,0016	0,0398	0,0509
1723,90	-0,0409	0,0285	0,0215	0,0892
1724,77	-0,0629	0,0208	0,0171	0,0985
1724,92	-0,0783	0,0406	0,0090	0,1233
1725,46	-0,0369	0,0253	-0,0585	0,0060
1725,71	-0,0808	0,0431	-0,0433	0,0818
1725,88	-0,0970	0,0575	-0,0376	0,1164
1726,65	-0,0746	0,0190	0,0084	0,1006
1726,85	-0,0404	0,0064	0,0562	0,0986
1727,84	-0,1545	0,0673	-0,0196	0,1988
1728,74	0,1160	0,0018	0,1731	0,0281
1728,82	0,0924	0,0242	0,1519	0,0581
1729,36	-0,0090	0,0294	-0,0314	0,0106
1729,82	0,0096	0,0263	0,0758	0,0873
1730,85	-0,0517	0,0919	-0,0065	0,1298
1731,74	-0,0436	0,0271	0,0091	0,0798
1731,93	-0,0927	0,0518	-0,0194	0,1220
1732,74	-0,0508	0,0220	0,0215	0,0903
1732,88	-0,0911	0,0847	-0,0029	0,1668
1734,00	0,4627	0,0202	-0,0558	-0,4761
1734,99	0,4874	-0,0108	-0,0368	-0,5031
1735,78	0,1601	0,0132	0,0184	-0,1329
1735,96	0,4192	0,0095	-0,0304	-0,4252
1736,37	0,1202	0,0174	-0,0009	-0,0994
1736,80	0,0389	0,0479	0,0108	0,0124
1736,93	0,1744	0,0483	-0,0105	-0,1414
1737,83	-0,0384	0,0436	0,0203	0,1053
1737,91	-0,0143	0,0389	0,0223	0,0887
1738,82	-0,0035	0,0371	0,1067	0,1264
1739,81	0,0040	0,0270	0,0968	0,1122
1740,83	-0,0517	0,0566	0,0540	0,1530
1741,85	-0,1280	0,0445	0,0423	0,2332
1742,76	0,0364	-0,0194	0,3145	0,2079
1743,77	-0,0160	0,2170	0,8021	0,9239
1743,80	-0,0176	0,2187	0,8016	0,9275
1744,79	-0,2653	0,2979	0,7945	1,1002

1745,78	-0,3425	0,2715	0,5032	0,9881
1745,81	-0,3424	0,2749	0,4952	0,9889
1746,82	-0,2554	0,1720	0,2496	0,6444
1747,84	-0,1685	0,1012	0,0924	0,3488
1748,85	-0,1458	0,0893	0,0536	0,2884
1749,86	-0,1337	0,0712	0,0414	0,2380
1750,85	-0,1400	0,1217	-0,0048	0,2441
1751,83	-0,0352	0,0320	0,0860	0,1439
1752,34	-0,0638	0,0112	0,0045	0,0772
1752,84	-0,0828	0,0428	0,0716	0,1782
1753,36	-0,0522	0,0062	-0,0032	0,0540
1753,85	-0,1680	0,0659	0,0137	0,2531
1754,83	-0,1195	0,0727	0,0075	0,2050
1754,85	-0,1229	0,0809	0,0095	0,2155
1755,81	0,0439	0,0460	0,0004	0,0018
1755,91	0,1601	0,0298	0,0062	-0,1275
1756,78	0,0557	0,0164	0,0508	0,0109
1756,93	0,2089	0,0084	0,0170	-0,1800
1757,95	0,5880	-0,2095	-0,0243	-0,6082
1758,91	0,5857	-0,2116	-0,0277	-0,6061
1758,95	0,5902	-0,2139	-0,0308	-0,6107
1759,94	0,5890	-0,1065	-0,0119	-0,6123
1760,90	0,4335	0,0122	0,0282	-0,4102
1761,43	0,0281	0,0184	-0,0183	-0,0238
1761,85	0,0629	0,0494	0,0565	0,0382
1762,57	-0,0403	0,0192	0,0636	0,1180
1762,90	-0,0771	0,0917	0,0871	0,2386
1763,88	-0,1527	0,0689	0,0706	0,3092
1764,72	-0,1017	0,0603	0,0301	0,1837
1764,90	-0,1411	0,1320	0,0323	0,2960
1765,83	-0,2426	0,1248	0,0937	0,4646
1766,81	-0,0210	-0,0484	0,3007	0,2302
1767,82	-0,0877	0,0230	0,1572	0,2555
1768,85	-0,1894	0,0935	0,0016	0,2790
1769,87	-0,1487	0,0689	0,0045	0,2192
1770,89	-0,1201	0,0482	0,0318	0,1908
1771,91	0,0071	0,0456	0,0177	0,0523
1772,89	0,0681	0,0823	0,1173	0,1154
1773,88	0,0438	0,0581	0,1840	0,1881
1774,88	-0,0437	0,0781	0,1414	0,2528
1775,86	-0,0061	0,0865	0,2209	0,2611
1775,88	-0,0078	0,0877	0,2209	0,2658
1776,87	-0,0828	0,0856	0,2200	0,3403
1777,87	-0,1726	0,1076	0,0480	0,3148
1778,93	-0,1955	0,1145	-0,0149	0,2899
1779,94	-0,0488	0,0614	-0,0121	0,0995
1780,92	0,0261	0,0706	-0,0009	0,0392
1781,86	-0,0441	0,0807	0,0227	0,1427
1782,86	-0,0907	0,0537	0,0663	0,2171
1783,87	-0,1143	0,0731	0,0385	0,2116
1784,90	-0,1337	0,0963	0,0330	0,2488
1785,91	-0,1431	0,0901	0,0178	0,2491
1786,91	-0,1342	0,0582	0,0543	0,2318
1787,88	-0,1092	0,0657	0,0576	0,2199
1788,87	-0,1206	0,0731	0,0593	0,2390
1789,86	-0,1703	0,1286	0,0645	0,3379
1790,88	-0,0034	0,3087	0,9246	1,0768
1791,88	-0,2029	0,3870	0,8434	1,2239
1792,88	-0,3157	0,3263	0,5153	1,0913
1793,89	-0,2295	0,1636	0,2476	0,6254
1794,92	-0,1491	0,1359	0,0857	0,3596
1795,92	-0,1203	0,0629	0,0708	0,2483
1796,89	-0,1145	0,0811	0,0319	0,2191
1797,89	-0,1290	0,0505	0,0676	0,2407
1798,89	-0,1587	0,0919	-0,0039	0,2476
1799,90	-0,1612	0,0515	0,0230	0,2294
1800,91	-0,2795	-0,0259	-0,0832	0,1663
1801,87	-0,2635	0,0038	-0,0962	0,1641
1801,92	-0,2625	0,0118	-0,0897	0,1796
1802,91	-0,2003	0,0440	0,0048	0,2426
1803,89	-0,1506	0,0892	0,0029	0,2371
1804,75	-0,0815	0,0243	0,0379	0,1391
1804,90	-0,1147	0,0659	0,0554	0,2319
1805,76	-0,0753	0,0535	0,0166	0,1403
1805,91	-0,1117	0,0685	0,0580	0,2271
1806,79	-0,0771	0,0570	0,0249	0,1523
1806,93	-0,1105	0,0624	0,0590	0,2313
1807,90	-0,1071	0,0603	0,0496	0,2106
1808,90	-0,1154	0,0635	0,0407	0,2060
1809,85	-0,0753	0,0402	0,0509	0,1500
1809,96	-0,0964	0,0235	0,0757	0,1853
1810,80	-0,0619	0,0617	0,0359	0,1523

1810,96	-0,1156	0,0802	0,0336	0,2256
1811,81	-0,1028	0,0298	0,0749	0,1978
1811,96	-0,1044	0,0900	0,0324	0,2113
1812,90	-0,1529	0,1141	0,1621	0,4633
1813,87	-0,1707	0,1496	0,1507	0,4632
1814,86	-0,1792	0,0964	0,0798	0,3440
1815,89	-0,2183	0,0552	-0,0119	0,2550
1816,85	-0,2767	-0,3619	0,0472	-0,0707
1817,86	-0,4104	-0,2740	-0,1058	0,0007
1818,86	-0,5740	-0,1389	-0,2830	0,1279
1819,87	-0,4806	-0,0244	-0,2558	0,1884
1820,88	-0,0861	0,0298	-0,1358	0,0291
1821,88	-0,0139	0,0359	-0,0412	0,0113
1822,87	-0,0417	0,0313	-0,0266	0,0468
1823,89	0,3444	0,0155	-0,0580	-0,3647
1824,41	0,1024	-0,0209	0,0210	-0,1022
1824,90	0,3628	0,0330	-0,0396	-0,3665
1825,37	0,0484	-0,0120	0,0140	-0,0424
1825,90	0,2746	0,0359	0,0068	-0,2307
1826,87	0,0865	0,0245	0,0621	-0,0055
1827,77	-0,0059	0,0086	0,0423	0,0713
1827,91	-0,0261	0,0539	0,0471	0,1196
1828,88	-0,0770	0,0366	0,0613	0,1817
1829,89	-0,0966	0,0536	0,0543	0,1874
1830,90	-0,0725	0,0461	0,0251	0,1331
1831,89	-0,0827	0,0880	-0,0049	0,1646
1832,83	-0,2170	0,0791	0,0454	0,3139
1832,85	-0,2170	0,0807	0,0426	0,3138
1833,86	0,0518	0,0325	0,4039	0,2879
1834,85	0,1057	-0,0676	0,4895	0,2285
1834,86	0,1058	-0,0667	0,4882	0,2285
1835,86	-0,1249	0,1281	0,0670	0,3199
1836,87	-0,1624	0,1502	-0,0305	0,2819
1837,87	-0,0457	0,1003	-0,0500	0,0964
1838,86	-0,0429	-0,0038	-0,1156	-0,0569
1839,86	-0,1026	-0,0046	-0,1204	-0,0041
1840,44	-0,0035	0,0230	0,0059	0,0292
1840,87	-0,1280	-0,0061	-0,0435	0,0784
1841,38	-0,0012	-0,0154	0,0501	0,0345
1841,88	-0,1080	0,0484	-0,0210	0,1342
1842,88	-0,1282	0,0050	0,0354	0,1699
1843,90	-0,1038	0,0107	0,0630	0,1692
1844,77	0,0411	0,0092	0,0489	0,0060
1844,92	-0,0501	0,0154	0,0627	0,1155
1845,82	0,0726	0,0234	0,0457	-0,0113
1845,90	0,0285	0,0378	0,0321	0,0307
1846,74	0,0828	0,0488	0,0534	0,0119
1846,92	0,0626	0,0519	0,0477	0,0214
1847,89	0,0113	0,0508	0,0431	0,0763
1848,89	-0,0163	0,0805	0,0346	0,1220
1849,95	-0,0480	0,1987	0,0346	0,2762
1850,90	-0,0199	0,1498	0,0960	0,2437
1851,85	-0,0689	0,0904	0,0593	0,2162
1851,92	-0,0615	0,1321	0,0671	0,2586
1852,86	-0,1302	0,1174	-0,0234	0,2227
1853,89	-0,1375	0,0618	-0,0002	0,1974
1854,86	-0,1750	0,1131	-0,0037	0,2721
1855,87	0,1031	0,0401	0,2902	0,1828
1856,88	0,0079	0,0758	0,2347	0,2932
1857,89	-0,0850	0,1107	0,0792	0,2628
1858,86	-0,0801	0,0696	0,0512	0,2030
1859,90	-0,0939	0,0388	0,0554	0,1785
1860,89	-0,0981	0,0243	0,0436	0,1577
1861,84	0,1345	0,0211	0,0224	-0,1014
1861,99	0,1604	0,0407	0,0648	-0,0818
1862,93	0,1541	0,0295	0,0723	-0,0766
1863,94	0,0975	0,0399	0,0406	-0,0288
1864,91	0,0289	0,0101	0,0430	0,0173
1865,95	0,2500	-0,0307	0,0221	-0,2551
1866,19	0,3603	-0,0576	0,1404	-0,3531
1866,95	0,2384	-0,0459	0,0386	-0,2436
1867,19	0,3495	-0,0501	0,1125	-0,3456
1868,02	0,2901	0,0546	-0,0091	-0,2736
1868,95	0,0597	0,0458	-0,0254	-0,0504
1869,87	0,2781	0,0367	0,1581	-0,2445
1870,86	0,2647	0,0163	0,2128	-0,2193
1871,88	0,1779	0,0655	0,0791	-0,1062
1872,90	-0,0265	0,0464	0,0484	0,1243
1873,92	-0,1257	0,0335	0,0326	0,1810
1874,93	-0,1229	0,0220	0,0308	0,1662
1875,94	-0,1075	0,0392	0,0164	0,1522
1876,90	-0,1070	0,0088	0,0559	0,1649

1877,91	-0,1070	0,0335	0,0682	0,1917
1878,92	-0,0908	0,0266	0,0654	0,1750
1879,93	-0,0880	0,0679	0,0096	0,1550
1880,93	-0,0924	0,0182	0,0367	0,1398
1881,94	-0,0943	-0,0017	0,0479	0,1354
1882,93	-0,1230	0,0011	0,0355	0,1532
1883,95	-0,1002	0,0158	0,0388	0,1526
1884,96	-0,1037	0,0268	0,0440	0,1609
1885,86	-0,0931	0,0203	0,0366	0,1471
1885,98	-0,1202	0,0513	0,0164	0,1814
1886,91	-0,1248	0,0298	0,0428	0,2081
1887,96	-0,0621	0,0431	-0,0098	0,0933
1888,93	0,0754	-0,0428	0,0805	-0,0432
1889,92	0,0073	-0,0340	0,0488	0,0009
1890,92	-0,1016	-0,0196	0,0239	0,1032
1891,94	-0,1223	0,0232	0,0187	0,1560
1892,91	-0,1154	0,0118	0,0534	0,1715
1893,86	-0,0951	0,0139	0,0353	0,1411
1893,99	-0,1103	0,0020	0,0582	0,1645
1894,94	-0,1145	0,0038	0,0565	0,1630
1895,95	-0,0983	-0,0234	0,0545	0,1171
1896,96	-0,1107	0,0124	0,0083	0,1232
1897,96	-0,1255	-0,0224	0,0276	0,1238
1898,96	-0,1207	-0,0134	0,0290	0,1250
1899,97	-0,1149	-0,0283	0,0496	0,1349
1900,95	-0,1143	0,0101	0,0274	0,1422
1901,96	-0,1214	-0,0076	0,0496	0,1575
1902,96	-0,0962	0,0329	0,0035	0,1253
1903,96	-0,0778	0,0199	0,0213	0,1103
1904,96	-0,1078	0,0189	0,0048	0,1268
1905,97	-0,0916	-0,0048	0,0246	0,1085
1906,98	-0,1308	0,0323	-0,0091	0,1470
1907,97	-0,1274	0,0090	-0,0026	0,1305
1908,97	-0,1559	-0,0089	0,0084	0,1460
1909,96	-0,1299	0,0046	0,0255	0,1624
1910,89	-0,1152	0,0311	0,0041	0,1431
1910,98	-0,1525	0,0110	0,0145	0,1692
1911,96	-0,2052	0,0221	-0,0382	0,1826
1912,97	-0,2067	-0,0140	-0,0896	0,1047
1913,97	-0,1572	-0,0659	-0,0071	0,0793
1914,97	-0,1654	0,0178	-0,0241	0,1480
1915,99	-0,1443	0,0478	0,0088	0,1851
1916,95	-0,1597	0,0532	-0,0069	0,1987
1917,96	-0,1415	0,0511	-0,0180	0,1670
1918,98	-0,1848	0,0205	0,0236	0,2173
1919,99	-0,1829	0,0334	0,0186	0,2229
1921,00	-0,1671	0,0296	0,0097	0,1989
1921,97	-0,1476	0,0202	0,0089	0,1740
1922,95	-0,1077	0,0525	0,0097	0,1614
1923,98	-0,1052	0,0553	0,0048	0,1602
1924,95	-0,1330	0,0330	-0,0118	0,1513
1926,01	-0,4439	-0,0437	-0,2794	0,1019
1927,02	-0,4450	-0,1246	-0,2955	0,0107
1927,52	-0,2963	-0,0412	-0,2091	0,0486
1928,01	-0,4461	-0,0828	-0,3005	0,0565
1928,45	-0,2682	-0,0226	-0,1830	0,0637
1929,01	-0,3845	-0,0235	-0,1460	0,1498
1929,90	-0,2205	-0,0321	-0,0297	0,1444
1930,00	-0,2346	0,0083	-0,0863	0,1538
1930,99	-0,2167	0,0193	-0,0420	0,1811
1932,06	0,4408	-0,0447	0,0880	-0,4241
1933,06	0,4437	-0,0339	0,0584	-0,4385
1934,04	0,2577	-0,0188	-0,0005	-0,2689
1934,99	-0,0210	0,0231	-0,0407	0,0089
1935,04	-0,0263	0,0337	-0,0507	0,0156
1936,03	-0,0846	0,0022	0,0067	0,0890
1937,02	-0,1024	0,0611	-0,0301	0,1310
1938,02	-0,1320	0,0983	0,0005	0,2197
1938,96	-0,1267	0,0627	0,0535	0,2307
1939,97	-0,1435	0,0475	0,0277	0,2126
1940,98	-0,1576	0,0020	0,0291	0,1865
1941,98	-0,1444	0,0129	0,0160	0,1637
1942,56	-0,0505	-0,0303	0,0184	0,0362
1943,03	-0,1271	0,0037	0,0113	0,1351
1943,55	-0,0401	-0,0229	0,0006	0,0173
1943,96	-0,1176	0,0033	0,0142	0,1300
1945,00	-0,1304	0,0169	0,0117	0,1555
1945,99	-0,1721	0,0384	0,0082	0,2127
1946,93	-0,1747	0,0458	0,0152	0,2268
1946,99	-0,1865	0,0580	-0,0038	0,2333
1947,97	-0,2080	0,0097	0,0010	0,2117
1948,89	-0,1734	0,0281	-0,0341	0,1640

1949,01	-0,2131	0,0139	-0,0533	0,1719
1949,99	-0,2407	0,0634	-0,0324	0,2693
1950,99	-0,2174	0,0961	0,1473	0,4416
1951,97	-0,1833	0,0654	0,1303	0,4311
1953,13	0,0978	0,5045	1,1100	1,0923
1954,11	0,3732	0,5012	1,1549	1,0304
1954,12	0,3735	0,5020	1,1540	1,0311
1955,10	0,1516	0,5143	0,7561	1,0162
1956,08	0,0194	0,2685	0,2397	0,4906
1957,05	-0,0520	0,1007	0,0518	0,2002
1957,71	0,0209	0,0684	0,0849	0,1252
1957,99	-0,0702	0,0084	0,0564	0,1480
1958,72	-0,0166	0,0721	0,0909	0,1609
1958,97	-0,1141	0,0397	0,0343	0,1756
1959,99	-0,1399	0,0346	0,0298	0,1920
1960,95	-0,1331	0,0660	0,0336	0,2218
1961,97	-0,1759	0,0760	-0,0900	0,1616
1963,00	-0,1809	0,0553	-0,0886	0,1482
1963,97	-0,1856	0,0480	-0,0387	0,1924
1965,01	-0,1704	0,0696	-0,0100	0,2226
1966,00	-0,1498	0,0555	0,0278	0,2348
1967,02	-0,1414	0,0756	0,0477	0,2561
1968,02	-0,1467	0,0398	0,0553	0,2381
1968,89	-0,1341	0,0567	0,0819	0,2668
1969,07	-0,1545	0,2244	0,1612	0,5176
1969,89	-0,1066	0,0786	0,0331	0,2320
1970,08	-0,1206	0,2798	0,1189	0,4960
1971,07	0,5585	0,0009	0,0028	-0,5642
1972,05	0,5479	-0,0791	-0,0345	-0,5628
1972,46	0,3361	-0,0332	0,0708	-0,3226
1973,05	0,5229	-0,0137	-0,0564	-0,5412
1973,48	0,1579	-0,0095	0,0355	-0,1480
1974,06	0,2921	0,0332	-0,0106	-0,2846
1974,91	0,0500	0,1046	0,0269	0,0219
1975,07	0,0690	0,2134	0,0992	0,1120
1976,03	0,1212	0,5683	0,5753	0,3283
1977,04	0,0339	0,5746	0,6020	0,9155
1978,04	-0,0565	0,4427	0,3538	0,8222
1979,01	-0,0793	0,2436	0,1509	0,4496
1980,00	-0,0864	0,0954	0,0574	0,2436
1980,99	-0,1023	0,0368	0,0510	0,1692
1981,98	-0,1183	0,0393	0,0415	0,1875
1982,98	-0,1317	0,0334	0,0631	0,2156
1983,97	-0,1554	0,0665	0,0317	0,2463
1984,96	-0,1674	0,0575	-0,0068	0,2137
1984,96	-0,1674	0,0575	-0,0068	0,2137
1985,96	-0,1729	0,0451	-0,0145	0,1954
1986,96	-0,1329	0,0275	-0,0099	0,1487
1987,99	-0,1290	0,0074	0,0081	0,1367
1989,00	-0,1320	0,0221	0,0152	0,1624
1990,00	-0,1293	0,0349	0,0249	0,1879
1991,02	-0,1364	0,0296	0,0701	0,2396
1992,01	-0,0703	0,2355	0,1016	0,3831
1993,01	0,1983	0,1445	0,1086	0,0371
1994,01	0,2435	0,1280	0,0323	-0,1072
1995,01	0,1102	0,0533	0,0312	-0,0282
1996,00	-0,0159	0,0097	0,0579	0,0791
1996,99	-0,0779	0,0025	0,0596	0,1233
1997,99	-0,0753	0,0575	0,0742	0,1981
1999,00	-0,1161	0,0788	0,0536	0,2390
2000,00	-0,1242	-0,0003	0,0680	0,1920
2001,01	-0,1317	0,0230	0,0158	0,1627
2002,02	-0,1054	0,0050	0,0338	0,1361
2003,02	-0,1268	0,0413	-0,0026	0,1691
2003,98	-0,0453	0,0438	0,0129	0,0961
2004,98	-0,0380	-0,0130	0,0515	0,0700
2005,98	-0,1015	0,0171	0,0098	0,1220
2006,99	-0,1610	0,0084	-0,0160	0,1439
2007,44	-0,1080	0,0017	-0,1052	0,0187
2007,61	-0,1224	-0,0223	-0,0914	0,0169
2007,99	-0,1263	-0,0091	0,0025	0,1125
2008,54	-0,1363	-0,0203	-0,0866	0,0292
2009,00	-0,0682	-0,0070	-0,0228	0,0376
2009,99	-0,0506	-0,0193	0,0101	0,0391
2011,00	-0,0768	0,0313	-0,0186	0,0888
2012,01	-0,0974	-0,0040	0,0147	0,1040
2013,01	-0,1057	-0,0042	0,0225	0,1199
2014,00	-0,0827	0,0238	0,0285	0,1250
2015,00	-0,0524	0,0340	0,0126	0,0928
2015,99	-0,0455	0,0016	0,0329	0,0749
2017,00	-0,0589	0,0257	-0,0068	0,0733
2017,99	-0,0684	0,0115	0,0274	0,0944

2019,00	-0,0921	0,0036	0,0395	0,1229
2020,02	-0,1072	0,0221	0,0306	0,1514
2021,03	-0,1097	0,0090	0,0344	0,1455
2021,49	-0,1062	-0,0106	-0,0442	0,0499
2022,02	-0,0928	0,0244	0,0063	0,1181
2022,45	-0,0763	-0,0117	-0,0266	0,0317
2023,03	-0,1145	0,0274	-0,0205	0,1188
2024,02	0,0089	0,0314	-0,0349	-0,0080
2025,03	-0,0009	-0,0281	0,0082	-0,0200
2026,04	-0,0477	0,0201	-0,0418	0,0292
2027,07	-0,0858	-0,0058	-0,0290	0,0511
2028,11	-0,1221	-0,0203	-0,0254	0,0746
2029,09	-0,1609	0,0235	-0,0642	0,1197
2030,02	-0,1382	0,0228	-0,0287	0,1300
2031,01	-0,1080	-0,0090	0,0121	0,1033
2032,01	-0,0917	-0,0157	0,0304	0,0985
2033,01	-0,1010	-0,0072	0,0282	0,1119
2034,01	-0,1032	-0,0196	0,0519	0,1264
2035,00	-0,1033	-0,0302	0,0799	0,1443
2035,99	-0,0951	0,0017	0,0457	0,1361
2037,00	-0,0938	-0,0120	0,0452	0,1197
2038,02	-0,1030	-0,0055	0,0144	0,1006
2039,01	-0,1183	0,0167	-0,0274	0,1013
2039,01	-0,1183	0,0167	-0,0274	0,1013
2040,00	-0,1566	0,0180	-0,0509	0,1227
2040,00	-0,1566	0,0180	-0,0509	0,1227
2041,00	-0,2133	0,0118	-0,1086	0,1194
2041,70	-0,2520	-0,0211	-0,1838	0,0500
2042,02	-0,1755	-0,0208	-0,0725	0,0830
2042,58	-0,1566	-0,0540	-0,1165	-0,0132
2042,62	-0,0947	-0,0624	-0,0700	-0,0366
2043,00	-0,1598	0,0025	-0,1098	0,0660
2043,72	-0,2303	-0,0162	-0,1552	0,0693
2044,56	-0,1907	-0,0023	-0,1083	0,0653
2045,00	-0,1650	0,0165	-0,0571	0,1242
2045,51	-0,1661	0,0237	-0,1026	0,0906
2046,00	-0,1245	0,0204	-0,0228	0,1193
2047,00	-0,1205	-0,0066	0,0038	0,1145
2048,03	-0,1367	-0,0053	0,0018	0,1254
2049,09	-0,1489	-0,0275	0,0051	0,1231
2050,02	-0,1368	-0,0096	0,0042	0,1206
2050,97	-0,1171	0,0129	-0,0133	0,1106
2051,10	-0,1250	0,0038	-0,0141	0,1090
2052,00	-0,1146	0,0037	-0,0084	0,1049
2053,02	-0,1306	-0,0095	0,0051	0,1216
2054,03	-0,1504	0,0136	-0,0339	0,1273
2054,98	-0,2040	-0,0127	-0,0290	0,1463
2055,03	-0,2045	-0,0088	-0,0330	0,1489
2056,08	-0,4555	-0,0027	-0,3204	0,1252
2056,68	-0,1664	0,0108	-0,1083	0,0686
2057,00	-0,2501	0,0365	-0,0255	0,2426
2057,43	-0,1291	-0,0163	-0,0981	0,0201
2057,63	-0,2060	0,0363	-0,1787	0,0611
2057,98	-0,0731	0,0100	0,1073	0,1776
2058,97	-0,2837	0,1249	-0,1058	0,2998
2060,02	-0,2714	0,1053	-0,1191	0,2572
2060,99	-0,2133	0,0247	-0,0451	0,1848
2061,97	-0,1850	0,0332	-0,0343	0,1724
2063,00	-0,1885	0,0144	-0,0219	0,1704
2063,62	-0,1299	-0,0026	-0,0487	0,0766
2064,59	-0,2389	-0,0096	-0,0215	0,1944
2065,65	-0,1072	-0,0214	0,0055	0,0852
2065,97	-0,1300	-0,0170	0,0224	0,1297
2066,55	-0,1205	-0,0247	0,0196	0,1092
2067,02	-0,1314	-0,0177	0,0299	0,1367
2068,04	-0,1181	-0,0155	0,0200	0,1156
2068,91	-0,0964	-0,0063	-0,0115	0,0807
2069,05	-0,1300	-0,0146	0,0043	0,1143
2069,97	-0,1322	-0,0408	0,0265	0,1063
2070,06	-0,1357	-0,0390	0,0290	0,1093
2070,99	-0,1744	-0,0114	0,0104	0,1551
2072,08	-0,1601	-0,0230	0,0060	0,1271
2073,08	-0,0600	-0,0482	0,0660	0,0635
2074,07	-0,2075	-0,0008	-0,0253	0,1701
2075,04	-0,1829	0,0221	-0,0331	0,1664
2075,94	-0,1332	-0,0009	0,0029	0,1308
2076,07	-0,1241	-0,0134	0,0188	0,1234
2077,05	-0,1462	-0,0242	0,0307	0,1398
2078,05	-0,1945	0,0210	-0,0505	0,1615
2079,04	-0,1698	0,0363	0,0077	0,2037
2079,69	-0,1122	-0,0005	-0,0227	0,0867
2080,01	-0,1659	0,0410	0,0100	0,2094

2080,66	-0,1108	0,0110	-0,0231	0,0973
2081,01	-0,1181	0,0303	0,0849	0,2219
2082,02	-0,1292	0,0304	0,1009	0,2455
2083,03	-0,1586	0,0127	0,0716	0,2213
2084,01	-0,1116	-0,0017	0,0775	0,1698
2084,99	-0,0980	0,0155	0,0425	0,1447
2086,00	-0,1358	0,0113	0,0237	0,1583
2086,63	-0,0930	-0,0034	-0,0011	0,0873
2086,94	-0,1491	0,0253	-0,0140	0,1572
2087,10	-0,1704	0,0309	-0,0065	0,1872
2088,05	-0,1936	-0,0122	-0,0270	0,1471
2088,39	-0,1672	0,0128	-0,0213	0,1503
2089,05	-0,1328	-0,1196	0,0784	0,0735
2090,03	-0,2437	-0,0409	-0,0234	0,1683
2091,00	-0,2370	-0,0369	0,0226	0,2086
2091,01	-0,2233	-0,0120	-0,0288	0,1663
2092,00	-0,1787	0,0205	-0,0196	0,1714
2092,99	-0,1539	-0,0144	0,0342	0,1749
2094,02	-0,1648	0,0399	-0,0097	0,1901
2095,03	-0,1785	0,0400	0,0418	0,2482
2096,02	-0,1781	0,0299	0,0631	0,2666
2096,91	-0,1223	0,0611	0,0033	0,1794
2097,07	-0,1521	0,0515	0,0033	0,1977
2098,02	-0,1725	0,0096	0,0361	0,2026
2098,93	-0,1051	0,0321	0,0150	0,1457
2099,08	-0,1386	0,0287	-0,0240	0,1396
2099,92	-0,1136	0,0032	0,0381	0,1439
2100,07	-0,1264	-0,0101	0,0291	0,1310
2100,98	-0,1524	0,0260	0,0123	0,1725
2101,98	-0,1699	0,0129	0,0238	0,1876
2102,97	-0,1779	0,0246	0,0233	0,2146
2104,07	-0,1406	0,1587	0,2547	0,4988
2105,04	0,0387	0,0307	0,3161	0,2819
2106,01	-0,1186	0,0944	0,1629	0,3185
2106,04	-0,1232	0,0990	0,1629	0,3287
2106,98	-0,2027	0,1342	0,0663	0,3839
2107,02	-0,2121	0,1345	0,0689	0,3967
2108,01	-0,1905	0,1096	0,0334	0,3188
2109,06	-0,1876	0,0605	0,0595	0,2929
2110,03	-0,2678	0,0725	0,0205	0,3423
2111,05	-0,3252	0,0816	-0,0125	0,3841
2112,03	-0,2832	0,0604	-0,0039	0,3281
2113,03	-0,2244	0,0316	0,0143	0,2588
2114,03	-0,2707	0,0405	-0,0297	0,2689
2115,10	-0,3607	-0,1522	-0,0690	0,0670
2116,10	-0,2373	-0,2119	0,0368	-0,0028
2117,10	-0,4381	-0,1801	-0,0354	0,1382
2118,09	-0,3849	-0,0859	-0,1123	0,1765
2118,09	-0,3849	-0,0859	-0,1123	0,1765
2119,08	-0,2672	0,0167	-0,1299	0,1642
2120,07	-0,1862	0,0436	-0,0555	0,1771
2121,01	-0,1180	0,0521	0,0636	0,2092
2121,99	-0,0592	0,0485	0,0852	0,1738
2122,98	-0,0990	0,0201	0,0777	0,1887
2123,98	-0,1285	0,0380	0,0191	0,1801
2125,02	-0,1485	0,0456	0,0048	0,1904
2126,05	-0,1555	0,0658	0,0785	0,2901
2127,06	-0,0623	0,0880	0,1110	0,2408
2128,05	-0,1004	0,0263	0,1094	0,2270
2129,02	-0,1230	0,0243	0,0571	0,1901
2130,05	-0,1231	-0,0051	0,0555	0,1680
2131,06	-0,1441	0,0306	0,0090	0,1748
2132,07	-0,1489	0,0570	0,0583	0,2539
2133,07	-0,1560	0,0553	0,0546	0,2584
2134,05	-0,1585	0,0284	0,0300	0,2141
2135,04	-0,1603	0,0008	0,0252	0,1913
2137,08	-0,1490	-0,0513	0,0654	0,1468
2138,08	-0,0174	-0,1203	0,1706	0,0577
2139,07	-0,2199	-0,0097	0,0186	0,2153
2140,07	-0,1547	0,0073	-0,0043	0,1595
2141,06	-0,1760	-0,0045	0,0130	0,1756
2142,05	-0,1532	0,0007	0,0397	0,1793
2143,02	-0,1312	0,0099	0,0519	0,1819
2144,03	-0,1164	0,0273	0,0284	0,1639
2145,03	-0,1204	0,0030	0,0385	0,1455
2146,05	-0,1241	-0,0001	0,0244	0,1370
2147,05	-0,1192	-0,0078	0,0203	0,1120
2148,05	-0,1368	-0,0169	0,0396	0,1520
2149,05	-0,1483	0,0036	0,0395	0,1732
2150,04	-0,1400	-0,0012	0,0348	0,1456
2151,04	-0,1333	0,0199	0,0030	0,1502
2152,05	-0,1411	-0,0069	0,0198	0,1505

2153,06	-0,1398	-0,0095	-0,0030	0,1210
2154,06	-0,1438	0,0190	-0,0136	0,1446
2155,06	-0,1449	0,0040	0,0263	0,1628
2156,01	-0,1516	-0,0002	0,0159	0,1604
2157,02	-0,1381	0,0038	0,0609	0,1842
2158,05	-0,1717	0,0094	0,0206	0,1870
2159,05	-0,1563	-0,0071	0,0299	0,1711
2160,06	-0,1756	-0,0085	0,0246	0,1747
2161,06	-0,1775	0,0107	-0,0175	0,1657
2162,06	-0,1933	-0,0246	0,0217	0,1809
2163,99	-0,0683	-0,0049	0,1569	0,2007
2164,98	0,0788	-0,0389	0,2572	0,0931
2166,00	-0,1574	0,0322	0,0557	0,2273
2167,02	-0,1764	0,0024	0,0156	0,1874
2167,99	-0,1506	0,0005	0,0424	0,1905
2168,98	-0,1309	0,0016	0,0576	0,1812
2169,99	-0,1053	0,0180	0,0377	0,1512
2171,02	-0,1197	0,0079	0,0326	0,1546
2172,02	-0,1215	-0,0026	0,0727	0,1731
2173,01	-0,0996	-0,0055	0,0656	0,1553
2173,98	-0,1187	0,0100	0,0281	0,1514
2175,03	-0,1016	-0,0315	0,0455	0,1057
2176,04	-0,1022	-0,0368	0,0312	0,0928
2177,06	-0,1156	-0,0014	0,0021	0,1162
2178,06	-0,1526	-0,0013	0,0204	0,1649
2179,07	-0,1456	-0,0245	0,0573	0,1691
2180,04	-0,1409	0,0076	0,0276	0,1690
2181,03	-0,1191	-0,0111	0,0440	0,1423
2182,04	-0,1331	-0,0241	0,0439	0,1404
2183,05	-0,1401	-0,0150	0,0278	0,1429
2184,03	-0,1432	-0,0192	0,0346	0,1502
2185,04	-0,1444	0,0266	0,0007	0,1678
2186,01	-0,1318	-0,0029	0,0625	0,1629
2186,98	-0,0777	0,0073	0,0809	0,1500
2187,97	-0,0990	-0,0005	0,0682	0,1488
2188,99	-0,1380	0,0129	0,0200	0,1619
2189,97	-0,1703	0,0146	0,0339	0,2070
2191,00	-0,1717	0,0112	0,0413	0,2067
2191,99	-0,1212	0,0168	0,0486	0,1724
2192,99	-0,1436	0,0259	0,0095	0,1614
2193,98	-0,1387	0,0081	0,0215	0,1575
2194,99	-0,1573	-0,0128	0,0242	0,1713
2196,01	-0,1609	0,0080	-0,0072	0,1523
2197,08	-0,1939	0,0281	-0,0308	0,1861
2198,08	-0,2149	0,0086	-0,0378	0,1769
2198,97	-0,0779	0,0006	0,1233	0,1937
2199,96	0,1645	-0,0973	0,3233	0,0250
2200,92	-0,1734	0,0513	0,0234	0,2287
2200,98	-0,1885	0,0523	0,0196	0,2386
2201,96	-0,1919	0,0328	-0,0290	0,1909
2203,03	-0,2282	0,0071	-0,0350	0,1938
2203,97	-0,1747	0,0046	-0,0290	0,1451
2205,01	-0,1554	-0,0081	-0,0005	0,1371
2206,99	-0,1417	0,0018	0,0310	0,1642
2207,99	-0,1234	0,0042	0,0432	0,1640
2209,00	-0,1355	0,0367	0,0155	0,1757
2209,99	-0,1318	0,0287	0,0050	0,1601
2215,04	-0,4217	0,1306	0,0215	0,5611
2216,04	-0,1167	0,1374	0,3780	0,5487
2217,03	0,1069	0,0215	0,4553	0,3156
2218,03	-0,2160	0,1504	0,1441	0,4565
2219,02	-0,2613	0,0924	0,0385	0,3829
2220,01	-0,2438	0,0280	0,0067	0,2577
2221,02	-0,2265	0,0211	0,0059	0,2346
2222,02	-0,1884	0,0166	0,0075	0,2029
2223,02	-0,1476	-0,0055	0,0461	0,1662
2224,05	-0,1598	-0,0172	0,0249	0,1700
2225,05	-0,1541	-0,0055	0,0042	0,1483
2226,05	-0,1426	-0,0257	0,0187	0,1238
2227,09	-0,1327	0,0191	-0,0308	0,1206
2228,06	-0,1368	-0,0051	0,0114	0,1383
2229,06	-0,1024	-0,0119	0,0494	0,1282
2230,04	-0,1240	0,0286	-0,0126	0,1374
2231,08	-0,1374	-0,0018	0,0355	0,1565
2232,05	-0,1405	-0,0163	0,0444	0,1580
2233,06	-0,1434	0,0084	-0,0013	0,1496
2234,07	-0,1472	0,0036	-0,0033	0,1424
2235,01	-0,1526	0,0117	-0,0061	0,1506
2236,04	-0,1525	0,0068	-0,0022	0,1519
2237,06	-0,1952	0,0119	-0,0159	0,1795
2238,06	-0,0630	0,0136	0,1335	0,1913
2239,06	0,0371	-0,0208	0,1681	0,1141

2240,09	-0,1230	0,0009	0,0690	0,1719
2241,05	-0,1157	0,0084	-0,0013	0,1193
2242,06	-0,1227	0,0175	-0,0109	0,1201
2242,18	-0,1320	0,0317	-0,0096	0,1465
2242,99	-0,1102	-0,0374	0,0513	0,1187
2243,17	-0,1081	-0,0063	0,0613	0,1462
2244,12	-0,1562	-0,0286	0,0495	0,1661
2245,01	-0,1245	-0,0075	0,0225	0,1326
2245,17	-0,1442	0,0086	0,0029	0,1470
2246,12	-0,1276	-0,0128	-0,0035	0,1040
2247,12	-0,1279	-0,0160	-0,0045	0,1027
2248,13	-0,1326	-0,0208	-0,0067	0,1066
2249,11	-0,1251	-0,0238	0,0285	0,1195
2250,11	-0,1270	-0,0098	0,0176	0,1238
2251,09	-0,1183	0,0051	0,0056	0,1238
2252,09	-0,1068	-0,0037	0,0182	0,1119
2253,10	-0,1223	-0,0100	-0,0013	0,1069
2254,06	-0,1147	-0,0062	0,0189	0,1181
2255,06	-0,0898	-0,0299	0,0437	0,0985
2256,08	-0,1022	-0,0411	0,0455	0,1020
2257,11	-0,1007	-0,0431	0,0562	0,1219
2258,13	0,0077	-0,0156	0,0386	0,0096
2259,15	0,0551	-0,0268	0,0379	-0,0459
2260,09	-0,0130	-0,0254	0,0336	0,0195
2261,10	-0,0456	-0,0548	0,0680	0,0534
2262,12	-0,0808	-0,0368	0,0479	0,0829
2263,12	-0,0951	-0,0190	0,0167	0,0865
2264,14	-0,0982	-0,0481	0,0489	0,0937
2265,15	-0,0981	-0,0149	0,0296	0,0938
2266,10	-0,1424	-0,0056	0,0056	0,1346
2267,10	-0,1471	-0,0067	0,0026	0,1326
2268,11	-0,1713	-0,0389	0,0094	0,1289
2269,10	-0,1517	-0,0296	-0,0132	0,1092
2270,10	-0,1334	-0,0464	0,0351	0,1119
2270,10	-0,1334	-0,0464	0,0351	0,1119
2271,10	-0,1301	-0,0282	0,0226	0,1149
2272,11	-0,1223	0,0024	-0,0020	0,1192
2273,13	-0,1106	-0,0096	-0,0057	0,0906
2274,15	-0,1143	-0,0288	-0,0003	0,0816
2275,16	-0,1268	-0,0267	-0,0085	0,0866
2276,15	-0,1227	-0,0466	0,0178	0,0943
2277,07	-0,1191	-0,0294	0,0169	0,0944
2278,10	-0,1090	-0,0193	0,0129	0,0999
2279,12	-0,1243	0,0040	-0,0108	0,1132
2280,12	-0,0982	-0,0077	0,0141	0,1023
2281,12	-0,0842	-0,0381	0,0387	0,0745
2282,12	-0,1164	-0,0233	0,0076	0,0961
2283,10	-0,1076	-0,0043	-0,0172	0,0816
2284,11	-0,1354	-0,0567	0,0121	0,0861
2285,09	-0,1240	-0,0692	0,0414	0,0871
2286,09	-0,0884	-0,0343	0,0560	0,0897
2286,09	-0,0885	-0,0343	0,0560	0,0897
2287,15	-0,1142	-0,0485	0,0267	0,0824
2288,15	-0,1254	-0,0094	-0,0330	0,0726
2289,11	-0,1114	-0,0098	-0,0371	0,0656
2290,11	-0,1331	-0,0188	-0,0378	0,0784
2291,11	-0,1428	-0,0451	0,0149	0,1076
2292,11	-0,1391	-0,0128	-0,0095	0,1089
2293,10	-0,1409	0,0102	-0,0280	0,1073
2294,09	-0,1453	-0,0216	0,0104	0,1240
2295,10	-0,1442	-0,0007	-0,0035	0,1297
2296,08	-0,1043	-0,0170	0,0337	0,1099
2297,08	-0,0720	-0,0211	0,0264	0,0709
2298,10	-0,0885	-0,0032	-0,0027	0,0789
2299,09	-0,0888	-0,0273	0,0179	0,0706
2300,09	-0,1034	-0,0284	0,0081	0,0829
2301,10	-0,1338	0,0013	-0,0366	0,0979
2302,08	-0,1431	0,0082	-0,0384	0,1121
2303,13	-0,1193	0,0130	0,0351	0,1581
2304,12	-0,1722	0,0146	0,0334	0,2081
2305,11	-0,1186	0,0822	0,0973	0,2802
2306,11	0,0103	-0,0087	0,2501	0,2006
2307,13	-0,1469	0,0351	0,0805	0,2465
2308,14	-0,2498	0,0577	-0,0699	0,2296
2309,11	-0,2420	0,0489	-0,0592	0,2275
2310,13	-0,2256	0,0094	-0,0091	0,2178
2311,20	-0,1849	-0,0099	0,0105	0,1776
2312,19	-0,1521	-0,0346	0,0259	0,1364
2313,12	-0,1508	-0,0222	0,0020	0,1212
2314,12	-0,1406	-0,0014	-0,0363	0,1039
2315,14	-0,1640	-0,0142	-0,0540	0,1000
2316,12	-0,1724	-0,0461	0,0003	0,1173

2317,12	-0,1833	-0,0166	-0,0199	0,1218
2317,12	-0,1834	-0,0166	-0,0199	0,1218
2318,10	-0,1863	-0,0247	-0,0010	0,1439
2319,13	-0,1665	-0,0276	-0,0055	0,1305
2320,14	-0,1749	-0,0529	0,0138	0,1257
2321,13	-0,1606	-0,0374	0,0320	0,1373
2322,12	-0,1041	-0,0196	0,0485	0,1164
2323,13	-0,1606	-0,0026	0,0053	0,1477
2324,09	-0,1729	-0,0225	0,0128	0,1494
2325,10	-0,1731	0,0040	-0,0157	0,1523
2326,11	-0,1708	-0,0065	-0,0108	0,1501
2327,11	-0,1604	0,0037	0,0048	0,1564
2328,11	-0,1447	-0,0477	0,0565	0,1447
2329,12	-0,1221	-0,0022	0,0012	0,1170
2330,13	-0,1241	-0,0180	-0,0167	0,0800
2331,14	-0,1547	-0,0456	0,0127	0,0994
2332,12	-0,1569	-0,0310	-0,0253	0,0880
2333,11	-0,1368	-0,0952	0,0380	0,0706
2334,11	-0,1369	-0,0074	-0,0394	0,0819
2335,11	-0,1560	-0,0340	-0,0233	0,0949
2336,11	-0,1643	-0,0237	-0,0227	0,1077
2337,13	-0,1890	-0,0272	-0,0143	0,1351
2338,09	-0,1104	-0,0283	0,0494	0,1163
2339,03	-0,0276	-0,0552	0,1119	0,0733
2340,05	-0,0783	-0,0433	0,0825	0,1009
2341,07	-0,1188	-0,0280	0,0186	0,1079
2342,10	-0,1334	0,0000	-0,0121	0,1186
2343,14	-0,1752	-0,0302	0,0048	0,1409
2344,15	-0,1923	-0,0256	-0,0302	0,1348
2345,16	-0,1621	-0,0272	-0,0194	0,1106
2346,16	-0,1410	-0,0761	0,0303	0,0794
2347,16	-0,1313	-0,0452	0,0074	0,0798
2348,15	-0,1254	-0,0244	-0,0175	0,0835
2349,13	-0,1265	-0,0266	0,0050	0,0916
2350,16	-0,1360	-0,0006	-0,0378	0,0969
2351,19	-0,1450	-0,0266	-0,0084	0,1080
2352,17	-0,1610	-0,0433	-0,0019	0,1159
2353,15	-0,1610	-0,0585	0,0378	0,1270
2354,15	-0,1578	-0,0457	0,0452	0,1362
2355,13	-0,1404	-0,0091	0,0012	0,1243
2356,10	-0,1436	-0,0102	0,0045	0,1140
2357,15	-0,1495	-0,0613	0,0462	0,1236
2358,18	-0,1396	-0,0290	0,0175	0,1142
2359,16	-0,1030	-0,0555	0,0564	0,0889
2360,12	-0,1241	-0,0303	0,0256	0,1082
2361,13	-0,1006	-0,0591	0,0481	0,0796
2362,14	-0,1200	-0,0138	-0,0182	0,0827
2363,19	0,0029	-0,0440	0,0303	-0,0190
2364,20	0,0730	-0,0501	0,0465	-0,0768
2365,20	0,0026	-0,0191	0,0142	-0,0100
2366,19	-0,0695	-0,0368	0,0107	0,0429
2367,20	-0,0996	-0,0588	0,0357	0,0668
2368,21	-0,1075	-0,0286	0,0087	0,0777
2369,20	-0,1354	-0,0416	0,0159	0,0985
2370,19	-0,1272	-0,0161	0,0123	0,1151
2371,18	-0,1240	-0,0441	0,0646	0,1303
2372,19	-0,1337	-0,0223	0,0395	0,1383
2373,19	-0,1304	-0,0158	0,0209	0,1225
2374,20	-0,1328	-0,0173	0,0071	0,1173
2375,20	-0,1265	-0,0121	-0,0113	0,0998
2376,19	-0,1243	-0,0258	-0,0007	0,0949
2377,19	-0,1252	-0,0366	0,0065	0,0878
2378,17	-0,1402	-0,0587	0,0232	0,0875
2379,17	-0,1398	-0,0427	-0,0106	0,0807
2380,19	-0,1177	-0,0476	0,0099	0,0647
2381,21	0,0459	-0,0966	0,0558	-0,0911
2382,22	0,1295	-0,0657	0,0259	-0,1664
2383,21	0,0703	-0,0614	0,0551	-0,0801
2384,21	-0,0300	-0,0327	0,0118	0,0104
2385,20	-0,0763	-0,0323	0,0246	0,0620
2386,19	-0,1069	-0,0475	0,0222	0,0851
2387,16	-0,1066	-0,0240	0,0285	0,0994
2388,16	-0,1106	-0,0527	0,0484	0,1014
2389,18	-0,1139	-0,0276	0,0196	0,0979
2390,20	-0,1165	-0,0329	0,0180	0,0937
2391,21	-0,1130	-0,0463	0,0304	0,0837
2392,20	-0,1444	-0,0393	0,0219	0,1138
2393,19	-0,1326	-0,0118	-0,0187	0,0996
2394,18	-0,1449	-0,0576	0,0231	0,1003
2395,32	0,2713	-0,0825	0,0239	-0,3023
2396,34	0,3239	-0,1220	0,0413	-0,3511
2397,25	0,2847	-0,0700	-0,0118	-0,3252

2398,23	0,0720	-0,0585	-0,0230	-0,1421
2399,19	-0,0709	-0,0484	-0,0053	0,0147
2400,19	-0,1144	-0,0501	0,0137	0,0682
2401,17	-0,1221	-0,0617	0,0190	0,0851
2402,18	-0,1245	-0,0563	0,0247	0,0850
2403,18	-0,1072	-0,0324	0,0048	0,0751
2404,17	-0,1158	-0,0369	0,0134	0,0751
2405,17	-0,1269	-0,0129	-0,0001	0,1077
2406,17	-0,1430	-0,0383	0,0318	0,1247
2407,19	-0,1724	-0,0266	-0,0227	0,1163
2408,20	-0,2036	-0,0462	-0,0333	0,1104
2409,17	-0,1787	-0,0565	-0,0104	0,0934
2410,17	-0,1489	-0,0826	0,0261	0,0732
2411,17	-0,1764	-0,0237	-0,0636	0,0865
2412,18	-0,1852	-0,0469	-0,0286	0,0930
2413,19	-0,1518	-0,0344	-0,0229	0,0743
2414,20	-0,1485	-0,0474	-0,0048	0,0835
2415,19	-0,1452	-0,0550	0,0065	0,0885
2416,20	-0,1577	-0,0506	0,0022	0,0992
2417,22	-0,1027	-0,0586	0,0054	0,0409
2418,21	-0,0748	-0,0448	-0,0123	0,0166
2419,20	-0,0866	-0,0581	0,0055	0,0254
2420,19	-0,1241	-0,0370	-0,0143	0,0535
2421,19	-0,1491	-0,0386	-0,0112	0,0802
2422,19	-0,1909	-0,0025	-0,0863	0,1049
2423,18	-0,1740	-0,0552	-0,0280	0,0785
2424,18	-0,1302	-0,0841	0,0211	0,0554
2425,18	-0,1629	-0,0721	0,0045	0,0855
2426,19	-0,1848	-0,0454	-0,0191	0,1054
2427,17	-0,1778	-0,0369	-0,0200	0,1057
2428,17	-0,1463	-0,0294	-0,0191	0,0940
2429,18	-0,1775	-0,0555	-0,0048	0,1143
2430,19	-0,1726	-0,0185	-0,0485	0,1047
2431,20	-0,1675	-0,0172	-0,0452	0,0978
2432,20	-0,1636	-0,0571	-0,0120	0,0854
2433,20	-0,1677	-0,0325	-0,0541	0,0793
2434,20	-0,1414	-0,0495	-0,0095	0,0760
2435,19	-0,1409	-0,0107	-0,0523	0,0766
2436,18	-0,1633	-0,0420	-0,0355	0,0769
2437,18	-0,1715	-0,0443	-0,0530	0,0767
2438,20	-0,2068	-0,0600	-0,0569	0,0840
2439,20	-0,2306	-0,0651	-0,0556	0,1013
2440,25	-0,1541	-0,0614	0,0339	0,1093
2441,25	-0,1031	-0,0348	0,0500	0,1078
2442,20	-0,1306	-0,0082	-0,0072	0,1108
2443,20	-0,1493	-0,0275	-0,0181	0,0990
2444,19	-0,1675	-0,0266	-0,0446	0,1006
2445,19	-0,1818	-0,0375	-0,0292	0,0975
2446,20	-0,1794	-0,0464	-0,0475	0,0832
2447,20	-0,2089	-0,0473	-0,0466	0,1035
2448,21	-0,1742	-0,0361	-0,0377	0,0945
2449,20	-0,1715	-0,0415	-0,0347	0,0926
2450,20	-0,1644	-0,0770	-0,0189	0,0707
2451,20	-0,1746	-0,0272	-0,0662	0,0761
2452,22	-0,1823	-0,0641	-0,0317	0,0757
2453,21	-0,2188	-0,0247	-0,0878	0,0943
2454,24	-0,2050	-0,0665	-0,0601	0,0837
2455,24	-0,1991	-0,0816	-0,0483	0,0657
2456,28	-0,2294	-0,0602	-0,0751	0,0880
2457,23	-0,2059	-0,0652	-0,0414	0,0908
2458,23	-0,2269	-0,0527	-0,0502	0,1018
2459,21	-0,2244	-0,0506	-0,0391	0,1071
2460,21	-0,2366	-0,0489	-0,0471	0,1147
2460,21	-0,2366	-0,0489	-0,0471	0,1147
2461,21	-0,2075	-0,0130	-0,0359	0,1522
2462,21	-0,1582	-0,0286	-0,0125	0,1138
2463,23	-0,2586	-0,0347	-0,0828	0,1365
2464,15	-0,2245	-0,0173	-0,0837	0,1192
2464,21	-0,2645	-0,0132	-0,1253	0,1242
2465,24	-0,2596	-0,0242	-0,1161	0,1181
2466,24	-0,0098	-0,0736	-0,0529	-0,1125
2467,27	0,1511	-0,0896	-0,0709	-0,2741
2468,28	0,1178	-0,0815	-0,0453	-0,2125
2469,24	-0,0440	-0,0794	-0,0457	-0,0706
2470,25	-0,0986	-0,0231	-0,0174	0,0524
2471,24	-0,1570	-0,0108	-0,0070	0,1275
2471,24	-0,1570	-0,0108	-0,0070	0,1275
2472,24	-0,1658	-0,0130	-0,0191	0,1337
2473,23	-0,1759	-0,0099	-0,0443	0,1201
2474,23	-0,1739	-0,0317	-0,0273	0,1072
2475,23	-0,2022	-0,0489	-0,0367	0,1146
2476,25	-0,1854	-0,0594	-0,0099	0,1117

2477,22	-0,1461	-0,0348	0,0105	0,1148
2478,22	-0,1327	-0,0162	0,0018	0,1123
2478,22	-0,1327	-0,0162	0,0018	0,1122
2479,21	-0,1449	-0,0261	0,0024	0,1119
2480,23	-0,1523	-0,0307	0,0008	0,1054
2481,23	-0,1881	-0,0645	-0,0013	0,1041
2482,23	-0,1922	-0,0441	-0,0506	0,0827
2483,24	-0,1807	-0,0627	-0,0242	0,0886
2484,24	-0,1773	-0,0406	-0,0272	0,1028
2485,26	-0,1857	-0,0501	-0,0144	0,1076
2486,26	-0,2045	-0,0623	-0,0087	0,1124
2487,26	-0,1905	-0,0588	-0,0052	0,1147
2488,26	-0,1831	-0,0701	0,0079	0,0995
2489,25	-0,1594	-0,0787	0,0038	0,0705
2490,25	-0,1404	-0,0774	0,0005	0,0626
2491,24	-0,1389	-0,0409	0,0041	0,0894
2492,25	-0,1399	-0,0318	0,0086	0,1069
2493,23	-0,1257	-0,0571	0,0554	0,1152
2494,23	-0,1380	-0,0147	0,0121	0,1245
2495,23	-0,1282	-0,0164	-0,0092	0,1015
2496,25	-0,1563	-0,0631	0,0389	0,1181
2497,24	-0,1642	-0,0345	-0,0030	0,1121
2498,24	-0,1367	-0,0577	0,0240	0,1025
2499,25	-0,1529	-0,0433	0,0313	0,1266
2500,24	-0,1576	-0,0614	0,0279	0,1226
2501,24	-0,1423	-0,0418	0,0088	0,1016
2504,25	-0,1473	-0,0648	0,0294	0,0947
2505,24	-0,1510	-0,0586	0,0301	0,1052
2506,24	-0,1483	-0,0602	0,0193	0,0979
2507,24	-0,1479	-0,0497	0,0100	0,1011
2508,23	-0,1607	-0,0711	0,0357	0,1174
2509,22	-0,1586	-0,0421	0,0043	0,1152
2510,22	-0,1608	-0,0686	0,0193	0,1097
2511,24	-0,1637	-0,0807	0,0367	0,1049
2512,24	-0,1703	-0,0403	-0,0073	0,1121
2513,23	-0,1349	-0,0534	0,0352	0,1037
2514,23	-0,1196	-0,0457	0,0447	0,1069
2515,25	-0,1337	-0,0514	0,0522	0,1181
2516,26	-0,1301	-0,0399	0,0277	0,1042
2517,26	-0,1274	-0,0681	0,0580	0,0942
2519,25	-0,1446	-0,0427	0,0199	0,1074
2520,25	-0,1317	-0,0486	0,0396	0,1090
2521,24	-0,1096	-0,0593	0,0514	0,0881
2522,23	-0,1026	-0,0330	0,0062	0,0757
2523,25	-0,1149	-0,0816	0,0649	0,0884
2524,26	-0,1216	-0,0495	0,0120	0,0767
2525,26	-0,1266	-0,0662	0,0286	0,0725
2526,28	-0,1414	-0,0548	0,0144	0,0919
2527,26	-0,1369	-0,0599	0,0440	0,0949
2528,25	-0,1163	-0,0512	0,0225	0,0840
2529,25	-0,1277	-0,0605	0,0396	0,0911
2530,28	-0,1381	-0,0486	0,0164	0,0954
2531,25	-0,1271	-0,0855	0,0773	0,0916
2532,25	-0,1434	-0,0674	0,0294	0,0963
2533,25	-0,1414	-0,0713	0,0418	0,0992
2534,26	-0,1519	-0,0466	0,0173	0,1136
2535,25	-0,1513	-0,0455	0,0123	0,1154
2536,26	-0,1380	-0,0308	0,0040	0,0986
2537,27	-0,1248	-0,0584	0,0354	0,0945
2538,30	-0,1440	-0,0421	0,0220	0,1143
2539,22	-0,1327	-0,0482	0,0334	0,1088
2540,20	-0,1218	-0,0646	0,0435	0,0907
2541,21	-0,1343	-0,0386	0,0266	0,0831
2542,25	-0,1509	-0,0428	0,0094	0,1020
2543,26	-0,1463	-0,0689	0,0112	0,0916
2544,27	-0,1428	-0,0523	0,0106	0,0990
2545,26	-0,1372	-0,0581	0,0262	0,0945
2546,27	-0,1417	-0,0648	0,0427	0,1016
2547,27	-0,1326	-0,0733	0,0477	0,0962
2548,26	-0,1347	-0,0346	0,0240	0,1093
2549,26	-0,1483	-0,0334	0,0113	0,1183
2550,25	-0,1491	-0,0773	0,0308	0,0894
2551,24	-0,1608	-0,0836	0,0097	0,0787
2552,24	-0,1560	-0,0574	-0,0206	0,0756
2553,21	-0,1487	-0,0736	0,0106	0,0833
2554,19	-0,0948	-0,0451	0,0428	0,0848
2555,20	-0,0963	-0,0772	0,0775	0,0850
2556,22	-0,1626	-0,0608	0,0204	0,1076
2557,23	-0,1592	-0,0315	-0,0153	0,0946
2558,25	-0,1535	-0,0686	0,0251	0,0890
2559,26	-0,1334	-0,0662	0,0175	0,0798
2560,24	-0,1434	-0,0410	0,0022	0,0810

2561,26	-0,1690	-0,0638	0,0047	0,0940
2562,23	-0,1604	-0,0407	-0,0208	0,0916
2563,26	-0,1657	-0,0599	-0,0027	0,0945
2565,26	-0,1889	-0,0644	0,0020	0,1135
2566,25	-0,2288	-0,0440	-0,0431	0,1212
2567,24	-0,1684	-0,0401	-0,0564	0,0753
2568,28	-0,0750	-0,1026	0,0422	0,0045
2569,25	-0,1803	-0,0628	-0,0234	0,0776
2570,27	-0,1630	-0,0347	0,0173	0,1313
2571,27	-0,1000	-0,0240	0,0730	0,1252
2572,27	-0,1623	-0,0439	0,0359	0,1371
2573,23	-0,1735	-0,0335	-0,0182	0,1110
2574,23	-0,1889	-0,0630	-0,0027	0,1036
2575,24	-0,1800	-0,0549	-0,0287	0,0921
2576,29	-0,1828	-0,0568	0,0162	0,1227
2577,32	-0,1782	-0,0469	0,0351	0,1406
2578,31	-0,1668	-0,0427	0,0066	0,1229
2579,31	-0,1449	-0,0464	0,0099	0,0989
2580,30	-0,1568	-0,0677	0,0107	0,0929
2581,28	-0,1687	-0,0564	-0,0161	0,0954
2582,24	-0,1668	-0,0621	-0,0222	0,0795
2583,23	-0,1660	-0,0702	0,0014	0,0864
2584,37	-0,2167	-0,0295	0,1149	0,2775
2585,42	-0,1593	-0,0246	0,1650	0,3459
2586,22	-0,2016	-0,0709	0,0723	0,1760
2586,43	-0,2021	-0,0253	0,1589	0,3046
2587,33	-0,2370	-0,0470	0,0532	0,2104
2588,23	-0,1991	-0,0459	0,0098	0,1360
2589,25	-0,1398	-0,0691	0,0184	0,0930
2590,26	-0,1449	-0,0795	0,0304	0,0816
2591,26	-0,1308	-0,0381	-0,0140	0,0734
2592,27	-0,1320	-0,0699	0,0261	0,0722
2593,27	-0,1306	-0,0880	0,0542	0,0786
2594,28	-0,1376	-0,0638	0,0130	0,0760
2595,29	-0,1366	-0,0609	0,0246	0,0859
2596,30	-0,1747	-0,0854	0,0152	0,0947
2596,90	-0,1778	-0,0859	-0,0169	0,0552
2597,28	-0,1612	-0,0745	0,0059	0,0763
2597,91	-0,1748	-0,0781	-0,0362	0,0459
2598,27	-0,1503	-0,1115	0,0513	0,0584
2598,91	-0,1723	-0,0933	-0,0191	0,0507
2599,28	-0,1573	-0,0728	-0,0225	0,0644
2600,26	-0,1482	-0,0758	0,0151	0,0697
2601,30	-0,1272	-0,0770	-0,0068	0,0523
2602,30	-0,1491	-0,0626	-0,0004	0,0709
2603,29	-0,1509	-0,0579	-0,0012	0,0754
2606,31	-0,1556	-0,0737	0,0167	0,0866
2607,30	-0,1394	-0,0863	0,0422	0,0841
2608,30	-0,1595	-0,0815	0,0450	0,1038
2609,29	-0,1431	-0,1025	0,0670	0,0905
2610,28	-0,1283	-0,0606	0,0038	0,0713
2611,28	-0,1214	-0,0943	0,0532	0,0713
2612,28	-0,1485	-0,0628	0,0216	0,0888
2613,32	-0,1216	-0,0550	-0,0001	0,0665
2614,30	-0,1321	-0,0747	0,0152	0,0588
2617,32	-0,1396	-0,0870	0,0429	0,0689
2618,32	-0,1384	-0,0637	-0,0030	0,0648
2619,33	-0,1478	-0,0833	0,0133	0,0674
2623,34	-0,1307	-0,0946	0,0199	0,0471
2625,32	-0,1384	-0,0740	0,0019	0,0634
2626,32	-0,1301	-0,0901	0,0184	0,0507
2628,31	-0,1308	-0,0706	0,0191	0,0622
2629,32	-0,1371	-0,0825	0,0375	0,0643
2636,34	-0,1576	-0,0826	-0,0289	0,0428
2637,32	-0,1397	-0,0919	0,0093	0,0407
2638,33	-0,1302	-0,0781	-0,0158	0,0305
2639,33	-0,1129	-0,0996	-0,0043	0,0132
2640,33	-0,1154	-0,0848	-0,0088	0,0202
2641,32	-0,1384	-0,0890	0,0086	0,0365
2642,30	-0,1597	-0,1060	-0,0068	0,0376
2643,31	-0,1625	-0,0968	-0,0312	0,0285
2644,32	-0,1926	-0,1259	-0,0197	0,0394
2645,33	-0,1818	-0,0876	-0,0451	0,0365
2646,34	-0,1752	-0,0681	-0,0586	0,0426
2648,33	-0,1682	-0,0712	-0,0494	0,0442
2649,32	-0,1685	-0,0829	-0,0347	0,0420
2651,34	-0,1690	-0,0936	-0,0313	0,0461
2655,31	-0,1524	-0,1035	-0,0080	0,0328
2656,31	-0,1695	-0,0965	-0,0305	0,0333
2658,30	-0,2530	-0,1475	-0,1055	-0,0049
2659,29	-0,2068	-0,1811	-0,0943	-0,0793
2660,30	-0,2513	-0,1305	-0,1646	-0,0450

2660,39	-0,2674	-0,1422	-0,1756	-0,0504
2661,44	-0,2559	-0,1377	-0,1249	-0,0252
2662,68	-0,2973	-0,1607	-0,1036	0,0141
2664,30	-0,1756	-0,0918	-0,0145	0,0300
2665,29	-0,1709	-0,0972	-0,0349	0,0306
2666,30	-0,1890	-0,0752	-0,0548	0,0480
2667,33	-0,2113	-0,1070	-0,0222	0,0500
2668,36	-0,2098	-0,1088	-0,0116	0,0377
2670,31	-0,1885	-0,1256	-0,0145	0,0363
2671,32	-0,2286	-0,0891	-0,0791	0,0505
2672,33	-0,2542	-0,0782	-0,0658	0,0578
2673,31	-0,3026	-0,0990	-0,1336	0,0512
2674,29	-0,4755	-0,1736	-0,2276	0,0156
2675,28	-0,2551	-0,2753	-0,0670	-0,0860
2675,71	-0,2372	-0,1192	-0,1197	-0,0165
2676,29	-0,3817	-0,1770	-0,1971	-0,0136
2676,43	-0,4036	-0,1975	-0,2119	-0,0189
2677,43	-0,3741	-0,1460	-0,2395	0,0024
2678,39	-0,2924	-0,1145	-0,1318	0,0265
2679,29	-0,2305	-0,0979	-0,1089	0,0273
2679,78	-0,1857	-0,0948	-0,0824	0,0147
2680,48	-0,2734	-0,1123	-0,1243	0,0352
2681,29	-0,2228	-0,1169	-0,0744	0,0351
2681,73	-0,2210	-0,1218	-0,0970	0,0200
2682,30	-0,2393	-0,0995	-0,0719	0,0460
2683,30	-0,1948	-0,1149	-0,0580	0,0389
2684,34	-0,1899	-0,0732	-0,0612	0,0543
2687,28	-0,2215	-0,0794	-0,0768	0,0400
2688,28	-0,2369	-0,0876	-0,1208	0,0277
2689,29	-0,5488	-0,1551	-0,3930	-0,0333
2690,31	-0,5568	-0,2535	-0,2722	-0,0150
2691,31	-0,3691	-0,2171	-0,1406	0,0060
2691,88	-0,2399	-0,0696	-0,1686	-0,0092
2692,37	-0,5133	-0,1444	-0,2733	0,0669
2693,36	-0,5027	-0,1317	-0,2994	0,0683
2694,45	-0,4627	-0,1368	-0,2455	0,0667
2695,32	-0,3460	-0,0999	-0,1598	0,0643
2696,29	-0,3345	-0,1201	-0,1213	0,0703
2697,28	-0,3052	-0,1052	-0,1209	0,0716
2697,28	-0,3052	-0,1052	-0,1209	0,0716
2697,73	-0,2933	-0,1273	-0,1179	0,0351
2698,68	-0,3600	-0,1540	-0,1042	0,0822
2700,31	-0,2196	-0,0894	-0,0537	0,0730
2701,32	-0,2006	-0,0463	-0,0860	0,0667
2703,30	-0,2487	-0,0860	-0,0792	0,0688
2704,29	-0,3053	-0,0709	-0,1584	0,0729
2705,30	-0,3944	-0,1595	-0,1911	0,0169
2706,28	-0,1712	-0,2853	0,0815	-0,0669
2706,29	-0,1718	-0,2856	0,0805	-0,0674
2707,28	-0,3072	-0,1744	-0,1325	-0,0232
2707,30	-0,3079	-0,1747	-0,1342	-0,0241
2708,29	-0,3338	-0,1130	-0,2247	-0,0086
2708,33	-0,3405	-0,1187	-0,2294	-0,0108
2709,37	-0,3660	-0,1313	-0,2007	0,0279
2710,29	-0,2799	-0,0857	-0,1378	0,0516
2711,29	-0,3297	-0,1038	-0,1445	0,0483
2711,89	-0,2133	-0,1015	-0,0668	0,0354
2712,28	-0,3791	-0,1327	-0,1432	0,0834
2712,80	-0,2891	-0,1119	-0,1420	0,0289
2713,91	-0,4595	-0,1678	-0,1870	0,1014
2715,29	-0,2689	-0,0830	-0,1070	0,0779
2716,33	-0,2252	-0,0921	-0,0657	0,0688
2717,34	-0,2206	-0,0873	-0,0290	0,0748
2719,30	-0,1913	-0,0376	-0,0681	0,0821
2720,30	-0,1914	-0,0567	-0,0267	0,0926
2721,29	-0,1995	-0,0359	0,0080	0,1568
2722,31	-0,2288	-0,0254	0,0077	0,1817
2723,31	-0,1839	-0,0771	0,0395	0,1461
2727,31	-0,3494	-0,1106	-0,0944	0,1339
2728,34	-0,2077	-0,1956	0,0735	0,0692
2729,35	-0,2821	-0,1163	-0,1052	0,0652
2730,32	-0,2572	-0,0756	-0,0967	0,0853
2731,33	-0,2194	-0,0609	-0,0704	0,0878
2743,30	-0,1779	-0,0897	0,0022	0,0828
2744,31	-0,1806	-0,1076	0,0240	0,0754
2745,32	-0,1841	-0,0707	-0,0222	0,0777
2750,33	-0,1408	-0,0425	-0,0069	0,0739
2751,34	-0,1419	-0,0787	0,0179	0,0695
2762,41	-0,1626	-0,1022	0,0161	0,0657
2763,41	-0,1315	-0,0802	0,0236	0,0593
2764,41	-0,1797	-0,0781	-0,0328	0,0622
2765,40	-0,1710	-0,0940	0,0044	0,0699

2777,40	-0,1449	-0,1103	0,0183	0,0537
2778,41	-0,1588	-0,0967	0,0272	0,0618
2798,40	-0,1984	-0,1024	-0,0316	0,0611
2799,41	-0,1921	-0,1190	-0,0052	0,0644
2800,41	-0,1930	-0,1523	0,0259	0,0592
2801,41	-0,1950	-0,0777	-0,0676	0,0612
2803,48	-0,2053	-0,0931	-0,0298	0,0581
2832,42	-0,2111	-0,0848	-0,0232	0,0778
2833,41	-0,1490	-0,0985	0,0039	0,0452
2833,41	-0,1491	-0,0984	0,0037	0,0452
2834,41	-0,1882	-0,0969	-0,0065	0,0603
2835,42	-0,1983	-0,0858	-0,0614	0,0547
2836,43	-0,1920	-0,0869	-0,0759	0,0327
2837,43	-0,1828	-0,0975	-0,0305	0,0357
2846,45	-0,1680	-0,0770	-0,0628	0,0247
2847,45	-0,1906	-0,0988	-0,0566	0,0280
2848,47	-0,2016	-0,1215	-0,0671	0,0116
2849,46	-0,2147	-0,1093	-0,0767	0,0164
2850,61	-0,2724	-0,1606	-0,0864	0,0171
2851,60	-0,2736	-0,1387	-0,1112	0,0104
2852,61	-0,2624	-0,1093	-0,1288	0,0097
2853,46	-0,2290	-0,0921	-0,1289	0,0120
2854,45	-0,2300	-0,1226	-0,0800	0,0156
2855,44	-0,2208	-0,1166	-0,0524	0,0277
2856,44	-0,2113	-0,0835	-0,0748	0,0324
2857,43	-0,1968	-0,0999	-0,0545	0,0308
2858,45	-0,1904	-0,0637	-0,0998	0,0324
2865,49	-0,3206	-0,1096	-0,2206	-0,0217
2866,49	-0,3686	-0,1070	-0,2615	-0,0211
2867,49	-0,3848	-0,1033	-0,2727	0,0034
2868,49	-0,3407	-0,0905	-0,2254	0,0397
2869,50	-0,3393	-0,0245	-0,0983	0,1754
2870,48	-0,0376	-0,0875	0,1922	0,0997
2871,50	-0,2481	-0,0212	-0,0100	0,1737
2872,47	-0,2941	-0,0405	-0,0519	0,1364
2873,47	-0,2678	-0,0686	-0,0931	0,0868
2874,46	-0,2654	-0,1032	-0,0913	0,0478
2875,45	-0,2802	-0,1208	-0,1125	0,0312
2876,44	-0,2543	-0,0916	-0,1313	0,0371
2877,43	-0,2304	-0,1015	-0,0861	0,0221
2878,44	-0,2149	-0,0992	-0,0810	0,0279
2879,46	-0,1944	-0,0731	-0,0964	0,0195
2880,48	-0,2020	-0,1257	-0,0746	0,0112
2881,49	-0,2397	-0,1256	-0,0725	0,0166
2882,48	-0,2253	-0,0779	-0,0666	0,0268
2883,49	-0,2165	-0,1222	-0,0471	0,0369
2884,49	-0,1947	-0,0793	-0,0527	0,0423
2885,49	-0,2491	-0,1073	-0,0966	0,0450
2886,49	-0,2898	-0,1203	-0,0975	0,0519
2887,49	-0,3002	-0,1427	-0,0831	0,0435
2888,49	-0,2911	-0,1231	-0,1083	0,0528
2889,48	-0,2405	-0,1053	-0,1034	0,0419
2891,47	-0,2088	-0,0881	-0,0224	0,0859
2892,47	-0,1649	-0,0987	0,0313	0,0740
2893,48	-0,2001	-0,1227	0,0246	0,0846
2894,51	-0,1945	-0,1088	-0,0035	0,0715
2895,49	-0,2016	-0,1252	-0,0108	0,0582
2896,47	-0,2024	-0,0947	-0,0146	0,0555
2897,45	-0,1868	-0,1006	-0,0220	0,0418
2908,47	-0,1720	-0,0794	-0,0119	0,0548
2909,47	-0,1629	-0,0565	-0,0406	0,0561
2915,59	-0,2140	-0,0923	-0,0351	0,0748
2916,63	-0,2144	-0,1182	0,0026	0,0849
2917,63	-0,2396	-0,0968	-0,0288	0,0876
2918,58	-0,2389	-0,0929	-0,0755	0,0671
2934,58	-0,1824	-0,0815	-0,0533	0,0471
2935,57	-0,1919	-0,0930	-0,0434	0,0499
2936,57	-0,1790	-0,0901	-0,0546	0,0472
2937,58	-0,1804	-0,1029	-0,0165	0,0481
2950,56	-0,2536	-0,0833	-0,0993	0,0558
2951,55	-0,1679	-0,0976	-0,0222	0,0375
2952,53	-0,1871	-0,0714	-0,0731	0,0315
2952,55	-0,1880	-0,0705	-0,0783	0,0304
2953,56	-0,2193	-0,0846	-0,0545	0,0400
2954,55	-0,2001	-0,0892	-0,0757	0,0326
2955,54	-0,1767	-0,0813	-0,0635	0,0279
2957,64	-0,2798	-0,1291	-0,1323	0,0075
2958,63	-0,1926	-0,1858	-0,0731	-0,0602
2959,56	-0,2695	-0,1817	-0,1523	-0,0549
2960,51	-0,2113	-0,2004	-0,0566	-0,0607
2961,51	-0,3597	-0,1314	-0,1971	0,0092
2962,46	-0,3579	-0,1185	-0,2009	0,0217

2962,53	-0,3691	-0,1288	-0,2083	0,0164
2963,46	-0,2819	-0,1202	-0,1264	0,0111
2964,49	-0,2234	-0,0956	-0,0695	0,0176
2965,53	-0,2268	-0,0756	-0,1059	0,0341
2966,01	-0,2162	-0,1303	-0,0592	0,0183
2966,54	-0,2218	-0,1238	-0,0576	0,0297
2967,98	-0,3579	-0,1812	-0,0876	0,0403
2972,55	-0,2001	-0,0812	-0,0685	0,0520
2973,55	-0,1947	-0,1015	-0,0056	0,0652
2974,55	-0,1883	-0,1181	-0,0064	0,0476
2975,55	-0,2166	-0,1070	-0,0224	0,0338
2976,55	-0,2208	-0,0925	-0,1015	0,0139
2977,54	-0,1833	-0,1247	-0,0603	0,0100
2979,58	-0,1979	-0,1129	-0,0319	0,0317
2980,59	-0,1918	-0,1014	-0,0530	0,0385
2981,51	-0,2350	-0,1257	-0,0805	0,0432
2982,53	-0,2535	-0,1438	-0,0710	0,0239
2983,47	-0,1894	-0,1636	-0,0383	0,0128
2984,47	-0,2207	-0,1184	-0,0513	0,0365
2989,55	-0,1680	-0,1078	0,0075	0,0484
2992,60	-0,1752	-0,0824	-0,0677	0,0052
2997,55	-0,1604	-0,0901	0,0150	0,0630
3019,57	-0,1211	-0,0638	0,0319	0,0835
3052,57	-0,2068	-0,0942	-0,0943	-0,0064
3053,55	-0,2459	-0,1256	-0,1308	-0,0138
3054,56	-0,2400	-0,1175	-0,1300	-0,0188
3055,57	-0,2488	-0,1275	-0,1291	-0,0155
3056,58	-0,2362	-0,1379	-0,1025	-0,0200
3057,57	-0,2294	-0,0894	-0,1107	-0,0064
3068,55	-0,3866	-0,1316	-0,2650	-0,0523
3069,54	-0,3964	-0,2094	-0,2643	-0,1124
3070,55	-0,4068	-0,2176	-0,2671	-0,1125
3071,55	-0,3957	-0,1737	-0,2369	-0,0872
3072,54	-0,3039	-0,1335	-0,2200	-0,0574
3084,54	-0,4683	-0,2258	-0,3775	-0,1666
3085,57	-0,3689	-0,3553	-0,2714	-0,2710
3086,54	-0,4536	-0,3100	-0,3519	-0,2500
3086,61	-0,4605	-0,3146	-0,3579	-0,2543
3087,55	-0,4721	-0,2150	-0,3715	-0,1797
3088,55	-0,3982	-0,1699	-0,2892	-0,1169
3089,65	-0,3239	-0,1438	-0,2385	-0,0690
3090,56	-0,2924	-0,0981	-0,1909	-0,0303
3091,54	-0,3004	-0,1392	-0,1740	-0,0373
3092,54	-0,3023	-0,1281	-0,1797	-0,0273
3093,57	-0,2481	-0,1384	-0,1515	-0,0287
3100,55	-0,3449	-0,2092	-0,3048	-0,1776
3101,55	-0,1414	-0,2654	-0,1837	-0,2804
3102,54	-0,1978	-0,2208	-0,2527	-0,2567
3102,55	-0,1977	-0,2187	-0,2549	-0,2580
3103,56	-0,2798	-0,1795	-0,3125	-0,2047
3104,56	-0,2748	-0,1404	-0,2844	-0,1398
3105,57	-0,2532	-0,1382	-0,1889	-0,0698
3106,55	-0,3399	-0,1448	-0,2367	-0,0639
3107,66	-0,4142	-0,1864	-0,2234	-0,0976
3108,68	-0,3973	-0,1824	-0,2163	-0,0873
3109,70	-0,3512	-0,1644	-0,2727	-0,0725
3110,56	-0,2460	-0,0849	-0,1448	-0,0259
3122,55	-0,2880	-0,1840	-0,1411	-0,0263
3123,55	-0,2651	-0,2292	-0,1303	-0,0817
3124,55	-0,3028	-0,2015	-0,1753	-0,0872
3125,57	-0,2715	-0,1237	-0,2239	-0,0460
3126,62	-0,2197	-0,1303	-0,1109	-0,0274
3139,57	-0,1627	-0,0822	-0,0977	-0,0121
3145,56	-0,1883	-0,1128	-0,0491	0,0113
3146,58	-0,1682	-0,1169	-0,0419	0,0066
3151,77	0,2450	-0,1247	-0,0203	-0,3399
3152,78	0,2393	-0,1449	-0,0084	-0,3395
3213,75	-0,2199	-0,0777	-0,0697	0,0397
3214,74	-0,2009	-0,1212	-0,0487	0,0314
3215,73	-0,2029	-0,1134	-0,0503	0,0256
3397,98	-0,2293	-0,1239	-0,1612	-0,0423
3398,97	-0,2588	-0,1504	-0,1623	-0,0329
3399,98	-0,2570	-0,1269	-0,1641	-0,0474
3411,91	-0,2188	-0,1101	-0,0900	-0,0226
3412,92	-0,2272	-0,1184	-0,1410	-0,0320
3413,93	-0,2709	-0,1406	-0,1379	-0,0272
3414,94	-0,2653	-0,1244	-0,1267	-0,0297
3427,92	-0,1972	-0,1125	-0,0657	-0,0115
3428,92	-0,2275	-0,1644	-0,0939	-0,0065

Table S2.A. Hypothetical identity of molecular components detected by MSI; annotation with peptides identified in samples of cancer-containing thyroid gland; empty spaces in LC-MS/MS - related information denote no match found for a given MSI component.

MSI molecular component (m/z)	m/z tolerance - minimum	m/z tolerance - maximum	LC-MS/MS measured peptide m/z	Δ delta m/z	amino acid sequence	entry ID	entry name	protein name	primary gene name
699,45	699,102	699,802							
699,62	699,272	699,972							
699,87	699,518	700,218							
700,18	699,830	700,530							
700,38	700,028	700,728							
701,31	700,964	701,665							
701,40	701,052	701,753							
702,33	701,982	702,685							
702,40	702,052	702,754							
703,39	703,034	703,738							
704,39	704,042	704,747							
705,40	705,049	705,754							
706,39	706,035	706,741							
707,39	707,039	707,747							
708,33	707,974	708,683							
708,38	708,021	708,729							
709,34	708,983	709,693							
710,36	710,009	710,719							
711,42	711,069	711,781							
712,40	712,041	712,753							
713,42	713,065	713,779							
714,42	714,065	714,779							
715,42	715,063	715,778							
716,33	715,976	716,692							
716,44	716,079	716,795							
717,42	717,057	717,775							
718,38	718,017	718,735							
718,41	718,054	718,772							
719,41	719,046	719,765							
720,41	720,052	720,773							
721,42	721,062	721,784							
722,39	722,030	722,752							
723,37	723,010	723,733							
723,46	723,102	723,825							
724,36	724,001	724,725							
724,41	724,051	724,776							
725,42	725,061	725,786							
726,40	726,040	726,766							
727,42	727,061	727,788							
728,42	728,058	728,786							
729,43	729,065	729,795							
730,38	730,018	730,749							
731,40	731,030	731,761							
731,43	731,065	731,796							
731,72	731,356	732,088							
732,41	732,047	732,779							
733,18	732,815	733,549							
733,42	733,049	733,783							
733,42	733,055	733,788							
734,43	734,063	734,798							
735,31	734,942	735,677							
735,42	735,055	735,790							
735,60	735,235	735,971							
736,33	735,958	736,694							
736,42	736,048	736,784							
737,42	737,046	737,784							
737,79	737,418	738,156							
738,39	738,022	738,760							
739,38	739,009	739,748							
739,44	739,071	739,810							
740,40	740,033	740,773							
741,43	741,055	741,796							
742,38	742,012	742,754							
742,45	742,080	742,823							
743,46	743,088	743,832							
744,41	744,040	744,784							
745,44	745,071	745,816							
746,34	745,964	746,710							
746,42	746,051	746,797							
747,52	747,144	747,892							
748,42	748,048	748,797							
749,42	749,047	749,796							
750,42	750,042	750,792							
751,42	751,049	751,800							
752,40	752,020	752,772							
753,42	753,042	753,796							
754,42	754,048	754,802							
755,40	755,025	755,780							
755,53	755,155	755,910							
756,45	756,076	756,833							
757,43	757,054	757,812							
757,44	757,064	757,822							
758,41	758,034	758,792							
759,39	759,005	759,765							
759,45	759,069	759,829							
760,42	760,038	760,798							
761,41	761,032	761,793							
762,40	762,014	762,777							
763,51	763,130	763,894							
764,41	764,028	764,792							
764,45	764,070	764,835							
765,44	765,054	765,819							
766,42	766,039	766,805							
767,42	767,041	767,808							
768,35	767,965	768,734							
768,43	768,042	768,811							
769,31	768,925	769,694							
769,44	769,057	769,826							
770,42	770,036	770,806							
771,42	771,033	771,805							
772,43	772,045	772,817							
773,43	773,045	773,818							
774,42	774,030	774,805							
775,37	774,987	775,762							
775,49	775,104	775,879							
776,36	775,975	776,751							
776,50	776,109	776,886							

[illegible]

803,46	803,056	803,859	803,40	0,061	K.WIDDVR.T	Q9NRW1	RAB6B_HUMAN	Ras-related protein Rab-6B	RAB6B
804,47 805,44	804,064 805,034	804,868 805,840	805,46	0,023	K.LMGISIR.N	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
806,45	806,045	806,851	806,44	0,004	K.YNQLLR.I	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro- ENO1 lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			806,36	0,087	R.LEEEMR.K	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like CORO1A protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
807,43	807,024	807,832	807,40	0,032	K.KLEDFR.D	P35609	ACTN2_HUMAN	Alpha-actinin-2 (Alpha-actinin skeletal muscle isoform 2) (F ACTN2 actin cross-linking protein)	ACTN2
			807,40	0,032	K.LKEDFR.L	Q96HE7	ERO1A_HUMAN	ERO1-like protein alpha (ERO1-L) (ERO1-L-alpha) (EC 1.8.4.- ERO1A) (Endoplasmic oxidoreductin-1-like protein) (Endoplasmic reticulum oxidoreductase alpha) (Oxidoreductin-1-L-alpha)	ERO1A
			807,39	0,037	R.LAADDFR.V	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing KRT18 gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
			807,39	0,037	R.LAADDFR.T	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			807,39	0,037	R.LAADDFR.L	P13645	K1C10_HUMAN	Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KRT10
			807,39	0,037	R.LAADDFR.T	P08779	K1C16_HUMAN	Keratin, type I cytoskeletal 16 (Cytokeratin-16) (CK-16) (Keratin-16) (K16)	KRT16
808,43	808,024	808,832	808,37	0,061	K.IEFDER.G	P21589	5NTD_HUMAN	5'-nucleotidase (5'-NT) (EC 3.1.3.5) (Ecto-5'-nucleotidase) NT5E (CD antigen CD73)	NT5E
			808,34	0,087	R.EEYPDR.I	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			808,34	0,087	R.EEYPDR.I	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta- TUBB4B 2C chain)	TUBB4B
808,71	808,310	809,119	808,37	0,347	K.IEFDER.G	P21589	5NTD_HUMAN	5'-nucleotidase (5'-NT) (EC 3.1.3.5) (Ecto-5'-nucleotidase) NT5E (CD antigen CD73)	NT5E
			808,34	0,374	R.EEYPDR.I	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			808,34	0,374	R.EEYPDR.I	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta- TUBB4B 2C chain)	TUBB4B
809,47	809,068	809,878	809,41	0,059	K.YAEAVTR.A	P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1
			809,38	0,097	K.DYAEVGR.V	P00738	HPT_HUMAN	Haptoglobin (Zonulin) [Cleaved into: Haptoglobin alpha chain; Haptoglobin beta chain]	HP
810,46 811,44 812,46	810,050 811,039 812,053	810,860 811,850 812,865	812,45	0,006	R.YIEIFK.S	P31943	HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H (hnRNP H) [Cleaved into: Heterogeneous nuclear ribonucleoprotein H, N-terminally processed]	HNRNPH1
			812,45	0,006	R.YIEIFK.S	P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 (hnRNP H2) (FTP-3) (Heterogeneous nuclear ribonucleoprotein H') (hnRNP H') [Cleaved into: Heterogeneous nuclear ribonucleoprotein H2, N-terminally processed]	HNRNPH2
			812,45	0,006	K.FEELFK.T	Q8IVF7	FMNL3_HUMAN	Formin-like protein 3 (Formin homology 2 domain-containing protein 3) (WW domain-binding protein 3) (WBP-3)	FMNL3
			812,42	0,035	K.VYFDLR.I	P23284	PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) PPIB (CYP-51) (Cyclophilin B) (Rotamase B) (S-cyclophilin) (SCYLP)	PPIB
813,43	813,028	813,842	813,36	0,076	K.WGMEYK.G	P62306	RUXF_HUMAN	Small nuclear ribonucleoprotein F (snRNP-F) (Sm protein F) (Sm-F) (SmF)	SNRPF
813,46	813,052	813,865	813,36	0,100	K.WGMEYK.G	P62306	RUXF_HUMAN	Small nuclear ribonucleoprotein F (snRNP-F) (Sm protein F) (Sm-F) (SmF)	SNRPF
814,44 814,45 815,42	814,030 814,045 815,016	814,845 814,859 815,832	815,44	0,011	R.HFWGLR.V	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
			815,46	0,032	R.ELIIGDR.Q	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase ATP5F1A F1 subunit alpha)	ATP5F1A
			815,36	0,069	R.DFGSFDK.F	P04179	SODM_HUMAN	Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1)	SOD2
816,44	816,035	816,851	816,42	0,019	R.LAEQAER.Y	P61981	1433G_HUMAN	14-3-3 protein gamma (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein gamma, N-terminally processed]	YWHAH
			816,42	0,019	K.LAEQAER.Y	P31946	1433B_HUMAN	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHAH
			816,42	0,019	R.LAEQAER.Y	Q04917	1433F_HUMAN	14-3-3 protein eta (Protein AS1)	YWHAH
			816,42	0,019	K.LAEQAER.Y	P27348	1433T_HUMAN	14-3-3 protein theta (14-3-3 protein T-cell) (14-3-3 protein tau) (Protein HS1)	YWHAQ
			816,42	0,019	K.LAEQAER.Y	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
			816,42	0,019	K.LAEQAER.Y	P62258	1433E_HUMAN	14-3-3 protein epsilon (14-3-3E)	YWHAH
			816,42	0,019	K.LAEQAER.Y	P31947	1433S_HUMAN	14-3-3 protein sigma (Epithelial cell marker protein 1) (Stratifin)	SFN
			816,46	0,022	R.EIQTAVR.L	O60814	H2B1K_HUMAN	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK
			816,46	0,022	R.EIQTAVR.L	Q16778	H2B2E_HUMAN	Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q)	HIST2H2BE
			816,46	0,022	K.AAATVAVR.A	Q9NP81	SYSM_HUMAN	Serine-tRNA ligase, mitochondrial (EC 6.1.1.11) (SerRSmt) (Seryl-tRNA synthetase) (SerRS) (Seryl-tRNA(Ser/Sec) synthetase)	SARS2
			816,47	0,023	R.GFIPNIR.T	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			816,42	0,025	R.FIDFFK.R	P49588	SYAC_HUMAN	Alanine-tRNA ligase, cytoplasmic (EC 6.1.1.7) (Alanyl-tRNA synthetase) (AlaRS) (Renal carcinoma antigen NY-REN-42)	AARS
			816,39	0,050	R.IFYDMK.V	P60981	DEST_HUMAN	Destrin (Actin-depolymerizing factor) (ADF)	DSTN
			816,39	0,052	R.EDHLFR.K	P01903	DRA_HUMAN	HLA class II histocompatibility antigen, DR alpha chain (MHC class II antigen DRA)	HLA-DRA
817,35 817,44 818,43	816,942 817,035 818,018	817,759 817,852 818,836	818,44	0,014	K.FYTFLK.N	P22352	GPX3_HUMAN	Glutathione peroxidase 3 (GPx-3) (GSHPx-3) (EC 1.11.1.9) (Extracellular glutathione peroxidase) (Plasma glutathione peroxidase) (GPx-Pl) (GSHPx-Pl)	GPX3

			818,44	0,015	R.VDPVNF.K.L	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2			
			818,40	0,023	R.VAAEDWK.K	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1			
			819,43	819,021	819,840	819,42	0,008	R.SVDETLR.L	Q06830	PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
			819,42	0,008	R.SVDETLR.L	Q13162	PRDX4_HUMAN	Peroxiredoxin-4 (EC 1.11.1.15) (Antioxidant enzyme AOE372) (AOE37-2) (Peroxiredoxin IV) (Prx-IV) (Thioredoxin peroxidase AO372) (Thioredoxin-dependent peroxide reductase A0372)	PRDX4			
			819,47	0,036	K.FIEIAR.K	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU			
			820,42	820,014	820,834	820,42	0,001	R.VGFAEAAR.L	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
820,48	820,073	820,894	820,42	0,061	R.VGFAEAAR.L	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD			
821,22	820,809	821,631	821,42	0,201	R.AKQMAEK.S	Q9NQ55	GPR84_HUMAN	G-protein coupled receptor 84 (Inflammation-related G-protein coupled receptor EX33)	GPR84			
821,42	821,010	821,832	821,42	0,000	R.AKQMAEK.S	Q9NQ55	GPR84_HUMAN	G-protein coupled receptor 84 (Inflammation-related G-protein coupled receptor EX33)	GPR84			
821,83	821,423	822,245	822,36	0,191	R.LEEEMR.K	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A			
822,17	821,760	822,582		0,211	K.EELMER.L	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN			
				0,242	K.GADVWFK.E	P05109	S10A8_HUMAN	Protein S100-A8 (Calgranulin-A) (Calprotectin L1L subunit) (Cystic fibrosis antigen) (CFAG) (Leukocyte L1 complex light chain) (Migration inhibitory factor-related protein 8) (MRP-8) (p8) (S100 calcium-binding protein A8) (Urinary stone protein band A)	S100A8			
			822,42	822,004	822,826	822,41	0,002	K.GADVWFK.E	P05109	S10A8_HUMAN	Protein S100-A8 (Calgranulin-A) (Calprotectin L1L subunit) (Cystic fibrosis antigen) (CFAG) (Leukocyte L1 complex light chain) (Migration inhibitory factor-related protein 8) (MRP-8) (p8) (S100 calcium-binding protein A8) (Urinary stone protein band A)	S100A8
			822,38	0,033	K.EELMER.L	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN			
			822,36	0,053	R.LEEEMR.K	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A			
			822,48	822,069	822,891	822,41	0,067	K.GADVWFK.E	P05109	S10A8_HUMAN	Protein S100-A8 (Calgranulin-A) (Calprotectin L1L subunit) (Cystic fibrosis antigen) (CFAG) (Leukocyte L1 complex light chain) (Migration inhibitory factor-related protein 8) (MRP-8) (p8) (S100 calcium-binding protein A8) (Urinary stone protein band A)	S100A8
			822,38	0,098	K.EELMER.L	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN			
			822,36	0,118	R.LEEEMR.K	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A			
			823,11	822,695	823,518	823,36	0,258	R.WDEAFR.K	P27695	APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase (EC 3.1.-.-) (EC 4.2.99.18) (APEX nuclease) (APEN) (Apurinic-apyrimidinic endonuclease 1) (AP endonuclease 1) (APE-1) (REF-1) (Redox factor-1) [Cleaved into: DNA-(apurinic or apyrimidinic site) lyase, mitochondrial]	APEX1
			823,41	822,996	823,820	823,36	0,044	R.WDEAFR.K	P27695	APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase (EC 3.1.-.-) (EC 4.2.99.18) (APEX nuclease) (APEN) (Apurinic-apyrimidinic endonuclease 1) (AP endonuclease 1) (APE-1) (REF-1) (Redox factor-1) [Cleaved into: DNA-(apurinic or apyrimidinic site) lyase, mitochondrial]	APEX1
823,44	823,028	823,852	823,36	0,076	R.WDEAFR.K	P27695	APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase (EC 3.1.-.-) (EC 4.2.99.18) (APEX nuclease) (APEN) (Apurinic-apyrimidinic endonuclease 1) (AP endonuclease 1) (APE-1) (REF-1) (Redox factor-1) [Cleaved into: DNA-(apurinic or apyrimidinic site) lyase, mitochondrial]	APEX1			
824,47	824,058	824,882	825,37	0,250	K.DWYDVK.A	P61247	RS3A_HUMAN	40S ribosomal protein S3a (Small ribosomal subunit protein eS1) (v-fos transformation effector protein) (Fte-1)	RPS3A			
824,70	824,289	825,114		825,37	0,004	K.DWYDVK.A	P61247	RS3A_HUMAN	40S ribosomal protein S3a (Small ribosomal subunit protein eS1) (v-fos transformation effector protein) (Fte-1)	RPS3A		
825,12	824,709	825,534		825,37	0,128	K.DWYDVK.A	P61247	RS3A_HUMAN	40S ribosomal protein S3a (Small ribosomal subunit protein eS1) (v-fos transformation effector protein) (Fte-1)	RPS3A		
825,37	824,955	825,780	825,37	0,004	K.DWYDVK.A	P61247	RS3A_HUMAN	40S ribosomal protein S3a (Small ribosomal subunit protein eS1) (v-fos transformation effector protein) (Fte-1)	RPS3A			
825,50	825,086	825,912	825,37	0,128	K.DWYDVK.A	P61247	RS3A_HUMAN	40S ribosomal protein S3a (Small ribosomal subunit protein eS1) (v-fos transformation effector protein) (Fte-1)	RPS3A			
826,45	826,033	826,859	826,44	0,008	R.VEIFYR.G	Q08380	LG3BP_HUMAN	Galectin-3-binding protein (Basement membrane autoantigen p105) (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (MAC2BP) (Mac-2 BP) (Tumor-associated antigen 90K)	LGALS3BP			
			826,34	0,108	K.DFEEMR.K	P09669	COX6C_HUMAN	Cytochrome c oxidase subunit 6C (Cytochrome c oxidase polypeptide VIc)	COX6C			
			826,47	826,059	826,886	826,44	0,035	R.VEIFYR.G	Q08380	LG3BP_HUMAN	Galectin-3-binding protein (Basement membrane autoantigen p105) (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (MAC2BP) (Mac-2 BP) (Tumor-associated antigen 90K)	LGALS3BP
			826,34	0,135	K.DFEEMR.K	P09669	COX6C_HUMAN	Cytochrome c oxidase subunit 6C (Cytochrome c oxidase polypeptide VIc)	COX6C			
827,39	826,974	827,801	827,43	0,039	K.FASFDK.V	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8			

827,51	827,092	827,919	827,43	0,039	K.FASFDK.V	P35908	K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (CK-2e) (Epithelial keratin-2e) (Keratin-2 epidermis) (Keratin-2e) (K2e) (Type-II keratin Kb2)	KRT2
			827,43	0,039	K.FASFDK.V	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7)	KRT7
			827,43	0,079	K.FASFDK.V	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
			827,43	0,079	K.FASFDK.V	P35908	K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (CK-2e) (Epithelial keratin-2e) (Keratin-2 epidermis) (Keratin-2e) (K2e) (Type-II keratin Kb2)	KRT2
			827,43	0,079	K.FASFDK.V	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7)	KRT7
828,40	827,981	828,810	829,47	0,009	K.LADLIER.D	P00352	AL1A1_HUMAN	Retinal dehydrogenase 1 (RALDH 1) (RaldH1) (EC 1.2.1.-) (EC 1.2.1.36) (ALDH-E1) (ALHDII) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic)	ALDH1A1
828,48	828,068	828,897							
829,46	829,049	829,879							
			829,47	0,009	R.LADLIER.D	P05091	ALDH2_HUMAN	Aldehyde dehydrogenase, mitochondrial (EC 1.2.1.3) (ALDH class 2) (ALDH-E2) (ALDH1)	ALDH2
			829,45	0,010	K.FLQFFK.H	Q92973	TNPO1_HUMAN	Transportin-1 (Importin beta-2) (Karyopherin beta-2) (M9 region interaction protein) (MIP)	TNPO1
			829,50	0,038	K.VLDLELK.G	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
			829,51	0,046	R.NALLSLAK.G	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
			829,51	0,046	K.GAAVIRS.R	O00468	AGRIN_HUMAN	Aggrin [Cleaved into: Aggrin N-terminal 110 kDa subunit; Aggrin C-terminal 110 kDa subunit; Aggrin C-terminal 90 kDa fragment (C90); Aggrin C-terminal 22 kDa fragment (C22)]	AGRIN
			829,52	0,060	R.ALLFIP.R	P08238	HSP90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			829,40	0,069	K.HWMLDK.L	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein eS4)	RPS4X
830,47	830,053	830,884	830,32	0,145	R.DDFYDR.L	Q9UKM9	RALY_HUMAN	RNA-binding protein Raly (Autoantigen p542) (Heterogeneous nuclear ribonucleoprotein C-like 2) (hnRNP core protein C-like 2) (hnRNP associated with lethal yellow protein homolog)	RALY
831,48	831,068	831,899	831,49	0,005	K.STELLIR.K	P84243	H33_HUMAN	Histone H3.3	H3F3A; H3F3B
			831,45	0,034	K.AVAASKER.S	P16403	H12_HUMAN	Histone H1.2 (Histone H1c) (Histone H1d) (Histone H1s-1)	HIST1H1C
			831,43	0,049	R.DLIDDLK.S	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedin) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4
			831,43	0,049	R.DLIDDLK.S	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
			832,47	0,091	K.LHFIFR.H	P27824	CALX_HUMAN	Calnexin (IP90) (Major histocompatibility complex class I antigen-binding protein p88) (p90)	CANX
832,49	832,071	832,904	832,47	0,014	K.LHFIFR.H	P27824	CALX_HUMAN	Calnexin (IP90) (Major histocompatibility complex class I antigen-binding protein p88) (p90)	CANX
833,07	832,654	833,487	833,42	0,353	K.WFPEVR.H	P15153	RAC2_HUMAN	Ras-related C3 botulinum toxin substrate 2 (GX) (Small G protein) (p21-Rac2)	RAC2
			833,43	0,358	R.SVEETLR.L	P30048	PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial (EC 1.11.1.15) (Antioxidant protein 1) (AOP-1) (HBC189) (Peroxiredoxin III) (Prx-III) (Peroxiredoxin-3) (Protein MER5 homolog)	PRDX3
			833,44	0,366	R.SEVTELR.R	P08779	K1C16_HUMAN	Keratin, type I cytoskeletal 16 (Cytokeratin-16) (CK-16) (Keratin-16) (K16)	KRT16
			833,48	0,414	K.KNLMALK.K	P50897	PPT1_HUMAN	Palmitoyl-protein thioesterase 1 (PPT-1) (EC 3.1.2.22) (Palmitoyl-protein hydrolase 1)	PPT1
			833,42	0,065	K.WFPEVR.H	P15153	RAC2_HUMAN	Ras-related C3 botulinum toxin substrate 2 (GX) (Small G protein) (p21-Rac2)	RAC2
833,36	832,942	833,775	833,43	0,070	R.SVEETLR.L	P30048	PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial (EC 1.11.1.15) (Antioxidant protein 1) (AOP-1) (HBC189) (Peroxiredoxin III) (Prx-III) (Peroxiredoxin-3) (Protein MER5 homolog)	PRDX3
			833,44	0,078	R.SEVTELR.R	P08779	K1C16_HUMAN	Keratin, type I cytoskeletal 16 (Cytokeratin-16) (CK-16) (Keratin-16) (K16)	KRT16
			833,48	0,126	K.KNLMALK.K	P50897	PPT1_HUMAN	Palmitoyl-protein thioesterase 1 (PPT-1) (EC 3.1.2.22) (Palmitoyl-protein hydrolase 1)	PPT1
			833,48	0,008	K.KNLMALK.K	P50897	PPT1_HUMAN	Palmitoyl-protein thioesterase 1 (PPT-1) (EC 3.1.2.22) (Palmitoyl-protein hydrolase 1)	PPT1
			833,44	0,041	R.SEVTELR.R	P08779	K1C16_HUMAN	Keratin, type I cytoskeletal 16 (Cytokeratin-16) (CK-16) (Keratin-16) (K16)	KRT16
833,48	833,060	833,894	833,43	0,049	R.SVEETLR.L	P30048	PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial (EC 1.11.1.15) (Antioxidant protein 1) (AOP-1) (HBC189) (Peroxiredoxin III) (Prx-III) (Peroxiredoxin-3) (Protein MER5 homolog)	PRDX3
			833,42	0,054	K.WFPEVR.H	P15153	RAC2_HUMAN	Ras-related C3 botulinum toxin substrate 2 (GX) (Small G protein) (p21-Rac2)	RAC2
			834,46	0,053	R.ALFDQIK.K	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
			834,46	0,025	R.ALFDQIK.K	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
			835,42	0,005	K.DTLMISR.T	P01859	IGHG2_HUMAN	Immunoglobulin heavy constant gamma 2 (Ig gamma-2 chain C region) (Ig gamma-2 chain C region DOT) (Ig gamma-2 chain C region TIL) (Ig gamma-2 chain C region ZIE)	IGHG2
			835,42	0,005	K.DTLMISR.T	P01857	IGHG1_HUMAN	Immunoglobulin heavy constant gamma 1 (Ig gamma-1 chain C region) (Ig gamma-1 chain C region EU) (Ig gamma-1 chain C region KOL) (Ig gamma-1 chain C region NIE)	IGHG1
			835,42	0,005	K.DTLMISR.T	P01861	IGHG4_HUMAN	Immunoglobulin heavy constant gamma 4 (Ig gamma-4 chain C region)	IGHG4

			835,44	0,021	K.WIDFVR.G	P05455	LA_HUMAN	Lupus La protein (La autoantigen) (La ribonucleoprotein) (Sjogren syndrome type B antigen) (SS-B)	SSB
			835,46	0,048	K.LVGVLDR.N	P07602	SAP_HUMAN	Prosaposin (Proactivator polypeptide) [Cleaved into: Saposin-A (Protein A); Saposin-B-Val; Saposin-B (Cerebroside sulfate activator) (CSAct) (Dispersin) (Sphingolipid activator protein 1) (SAP-1) (Sulfatide/GM1 activator); Saposin-C (A1 activator) (Co-beta-glucosidase) (Glucosylceramidase activator) (Sphingolipid activator protein 2) (SAP-2); Saposin-D (Component C) (Protein C)]	PSAP
835,44	835,025	835,861	835,44	0,006	K.WIDFVR.G	P05455	LA_HUMAN	Lupus La protein (La autoantigen) (La ribonucleoprotein) (Sjogren syndrome type B antigen) (SS-B)	SSB
			835,46	0,020	K.LVGVLDR.N	P07602	SAP_HUMAN	Prosaposin (Proactivator polypeptide) [Cleaved into: Saposin-A (Protein A); Saposin-B-Val; Saposin-B (Cerebroside sulfate activator) (CSAct) (Dispersin) (Sphingolipid activator protein 1) (SAP-1) (Sulfatide/GM1 activator); Saposin-C (A1 activator) (Co-beta-glucosidase) (Glucosylceramidase activator) (Sphingolipid activator protein 2) (SAP-2); Saposin-D (Component C) (Protein C)]	PSAP
			835,42	0,023	K.DTLMISR.T	P01859	IGHG2_HUMAN	Immunoglobulin heavy constant gamma 2 (Ig gamma-2 chain C region) (Ig gamma-2 chain C region DOT) (Ig gamma-2 chain C region TIL) (Ig gamma-2 chain C region ZIE)	IGHG2
			835,42	0,023	K.DTLMISR.T	P01857	IGHG1_HUMAN	Immunoglobulin heavy constant gamma 1 (Ig gamma-1 chain C region) (Ig gamma-1 chain C region EU) (Ig gamma-1 chain C region KOL) (Ig gamma-1 chain C region NIE)	IGHG1
			835,42	0,023	K.DTLMISR.T	P01861	IGHG4_HUMAN	Immunoglobulin heavy constant gamma 4 (Ig gamma-4 chain C region)	IGHG4
			836,43	0,012	R.GPAGPQGPR.G	P02452	CO1A1_HUMAN	Collagen alpha-1(I) chain (Alpha-1 type I collagen)	COL1A1
836,43	836,012	836,848	836,41	0,022	K.EQFAWR.H	P46783	RS10_HUMAN	40S ribosomal protein S10 (Small ribosomal subunit protein eS10)	RPS10
			836,35	0,077	R.DHFFDR.G	O43776	SYNC_HUMAN	Asparagine--tRNA ligase, cytoplasmic (EC 6.1.1.22) (Asparaginyl-tRNA synthetase) (AsnRS)	NARS
			837,29	0,131	K.FVEWTR.L	P35237	SPB6_HUMAN	Serin B6 (Cytoplasmic antiproteinase) (CAP) (Peptidase inhibitor 6) (Pi-6) (Placental thrombin inhibitor)	SERPINB6
			837,46	0,166	R.DSFDIIR	P23142	FBLN1_HUMAN	Fibulin-1 (FIBL-1)	FBLN1
			837,46	0,166	R.ISWYLR.D	Q13011	ECH1_HUMAN	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial (EC 5.3.3.-)	ECH1
			837,43	0,011	K.FVEWTR.L	P35237	SPB6_HUMAN	Serin B6 (Cytoplasmic antiproteinase) (CAP) (Peptidase inhibitor 6) (Pi-6) (Placental thrombin inhibitor)	SERPINB6
837,43	837,015	837,852	837,46	0,024	R.DSFDIIR	P23142	FBLN1_HUMAN	Fibulin-1 (FIBL-1)	FBLN1
			837,46	0,024	R.ISWYLR.D	Q13011	ECH1_HUMAN	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial (EC 5.3.3.-)	ECH1
			837,60	0,145	R.DSFDIIR	P23142	FBLN1_HUMAN	Fibulin-1 (FIBL-1)	FBLN1
			837,46	0,145	R.ISWYLR.D	Q13011	ECH1_HUMAN	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial (EC 5.3.3.-)	ECH1
			837,42	0,180	K.FVEWTR.L	P35237	SPB6_HUMAN	Serin B6 (Cytoplasmic antiproteinase) (CAP) (Peptidase inhibitor 6) (Pi-6) (Placental thrombin inhibitor)	SERPINB6
			838,44	0,011	K.ATSGSLR.C	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
838,44	838,023	838,861	838,48	0,037	R.LLHGVGDK.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			839,08						
			839,21						
			839,36						
			839,51						
			839,89						
840,16	839,745	840,585	840,35	0,183	--MNYEGAR.S	P54829	PTN5_HUMAN	Tyrosine-protein phosphatase non-receptor type 5 (EC 3.1.3.48) (Neural-specific protein-tyrosine phosphatase) (Striatum-enriched protein-tyrosine phosphatase) (STEP)	PTPN5
			840,43	0,264	K.YNQLMR.I	P13929	ENOB_HUMAN	Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 3) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase)	ENO3
			840,43	0,264	K.YNQLMR.I	P09104	ENOG_HUMAN	Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 2) (Neural enolase) (Neuron-specific enolase) (NSE)	ENO2
			840,46	0,292	R.YIEIFR.S	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNPH3
			840,47	0,306	R.GVVGPGGAR.G	P08123	CO1A2_HUMAN	Collagen alpha-2(I) chain (Alpha-2 type I collagen)	COL1A2
			840,34	0,006	--MNYEGAR.S	P54829	PTN5_HUMAN	Tyrosine-protein phosphatase non-receptor type 5 (EC 3.1.3.48) (Neural-specific protein-tyrosine phosphatase) (Striatum-enriched protein-tyrosine phosphatase) (STEP)	PTPN5
840,34	839,922	840,762	840,43	0,087	K.YNQLMR.I	P13929	ENOB_HUMAN	Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 3) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase)	ENO3
			840,43	0,087	K.YNQLMR.I	P09104	ENOG_HUMAN	Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 2) (Neural enolase) (Neuron-specific enolase) (NSE)	ENO2
			840,46	0,115	R.YIEIFR.S	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNPH3
			840,47	0,129	R.GVVGPGGAR.G	P08123	CO1A2_HUMAN	Collagen alpha-2(I) chain (Alpha-2 type I collagen)	COL1A2
			840,47	0,008	R.GVVGPGGAR.G	P08123	CO1A2_HUMAN	Collagen alpha-2(I) chain (Alpha-2 type I collagen)	COL1A2
			840,46	0,021	R.YIEIFR.S	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNPH3
840,48	840,058	840,899	840,43	0,049	K.YNQLMR.I	P13929	ENOB_HUMAN	Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 3) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase)	ENO3
			840,43	0,049	K.YNQLMR.I	P09104	ENOG_HUMAN	Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 2) (Neural enolase) (Neuron-specific enolase) (NSE)	ENO2
			840,35	0,131	--MNYEGAR.S	P54829	PTN5_HUMAN	Tyrosine-protein phosphatase non-receptor type 5 (EC 3.1.3.48) (Neural-specific protein-tyrosine phosphatase) (Striatum-enriched protein-tyrosine phosphatase) (STEP)	PTPN5

840,82	840,404	841,245	840,47	0,354	R.GVVGPQGARG	P08123	CO1A2_HUMAN	Collagen alpha-2(I) chain (Alpha-2 type I collagen)	COL1A2
			840,46	0,368	R.YIEIFR.S	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNP3
			840,43	0,395	K.YNQLMR.I	P13929	ENOB_HUMAN	Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 3) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase)	ENO3
			840,43	0,395	K.YNQLMR.I	P09104	ENOG_HUMAN	Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 2) (Neural enolase) (Neuron-specific enolase) (NSE)	ENO2
841,09	840,670	841,511	841,38	0,287	R.QFFDER.W	Q13409	DC1I2_HUMAN	Cytoplasmic dynein 1 intermediate chain 2 (Cytoplasmic dynein intermediate chain 2) (Dynein intermediate chain 2, cytosolic) (DH IC-2)	DYNC1I2
			841,40	0,305	K.FAAEEFK.V	P61960	UFM1_HUMAN	Ubiquitin-fold modifier 1	UFM1
841,32	840,896	841,737	841,38	0,061	R.QFFDER.W	Q13409	DC1I2_HUMAN	Cytoplasmic dynein 1 intermediate chain 2 (Cytoplasmic dynein intermediate chain 2) (Dynein intermediate chain 2, cytosolic) (DH IC-2)	DYNC1I2
			841,40	0,079	K.FAAEEFK.V	P61960	UFM1_HUMAN	Ubiquitin-fold modifier 1	UFM1
841,51	841,088	841,929	841,40	0,112	K.FAAEEFK.V	P61960	UFM1_HUMAN	Ubiquitin-fold modifier 1	UFM1
			841,38	0,131	R.QFFDER.W	Q13409	DC1I2_HUMAN	Cytoplasmic dynein 1 intermediate chain 2 (Cytoplasmic dynein intermediate chain 2) (Dynein intermediate chain 2, cytosolic) (DH IC-2)	DYNC1I2
842,10	841,677	842,519							
842,44	842,024	842,866							
842,57	842,149	842,991							
843,46	843,035	843,878							
843,48	843,061	843,904							
843,59	843,171	844,015							
844,48	844,059	844,903	844,46	0,026	R.LLDVDNR.V	P00403	COX2_HUMAN	Cytochrome c oxidase subunit 2 (Cytochrome c oxidase polypeptide II)	MT-CO2
844,57	844,145	844,989	844,46	0,112	R.LLDVDNR.V	P00403	COX2_HUMAN	Cytochrome c oxidase subunit 2 (Cytochrome c oxidase polypeptide II)	MT-CO2
845,50	845,075	845,921	845,50	0,001	R.SGVSLAALK.K	P16403	H12_HUMAN	Histone H1.2 (Histone H1c) (Histone H1d) (Histone H1s-1)	HIST1H1C
			845,44	0,062	K.WFAFFK.Y	P53634	CATC_HUMAN	Dipeptidyl peptidase 1 (EC 3.4.14.1) (Cathepsin C) (Cathepsin J) (Dipeptidyl peptidase I) (DPP-I) (DPP1) (Dipeptidyl transferase) [Cleaved into: Dipeptidyl peptidase 1 exclusion domain chain (Dipeptidyl peptidase I exclusion domain chain); Dipeptidyl peptidase 1 heavy chain (Dipeptidyl peptidase I heavy chain); Dipeptidyl peptidase 1 light chain (Dipeptidyl peptidase I light chain)]	CTSC
846,48	846,059	846,905	846,33	0,156	R.YDDYDR.Y	O75494	SRS10_HUMAN	Serine/arginine-rich splicing factor 10 (40 kDa SR-repressor protein) (SRp40) (FUS-interacting serine-arginine-rich protein 1) (Splicing factor SRp38) (Splicing factor, arginine/serine-rich 13A) (TLS-associated protein with Ser-Arg repeats) (TASR) (TLS-associated protein with SR repeats) (TLS-associated serine-arginine protein) (TLS-associated SR protein)	SRSF10
			847,42	0,055	K.SEITELR.R	P13645	K1C10_HUMAN	Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KRT10
847,47	847,047	847,894	847,42	0,055	R.SLEDDIR.S	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedien) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4
			847,40	0,069	R.RCQDLR.M	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			848,46	0,022	K.GFQLDLR.G	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			848,46	0,025	K.ASTTLDIK.D	P46821	MAP1B_HUMAN	Microtubule-associated protein 1B (MAP-1B) [Cleaved into: MAP1B heavy chain; MAP1 light chain LC1]	MAP1B
848,48	848,056	848,904	848,41	0,074	M.ATDELATK.L	Q96C19	EFHD2_HUMAN	EF-hand domain-containing protein D2 (Swi/psrosin-1)	EFHD2
			848,41	0,074	R.EASSGAACK.R	P12109	CO6A1_HUMAN	Collagen alpha-1(VI) chain	COL6A1
			848,41	0,074	K.SAEREK.L	P40227	TCPZ_HUMAN	T-complex protein 1 subunit zeta (TCP-1-zeta) (Acute morphine dependence-related protein 2) (CCT-zeta-1) (HTR3) (Tcp20)	CCT6A
			848,41	0,074	K.ETADAITK.E	Q00765	REEP5_HUMAN	Receptor expression-enhancing protein 5 (Polyposis locus protein 1) (Protein TB2)	REEP5
848,48	848,056	848,904	848,40	0,078	K.TEWLDGK.H	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
			848,40	0,084	R.TWDAER.E	P13611	CSPG2_HUMAN	Versican core protein (Chondroitin sulfate proteoglycan core protein 2) (Chondroitin sulfate proteoglycan 2) (Glial hyaluronate-binding protein) (GHAP) (Large fibroblast proteoglycan) (PG-M)	VCAN
			848,39	0,088	R.AYYEFR.E	Q1KMD3	HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 2 (Scaffold-attachment factor A2) (SAF-A2)	HNRNPUL2
			848,33	0,155	R.DQWEDR.I	P15311	EZRI_HUMAN	Ezrin (Cyto villin) (Villin-2) (p81)	EZR
849,45	849,022	849,871	849,46	0,011	R.FAEIEK.N	P28838	AMPL_HUMAN	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase 3) (LAP-3) (Leucyl aminopeptidase) (Peptidase 5) (Proline aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase)	LAP3
850,49	850,066	850,916	850,52	0,033	K.HLLSPQR.A	P24043	LAMA2_HUMAN	Laminin subunit alpha-2 (Laminin M chain) (Laminin-12 subunit alpha) (Laminin-2 subunit alpha) (Laminin-4 subunit alpha) (Merosin heavy chain)	LAMA2
			850,46	0,034	R.FGPGVAFR.A	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			850,53	0,043	R.HLQLAIR.G	Q71UI9	H2AV_HUMAN	Histone H2A.V (H2A.F/Z)	H2AFV
			850,53	0,043	R.HLQLAIR.N	Q96KK5	H2A1H_HUMAN	Histone H2A type 1-H (Histone H2A/s)	HIST1H2AH
850,51	850,082	850,932	850,42	0,068	R.EIAQDFK.T	P84243	H33_HUMAN	Histone H3.3	H3F3A; H3F3B
			850,52	0,017	K.HLLSPQR.A	P24043	LAMA2_HUMAN	Laminin subunit alpha-2 (Laminin M chain) (Laminin-12 subunit alpha) (Laminin-2 subunit alpha) (Laminin-4 subunit alpha) (Merosin heavy chain)	LAMA2
			850,53	0,027	R.HLQLAIR.G	Q71UI9	H2AV_HUMAN	Histone H2A.V (H2A.F/Z)	H2AFV
			850,53	0,027	R.HLQLAIR.N	Q96KK5	H2A1H_HUMAN	Histone H2A type 1-H (Histone H2A/s)	HIST1H2AH
			850,46	0,050	R.FGPGVAFR.A	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19

			850,42	0,084	R.EIAQDFK.T	P84243	H33_HUMAN	Histone H3.3	H3F3A; H3F3B
850,80	850,378	851,229	850,53	0,270	R.HLQLAIR.G	Q71UI9	H2AV_HUMAN	Histone H2A.V (H2A.F/Z)	H2AFV
			850,53	0,270	R.HLQLAIR.N	Q96KK5	H2A1H_HUMAN	Histone H2A type 1-H (Histone H2A/s)	HIST1H2AH
			850,52	0,279	K.HLLSPQR.A	P24043	LAMA2_HUMAN	Laminin subunit alpha-2 (Laminin M chain) (Laminin-12 subunit alpha) (Laminin-2 subunit alpha) (Laminin-4 subunit alpha) (Merosin heavy chain)	LAMA2
			850,46	0,346	R.FGPGVAFR.A	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			850,42	0,380	R.EIAQDFK.T	P84243	H33_HUMAN	Histone H3.3	H3F3A; H3F3B
851,44	851,015	851,866							
851,51	851,082	851,933							
852,42	851,992	852,844	852,39	0,026	R.FWEWGK.N	Q6P587	FAHD1_HUMAN	Acylpyruvase FAHD1, mitochondrial (EC 3.7.1.5) (Fumarylacetoacetate hydrolase domain-containing protein 1) (FAH domain-containing protein 1) (Oxaloacetate decarboxylase) (OAA decarboxylase) (EC 4.1.1.112) (YisK-like protein)	FAHD1
			852,56	0,138	R.GLVVPVIR.N	P36957	ODO2_HUMAN	Dihydrolipoylysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex) (E2K)	DLST
852,42	851,997	852,849	852,39	0,032	R.FWEWGK.N	Q6P587	FAHD1_HUMAN	Acylpyruvase FAHD1, mitochondrial (EC 3.7.1.5) (Fumarylacetoacetate hydrolase domain-containing protein 1) (FAH domain-containing protein 1) (Oxaloacetate decarboxylase) (OAA decarboxylase) (EC 4.1.1.112) (YisK-like protein)	FAHD1
			852,56	0,133	R.GLVVPVIR.N	P36957	ODO2_HUMAN	Dihydrolipoylysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex) (E2K)	DLST
852,69	852,262	853,114	852,56	0,132	R.GLVVPVIR.N	P36957	ODO2_HUMAN	Dihydrolipoylysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex) (E2K)	DLST
			852,39	0,296	R.FWEWGK.N	Q6P587	FAHD1_HUMAN	Acylpyruvase FAHD1, mitochondrial (EC 3.7.1.5) (Fumarylacetoacetate hydrolase domain-containing protein 1) (FAH domain-containing protein 1) (Oxaloacetate decarboxylase) (OAA decarboxylase) (EC 4.1.1.112) (YisK-like protein)	FAHD1
853,43	853,003	853,856							
854,43	854,007	854,862							
855,05	854,619	855,474	855,44	0,390	K.TDFGIFR.M	Q9HCC0	MCCB_HUMAN	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial (MCCase subunit beta) (EC 6.4.1.4) (3-methylcrotonyl-CoA carboxylase 2) (3-methylcrotonyl-CoA carboxylase non-biotin-containing subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase subunit beta)	MCCC2
			855,45	0,407	R.LYDGLFK.V	Q16531	DDB1_HUMAN	DNA damage-binding protein 1 (DDB p127 subunit) (DNA damage-binding protein a) (DDBa) (Damage-specific DNA-binding protein 1) (HBV X-associated protein 1) (XAP-1) (UV-damaged DNA-binding factor) (UV-damaged DNA-binding protein 1) (UV-DDB 1) (XPE-binding factor) (XPE-BF) (Xeroderma pigmentosum group E-complementing protein) (XPCE)	DDB1
855,40	854,972	855,828	855,44	0,036	K.TDFGIFR.M	Q9HCC0	MCCB_HUMAN	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial (MCCase subunit beta) (EC 6.4.1.4) (3-methylcrotonyl-CoA carboxylase 2) (3-methylcrotonyl-CoA carboxylase non-biotin-containing subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase subunit beta)	MCCC2
			855,45	0,053	R.LYDGLFK.V	Q16531	DDB1_HUMAN	DNA damage-binding protein 1 (DDB p127 subunit) (DNA damage-binding protein a) (DDBa) (Damage-specific DNA-binding protein 1) (HBV X-associated protein 1) (XAP-1) (UV-damaged DNA-binding factor) (UV-damaged DNA-binding protein 1) (UV-DDB 1) (XPE-binding factor) (XPE-BF) (Xeroderma pigmentosum group E-complementing protein) (XPCE)	DDB1
855,45	855,018	855,873	855,45	0,008	R.LYDGLFK.V	Q16531	DDB1_HUMAN	DNA damage-binding protein 1 (DDB p127 subunit) (DNA damage-binding protein a) (DDBa) (Damage-specific DNA-binding protein 1) (HBV X-associated protein 1) (XAP-1) (UV-damaged DNA-binding factor) (UV-damaged DNA-binding protein 1) (UV-DDB 1) (XPE-binding factor) (XPE-BF) (Xeroderma pigmentosum group E-complementing protein) (XPCE)	DDB1
			855,44	0,009	K.TDFGIFR.M	Q9HCC0	MCCB_HUMAN	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial (MCCase subunit beta) (EC 6.4.1.4) (3-methylcrotonyl-CoA carboxylase 2) (3-methylcrotonyl-CoA carboxylase non-biotin-containing subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase subunit beta)	MCCC2
856,07	855,642	856,498							
856,34	855,916	856,772							
856,49	856,060	856,916							
856,57	856,141	856,998							
857,52	857,095	857,953	857,49	0,039	R.YAHVVL.R.K	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
857,54	857,108	857,966	857,49	0,051	R.YAHVVL.R.K	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
858,46	858,034	858,892							
859,42	858,992	859,851	859,36	0,066	R.DYEYNR.Y	Q1KMD3	HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 2 (Scaffold-attachment factor A2) (SAF-A2)	HNRNPU2
859,49	859,057	859,916	859,36	0,131	R.DYEYNR.Y	Q1KMD3	HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 2 (Scaffold-attachment factor A2) (SAF-A2)	HNRNPU2

860,43	860,001	860,862	860,44	0,008	K.IWDLEGK.I	P63244	RACK1_HUMAN	Receptor of activated protein C kinase 1 (Cell proliferation-inducing gene 21 protein) (Guanine nucleotide-binding protein subunit beta-2-like 1) (Guanine nucleotide-binding protein subunit beta-like protein 12.3) (Human lung cancer oncogene 7 protein, HLC-7) (Receptor for activated C kinase) (Small ribosomal subunit protein RACK1) [Cleaved into: Receptor of activated protein C kinase 1, N-terminally processed (Guanine nucleotide-binding protein subunit beta-2-like 1, N-terminally processed)]	RACK1
			860,42	0,015	R.IGDEDVGR.V	P23284	PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) PPIB (CYP-S1) (Cyclophilin B) (Rotamase B) (S-cyclophilin) (SCYLP)	PPIB
			860,42	0,016	K.DYFLFR.D	P61604	CH10_HUMAN	10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperonin) (Chaperonin 10) (CPN10) (Early-pregnancy factor) (EPF)	HSPE1
			860,41	0,024	R.DDDLNL.R.A	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
860,49	860,059	860,919	860,44	0,049	K.IWDLEGK.I	P63244	RACK1_HUMAN	Receptor of activated protein C kinase 1 (Cell proliferation-inducing gene 21 protein) (Guanine nucleotide-binding protein subunit beta-2-like 1) (Guanine nucleotide-binding protein subunit beta-like protein 12.3) (Human lung cancer oncogene 7 protein, HLC-7) (Receptor for activated C kinase) (Small ribosomal subunit protein RACK1) [Cleaved into: Receptor of activated protein C kinase 1, N-terminally processed (Guanine nucleotide-binding protein subunit beta-2-like 1, N-terminally processed)]	RACK1
			860,42	0,072	R.IGDEDVGR.V	P23284	PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) PPIB (CYP-S1) (Cyclophilin B) (Rotamase B) (S-cyclophilin) (SCYLP)	PPIB
			860,42	0,074	K.DYFLFR.D	P61604	CH10_HUMAN	10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperonin) (Chaperonin 10) (CPN10) (Early-pregnancy factor) (EPF)	HSPE1
			860,41	0,081	R.DDDLNL.R.A	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
861,13	860,699	861,560	861,41	0,282	R.IGDQWDK.Q	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
861,44	861,006	861,867	861,41	0,026	R.IGDQWDK.Q	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
862,13	861,703	862,565	862,35	0,216	K.DQWEER.I	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			862,48	0,343	R.IALDFQR.G	P17931	LEG3_HUMAN	Galectin-3 (Gal-3) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Galactose-specific lectin 3) (Galactoside-binding protein) (GALBP) (IgE-binding protein) (L-31) (Laminin-binding protein) (Lectin L-29) (Mac 2 antigen)	LGALS3
862,45	862,014	862,877	862,48	0,031	R.IALDFQR.G	P17931	LEG3_HUMAN	Galectin-3 (Gal-3) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Galactose-specific lectin 3) (Galactoside-binding protein) (GALBP) (IgE-binding protein) (L-31) (Laminin-binding protein) (Lectin L-29) (Mac 2 antigen)	LGALS3
			862,35	0,095	K.DQWEER.I	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
862,51	862,084	862,946	862,48	0,038	R.IALDFQR.G	P17931	LEG3_HUMAN	Galectin-3 (Gal-3) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Galactose-specific lectin 3) (Galactoside-binding protein) (GALBP) (IgE-binding protein) (L-31) (Laminin-binding protein) (Lectin L-29) (Mac 2 antigen)	LGALS3
			862,35	0,165	K.DQWEER.I	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
863,06	862,631	863,494	863,37	0,306	K.EVTEEEK.T	Q13547	HDAC1_HUMAN	Histone deacetylase 1 (HD1) (EC 3.5.1.98)	HDAC1
			863,42	0,358	-MAAGDGDVK.L	O15173	PGR2_HUMAN	Membrane-associated progesterone receptor component 2 (Progesterone membrane-binding protein) (Steroid receptor protein DG6)	PGRMC2
863,13	862,701	863,564	863,37	0,236	K.EVTEEEK.T	Q13547	HDAC1_HUMAN	Histone deacetylase 1 (HD1) (EC 3.5.1.98)	HDAC1
			863,42	0,288	-MAAGDGDVK.L	O15173	PGR2_HUMAN	Membrane-associated progesterone receptor component 2 (Progesterone membrane-binding protein) (Steroid receptor protein DG6)	PGRMC2
863,49	863,054	863,918	863,42	0,066	-MAAGDGDVK.L	O15173	PGR2_HUMAN	Membrane-associated progesterone receptor component 2 (Progesterone membrane-binding protein) (Steroid receptor protein DG6)	PGRMC2
			863,37	0,117	K.EVTEEEK.T	Q13547	HDAC1_HUMAN	Histone deacetylase 1 (HD1) (EC 3.5.1.98)	HDAC1
864,46	864,031	864,896	864,37	0,095	R.DEQSEEK.K	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
			864,37	0,098	K.WGTDEEK.F	P08758	ANXA5_HUMAN	Annexin A5 (Anchoring CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
864,56	864,128	864,993	864,37	0,192	R.DEQSEEK.K	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
			864,37	0,195	K.WGTDEEK.F	P08758	ANXA5_HUMAN	Annexin A5 (Anchoring CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
865,41	864,981	865,847							
865,53	865,094	865,959							
866,49	866,053	866,920							
867,45	867,015	867,882	867,42	0,029	R.WYEIEK.I	P05090	APOD_HUMAN	Apolipoprotein D (Apo-D) (ApoD)	APOD
868,45	868,015	868,884	868,47	0,024	R.GPSGPQGR.G	P08123	CO1A2_HUMAN	Collagen alpha-2(I) chain (Alpha-2 type I collagen)	COL1A2
869,34	868,904	869,774	869,43	0,096	K.LEEMGFK.D	Q9NVA2	SEP11_HUMAN	Septin-11	SEPT11

			869,44	0,100	K.LGFEEFK.Y	P04632	CPNS1_HUMAN	Calpain small subunit 1 (CSS1) (Calcium-activated neutral proteinase small subunit) (CANP small subunit) (Calcium-dependent protease small subunit) (CDPS) (Calcium-dependent protease small subunit 1) (Calpain regulatory subunit)	CAPNS1
869,46	869,021	869,891	869,44	0,017	K.LGFEEFK.Y	P04632	CPNS1_HUMAN	Calpain small subunit 1 (CSS1) (Calcium-activated neutral proteinase small subunit) (CANP small subunit) (Calcium-dependent protease small subunit) (CDPS) (Calcium-dependent protease small subunit 1) (Calpain regulatory subunit)	CAPNS1
			869,43	0,021	K.LEEMGFK.D	Q9NVA2	SEP11_HUMAN	Septin-11	SEPT11
870,48	870,050	870,920	870,44 870,41	0,045 0,077	R.FANYDK.V R.ISSSSF.SR.V	P08670 P05787	VIME_HUMAN K2C8_HUMAN	Vimentin Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	VIM KRT8
870,55	870,110	870,980	870,44 870,41	0,106 0,138	R.FANYDK.V R.ISSSSF.SR.V	P08670 P05787	VIME_HUMAN K2C8_HUMAN	Vimentin Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	VIM KRT8
871,51	871,075	871,946	871,53 871,45	0,016 0,058	K.IVVNLTGR.L R.IDELEPR.R	P62244 Q14697	RS15A_HUMAN GANAB_HUMAN	40S ribosomal protein S15a (Small ribosomal subunit protein uS8) Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	RPS15A GANAB
872,41	871,976	872,848	872,38	0,032	R.FENYGD.K.F	Q9BUJ2	HNRL1_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 1 (Adenovirus early region 1B-associated protein 5) (E1B-55 kDa-associated protein 5) (E1B-AP5)	HNRNPUL1
872,49	872,053	872,925	872,38	0,108	R.FENYGD.K.F	Q9BUJ2	HNRL1_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 1 (Adenovirus early region 1B-associated protein 5) (E1B-55 kDa-associated protein 5) (E1B-AP5)	HNRNPUL1
873,46	873,024	873,898	873,46 873,46	0,003 0,004	R.LDLLED.R.S R.INRV.TDR.N	Q14697 Q02218	GANAB_HUMAN ODO1_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha) 2-oxoglutarate dehydrogenase, mitochondrial (EC 1.2.4.2) (2-oxoglutarate dehydrogenase complex component E1) (OGDC-E1) (Alpha-ketoglutarate dehydrogenase)	GANAB OGDH
874,42	873,982	874,857	874,43	0,005	K.LDLRDD.K.D	P15153	RAC2_HUMAN	Ras-related C3 botulinum toxin substrate 2 (GX) (Small G protein) (p21-Rac2)	RAC2
875,43	874,990	875,866	875,43 875,43	0,001 0,001	R.MIDVQNR.A R.EVMDLLR.E	Q13630 P11047	FCL_HUMAN LAMC1_HUMAN	GDP-L-fucose synthase (EC 1.1.1.271) (GDP-4-keto-6-deoxy D-mannose-3,5-epimerase-4-reductase) (Protein FX) (Red cell NADP(H)-binding protein) (Short-chain dehydrogenase/reductase family 4E member 1) Laminin subunit gamma-1 (Laminin B2 chain) (Laminin-1 subunit gamma) (Laminin-10 subunit gamma) (Laminin-11 subunit gamma) (Laminin-2 subunit gamma) (Laminin-3 subunit gamma) (Laminin-4 subunit gamma) (Laminin-6 subunit gamma) (Laminin-7 subunit gamma) (Laminin-8 subunit gamma) (Laminin-9 subunit gamma) (S-laminin subunit gamma) (S-LAM gamma)	TSTA3 LAMC1
			875,43 875,43 875,41	0,001 0,001 0,020	R.EDGEKAAR.E K.EDLTEIR.D R.AAASSSPER.S	P04899 P05388 Q562R1	GNAI2_HUMAN RLA0_HUMAN ACTBL_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2 (Adenylate cyclase-inhibiting G alpha protein) 60S acidic ribosomal protein P0 (60S ribosomal protein L10E) (Large ribosomal subunit protein uL10) Beta-actin-like protein 2 (Kappa-actin)	GNAI2 RPLP0 ACTBL2
876,46	876,021	876,898	876,44 876,44 876,52	0,017 0,017 0,017 0,063	K.LPASFDAR.E R.VSTEVDAR.L R.LEGEDSAR.E R.IFLQDIK.K	P07858 P37837 Q16822 P02794	CATB_HUMAN TALDO_HUMAN PCKGM_HUMAN FRIH_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain] Transaldolase (EC 2.2.1.2) Phosphoenolpyruvate carboxykinase [GTP], mitochondrial (PEPCK-M) (EC 4.1.1.32) Ferritin heavy chain (Ferritin H subunit) (EC 1.16.3.1) (Cell proliferation-inducing gene 15 protein) [Cleaved into: Ferritin heavy chain, N-terminally processed]	CTSB TALDO1 PCK2 FTH1
877,07 877,46	876,630 877,023	877,508 877,901	877,51	0,047	K.SFVLNLG.K.D	P09382	LEG1_HUMAN	Galectin-1 (Gal-1) (14 kDa laminin-binding protein) (HLBP14) (14 kDa lectin) (Beta-galactoside-binding lectin L-14-I) (Galaptin) (HBL) (HPL) (Lactose-binding lectin 1) (Lectin galactoside-binding soluble 1) (Putative MAPK-activating protein PM12) (S-Lac lectin 1)	LGALS1
878,07 878,43 878,53 879,05	877,629 877,992 878,089 878,967	878,507 878,870 878,967 879,485	879,38 879,45	0,331 0,405	K.DMEESIR.N K.DFLESIR.K	P14314 Q8TAG9	GLU2B_HUMAN EXOC6_HUMAN	Glucosidase 2 subunit beta (80K-H protein) (Glucosidase II subunit beta) (Protein kinase C substrate 60.1 kDa protein heavy chain) (PKCSH) Exocyst complex component 6 (Exocyst complex component Sec15A) (SEC15-like protein 1)	PRKCSH EXOC6
879,42	878,982	879,861	879,45 879,38	0,029 0,044	K.DFLESIR.K K.DMEESIR.N	Q8TAG9 P14314	EXOC6_HUMAN GLU2B_HUMAN	Exocyst complex component 6 (Exocyst complex component Sec15A) (SEC15-like protein 1) Glucosidase 2 subunit beta (80K-H protein) (Glucosidase II subunit beta) (Protein kinase C substrate 60.1 kDa protein heavy chain) (PKCSH)	EXOC6 PRKCSH
879,51	879,069	879,949	879,45 879,38	0,059 0,132	K.DFLESIR.K K.DMEESIR.N	Q8TAG9 P14314	EXOC6_HUMAN GLU2B_HUMAN	Exocyst complex component 6 (Exocyst complex component Sec15A) (SEC15-like protein 1) Glucosidase 2 subunit beta (80K-H protein) (Glucosidase II subunit beta) (Protein kinase C substrate 60.1 kDa protein heavy chain) (PKCSH)	EXOC6 PRKCSH
880,39	879,952	880,833	880,41 880,41 880,43 880,43	0,014 0,014 0,034 0,034	K.LQSEMEK.N K.NLTEMK.V R.HYELTYR.R R.DLYDAGVK.R	O95613 Q9Y2K3 Q9NVA2 P07355	PCNT_HUMAN MYH15_HUMAN SEP11_HUMAN ANXA2_HUMAN	Pericentrin (Kendrin) (Pericentrin-B) Myosin-15 (Myosin heavy chain 15) Septin-11 Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	PCNT MYH15 SEPT11 ANXA2
			880,43 880,52	0,036 0,126	K.AEFAEVSK.L R.VIFGLFGK.T	P02768 P23284	ALBU_HUMAN PPIB_HUMAN	Serum albumin Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) (CYP-51) (Cyclophilin B) (Rotamase B) (S-cyclophilin) (SCYLP)	ALB PPIB

880,50	880,063	880,943	880,52	0,015	R.VIFGLFGK.T	P23284	PP1B_HUMAN	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) PPIB (CYP-S1) (Cyclophilin B) (Rotamase B) (S-cyclophilin) (SCYLP)	
			880,43	0,075	K.AEFAEVSK.L	P02768	ALBU_HUMAN	Serum albumin	ALB
			880,43	0,076	R.DLYDAGVK.R	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			880,43	0,076	R.HYELYR.R	Q9NVA2	SEP11_HUMAN	Septin-11	SEPT11
			880,41	0,097	K.LQSEMEK.N	O95613	PCNT_HUMAN	Pericentrin (Kendrin) (Pericentrin-B)	PCNT
			880,41	0,097	K.NLTEMKE.V	Q9Y2K3	MYH15_HUMAN	Myosin-15 (Myosin heavy chain 15)	MYH15
881,40	880,956	881,837							
881,48	881,040	881,922							
882,44	881,997	882,879	882,61	0,172	R.VLGLVLLR.G	P14678	R5MB_HUMAN	Small nuclear ribonucleoprotein-associated proteins B and B' (snRNP-B) (Sm protein B/B') (Sm-B/B') (SmB/B')	SNRPB
882,50	882,057	882,939	882,61	0,112	R.VLGLVLLR.G	P14678	R5MB_HUMAN	Small nuclear ribonucleoprotein-associated proteins B and B' (snRNP-B) (Sm protein B/B') (Sm-B/B') (SmB/B')	SNRPB
883,41	882,972	883,856							
883,49	883,050	883,934							
884,46	884,016	884,900	884,45	0,007	R.LQYADFK.Q	Q9Y2K3	MYH15_HUMAN	Myosin-15 (Myosin heavy chain 15)	MYH15
			884,45	0,007	R.KLSFDFQ.-	P23381	SYWC_HUMAN	Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleared into: T1-TrpRS; T2-TrpRS]	WARS
884,48	884,037	884,922	884,45	0,029	R.LQYADFK.Q	Q9Y2K3	MYH15_HUMAN	Myosin-15 (Myosin heavy chain 15)	MYH15
			884,45	0,029	R.KLSFDFQ.-	P23381	SYWC_HUMAN	Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleared into: T1-TrpRS; T2-TrpRS]	WARS
885,47	885,030	885,916							
886,43	885,989	886,876	886,44	0,005	R.GSEGPQGV.R	P02452	CO1A1_HUMAN	Collagen alpha-1(I) chain (Alpha-1 type I collagen)	COL1A1
887,44	886,997	887,884	887,43	0,007	K.FDLMYAK.R	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
			887,43	0,007	K.FDLMYAK.R	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleared into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			887,43	0,007	K.FDLMYAK.R	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleared into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			887,47	0,033	K.HIDFSLR.S	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RPS9
			887,47	0,034	K.CSASPPLR.R	P46013	KI67_HUMAN	Proliferation marker protein Ki-67 (Antigen identified by monoclonal antibody Ki-67) (Antigen Ki-67) (Antigen Ki67)	MKI67
			887,47	0,034	K.GVSQMPLR.Y	P31939	PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH [Cleared into: Bifunctional purine biosynthesis protein PURH, N-terminally processed] [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (5-aminimidazole-4-carboxamide ribonucleotide formyltransferase) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (ATIC) (IMP synthase) (Inosinase)]	ATIC
888,46	888,011	888,900	888,44	0,011	K.IWGEDLR.H	P43490	NAMPT_HUMAN	Nicotinamide phosphoribosyltransferase (NAMPRase) (Nampt) (EC 2.4.2.12) (Pre-B-cell colony-enhancing factor 1) (Pre-B cell-enhancing factor) (Visfatin)	NAMPT
889,45	889,002	889,892	889,45	0,006	K.EQWWLK.L	Q01813	PFKAP_HUMAN	ATP-dependent 6-phosphofructokinase, platelet type (ATP- PFKP) (PFK-P) (EC 2.7.1.11) (6-phosphofructokinase type C) (Phosphofructo-1-kinase isozyme C) (PFK-C) (Phosphohexokinase)	
			889,47	0,020	R.DPLELFR.G	Q16401	PSMD5_HUMAN	26S proteasome non-ATPase regulatory subunit 5 (26S protease subunit S5 basic) (26S proteasome subunit S5B)	PSMD5
			889,39	0,056	R.EPTTEER.A	Q15056	IF4H_HUMAN	Eukaryotic translation initiation factor 4H (eIF-4H) (Williams-Beuren syndrome chromosomal region 1 protein)	EIF4H
			889,38	0,072	K.GFDEYMK.E	Q01469	FABP5_HUMAN	Fatty acid-binding protein 5 (Epidermal-type fatty acid-binding protein) (E-FABP) (Fatty acid-binding protein, epidermal) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP)	FABP5
890,43	889,981	890,871	890,50	0,075	R.ELPSFLGK.R	P26447	S10A4_HUMAN	Protein S100-A4 (Calvasculin) (Metastasin) (Placental calcium-binding protein) (Protein Mts1) (S100 calcium-binding protein A4)	S100A4
			890,53	0,109	K.VHPAVVIR.Q	P62829	RL23_HUMAN	60S ribosomal protein L23 (60S ribosomal protein L17) (Large ribosomal subunit protein uL14)	RPL23
891,43	890,989	891,880	891,42	0,011	K.FYEAFSK.N	P08238	H590B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			891,42	0,015	R.LMEDLDR.N	P06703	S10A6_HUMAN	Protein S100-A6 (Calcyclin) (Growth factor-inducible protein 2A9) (MLN 4) (Prolactin receptor-associated protein) (PRA) (S100 calcium-binding protein A6)	S100A6
			891,48	0,050	K.LLDDLFR.K	Q9UKV3	ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus (Acinus)	ACIN1
892,39	891,943	892,836	892,45	0,059	--MAQTQGTR.R	Q13547	HDAC1_HUMAN	Histone deacetylase 1 (HD1) (EC 3.5.1.98)	HDAC1
			892,48	0,093	K.LEMEAKR.K	Q9UM54	MYO6_HUMAN	Unconventional myosin-VI (Unconventional myosin-6)	MYO6
			892,48	0,093	K.LELAQYR.E	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
892,50	892,051	892,944	892,48	0,015	K.LEMEAKR.K	Q9UM54	MYO6_HUMAN	Unconventional myosin-VI (Unconventional myosin-6)	MYO6
			892,48	0,015	K.LELAQYR.E	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
			892,45	0,049	--MAQTQGTR.R	Q13547	HDAC1_HUMAN	Histone deacetylase 1 (HD1) (EC 3.5.1.98)	HDAC1
893,01	892,563	893,456							
893,40	892,957	893,850							
893,50	893,054	893,948							
894,39	893,941	894,835	894,43	0,040	K.ADEGISFR.G	Q06830	PRDX1_HUMAN	Peroxisiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
			894,44	0,048	K.MPSGEFAR.I	P12004	PCNA_HUMAN	Proliferating cell nuclear antigen (PCNA) (Cyclin)	PCNA

			894,45	0,063	R.VFDMLNR.R	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-1 (eIF-4A-I) (eIF4A-I) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
			894,47	0,082	K.YAWVLDK.L	P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1
			894,47	0,022	K.YAWVLDK.L	P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1
			894,45	0,041	R.VFDMLNR.R	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-1 (eIF-4A-I) (eIF4A-I) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
894,49	894,045	894,940	894,47	0,056	K.MPSGEFAR.I	P12004	PCNA_HUMAN	Proliferating cell nuclear antigen (PCNA) (Cyclin)	PCNA
			894,43	0,064	K.ADEGISFR.G	Q06830	PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
			895,45	0,000	K.SILYDER.S	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
			895,44	0,011	R.ELFEMAR.T	P35998	PR57_HUMAN	26S proteasome regulatory subunit 7 (26S proteasome AAA-ATPase subunit RPT1) (Proteasome 26S subunit ATPase 2) (Protein MSS1)	PSMC2
895,46	895,014	895,910	895,45	0,011	K.SILYDER.S	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
			895,44	0,022	R.ELFEMAR.T	P35998	PR57_HUMAN	26S proteasome regulatory subunit 7 (26S proteasome AAA-ATPase subunit RPT1) (Proteasome 26S subunit ATPase 2) (Protein MSS1)	PSMC2
			896,43	0,013	K.YLTWASR.Q	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
			896,47	0,040	K.FVADGIFK.A	P23396	RS3_HUMAN	40S ribosomal protein S3 (EC 4.2.99.18) (Small ribosomal subunit protein uS3)	RPS3
897,44	896,992	897,889	897,44	0,000	K.LEDFAR.N	P11413	G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	G6PD
			897,48	0,037	K.IGTVMTFL.-	P30046	DOPD_HUMAN	D-dopachrome decarboxylase (EC 4.1.1.84) (D-dopachrome tautomerase) (Phenylpyruvate tautomerase II)	DDT
			897,40	0,039	R.MTLDDFR.I	P35527	K1C9_HUMAN	Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9) (Keratin-9) (K9)	KRT9
			897,47	0,005	K.IGTVMTFL.-	P30046	DOPD_HUMAN	D-dopachrome decarboxylase (EC 4.1.1.84) (D-dopachrome tautomerase) (Phenylpyruvate tautomerase II)	DDT
897,47	897,024	897,921	897,44	0,032	K.LEDFAR.N	P11413	G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	G6PD
			897,40	0,071	R.MTLDDFR.I	P35527	K1C9_HUMAN	Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9) (Keratin-9) (K9)	KRT9
			898,50	0,073	R.FWDYLR.W	P02649	APOE_HUMAN	Apolipoprotein E (Apo-E)	APOE
			899,50	0,052	K.HFELGGDK.K	P83881	RL36A_HUMAN	60S ribosomal protein L36a (60S ribosomal protein L44) (Cell growth-inhibiting gene 15 protein) (Cell migration-inducing gene 6 protein) (Large ribosomal subunit protein eL42)	RPL36A
900,39	899,935	900,836	900,51	0,030	K.IWYEHR.L	P48735	IDHP_HUMAN	Isocitrate dehydrogenase [NADP], mitochondrial (IDH) (EC 1.1.1.42) (ICD-M) (IDP) (NADP(+)-specific ICDH) (Oxalosuccinate decarboxylase)	IDH2
			900,51	0,030	K.IWYEHR.L	Q75874	IDHC_HUMAN	Isocitrate dehydrogenase [NADP] cytoplasmic (IDH) (EC 1.1.1.42) (Cytosolic NADP-isocitrate dehydrogenase) (IDP) (NADP(+)-specific ICDH) (Oxalosuccinate decarboxylase)	IDH1
			900,98	0,040	K.FDLMYAK.R	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			901,51	0,040	K.FDLMYAK.R	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
901,51	901,056	901,957	901,51	0,040	K.FDLMYAK.R	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
			902,49	0,048	R.LSGQDVER.G	Q02218	ODO1_HUMAN	2-oxoglutarate dehydrogenase, mitochondrial (EC 1.2.4.2) (2-oxoglutarate dehydrogenase complex component E1) (OGDC-E1) (Alpha-ketoglutarate dehydrogenase)	OGDH
			904,48	0,019	R.IEEELGSK.A	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			904,45	0,037	K.EMPQDLR.S	Q43765	SGTA_HUMAN	Small glutamine-rich tetra-ricopeptide repeat-containing protein alpha (Alpha-SGT) (Vpu-binding protein) (UBP)	SGTA
905,28	904,825	905,731	905,42	0,138	K.AYADFYR.N	P09669	COX6C_HUMAN	Cytochrome c oxidase subunit 6C (Cytochrome c oxidase polypeptide VIc)	COX6C
			905,48	0,202	M.NLGVSMRL.I	Q57292	TM273_HUMAN	Transmembrane protein 273	TMEM273
			905,48	0,002	M.NLGVSMRL.I	Q57292	TM273_HUMAN	Transmembrane protein 273	TMEM273
			905,42	0,066	K.AYADFYR.N	P09669	COX6C_HUMAN	Cytochrome c oxidase subunit 6C (Cytochrome c oxidase polypeptide VIc)	COX6C
906,23	905,779	906,686	906,46	0,232	R.DVQEIFR.M	Q13838	DX39B_HUMAN	Spliceosome RNA helicase DDX39B (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	DDX39B
			906,47	0,235	R.NFDEILR.V	P30041	PRDX6_HUMAN	Peroxiredoxin-6 (EC 1.11.1.15) (1-Cys peroxiredoxin) (1-Cys PRX) (24 kDa protein) (Acidic calcium-independent phospholipase A2) (aiPLA2) (EC 3.1.1.4) (Antioxidant protein 2) (Liver 2D page spot 40) (Non-selenium glutathione peroxidase) (NSGPx) (Red blood cells page spot 12)	PRDX6

906,46	906,007	906,914	906,46	0,004	R.DVQEIFR.M	Q13838	DX39B_HUMAN	Spliceosome RNA helicase DDX39B (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	DDX39B
			906,47	0,007	R.NFDEILR.V	P30041	PRDX6_HUMAN	Peroxiredoxin-6 (EC 1.11.1.15) (1-Cys peroxiredoxin) (1-Cys PRX) (24 kDa protein) (Acidic calcium-independent phospholipase A2) (aiPLA2) (EC 3.1.1.4) (Antioxidant protein 2) (Liver 2D page spot 40) (Non-selenium glutathione peroxidase) (NSGPx) (Red blood cells page spot 12)	PRDX6
907,46	907,003	907,910	907,43	0,030	K.IIFEDDR.C	P49773	HINT1_HUMAN	Histidine triad nucleotide-binding protein 1 (EC 3.-.-.-) (Adenosine 5'-monophosphoramidase) (Protein kinase C inhibitor 1) (Protein kinase C-interacting protein 1) (PKCI-1)	HINT1
			907,49	0,037	K.FLPLFDR.V	P61604	CH10_HUMAN	10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperonin) (Chaperonin 10) (CPN10) (Early-pregnancy factor) (EPF)	HSPE1
			907,50	0,041	K.FEELTR.L	P06732	KCRM_HUMAN	Creatine kinase M-type (EC 2.7.3.2) (Creatine kinase M chain) (Creatine phosphokinase M-type) (CPK-M) (M-CK)	CKM
			907,41	0,050	R.LMEDLDR.N	P06703	S10A6_HUMAN	Protein S100-A6 (Calcyclin) (Growth factor-inducible protein 2A9) (MLN 4) (Prolactin receptor-associated protein) (PRA) (S100 calcium-binding protein A6)	S100A6
			907,52	0,065	R.NLLSVAYK.N	Q04917	1433F_HUMAN	14-3-3 protein eta (Protein AS1)	YWHAH
			907,52	0,065	R.NLLSVAYK.N	P31947	1433S_HUMAN	14-3-3 protein sigma (Epithelial cell marker protein 1) (Stratifin)	SFN
			907,52	0,065	R.NLLSVAYK.N	P61981	1433G_HUMAN	14-3-3 protein gamma (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein gamma, N-terminally processed]	YWHAH
			907,52	0,065	R.NLLSVAYK.N	P27348	1433T_HUMAN	14-3-3 protein theta (14-3-3 protein T-cell) (14-3-3 protein tau) (Protein HS1)	YWHAQ
			907,52	0,065	R.NLLSVAYK.N	P62258	1433E_HUMAN	14-3-3 protein epsilon (14-3-3E)	YWHAH
			907,52	0,065	R.NLLSVAYK.N	P31946	1433B_HUMAN	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHAH
			907,52	0,065	R.NLLSVAYK.N	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
908,48	908,022	908,930	908,48	0,003	K.YDWLLAK.I	P09917	LOX5_HUMAN	Arachidonate 5-lipoxygenase (5-LO) (5-lipoxygenase) (EC 1.13.11.34)	ALOX5
			908,49	0,010	R.ADLYLEGK.D	Q9NSE4	SYIM_HUMAN	Isoleucine-tRNA ligase, mitochondrial (EC 6.1.1.5) (Isoleucyl-tRNA synthetase) (IleRS)	IARS2
			908,49	0,010	K.FVSELWK.D	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
			908,45	0,028	R.ALYEAGER.R	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
909,40	908,950	909,859							
909,50	909,044	909,953							
910,49	910,036	910,946	910,54	0,044	K.LYNLFK.I	Q96199	SUCB2_HUMAN	Succinate-CoA ligase [GDP-forming] subunit beta, mitochondrial (EC 6.2.1.4) (GTP-specific succinyl-CoA synthetase subunit beta) (G-5CS) (GTPSCS) (Succinyl-CoA synthetase beta-G chain) (SCS-betaG)	SUCLG2
911,49	911,038	911,949	911,53	0,039	K.LYSLFR.R	Q9UDW1	QCR9_HUMAN	Cytochrome b-c1 complex subunit 9 (Complex III subunit 9) (Complex III subunit X) (Cytochrome c1 non-heme 7 kDa protein) (Ubiquinol-cytochrome c reductase complex 7.2 kDa protein)	UQCRC1
			911,42	0,074	R.FHEHWR.F	Q15631	TSN_HUMAN	Translin (EC 3.1.-.-) (Component 3 of promoter of RISC) (C3PO)	TSN
			911,37	0,127	R.DDFTFER.L	P21912	SDHB_HUMAN	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (EC 1.3.5.1) (Iron-sulfur subunit of complex II) (Ip)	SDHB
912,49	912,031	912,944	912,48	0,008	R.NYLSIFR.K	P07384	CAN1_HUMAN	Calpain-1 catalytic subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase 1) (CANP 1) (Calpain mu-type) (Calpain-1 large subunit) (Cell proliferation-inducing gene 30 protein) (Micromolar-calpain) (muCANP)	CAPN1
913,10	912,648	913,561	913,40	0,296	R.MTLDDFR.I	P35527	K1C9_HUMAN	Keratin, type I cytoskeletal 9 (Cyokeratin-9) (CK-9) (Keratin-9) (K9)	KRT9
			913,43	0,325	K.EVYFAER.V	P50238	CRIP1_HUMAN	Cysteine-rich protein 1 (CRP-1) (Cysteine-rich heart protein) (CRHP) (hCRHP) (Cysteine-rich intestinal protein) (CRIP)	CRIP1
913,43	912,969	913,882	913,43	0,003	K.EVYFAER.V	P50238	CRIP1_HUMAN	Cysteine-rich protein 1 (CRP-1) (Cysteine-rich heart protein) (CRHP) (hCRHP) (Cysteine-rich intestinal protein) (CRIP)	CRIP1
			913,40	0,026	R.MTLDDFR.I	P35527	K1C9_HUMAN	Keratin, type I cytoskeletal 9 (Cyokeratin-9) (CK-9) (Keratin-9) (K9)	KRT9
913,54	913,085	913,999	913,43	0,113	K.EVYFAER.V	P50238	CRIP1_HUMAN	Cysteine-rich protein 1 (CRP-1) (Cysteine-rich heart protein) (CRHP) (hCRHP) (Cysteine-rich intestinal protein) (CRIP)	CRIP1
			913,40	0,142	R.MTLDDFR.I	P35527	K1C9_HUMAN	Keratin, type I cytoskeletal 9 (Cyokeratin-9) (CK-9) (Keratin-9) (K9)	KRT9
914,49	914,034	914,948	914,52	0,026	R.GFGFVLFK.D	Q14979	HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like (hnRNP D-like) (hnRNP DL) (AU-rich element RNA-binding factor) (JKT41-binding protein) (Protein laAUF1)	HNRNDL
			914,52	0,026	R.GFGFVLFK.E	Q14103	HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1)	HNRNDP
			914,42	0,074	K.FNEYWR.L	Q99584	S10AD_HUMAN	Protein S100-A13 (S100 calcium-binding protein A13)	S100A13
915,51	915,048	915,964	915,50	0,010	K.QILSADLR.S	P55786	PSA_HUMAN	Puromycin-sensitive aminopeptidase (PSA) (EC 3.4.11.14) (Cytosol alanyl aminopeptidase) (AAP-S)	NPEPPS
			915,49	0,014	K.LQDAEIA.R	P06703	S10A6_HUMAN	Protein S100-A6 (Calcyclin) (Growth factor-inducible protein 2A9) (MLN 4) (Prolactin receptor-associated protein) (PRA) (S100 calcium-binding protein A6)	S100A6
			915,54	0,030	R.ISLQWLR.R	P27487	DPP4_HUMAN	Dipeptidyl peptidase 4 (EC 3.4.14.5) (ADABP) (Adenosine deaminase complexing protein 2) (ADCP-2) (Dipeptidyl peptidase IV) (DPP IV) (T-cell activation antigen CD26) (TP103) (CD antigen CD26) [Cleaved into: Dipeptidyl peptidase 4 membrane form (Dipeptidyl peptidase IV membrane form); Dipeptidyl peptidase 4 soluble form (Dipeptidyl peptidase IV soluble form)]	DPP4

916,58	916,126	917,042	916,50	0,083	K.IILEDWK.K	P14314	GLU2B_HUMAN	Glucosidase 2 subunit beta (80K-H protein) (Glucosidase II subunit beta) (Protein kinase C substrate 60.1 kDa protein heavy chain) (PKCSH)	PRKCSH
917,53	917,068	917,985	917,46	0,063	R.LSMYLMK.A	Q9Y6N5	SQOR_HUMAN	Sulfide:quinone oxidoreductase, mitochondrial, SQOR, EC 1.8.5.- (Sulfide dehydrogenase-like) (Sulfide quinone oxidoreductase)	SQOR
			917,45	0,078	R.QNESSQPK.V	P46013	KI67_HUMAN	Proliferation marker protein Ki-67 (Antigen identified by monoclonal antibody Ki-67) (Antigen Ki-67) (Antigen Ki67)	MKI67
			917,45	0,078	R.EHYAELR.E	Q13232	NDK3_HUMAN	Nucleoside diphosphate kinase 3 (NDK 3) (NDP kinase 3) (EC 2.7.4.6) (DR-nm23) (Nucleoside diphosphate kinase C) (NDPKC) (nm23-H3)	NME3
			917,44	0,084	R.YGDFFIR.Q	Q9Y262	EIF3L_HUMAN	Eukaryotic translation initiation factor 3 subunit L (eIF3L) (Eukaryotic translation initiation factor 3 subunit 6-interacting protein) (Eukaryotic translation initiation factor 3 subunit E-interacting protein)	EIF3L
918,44	917,984	918,902	918,45	0,002	R.DLEDLAR.E	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
			918,47	0,026	K.VLEDSDLK.K	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP, EC 3.6.4.10 (78 kDa glucose-regulated protein, GRP-78) (Binding-immunoglobulin protein, BiP) (Heat shock protein 70 family protein 5, HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			918,47	0,026	R.NKLTSEAR.G	P41218	MNDA_HUMAN	Myeloid cell nuclear differentiation antigen	MNDA
			918,47	0,031	R.DGTLVSGGGR.D	O95834	EMAL2_HUMAN	Echinoderm microtubule-associated protein-like 2 (EMAP-2) (HuEMAP-2)	EML2
918,48	918,020	918,938	918,47	0,005	R.DGTLVSGGGR.D	O95834	EMAL2_HUMAN	Echinoderm microtubule-associated protein-like 2 (EMAP-2) (HuEMAP-2)	EML2
			918,47	0,010	K.VLEDSDLK.K	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP, EC 3.6.4.10 (78 kDa glucose-regulated protein, GRP-78) (Binding-immunoglobulin protein, BiP) (Heat shock protein 70 family protein 5, HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			918,47	0,010	R.NKLTSEAR.G	P41218	MNDA_HUMAN	Myeloid cell nuclear differentiation antigen	MNDA
			918,45	0,034	R.DLEDLAR.E	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
919,50	919,036	919,955	919,46	0,031	R.YYFEGIK.Q	O95433	AHSA1_HUMAN	Activator of 90 kDa heat shock protein ATPase homolog 1 (AHA1) (p38)	AHSA1
920,49	920,030	920,951	920,50	0,005	R.GLFHDDK.G	Q13162	PRDX4_HUMAN	Peroxiredoxin-4 (EC 1.11.1.15) (Antioxidant enzyme AOE372) (AOE37-2) (Peroxiredoxin IV) (Prx-IV) (Thioredoxin peroxidase AO372) (Thioredoxin-dependent peroxide reductase AO372)	PRDX4
			920,50	0,005	R.GLFHDDK.G	Q06830	PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
			920,48	0,007	K.VGDVVEFR.G	Q9UHQ9	NBSR1_HUMAN	NADH-cytochrome b5 reductase 1 (b5R.1) (EC 1.6.2.2) (Humb5R2) (NAD(P)H:quinone oxidoreductase type 3 polypeptide A2)	CYB5R1
			920,52	0,030	K.LIGEYGLR.N	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RP59
921,50	921,043	921,965	921,46	0,046	K.IEDFLER.R	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RP59
			921,46	0,046	K.LDMEIER.I	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
922,51	922,051	922,973	922,51	0,005	K.IFNLYPR.K	Q14195	DPYL3_HUMAN	Dihydropyrimidinase-related protein 3 (DRP-3) (Collapsin response mediator protein 4) (CRMP-4) (Unc-33-like phosphoprotein 1) (ULIP-1)	DPYSL3
			922,46	0,053	K.KDEDLFR.E	O75531	BAF_HUMAN	Barrier-to-autointegration factor (Breakpoint cluster region protein 1) [Cleaved into: Barrier-to-autointegration factor, N-terminally processed]	BANF1
			922,45	0,060	R.DVCLYPR.F	O43776	SYNC_HUMAN	Asparagine--tRNA ligase, cytoplasmic (EC 6.1.1.22) (Asparaginyl-tRNA synthetase) (AsnRS)	NARS
			922,44	0,072	R.EDMAALEK.D	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
			922,44	0,072	R.EDMAALEK.D	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			922,44	0,072	R.EDMAALEK.D	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			922,42	0,095	K.FLENEDR.R	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiprotease) (Serpine A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
923,52	923,056	923,980	923,40	0,120	R.CTCVNGNR.G	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
924,38	923,914	924,838	924,42	0,043	R.LQDYEEK.T	P15311	EZRI_HUMAN	Ezrin (Cyto villin) (Villin-2) (p81)	EZR
			924,44	0,065	K.TDEGIAYR.G	P32119	PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
			924,45	0,077	R.VVWWMFR.V	Q16762	THTR_HUMAN	Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese)	TST
924,50	924,038	924,962	924,45	0,047	R.VVWWMFR.V	Q16762	THTR_HUMAN	Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese)	TST
			924,44	0,059	K.TDEGIAYR.G	P32119	PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
			924,42	0,081	R.LQDYEEK.T	P15311	EZRI_HUMAN	Ezrin (Cyto villin) (Villin-2) (p81)	EZR
925,48	925,016	925,942							
926,49	926,030	926,957							
927,51	927,050	927,978	927,50	0,012	K.AGPIWDLR.L	O43390	HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R)	HNRNPR
			927,48	0,034	K.YLYEIAR.R	P02768	ALBU_HUMAN	Serum albumin	ALB
			927,44	0,070	K.DYVDLFR.H	P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	PRKDC
928,43	927,967	928,895	928,54	0,104	R.GFGFILFK.D	Q99729	ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein A/B (hnRNP A/B) (APOBEC1-binding protein 1) (ABBP-1)	HNRNPAB

928,50	928,041	928,969	928,54	0,030	R.GFGFILFK.D	Q99729	ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein A/B (hnRNP A/B) (APOBEC1-binding protein 1) (ABBP-1)	HNRNPAB
929,40	928,934	929,863							
929,51	929,046	929,976							
930,48	930,020	930,950	930,51	0,029	K.AAAQERER.R	Q05682	CALD1_HUMAN	Caldesmon (CDM)	CALD1
			930,38	0,102	K.GGDAPAAAGEDA.-	P62851	RS25_HUMAN	40S ribosomal protein S25 (Small ribosomal subunit protein eS25)	RPS25
931,48	931,019	931,951							
932,51	932,045	932,978	932,52	0,005	K.QVMAIKSR.V	Q92616	GCN1_HUMAN	eIF-2-alpha kinase activator GCN1 (GCN1 eIF-2-alpha kinase activator homolog) (GCN1-like protein 1) (General control of amino-acid synthesis 1-like protein 1) (Translational activator GCN1) (HsGCN1)	GCN1
			932,52	0,010	K.SAVTALWGK.V	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			932,53	0,014	K.KPFGLRSK.M	Q658J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			932,48	0,030	R.YLNFFTK.A	P12004	PCNA_HUMAN	Proliferating cell nuclear antigen (PCNA) (Cyclin)	PCNA
			932,45	0,058	K.LLEGEESR.L	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin kb7)	KRT7
			932,45	0,058	K.LLEGEESR.I	P08670	VIME_HUMAN	Vimentin	VIM
			932,45	0,058	K.LLEGEESR.L	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
933,47	933,007	933,940	933,51	0,036	K.LCTVATLR.E	P02768	ALBU_HUMAN	Serum albumin	ALB
			933,54	0,062	K.VNLAEFLK.G	P30044	PRDX5_HUMAN	Peroxioredoxin-5, mitochondrial (EC 1.11.1.15) (Alu corepressor 1) (Antioxidant enzyme B166) (AOEB166) (Liver tissue 2D-page spot 718) (PLP) (Peroxioredoxin V) (Prx-V) (Peroxisomal antioxidant enzyme) (TPx type VI) (Thioredoxin peroxidase PMP20)	PRDX5
934,48	934,010	934,945	934,49	0,008	K.TFPAETIR.F	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			934,51	0,031	R.EIALWFR.A	Q13232	NDK3_HUMAN	Nucleoside diphosphate kinase 3 (NDK 3) (NDP kinase 3) (EC 2.7.4.6) (DR-nm23) (Nucleoside diphosphate kinase C) (NDPKC) (nm23-H3)	NME3
			934,43	0,043	R.LELCDER.V	P07919	QCR6_HUMAN	Cytochrome b-c1 complex subunit 6, mitochondrial (Complex III subunit 6) (Complex III subunit VIII) (Cytochrome c1 non-heme 11 kDa protein) (Mitochondrial hinge protein) (Ubiquinol-cytochrome c reductase complex 11 kDa protein)	UQCRH
			934,55	0,075	K.LDYILGLK.I	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RPS9
934,51	934,040	934,974	934,51	0,002	R.EIALWFR.A	Q13232	NDK3_HUMAN	Nucleoside diphosphate kinase 3 (NDK 3) (NDP kinase 3) (EC 2.7.4.6) (DR-nm23) (Nucleoside diphosphate kinase C) (NDPKC) (nm23-H3)	NME3
			934,49	0,021	K.TFPAETIR.F	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			934,55	0,046	K.LDYILGLK.I	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RPS9
			934,43	0,072	R.LELCDER.V	P07919	QCR6_HUMAN	Cytochrome b-c1 complex subunit 6, mitochondrial (Complex III subunit 6) (Complex III subunit VIII) (Cytochrome c1 non-heme 11 kDa protein) (Mitochondrial hinge protein) (Ubiquinol-cytochrome c reductase complex 11 kDa protein)	UQCRH
935,54	935,074	936,009	935,51	0,032	R.EEYLLLR.L	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
			935,49	0,051	R.DGYAQLR.D	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
936,52	936,049	936,986	936,48	0,040	R.ATNSQLFR.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			936,37	0,149	K.GDMDELEK.E	Q14683	SMC1A_HUMAN	Structural maintenance of chromosomes protein 1A (SMC protein 1A) (SMC-1-alpha) (SMC-1A) (Sb1.8)	SMC1A
			936,37	0,149	K.CDLEDER.V	P61224	RAP1B_HUMAN	Ras-related protein Rap-1b (GTP-binding protein smg p21B)	RAP1B
937,53	937,065	938,002	937,56	0,023	R.EFLLIFR.K	Q96C19	EFHD2_HUMAN	EF-hand domain-containing protein D2 (Swiprosin-1)	EFHD2
			937,47	0,065	K.LMFEELR.N	Q9Y310	RTCB_HUMAN	tRNA-splicing ligase RtcB homolog (EC 6.5.1.3)	RTCB
			937,47	0,067	R.WTKSMRL.R	Q9NV66	TYW1_HUMAN	S-adenosyl-L-methionine-dependent tRNA 4-demethylwyosine synthase (EC 4.1.3.44) (Radical S-adenosyl methionine and flavodoxin domain-containing protein 1) (tRNA wybutosine-synthesizing protein 1 homolog) (tRNA-yW-synthesizing protein)	TYW1
			937,41	0,124	R.EEEMMIR.Q	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
938,52	938,049	938,987	938,48	0,041	R.LETCFLR.Y	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			938,46	0,058	K.LYSESLAR.Y	P50395	GDI2_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
			938,46	0,058	K.LYSESLAR.Y	P31150	GDI1_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			938,45	0,067	R.DYLIDGSR.G	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL
939,49	939,020	939,959	939,52	0,029	R.SDIAPVPIK.D	Q08257	QOR_HUMAN	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-crystallin)	CRYZ
			939,57	0,078	R.LILPQMPK.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
940,50	940,031	940,971	940,46	0,043	K.HIAEEADR.K	P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	TPM4
			940,46	0,043	K.DISLSDYK.G	Q06830	PRDX1_HUMAN	Peroxioredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
			940,45	0,052	K.DDNPNLPR.L	P02768	ALBU_HUMAN	Serum albumin	ALB
941,50	941,029	941,970							
942,46	941,989	942,932	942,45	0,006	K.FTFEEAAK.E	P13611	CSPG2_HUMAN	Versican core protein (Chondroitin sulfate proteoglycan core protein 2) (Chondroitin sulfate proteoglycan 2) (Glial hyaluronate-binding protein) (GHAP) (Large fibroblast proteoglycan) (PG-M)	VCAN
			942,50	0,041	R.GARGQNALR.Q	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
942,52	942,048	942,990	942,50	0,018	R.GARGQNALR.Q	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
			942,45	0,065	K.FTFEEAAK.E	P13611	CSPG2_HUMAN	Versican core protein (Chondroitin sulfate proteoglycan core protein 2) (Chondroitin sulfate proteoglycan 2) (Glial hyaluronate-binding protein) (GHAP) (Large fibroblast proteoglycan) (PG-M)	VCAN

943,54	943,067	944,011	943,50	0,039	K.HELIEFR.R	Q00610	CLH1_HUMAN	Clathrin heavy chain 1 (Clathrin heavy chain on chromosome 17) (CLH-17)	CLTC
			943,45	0,092	K.LTFDEYR.N	P12429	ANXA3_HUMAN	Annexin A3 (35-alpha calcimedin) (Annexin III) (Annexin-3) (Inositol 1,2-cyclic phosphate 2-phosphohydrolase) (Lipocortin III) (Placental anticoagulant protein III) (PAP-III)	ANXA3 H2AFV
944,52	944,044	944,989	944,53	0,016	R.AGLQFPVGR.V	Q96KK5	H2A1H_HUMAN	Histone H2A type 1-H (Histone H2A/s)	HIST1H2AH
			944,53	0,016	R.AGLQFPVGR.I	Q71U19	H2AV_HUMAN	Histone H2A.V (H2A.F/Z)	H2AFV
944,74	944,266	945,211	944,53	0,206	R.AGLQFPVGR.V	Q96KK5	H2A1H_HUMAN	Histone H2A type 1-H (Histone H2A/s)	HIST1H2AH
			944,53	0,206	R.AGLQFPVGR.I	Q71U19	H2AV_HUMAN	Histone H2A.V (H2A.F/Z)	H2AFV
945,52	945,047	945,992	945,47	0,051	K.YLDIHER.M	P62072	TIM10_HUMAN	Mitochondrial import inner membrane translocase subunit Tim10	TIMM10
			945,45	0,070	R.SYEIMFR.E	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
			945,38	0,144	K.FDSEYER.M	P43243	MATR3_HUMAN	Matrin-3	MATR3
946,51	946,041	946,987							
946,52	946,044	946,991							
947,49	947,018	947,965	947,45	0,046	K.SLSAERER.W	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
			947,56	0,065	R.IIWQFIK.E	P48735	IDHP_HUMAN	Isocitrate dehydrogenase [NADP], mitochondrial (IDH) (EC 1.1.1.42) (ICD-M) (IDP) (NADP(+)-specific ICDH) (Oxalosuccinate decarboxylase)	IDH2
947,52	947,043	947,990	947,56	0,065	K.VTNLLMLK.G	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
			947,56	0,040	R.IIWQFIK.E	P48735	IDHP_HUMAN	Isocitrate dehydrogenase [NADP], mitochondrial (IDH) (EC 1.1.1.42) (ICD-M) (IDP) (NADP(+)-specific ICDH) (Oxalosuccinate decarboxylase)	IDH2
			947,56	0,040	K.VTNLLMLK.G	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
947,52	947,043	947,990	947,45	0,071	K.SLSAERER.W	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
948,50	948,022	948,971	948,48	0,020	R.DFTPAELR.R	O00264	PGRC1_HUMAN	Membrane-associated progesterone receptor component 1 (mPR) (Dap1) (IZA)	PGRCM1
			948,44	0,056	K.FYEQFSK.N	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP 2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
949,48	949,004	949,954	949,49	0,006	R.LGDQEFIK.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			949,50	0,023	K.GITEECK.K.Q	Q9UKV3	ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus (Acinus)	ACIN1
			949,50	0,023	K.KLSEFGIR.N	Q9UBT2	SAE2_HUMAN	SUMO-activating enzyme subunit 2 (EC 2.3.2.-) (Anthracycline-associated resistance ARX) (Ubiquitin-like 1-activating enzyme E18) (Ubiquitin-like modifier-activating enzyme 2)	UBA2
950,47	949,999	950,949	950,47	0,003	K.EILDAFDK.M	P07602	SAP_HUMAN	Prosaposin (Proactivator polypeptide) [Cleaved into: Saposin-A (Protein A); Saposin-B-Val; Saposin-B (Cerebroside sulfate activator) (CSAct) (Dispersin) (Sphingolipid activator protein 1) (SAP-1) (Sulfatide/GM1 activator); Saposin-C (A1 activator) (Co-beta-glucosidase) (Glucosylceramidase activator) (Sphingolipid activator protein 2) (SAP-2); Saposin-D (Component C) (Protein C)]	PSAP
			950,47	0,003	R.ELVEGEMK.E	Q15424	SAFB1_HUMAN	Scaffold attachment factor B1 (SAF-B) (SAF-B1) (HSP27 estrogen response element-TATA box-binding protein) (HSP27 ERE-TATA-binding protein)	SAFB
			950,48	0,005	R.LFWPEMK.V	P22352	GPX3_HUMAN	Glutathione peroxidase 3 (GPx-3) (GSHPx-3) (EC 1.11.1.9) (Extracellular glutathione peroxidase) (Plasma glutathione peroxidase) (GPx-P) (GSHPx-P)	GPX3
			950,49	0,013	R.GFSLEELR.V	P26373	RL13_HUMAN	60S ribosomal protein L13 (Breast basic conserved protein 1) (Large ribosomal subunit protein eL13)	RPL13
951,51	951,031	951,983	951,51	0,002	R.PFLFGGWK.T	P04843	RPN1_HUMAN	Ras-related C3 botulinum toxin substrate 2 (Gx) (Small G protein) (p21-Rac2)	RAC2
			951,43	0,075	K.DLGEENFK.A	P02768	ALBU_HUMAN	Serum albumin	ALB
			951,43	0,075	K.ERECETK.T	Q86T65	DAAM2_HUMAN	Disheveled-associated activator of morphogenesis 2	DAAM2
952,37	951,891	952,843	952,39	0,027	R.EMEEQMR.R	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMp100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
			952,42	0,058	R.SLDADEFK.Q	Q13938	CAYP1_HUMAN	Calcyphosin (Calcyphosine)	CAPS
			952,46	0,088	R.EVEMGPKF.H	Q86VP6	CAND1_HUMAN	Cullin-associated NEDD8-dissociated protein 1 (Cullin-associated and neddylation-dissociated protein 1) (TBP-interacting protein of 120 kDa A) (TBP-interacting protein 120A) (p120 CAND1)	CAND1
952,51	952,034	952,986	952,46	0,088	K.DLSLDDFK.G	P30048	PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial (EC 1.11.1.15) (Antioxidant protein 1) (AOP-1) (HBC189) (Peroxiredoxin III) (Prx-III) (Peroxiredoxin-3) (Protein MERS homolog)	PRDX3
			952,49	0,119	K.ELGIETYK.V	P21397	AOFA_HUMAN	Amine oxidase [flavin-containing] A (EC 1.4.3.4) (Monoamine oxidase type A) (MAO-A)	MAOA
			952,49	0,122	M.VHLTPEEK.T	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
			952,49	0,122	M.VHLTPEEK.S	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
952,51	952,034	952,986	952,49	0,021	M.VHLTPEEK.T	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
			952,49	0,021	M.VHLTPEEK.S	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			952,49	0,025	K.ELGIETYK.V	P21397	AOFA_HUMAN	Amine oxidase [flavin-containing] A (EC 1.4.3.4) (Monoamine oxidase type A) (MAO-A)	MAOA

953,44	952,959	953,912	952,46	0,055	R.EVEMGPFK.H	Q86VP6	CAND1_HUMAN	Cullin-associated NEDD8-dissociated protein 1 (Cullin-associated and neddylation-dissociated protein 1) (TBP-interacting protein of 120 kDa A) (TBP-interacting protein 120A) (p120 CAND1)	CAND1
			952,46	0,055	K.DLSLDDFK.G	P30048	PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial (EC 1.11.1.15) (Antioxidant protein 1) (AOP-1) (HBC189) (Peroxiredoxin III) (Prx-III) (Peroxiredoxin-3) (Protein MER5 homolog)	PRDX3
			952,42	0,085	R.SLDADEFK.Q	Q13938	CAYP1_HUMAN	Calcyphosin (Calcyphosine)	CAP5
			952,39	0,116	R.EMEEQMR.R	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMp100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
			953,46	0,026	K.KDWYDVK.A	P61247	RS3A_HUMAN	40S ribosomal protein S3a (Small ribosomal subunit protein eS1) (v-fos transformation effector protein) (Fte-1)	RPS3A
			953,39	0,043	R.MHVEHER.R	Q15424	SAFB1_HUMAN	Scaffold attachment factor B1 (SAF-B) (SAF-B1) (HSP27 estrogen response element-TATA box-binding protein) (HSP27 ERE-TATA-binding protein)	SAFB
			953,60	0,167	K.IPSGLPELK.Y	Q9BXN1	ASPN_HUMAN	Asporin (Periodontal ligament-associated protein 1) (PLAP-1)	ASPN
			953,60	0,167	K.IIPEIQK.V	P55060	XPO2_HUMAN	Exportin-2 (Exp2) (Cellular apoptosis susceptibility protein) (Chromosome segregation 1-like protein) (Importin-alpha re-exporter)	CSE1L
			953,60	0,167	R.LLLPGELAK.H	Q16778	H2B2E_HUMAN	Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q)	HIST2H2BE
			953,60	0,167	R.LLLPGELAK.H	O60814	H2B1K_HUMAN	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK
953,46	952,986	953,940	953,46	0,002	K.KDWYDVK.A	P61247	RS3A_HUMAN	40S ribosomal protein S3a (Small ribosomal subunit protein eS1) (v-fos transformation effector protein) (Fte-1)	RPS3A
			953,39	0,071	R.MHVEHER.R	Q15424	SAFB1_HUMAN	Scaffold attachment factor B1 (SAF-B) (SAF-B1) (HSP27 estrogen response element-TATA box-binding protein) (HSP27 ERE-TATA-binding protein)	SAFB
			953,60	0,139	K.IPSGLPELK.Y	Q9BXN1	ASPN_HUMAN	Asporin (Periodontal ligament-associated protein 1) (PLAP-1)	ASPN
			953,60	0,139	K.IIPEIQK.V	P55060	XPO2_HUMAN	Exportin-2 (Exp2) (Cellular apoptosis susceptibility protein) (Chromosome segregation 1-like protein) (Importin-alpha re-exporter)	CSE1L
			953,60	0,139	R.LLLPGELAK.H	Q16778	H2B2E_HUMAN	Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q)	HIST2H2BE
			953,60	0,139	R.LLLPGELAK.H	O60814	H2B1K_HUMAN	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK
			953,60	0,008	K.IPSGLPELK.Y	Q9BXN1	ASPN_HUMAN	Asporin (Periodontal ligament-associated protein 1) (PLAP-1)	ASPN
			953,60	0,008	K.IIPEIQK.V	P55060	XPO2_HUMAN	Exportin-2 (Exp2) (Cellular apoptosis susceptibility protein) (Chromosome segregation 1-like protein) (Importin-alpha re-exporter)	CSE1L
			953,60	0,008	R.LLLPGELAK.H	Q16778	H2B2E_HUMAN	Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q)	HIST2H2BE
			953,60	0,008	R.LLLPGELAK.H	O60814	H2B1K_HUMAN	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK
953,61	953,133	954,087	953,60	0,008	K.IPSGLPELK.Y	Q9BXN1	ASPN_HUMAN	Asporin (Periodontal ligament-associated protein 1) (PLAP-1)	ASPN
			953,60	0,008	K.IIPEIQK.V	P55060	XPO2_HUMAN	Exportin-2 (Exp2) (Cellular apoptosis susceptibility protein) (Chromosome segregation 1-like protein) (Importin-alpha re-exporter)	CSE1L
			953,60	0,008	R.LLLPGELAK.H	Q16778	H2B2E_HUMAN	Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q)	HIST2H2BE
			953,60	0,008	R.LLLPGELAK.H	O60814	H2B1K_HUMAN	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK
			953,46	0,149	K.KDWYDVK.A	P61247	RS3A_HUMAN	40S ribosomal protein S3a (Small ribosomal subunit protein eS1) (v-fos transformation effector protein) (Fte-1)	RPS3A
			953,39	0,217	R.MHVEHER.R	Q15424	SAFB1_HUMAN	Scaffold attachment factor B1 (SAF-B) (SAF-B1) (HSP27 estrogen response element-TATA box-binding protein) (HSP27 ERE-TATA-binding protein)	SAFB
			954,48	0,015	K.FFVGGNWK.M	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP11
			954,47	0,028	R.EQFVEFR.D	Q43852	CALU_HUMAN	Calumenin (Crocabin) (IEF SSP 9302)	CALU
			954,53	0,035	K.FITIFGTR.S	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein 1) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
			954,46	0,036	R.IFGSYDPR.R	P08311	CATG_HUMAN	Cathepsin G (CG) (EC 3.4.21.20)	CTSG
954,50	954,021	954,976	954,46	0,041	K.FMETVAEK.A	P10909	CLUS_HUMAN	Clusterin (Aging-associated gene 4 protein) (Apolipoprotein J) (Apo-J) (Complement cytotoxicity inhibitor) (CLI) (Complement-associated protein SP-40,40) (Ku70-binding protein 1) (NA1/NA2) (Sulfated glycoprotein 2) (SGP-2) (Testosterone-repressed prostate message 2) (TRPM-2) [Cleaved into: Clusterin beta chain (Apolalpha) (Complement cytotoxicity inhibitor a chain); Clusterin alpha chain (Apolbeta) (Complement cytotoxicity inhibitor b chain)]	CLU
			954,55	0,052	K.YFLWVVK.F	P62993	GRB2_HUMAN	Growth factor receptor-bound protein 2 (Adapter protein GRB2) (Protein Ash) (SH2/SH3 adapter GRB2)	GRB2
			955,52	0,008	R.YILDYLR.D	Q96CX2	KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 (Pfetin) (Predominantly fetal expressed T1 domain)	KCTD12
			956,46	0,046	K.EAFSLFDK.D	P0DP23	CALM1_HUMAN	Calmodulin-1	CALM1
			956,46	0,050	K.FAEYGEIK.N	Q9Y5S9	RBM8A_HUMAN	RNA-binding protein 8A (Binder of OVCA1-1) (BOV-1) (RNA-binding motif protein 8A) (RNA-binding protein Y14) (Ribonucleoprotein RBM8A)	RBM8A
			956,57	0,159	R.LLEEALLR.L	P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	PRKDC
			956,57	0,026	R.LLEEALLR.L	P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	PRKDC
			956,46	0,082	K.FAEYGEIK.N	Q9Y5S9	RBM8A_HUMAN	RNA-binding protein 8A (Binder of OVCA1-1) (BOV-1) (RNA-binding motif protein 8A) (RNA-binding protein Y14) (Ribonucleoprotein RBM8A)	RBM8A
			956,46	0,087	K.EAFSLFDK.D	P0DP23	CALM1_HUMAN	Calmodulin-1	CALM1
			957,61	0,180	K.FIIPQIVK.Y	P07195	LDHB_HUMAN	L-lactate dehydrogenase B chain (LDH-B) (EC 1.1.1.27) (LDH heart subunit) (LDH-H) (Renal carcinoma antigen NY-REN-46)	LDHB
			957,61	0,056	K.FIIPQIVK.Y	P07195	LDHB_HUMAN	L-lactate dehydrogenase B chain (LDH-B) (EC 1.1.1.27) (LDH heart subunit) (LDH-H) (Renal carcinoma antigen NY-REN-46)	LDHB
958,42	957,944	958,903	958,51	0,082	K.LVIEEAER.S	P50991	TCPD_HUMAN	T-complex protein 1 subunit delta (TCP-1-delta) (CCT-delta) (Stimulator of TAR RNA-binding)	CCT4

958,56	958,077	959,035	958,51	0,050	K.LVIEAER.S	P50991	TCPD_HUMAN	T-complex protein 1 subunit delta (TCP-1-delta) (CCT-delta) (Stimulator of TAR RNA-binding)	CCT4
959,44	958,965	959,924							
959,56	959,084	960,043							
960,45	959,965	960,926	960,43	0,014	R.DWYPHSR.L	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	HSPB1
			960,55	0,104	K.FQNALLVR.Y	P02768	ALBU_HUMAN	Serum albumin	ALB
			960,55	0,104	R.VTDALNATR.A	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
960,56	960,079	961,039	960,55	0,010	K.FQNALLVR.Y	P02768	ALBU_HUMAN	Serum albumin	ALB
			960,55	0,010	R.VTDALNATR.A	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
			960,43	0,127	R.DWYPHSR.L	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	HSPB1
961,50	961,024	961,985	961,46	0,047	R.FLYEMSR.I	Q86T65	DAAM2_HUMAN	Disheveled-associated activator of morphogenesis 2	DAAM2
			961,45	0,057	R.SYEIMFR.E	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleared into: Endorepellin; LG3 peptide]	HSPG2
			961,44	0,069	R.GPSWDPPFR.D	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	HSPB1
962,44	961,960	962,923	962,44	0,001	K.EMFGGFFK.S	Q9Y5X3	SNX5_HUMAN	Sorting nexin-5	SNX5
			962,47	0,023	R.ESIESEIR.R	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			962,47	0,027	R.LTEDEVEK.L	P08590	MYL3_HUMAN	Myosin light chain 3 (Cardiac myosin light chain 1) (CMLC1) MYL3 (Myosin light chain 1, slow-twitch muscle B/ventricular isoform) (MLC1Sb) (Ventricular myosin alkali light chain) (Ventricular myosin light chain 1) (VLCI) (Ventricular/slow twitch myosin alkali light chain) (MLC-IV/sb)	MYL3
962,53	962,046	963,009	962,47	0,058	R.LTEDEVEK.L	P08590	MYL3_HUMAN	Myosin light chain 3 (Cardiac myosin light chain 1) (CMLC1) MYL3 (Myosin light chain 1, slow-twitch muscle B/ventricular isoform) (MLC1Sb) (Ventricular myosin alkali light chain) (Ventricular myosin light chain 1) (VLCI) (Ventricular/slow twitch myosin alkali light chain) (MLC-IV/sb)	MYL3
			962,47	0,062	R.ESIESEIR.R	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			962,44	0,087	K.EMFGGFFK.S	Q9Y5X3	SNX5_HUMAN	Sorting nexin-5	SNX5
963,51	963,024	963,987	963,52	0,013	K.LTVNDFVR.D	Q9UJS0	CMC2_HUMAN	Calcium-binding mitochondrial carrier protein Aralar2 (Citrin) (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13)	SLC25A13
			963,52	0,013	K.YNLGLDLR.T	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			963,44	0,063	R.YYTVFDR.D	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleared into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
			963,40	0,106	R.GDPGFEGER.G	P12109	CO6A1_HUMAN	Collagen alpha-1(VI) chain	COL6A1
964,42	963,938	964,903	964,47	0,054	R.FEELAAAR.E	Q02818	NUCB1_HUMAN	Nucleobindin-1 (CALNUC)	NUCB1
964,53	964,049	965,014	964,47	0,057	R.FEELAAAR.E	Q02818	NUCB1_HUMAN	Nucleobindin-1 (CALNUC)	NUCB1
965,45	964,965	965,930	965,46	0,014	R.AQYDELAR.K	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
			965,47	0,026	K.AAEDYGVIK.T	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein WS3-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
965,55	965,069	966,034	965,47	0,078	K.AAEDYGVIK.T	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein WS3-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
			965,46	0,090	R.AQYDELAR.K	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
966,50	966,014	966,980	966,49	0,010	K.ITTDEMIK.R	Q29RF7	PD55A_HUMAN	Sister chromatid cohesion protein PD55 homolog A (Cell proliferation-inducing gene 54 protein) (Sister chromatid cohesion protein 112) (SCC-112)	PD55A
			966,51	0,010	K.LWYTLDR.A	P00387	NBSR3_HUMAN	NADH-cytochrome b5 reductase 3 (B5R) (Cytochrome b5 reductase) (EC 1.6.2.2) (Diaphorase-1) [Cleared into: NADH-cytochrome b5 reductase 3 membrane-bound form; NADH-cytochrome b5 reductase 3 soluble form]	CYB5R3
			966,48	0,014	R.DTYEAVR.E	P62906	RL10A_HUMAN	60S ribosomal protein L10a (CSA-19) (Large ribosomal subunit protein uL1) (Neural precursor cell expressed developmentally down-regulated protein 6) (NEDD-6)	RPL10A
			966,52	0,020	K.RSQYGSR.Q	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC XRCC6 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-drp lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	
			966,47	0,024	R.LFWPEPMK.V	P22352	GPX3_HUMAN	Glutathione peroxidase 3 (GPx-3) (GSHPx-3) (EC 1.1.1.1.9) (Extracellular glutathione peroxidase) (Plasma glutathione peroxidase) (GPx-P) (GSHPx-P)	GPX3
			966,46	0,035	K.AEIFEDR.K	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA

967,51 967,95 968,10	967,026 967,469 967,613	967,993 968,437 968,581	966,56	0,063	K.KQVFTSEK.F	Q92616	GCN1_HUMAN	eIF-2-alpha kinase activator GCN1 (GCN1 eIF-2-alpha kinase activator homolog) (GCN1-like protein 1) (General control of amino-acid synthesis 1-like protein 1) (Translational activator GCN1) (HsGCN1)	GCN1
			966,56	0,063	R.ILEFFGLK.K	P07237	PDIA1_HUMAN	Protein disulfide-isomerase (PDI) (EC 5.3.4.1) (Cellular thyroid hormone-binding protein) (Prolyl 4-hydroxylase subunit beta) (p55)	P4HB
			968,47	0,370	R.FEEFLQR.K	Q02218	ODO1_HUMAN	2-oxoglutarate dehydrogenase, mitochondrial (EC 1.2.4.2) (2-oxoglutarate dehydrogenase complex component E1) (OGDC-E1) (Alpha-ketoglutarate dehydrogenase)	OGDH
968,52	968,033	969,001	968,47	0,375	K.LPDGYEFK.F	P09382	LEG1_HUMAN	Galectin-1 (Gal-1) (14 kDa laminin-binding protein) (HLBP14) (14 kDa lectin) (Beta-galactoside-binding lectin L-14-I) (Galaptin) (HBL) (HPL) (Lactose-binding lectin 1) (Lectin galactoside-binding soluble 1) (Putative MAPK-activating protein PM12) (S-Lac lectin 1)	LGALS1
			968,48	0,384	R.SIISMFDR.E	O75340	PDCD6_HUMAN	Programmed cell death protein 6 (Apoptosis-linked gene 2 protein homolog) (ALG-2)	PDCD6
			968,48	0,035	R.SIISMFDR.E	O75340	PDCD6_HUMAN	Programmed cell death protein 6 (Apoptosis-linked gene 2 protein homolog) (ALG-2)	PDCD6
969,06	968,575	969,544	968,47	0,045	K.LPDGYEFK.F	P09382	LEG1_HUMAN	Galectin-1 (Gal-1) (14 kDa laminin-binding protein) (HLBP14) (14 kDa lectin) (Beta-galactoside-binding lectin L-14-I) (Galaptin) (HBL) (HPL) (Lactose-binding lectin 1) (Lectin galactoside-binding soluble 1) (Putative MAPK-activating protein PM12) (S-Lac lectin 1)	LGALS1
			968,47	0,050	R.FEEFLQR.K	Q02218	ODO1_HUMAN	2-oxoglutarate dehydrogenase, mitochondrial (EC 1.2.4.2) (2-oxoglutarate dehydrogenase complex component E1) (OGDC-E1) (Alpha-ketoglutarate dehydrogenase)	OGDH
			969,42	0,359	R.LMEEYER.L	P35609	ACTN2_HUMAN	Alpha-actinin-2 (Alpha-actinin skeletal muscle isoform 2) (F-actin cross-linking protein)	ACTN2
969,52	969,031	970,000	969,42	0,365	R.TDQYWEEK.I	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
			969,44	0,383	R.LLCNFM.R.Q	P25786	PSA1_HUMAN	Proteasome subunit alpha type-1 (EC 3.4.25.1) (30 kDa prosomal protein) (PROS-30) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome component C2) (Proteasome nu chain)	PSMA1
			969,44 969,50	0,383 0,436	R.EQFNEFR.D K.ELEFYLR.K	Q15293 P62241	RCN1_HUMAN RS8_HUMAN	Reticulocalbin-1 40S ribosomal protein S8 [Small ribosomal subunit protein eS8]	RCN1 RPS8
970,52	970,036	971,007	969,50	0,020	K.ELEFYLR.K	P62241	RS8_HUMAN	40S ribosomal protein S8 [Small ribosomal subunit protein eS8]	RPS8
			969,44	0,073	R.LLCNFM.R.Q	P25786	PSA1_HUMAN	Proteasome subunit alpha type-1 (EC 3.4.25.1) (30 kDa prosomal protein) (PROS-30) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome component C2) (Proteasome nu chain)	PSMA1
			969,44 969,42	0,073 0,092	R.EQFNEFR.D R.TDQYWEEK.I	Q15293 P07858	RCN1_HUMAN CATB_HUMAN	Reticulocalbin-1 Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	RCN1 CTSB
971,54	971,056	972,028	969,42	0,097	R.LMEEYER.L	P35609	ACTN2_HUMAN	Alpha-actinin-2 (Alpha-actinin skeletal muscle isoform 2) (F-actin cross-linking protein)	ACTN2
			970,56 970,47	0,043 0,048	R.NEALAALLR.D K.SWDIFFR.N	P13797 Q02218	PLST_HUMAN ODO1_HUMAN	Plastin-3 (T-plastin) 2-oxoglutarate dehydrogenase, mitochondrial (EC 1.2.4.2) (2-oxoglutarate dehydrogenase complex component E1) (OGDC-E1) (Alpha-ketoglutarate dehydrogenase)	PLS3 OGDH
			971,45	0,090	K.FSWFAGEK.L	P21266	GSTM3_HUMAN	Glutathione S-transferase Mu 3 (EC 2.5.1.18) (GST class-mu 3) (GSTM3-3) (hGSTM3-3)	GSTM3
972,45 972,55 973,53	971,967 972,068 973,041	972,940 973,040 974,014	973,54	0,015	K.TVALWDLR.N	Q09028	RBBP4_HUMAN	Histone-binding protein RBBP4 (Chromatin assembly factor 1 subunit C) (CAF-1 subunit C) (Chromatin assembly factor 1 p48 subunit) (CAF-1 48 kDa subunit) (CAF-1 p48) (Nucleosome-remodeling factor subunit RBAP48) (Retinoblastoma-binding protein 4) (RBBP-4) (Retinoblastoma-binding protein p48)	RBBP4
			973,55 973,46	0,019 0,064	R.LVWLDLK.S R.YYAGWADK.Y	P02790 P05091	HEMO_HUMAN ALDH2_HUMAN	Hemopexin (Beta-1B-glycoprotein) Aldehyde dehydrogenase, mitochondrial (EC 1.2.1.3) (ALDH class 2) (ALDH-E2) (ALDH)	HPX ALDH2
			973,46	0,072	R.FHFDH.R.D	Q15424	SAFB1_HUMAN	Scaffold attachment factor B1 (SAF-B) (SAF-B1) (HSP27 estrogen response element-TATA box-binding protein) (HSP27 ERE-TATA-binding protein)	SAFB
974,49	974,007	974,982	974,52	0,023	R.EILDES.L.R	Q8WUM4	PDC6_HUMAN	Programmed cell death 6-interacting protein (PDCD6-interacting protein) (ALG-2-interacting protein 1) (ALG-2-interacting protein X) (Hp95)	PDCD6IP
			974,47	0,027	R.FHVEEGK.G	P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1
			974,47	0,029	K.LLEGEER.L	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
975,45	974,959	975,935	974,41	0,082	R.SEGFDY.R.C	P12004	PCNA_HUMAN	Proliferating cell nuclear antigen (PCNA) (Cyclin)	PCNA
			975,45	0,001	R.NWQWWR.L	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
			975,55	0,102	R.LPLQDVYK.I	P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1
975,55	975,064	976,039	975,55	0,003	R.LPLQDVYK.I	P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1
			975,45	0,104	R.NWQWWR.L	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9

976,46	975,968	976,944	976,46	0,008	K.IEGEPEFR.L	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
			976,45	0,010	K.AGFAGDDAPR.A	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			976,45	0,010	K.AGFAGDDAPR.A	Q658J3	POTEE_HUMAN	POTE ankryrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			976,45	0,010	K.AGFAGDDAPR.A	P68133	ACT5_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			976,45	0,010	K.AGFAGDDAPR.A	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			976,45	0,010	K.AGFAGDDAPR.A	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			976,48	0,022	R.MLAEDEL.R.D	P61204	ARF3_HUMAN	ADP-ribosylation factor 3	ARF3
			976,53	0,077	R.LIEDFLAR.S	Q43617	TPPC3_HUMAN	Trafficking protein particle complex subunit 3 (BET3 homolog)	TRAPPC3
			976,54	0,087	K.QLFDQVVK.T	P15311	EZR1_HUMAN	Ezrin (Cytovillin) (Villin-2) (p81)	EZR
			976,54	0,087	K.QLFDQVVK.T	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
976,70	976,215	977,192	976,54	0,160	K.QLFDQVVK.T	P15311	EZR1_HUMAN	Ezrin (Cytovillin) (Villin-2) (p81)	EZR
			976,54	0,160	K.QLFDQVVK.T	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			976,53	0,170	R.LIEDFLAR.S	Q43617	TPPC3_HUMAN	Trafficking protein particle complex subunit 3 (BET3 homolog)	TRAPPC3
			976,48	0,226	R.MLAEDEL.R.D	P61204	ARF3_HUMAN	ADP-ribosylation factor 3	ARF3
			976,46	0,239	K.IEGEPEFR.L	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
			976,45	0,257	K.AGFAGDDAPR.A	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			976,45	0,257	K.AGFAGDDAPR.A	Q658J3	POTEE_HUMAN	POTE ankryrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			976,45	0,257	K.AGFAGDDAPR.A	P68133	ACT5_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			976,45	0,257	K.AGFAGDDAPR.A	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			976,45	0,257	K.AGFAGDDAPR.A	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
977,48	976,990	977,967	977,47	0,004	R.LVEDMENK.I	P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta (CapZ beta)	CAPZB
978,46	977,967	978,945	978,51	0,050	K.HMMFIQR.F	Q2M2D7	TBC28_HUMAN	TBC1 domain family member 28	TBC1D28
			978,52	0,069	R.TSGLSSWK.Q	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			978,52	0,069	K.HQPTAIAK.T	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
978,54	978,047	979,026	978,52	0,012	R.TSGLSSWK.Q	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			978,52	0,012	K.HQPTAIAK.T	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
			978,51	0,031	K.HMMFIQR.F	Q2M2D7	TBC28_HUMAN	TBC1 domain family member 28	TBC1D28
979,52	979,028	980,008	979,50	0,021	R.DYLHYIR.K	P62280	RS11_HUMAN	40S ribosomal protein S11 (Small ribosomal subunit protein uS17)	RPS11
			979,50	0,021	R.GFCQIQVK.T	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
980,50	980,012	980,993	980,45	0,050	R.QDGSVDFGR.K	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
981,44	980,952	981,934	981,45	0,002	R.DIQDSEK.G	P09917	LOX5_HUMAN	Arachidonate 5-lipoxygenase (5-LO) (5-lipoxygenase) (EC 1.13.11.34)	ALOX5
			981,43	0,018	K.YHEEFK.S	Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 (LASP-1) (Metastatic lymph node gene 50 protein) (MLN 50)	LASP1
			981,43	0,018	R.GENEEMK.D	P24043	LAMA2_HUMAN	Laminin subunit alpha-2 (Laminin M chain) (Laminin-12 subunit alpha) (Laminin-2 subunit alpha) (Laminin-4 subunit alpha) (Merosin heavy chain)	LAMA2
			981,42	0,020	K.MFEHDFR.W	P13611	CSPG2_HUMAN	Versican core protein (Chondroitin sulfate proteoglycan core protein 2) (Chondroitin sulfate proteoglycan 2) (Glial hyaluronate-binding protein) (GHAP) (Large fibroblast proteoglycan) (PG-M)	VCAN
			981,52	0,079	K.DVGRPOQGR.E	P37802	TAGL2_HUMAN	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	TAGLN2
981,54	981,049	982,031	981,52	0,018	K.DVGRPOQGR.E	P37802	TAGL2_HUMAN	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	TAGLN2
			981,45	0,095	R.DIQDSEK.G	P09917	LOX5_HUMAN	Arachidonate 5-lipoxygenase (5-LO) (5-lipoxygenase) (EC 1.13.11.34)	ALOX5
			981,43	0,115	K.YHEEFK.S	Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 (LASP-1) (Metastatic lymph node gene 50 protein) (MLN 50)	LASP1
			981,43	0,115	R.GENEEMK.D	P24043	LAMA2_HUMAN	Laminin subunit alpha-2 (Laminin M chain) (Laminin-12 subunit alpha) (Laminin-2 subunit alpha) (Laminin-4 subunit alpha) (Merosin heavy chain)	LAMA2
			981,42	0,117	K.MFEHDFR.W	P13611	CSPG2_HUMAN	Versican core protein (Chondroitin sulfate proteoglycan core protein 2) (Chondroitin sulfate proteoglycan 2) (Glial hyaluronate-binding protein) (GHAP) (Large fibroblast proteoglycan) (PG-M)	VCAN
982,51	982,016	982,999	982,48	0,025	K.DIMAEIVK.N	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
			982,48	0,026	R.VMFTDLK.L	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
			982,44	0,066	R.DWSHYFK.I	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
983,53	983,040	984,024	983,54	0,011	R.RYPAHLAR.S	Q9H773	DCTP1_HUMAN	dCTP pyrophosphatase 1 (EC 3.6.1.12) (Deoxycytidine-triphosphatase 1) (dCTPase 1) (RS21C6) (XTP3-transactivated gene A protein)	DCTPP1
			983,52	0,012	K.MDVHGRIR.E	Q8TAP6	CEP76_HUMAN	Centrosomal protein of 76 kDa (Cep76)	CEP76
			983,55	0,018	R.ILGDEPEAR.L.D	Q15582	BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3 (Beta ig-h3) (Kerato-epithelin) (RGD-containing collagen-associated protein) (RGD-CAP)	TGFB1
			983,55	0,022	R.HGSLGFLPR.K	P39023	RL3_HUMAN	60S ribosomal protein L3 (HIV-1 TAR RNA-binding protein B) (TARBP-B) (Large ribosomal subunit protein uL3)	RPL3
984,09	983,595	984,579	984,46	0,372	R.DEFEGLFK.Q	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
			984,48	0,391	R.AFFSEVER.R	Q9UQ80	PA2G4_HUMAN	Proliferation-associated protein 2G4 (Cell cycle protein p38-2G4 homolog) (hG4-1) (ErbB3-binding protein 1)	PA2G4
			984,49	0,401	K.TYETTLEK.C	P02768	ALBU_HUMAN	Serum albumin	ALB

984,52	984,027	985,012	984,49	0,032	K.TYETTLK.C	P02768	ALBU_HUMAN	Serum albumin	ALB
			984,48	0,041	R.AFFSEVER.R	Q9UQ80	PA2G4_HUMAN	Proliferation-associated protein 2G4 (Cell cycle protein p38-2G4 homolog) (hG4-1) (ErB3-binding protein 1)	PA2G4
			984,46	0,060	R.DEFEGFLK.Q	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.2.145) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
985,56	985,070	986,056	985,57	0,006	K.LLQLVEDR.G	P17844	DDX5_HUMAN	Probable ATP-dependent RNA helicase DDX5 (EC 3.6.4.13) (DEAD box protein 5) (RNA helicase p68)	DDX5
			985,50	0,068	K.EGWPLDIR.V	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
986,48	985,987	986,974	986,48	0,002	K.HFSPEELK.V	P02511	CRYAB_HUMAN	Alpha-crystallin B chain (Alpha(B)-crystallin) (Heat shock protein beta-5) (HspB5) (Renal carcinoma antigen NY-REN-27) (Rosenthal fiber component)	CRYAB
			986,50	0,017	R.LTPEEIER.M	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP, EC 3.6.4.10 (78 kDa glucose-regulated protein, GRP-78) (Binding-immunoglobulin protein, BiP) (Heat shock protein 70 family protein 5, HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			986,46	0,018	K.YDEEFQR.Y	P55060	XPO2_HUMAN	Exportin-2 (Exp2) (Cellular apoptosis susceptibility protein) (Chromosome segregation 1-like protein) (Importin-alpha re-exporter)	CSE1L
			986,51	0,032	K.KPEDSSAPR.C	Q9Y661	HS3S4_HUMAN	Heparan sulfate glucosamine 3-O-sulfotransferase 4 (EC 2.8.2.23) (Heparan sulfate D-glucosaminyl 3-O-sulfotransferase 4) (3-OST-4) (Heparan sulfate 3-O-sulfotransferase 4) (h3-OST-4)	HS3ST4
			986,60	0,118	R.DLPLLLFR.T	O43175	SERA_HUMAN	D-3-phosphoglycerate dehydrogenase (3-PGDH) (EC 1.1.1.95) (2-oxoglutarate reductase) (EC 1.1.1.399) (Malate dehydrogenase) (EC 1.1.1.37)	PHGDH
			986,60	0,039	R.DLPLLLFR.T	O43175	SERA_HUMAN	D-3-phosphoglycerate dehydrogenase (3-PGDH) (EC 1.1.1.95) (2-oxoglutarate reductase) (EC 1.1.1.399) (Malate dehydrogenase) (EC 1.1.1.37)	PHGDH
986,56	986,067	987,054	986,51	0,048	K.KPEDSSAPR.C	Q9Y661	HS3S4_HUMAN	Heparan sulfate glucosamine 3-O-sulfotransferase 4 (EC 2.8.2.23) (Heparan sulfate D-glucosaminyl 3-O-sulfotransferase 4) (3-OST-4) (Heparan sulfate 3-O-sulfotransferase 4) (h3-OST-4)	HS3ST4
			986,50	0,063	R.LTPEEIER.M	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP, EC 3.6.4.10 (78 kDa glucose-regulated protein, GRP-78) (Binding-immunoglobulin protein, BiP) (Heat shock protein 70 family protein 5, HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			986,48	0,078	K.HFSPEELK.V	P02511	CRYAB_HUMAN	Alpha-crystallin B chain (Alpha(B)-crystallin) (Heat shock protein beta-5) (HspB5) (Renal carcinoma antigen NY-REN-27) (Rosenthal fiber component)	CRYAB
			986,46	0,098	K.YDEEFQR.Y	P55060	XPO2_HUMAN	Exportin-2 (Exp2) (Cellular apoptosis susceptibility protein) (Chromosome segregation 1-like protein) (Importin-alpha re-exporter)	CSE1L
			987,55	0,018	R.IPLNDFR.C	P13473	LAMP2_HUMAN	Lysosome-associated membrane glycoprotein 2 (LAMP-2) (Lysosome-associated membrane protein 2) (CD107 antigen-like family member B) (LGP-96) (CD antigen CD107b)	LAMP2
			987,50	0,034	R.ALELEQER.K	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
988,52	988,021	989,010	987,44	0,096	R.AHSVEECR.C	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
			988,54	0,021	K.SDLERQLK.T	Q5M775	CYTSB_HUMAN	Cytospin-B (Nuclear structure protein 5) (NSP5) (Sperm antigen HCMOGT-1) (Sperm antigen with calponin homology and coiled-coil domains 1)	SPECC1
			988,49	0,022	K.LIEVDDER.K	P62753	RS6_HUMAN	40S ribosomal protein S6 (Phosphoprotein NP33) (Small ribosomal subunit protein eS6)	RPS6
			988,54	0,023	K.MLLVDEL.R	P18085	ARF4_HUMAN	ADP-ribosylation factor 4	ARF4
			988,43	0,081	R.KEEEDNPK.G	Q10570	CPSF1_HUMAN	Cleavage and polyadenylation specificity factor subunit 1 (Cleavage and polyadenylation specificity factor 160 kDa subunit) (CPSF 160 kDa subunit)	CPSF1
			988,43	0,081	K.AWEEYYK.K	Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1) (DNA helicase V) (hDH V)	FUBP1
989,54	989,041	990,031	989,58	0,040	K.VFLENVIR.D	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
			990,54	0,096	M.VLDLDFR.V	P49591	SYSC_HUMAN	Serine--tRNA ligase, cytoplasmic (EC 6.1.1.11) (Seryl-tRNA synthetase) (SerRS) (Seryl-tRNA(Ser/Sec) synthetase)	SARS
			990,55	0,101	R.QVCTDVIR.A	Q96P44	COLA1_HUMAN	Collagen alpha-1(XI) chain	COL21A1
			990,55	0,017	R.QVCTDVIR.A	Q96P44	COLA1_HUMAN	Collagen alpha-1(XI) chain	COL21A1
			990,54	0,022	M.VLDLDFR.V	P49591	SYSC_HUMAN	Serine--tRNA ligase, cytoplasmic (EC 6.1.1.11) (Seryl-tRNA synthetase) (SerRS) (Seryl-tRNA(Ser/Sec) synthetase)	SARS
			991,46	0,031	R.MGGEAEIR.F	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A (EC 3.6.4.13) (DEAH box protein 9) (DEXH-box helicase 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II) (RNA helicase A)	DHX9
			991,51	0,089	K.TSVFVDPK.E	P12882	MYH1_HUMAN	Myosin-1 (Myosin heavy chain 1) (Myosin heavy chain 2x) (MyHC-2x) (Myosin heavy chain IIX/d) (MYHC-IIX/d) (Myosin heavy chain, skeletal muscle, adult 1)	MYH1
			991,52	0,091	R.QLAEDFLR.D	Q92841	DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.4.13) (DEAD box protein 17) (DEAD box protein p72) (DEAD box protein p82) (RNA-dependent helicase p72)	DDX17
			991,54	0,112	K.ENLDFIK.H	P07237	PDIA1_HUMAN	Protein disulfide-isomerase (PDI) (EC 5.3.4.1) (Cellular thyroid hormone-binding protein) (Prolyl 4-hydroxylase subunit beta) (p55)	P4HB

991,55	991,051	992,042	991,54	0,010	K.ENLDFIK.H	P07237	PDIA1_HUMAN	Protein disulfide-isomerase (PDI) (EC 5.3.4.1) (Cellular thyroid hormone-binding protein) (Prolyl 4-hydroxylase subunit beta) (p55)	P4HB
			991,52	0,031	R.QLAEDFLR.D	Q92841	DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.4.13) (DEAD box protein 17) (DEAD box protein p72) (DEAD box protein p82) (RNA-dependent helicase p72)	DDX17
			991,51	0,032	K.TSVFVDPK.E	P12882	MYH1_HUMAN	Myosin-1 (Myosin heavy chain 1) (Myosin heavy chain 2x) (MyHC-2x) (Myosin heavy chain IIX/d) (MYHC-IIX/d) (Myosin heavy chain, skeletal muscle, adult 1)	MYH1
			991,46	0,091	R.MGGEAEIR.F	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A (EC 3.6.4.13) (DEAH box protein 9) (DEXH-box helicase 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II) (RNA helicase A)	DHX9
992,44	991,948	992,940	992,46	0,011	K.YADEEIPR.S	O75369	FLNB_HUMAN	Filamin-B (FLN-B) (ABP-278) (ABP-280 homolog) (Actin-binding-like protein) (Beta-filamin) (Filamin homolog 1) (Fh1) (Filamin-3) (Thyroid autoantigen) (Truncated actin-binding protein) (Truncated ABP)	FLNB
			992,46	0,019	R.MLAEDELR.D	P61204	ARF3_HUMAN	ADP-ribosylation factor 3	ARF3
			992,40	0,045	R.YDDYSSSR.D	Q96E39	RMXL1_HUMAN	RNA binding motif protein, X-linked-like-1 (Heterogeneous nuclear ribonucleoprotein G-like 1)	RBMXL1
			992,50	0,056	R.KCTQLNTK.V	Q72569	BRAP_HUMAN	BRCA1-associated protein (EC 2.3.2.27) (BRAP2) (Impedes mitogenic signal propagation) (IMP) (RING finger protein 52) (RING-type E3 ubiquitin transferase BRAP2) (Renal carcinoma antigen NY-REN-63)	BRAP
992,56	992,066	993,058	992,50	0,062	R.KCTQLNTK.V	Q72569	BRAP_HUMAN	BRCA1-associated protein (EC 2.3.2.27) (BRAP2) (Impedes mitogenic signal propagation) (IMP) (RING finger protein 52) (RING-type E3 ubiquitin transferase BRAP2) (Renal carcinoma antigen NY-REN-63)	BRAP
			992,46	0,099	R.MLAEDELR.D	P61204	ARF3_HUMAN	ADP-ribosylation factor 3	ARF3
			992,46	0,107	K.YADEEIPR.S	O75369	FLNB_HUMAN	Filamin-B (FLN-B) (ABP-278) (ABP-280 homolog) (Actin-binding-like protein) (Beta-filamin) (Filamin homolog 1) (Fh1) (Filamin-3) (Thyroid autoantigen) (Truncated actin-binding protein) (Truncated ABP)	FLNB
			992,40	0,163	R.YDDYSSSR.D	Q96E39	RMXL1_HUMAN	RNA binding motif protein, X-linked-like-1 (Heterogeneous nuclear ribonucleoprotein G-like 1)	RBMXL1
993,47	992,977	993,970	993,51	0,033	K.AGLVDDFEK.K	O75947	ATP5H_HUMAN	ATP synthase subunit d, mitochondrial (ATPase subunit d) (ATP synthase peripheral stalk subunit d)	ATP5PD
			993,52	0,042	R.DSFQEVLR.F	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			993,68	0,210	K.IIVLGLPR.G	P68402	PA1B2_HUMAN	Platelet-activating factor acetylhydrolase 1B subunit beta (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH subunit beta) (PAFAH subunit beta)	PAFAH1B2
993,56	993,064	994,057	993,52	0,045	R.DSFQEVLR.F	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			993,51	0,054	K.AGLVDDFEK.K	O75947	ATP5H_HUMAN	ATP synthase subunit d, mitochondrial (ATPase subunit d) (ATP synthase peripheral stalk subunit d)	ATP5PD
			993,68	0,123	K.IIVLGLPR.G	P68402	PA1B2_HUMAN	Platelet-activating factor acetylhydrolase 1B subunit beta (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH subunit beta) (PAFAH subunit beta)	PAFAH1B2
994,47	993,974	994,969	994,48	0,004	R.RMEEEER.L	Q15149	PLEC_HUMAN	Plectin (PCN) (PLTN) (Hemidesmosomal protein 1) (HD1) (Plectin-1)	PLEC
			994,48	0,004	R.LGLDYER.V	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
			994,44	0,033	R.GDPNWFMK.K	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein WS3-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
			994,51	0,036	K.HLTDAYFK.K	Q02878	RL6_HUMAN	60S ribosomal protein L6 (Large ribosomal subunit protein eL6) (Neoplasm-related protein C140) (Tax-responsive enhancer element-binding protein 107) (TaxREB107)	RPL6
			994,52	0,048	K.TEDTIFLR.E	P19652	A1AG2_HUMAN	Alpha-1-acid glycoprotein 2 (AGP 2) (Orosomucoid-2) (OMD 2)	ORM2
			994,52	0,048	K.TEDTIFLR.E	P02763	A1AG1_HUMAN	Alpha-1-acid glycoprotein 1 (AGP 1) (Orosomucoid-1) (OMD 1)	ORM1
994,58	994,079	995,074	994,52	0,058	K.TEDTIFLR.E	P19652	A1AG2_HUMAN	Alpha-1-acid glycoprotein 2 (AGP 2) (Orosomucoid-2) (OMD 2)	ORM2
			994,52	0,058	K.TEDTIFLR.E	P02763	A1AG1_HUMAN	Alpha-1-acid glycoprotein 1 (AGP 1) (Orosomucoid-1) (OMD 1)	ORM1
			994,51	0,069	K.HLTDAYFK.K	Q02878	RL6_HUMAN	60S ribosomal protein L6 (Large ribosomal subunit protein eL6) (Neoplasm-related protein C140) (Tax-responsive enhancer element-binding protein 107) (TaxREB107)	RPL6
			994,48	0,101	R.RMEEEER.L	Q15149	PLEC_HUMAN	Plectin (PCN) (PLTN) (Hemidesmosomal protein 1) (HD1) (Plectin-1)	PLEC
			994,48	0,101	R.LGLDYER.V	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
			994,44	0,138	R.GDPNWFMK.K	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein WS3-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
995,54	995,039	996,034	995,52	0,019	K.IKEWYEK.H	P13645	K1C10_HUMAN	Keratin, type I cytoskeletal 10 (Cytokeatin-10) (CK-10) (Keratin-10) (K10)	KRT10
			995,51	0,029	K.SDVEAIFSK.Y	P07910	HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1/C2)	HNRNPC
			995,43	0,102	R.DAEDAVYGR.D	Q07955	SRSF1_HUMAN	Serine/arginine-rich splicing factor 1 (Alternative-splicing factor 1) (ASF-1) (Splicing factor, arginine/serine-rich 1) (pre-mRNA-splicing factor SF2, P33 subunit)	SRSF1
996,53	996,028	997,025	996,50	0,024	R.EPPAYTYR.D	Q8IVL6	P3H3_HUMAN	Prolyl 3-hydroxylase 3 (EC 1.14.11.7) (Leprecan-like protein 2) (Protein B)	P3H3
			996,50	0,025	K.DIDIHEVR.I	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
			996,49	0,036	K.DLTEYLSR.F	O14979	HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like (hnRNP D-like) (hnRNP DL) (AU-rich element RNA-binding factor) (JKT41-binding protein) (Protein laAUF1)	HNRNDL
			996,45	0,073	K.FELDTSER.K	P04844	RPN2_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 (Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit) (RIBIIR) (Ribophorin II) (RPN-II) (Ribophorin-2)	RPN2
997,46	996,963	997,961	997,44	0,019	R.EWEMQFK.E	O15173	PGRMC2_HUMAN	Membrane-associated progesterone receptor component 2 (Progesterone membrane-binding protein) (Steroid receptor protein DG6)	PGRMC2

997,52	997,021	998,018	997,43	0,034	R.GGDLMAYDR.R	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
			997,42	0,045	K.MFEHDFR.W	P13611	CSPG2_HUMAN	Versican core protein (Chondroitin sulfate proteoglycan core protein 2) (Chondroitin sulfate proteoglycan 2) (Glial hyaluronate-binding protein) (GHAP) (Large fibroblast proteoglycan) (PG-M)	VCAN
			997,41	0,055	R.WDQDYDR.A	Q6I850	TWF2_HUMAN	Twinfilin-2 (A6-related protein) (hA6RP) (Protein tyrosine kinase 9-like) (Twinfilin-1-like protein)	TWF2
			997,59	0,128	K.DILADLPK.E	O75390	CISY_HUMAN	Citrate synthase, mitochondrial (EC 2.3.3.1) (Citrate (Si)-synthase)	CS
			997,59	0,070	K.DILADLPK.E	O75390	CISY_HUMAN	Citrate synthase, mitochondrial (EC 2.3.3.1) (Citrate (Si)-synthase)	CS
			997,44	0,076	R.EWEMQFK.E	O15173	PGRC2_HUMAN	Membrane-associated progesterone receptor component 2 (Progesterone membrane-binding protein) (Steroid receptor protein DG6)	PGRMC2
			997,43	0,091	R.GGDLMAYDR.R	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
			997,42	0,102	K.MFEHDFR.W	P13611	CSPG2_HUMAN	Versican core protein (Chondroitin sulfate proteoglycan core protein 2) (Chondroitin sulfate proteoglycan 2) (Glial hyaluronate-binding protein) (GHAP) (Large fibroblast proteoglycan) (PG-M)	VCAN
			997,41	0,113	R.WDQDYDR.A	Q6I850	TWF2_HUMAN	Twinfilin-2 (A6-related protein) (hA6RP) (Protein tyrosine kinase 9-like) (Twinfilin-1-like protein)	TWF2
			998,41	0,007	K.DVEDMFSR.F	Q15717	ELAV1_HUMAN	ELAV-like protein 1 (Hu-antigen R) (HuR)	ELAVL1
			998,37	0,049	R.DYDDMSPR.R	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
			998,49	0,068	K.GKVCFEMK.V	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
998,42	997,919	998,918	998,49	0,068	R.DLTDYLMK.I	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			998,49	0,068	R.DLTDYLMK.I	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			998,49	0,068	R.DLTDYLMK.I	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			998,49	0,068	R.DLTDYLMK.I	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			998,49	0,068	R.DLTDYLMK.I	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			998,51	0,092	R.ISFDEFIK.I	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
			998,54	0,122	K.EPGLQWR.V	P06396	GELS_HUMAN	Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF) (Brevin)	GSN
			998,54	0,007	K.EPGLQWR.V	P06396	GELS_HUMAN	Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF) (Brevin)	GSN
			998,51	0,037	R.ISFDEFIK.I	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
			998,49	0,061	K.GKVCFEMK.V	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
			998,49	0,061	R.DLTDYLMK.I	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			998,49	0,061	R.DLTDYLMK.I	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
998,55	998,048	999,047	998,49	0,061	R.DLTDYLMK.I	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			998,49	0,061	R.DLTDYLMK.I	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			998,49	0,061	R.DLTDYLMK.I	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			998,41	0,137	K.DVEDMFSR.F	Q15717	ELAV1_HUMAN	ELAV-like protein 1 (Hu-antigen R) (HuR)	ELAVL1
			998,37	0,178	R.DYDDMSPR.R	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
			999,50	0,068	R.ELPNIEER.I	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			999,51	0,078	R.HLMWDLGK.G	Q99643	C560_HUMAN	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial (Integral membrane protein CII-3) (QPs-1) (QPs1) (Succinate dehydrogenase complex subunit C) (Succinate-ubiquinone oxidoreductase cytochrome B large subunit) (CYBL)	SDHC
			999,51	0,062	R.HLMWDLGK.G	Q99643	C560_HUMAN	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial (Integral membrane protein CII-3) (QPs-1) (QPs1) (Succinate dehydrogenase complex subunit C) (Succinate-ubiquinone oxidoreductase cytochrome B large subunit) (CYBL)	SDHC
			999,50	0,072	R.ELPNIEER.I	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			999,51	0,396	R.HLMWDLGK.G	Q99643	C560_HUMAN	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial (Integral membrane protein CII-3) (QPs-1) (QPs1) (Succinate dehydrogenase complex subunit C) (Succinate-ubiquinone oxidoreductase cytochrome B large subunit) (CYBL)	SDHC
			999,50	0,406	R.ELPNIEER.I	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1000,37	0,467	R.DMDDAYDR.L	P07686	HEXB_HUMAN	Beta-hexosaminidase subunit beta (EC 3.2.1.52) (Beta-N-acetylhexosaminidase subunit beta) (Hexosaminidase subunit B) (Cervical cancer proto-oncogene 7 protein) (HCC-7) (N-acetyl-beta-glucosaminidase subunit beta) [Cleaved into: Beta-hexosaminidase subunit beta chain B; Beta-hexosaminidase subunit beta chain A]	HEXB
1000,06	999,556	1000,556	1000,37	0,319	R.DMDDAYDR.L	P07686	HEXB_HUMAN	Beta-hexosaminidase subunit beta (EC 3.2.1.52) (Beta-N-acetylhexosaminidase subunit beta) (Hexosaminidase subunit B) (Cervical cancer proto-oncogene 7 protein) (HCC-7) (N-acetyl-beta-glucosaminidase subunit beta) [Cleaved into: Beta-hexosaminidase subunit beta chain B; Beta-hexosaminidase subunit beta chain A]	HEXB
			1000,43	0,371	K.ADCSFWSK.Y	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1000,49	0,437	K.YLGEEYVK.A	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1000,59	0,044	K.QUALVELVK.H	P02768	ALBU_HUMAN	Serum albumin	ALB
			1000,49	0,051	K.YLGEEYVK.A	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1000,43	0,117	K.ADCSFWSK.Y	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1000,54	1000,043	1001,044	1000,59	0,044	K.QUALVELVK.H	P02768	ALBU_HUMAN	Serum albumin	ALB
			1000,49	0,051	K.YLGEEYVK.A	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1000,43	0,117	K.ADCSFWSK.Y	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1000,43	0,117	K.ADCSFWSK.Y	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG

			1000,37	0,169	R.DMDDAYDR.L	P07686	HEXB_HUMAN	Beta-hexosaminidase subunit beta (EC 3.2.1.52) (Beta-N-acetylhexosaminidase subunit beta) (Hexosaminidase subunit B) (Cervical cancer proto-oncogene 7 protein) (HCC-7) (N-acetyl-beta-glucosaminidase subunit beta) [Cleaved into: Beta-hexosaminidase subunit beta chain B; Beta-hexosaminidase subunit beta chain A]	HEXB
1001,00	1000,504	1001,505	1000,59	0,417	K.QTALVELVK.H	P02768	ALBU_HUMAN	Serum albumin	ALB
1001,47	1000,967	1001,969	1001,56	0,096	R.EKEEVVLR.C	O95613	PCNT_HUMAN	Pericentrin (Kendrin) (Pericentrin-B)	PCNT
1001,58	1001,077	1002,079	1001,56	0,014	R.EKEEVVLR.C	O95613	PCNT_HUMAN	Pericentrin (Kendrin) (Pericentrin-B)	PCNT
1002,54	1002,038	1003,040	1002,55	0,013	K.EMVLELR.D	Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1) (DNA helicase V) (hDH V)	FUBP1
			1002,52	0,020	R.LMHLEFGR.G	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1002,43	0,111	R.EIEDPEDR.K	P27824	CALX_HUMAN	Calnexin (IP90) (Major histocompatibility complex class I antigen-binding protein p88) (p90)	CANX
1003,53	1003,032	1004,035	1003,52	0,013	K.NDIPFELR.I	P30711	GSTT1_HUMAN	Glutathione S-transferase theta-1 (EC 2.5.1.18) (GST class-theta-1) (Glutathione transferase T1-1)	GSTT1
1004,53	1004,023	1005,027	1004,54	0,016	K.MLLVDEL.R	P18085	ARF4_HUMAN	ADP-ribosylation factor 4	ARF4
			1004,55	0,028	R.LQQNLFGGK.F	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1005,48	1004,975	1005,980	1005,54	0,067	R.ILELDQFK.G	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC XRCC6 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	
			1005,55	0,077	K.LIEIENFK.S	Q14683	SMC1A_HUMAN	Structural maintenance of chromosomes protein 1A (SMC protein 1A) (SMC-1-alpha) (SMC-1A) (Sb1.8)	SMC1A
			1005,55	0,055	K.LIEIENFK.S	Q14683	SMC1A_HUMAN	Structural maintenance of chromosomes protein 1A (SMC protein 1A) (SMC-1-alpha) (SMC-1A) (Sb1.8)	SMC1A
1005,61	1005,106	1006,112	1005,54	0,064	R.ILELDQFK.G	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC XRCC6 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	
1006,47	1005,964	1006,970	1006,47	0,006	K.TEIEDFPR.F	P06865	HEXA_HUMAN	Beta-hexosaminidase subunit alpha (EC 3.2.1.52) (Beta-N-acetylhexosaminidase subunit alpha) (Hexosaminidase subunit A) (N-acetyl-beta-glucosaminidase subunit alpha)	HEXA
			1006,52	0,055	K.YPSLELER.R	Q5SSJ5	HP1B3_HUMAN	Heterochromatin protein 1-binding protein 3 (Protein HP1- BP74)	HP1BP3
1006,56	1006,057	1007,064	1006,52	0,039	K.YPSLELER.R	Q5SSJ5	HP1B3_HUMAN	Heterochromatin protein 1-binding protein 3 (Protein HP1- BP74)	HP1BP3
			1006,47	0,087	K.TEIEDFPR.F	P06865	HEXA_HUMAN	Beta-hexosaminidase subunit alpha (EC 3.2.1.52) (Beta-N-acetylhexosaminidase subunit alpha) (Hexosaminidase subunit A) (N-acetyl-beta-glucosaminidase subunit alpha)	HEXA
1007,60	1007,097	1008,104	1007,56	0,037	R.LGLGHNQIR.M	P21810	PGS1_HUMAN	Biglycan (Bone/cartilage proteoglycan I) (PG-S1)	BGN
			1007,53	0,071	K.YIQELWR.K	P61313	RL15_HUMAN	60S ribosomal protein L15 (Large ribosomal subunit protein eL15)	RPL15
1008,58	1008,072	1009,081	1008,51	0,064	K.IFGSEAAWK.V	P49748	ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial (VLCAD) (EC 1.3.8.9)	ACADVL
			1008,51	0,070	K.ANYVWWLR.H	P31939	PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH [Cleaved into: Bifunctional purine biosynthesis protein PURH, N-terminally processed] [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (ATIC) (IMP synthase) (Inosinicase)]	ATIC
1009,56	1009,056	1010,065	1009,54	0,018	R.AENFFILR.R	P59998	ARPC4_HUMAN	Actin-related protein 2/3 complex subunit 4 (Arp2/3 complex 20 kDa subunit) (p20-ARC)	ARPC4
			1009,45	0,108	R.DAEDIAYGR.N	Q13242	SRSF9_HUMAN	Serine/arginine-rich splicing factor 9 (Pre-mRNA-splicing factor SRp30C) (Splicing factor, arginine/serine-rich 9)	SRSF9
			1009,42	0,144	R.MCEDLWR.W	Q14376	GALE_HUMAN	UDP-glucose 4-epimerase (EC 5.1.3.2) (Galactowaldenase) (UDP-N-acetylgalactosamine 4-epimerase) (UDP-GalNAc 4-epimerase) (UDP-N-acetylglucosamine 4-epimerase) (UDP-GlcNAc 4-epimerase) (EC 5.1.3.7) (UDP-galactose 4-epimerase)	GALE
1011,71 1012,59	1011,205 1012,081	1012,217 1013,093	1012,62	0,031	R.NEALIALLR.E	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
			1012,46	0,127	K.YETELAMR.Q	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
1012,72	1012,212	1013,225	1012,62	0,101	R.NEALIALLR.E	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
			1012,46	0,259	K.YETELAMR.Q	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
1013,50	1012,997	1014,011	1013,50	0,002	K.GQFETYLR.D	Q13510	ASAH1_HUMAN	Acid ceramidase (AC) (ACDase) (Acid CDease) (EC 3.5.1.23) (Acylsphingosine deacylase) (N-acyl ethanolamine hydrolase ASAH1) (EC 3.5.1.-) (N-acylsphingosine amidohydrolase) (Putative 32 kDa heart protein) (PHP32) [Cleaved into: Acid ceramidase subunit alpha; Acid ceramidase subunit beta]	ASAH1

1013,68	1013,178	1014,192	1013,48	0,025	K.YNLDFWR.K	Q13630	FCL_HUMAN	GDP-L-fucose synthase (EC 1.1.1.271) (GDP-4-keto-6-deoxy TSTA3 D-mannose-3,5-epimerase-4-reductase) (Protein FX) (Red cell NADP(H)-binding protein) (Short-chain dehydrogenase/reductase family 4E member 1)	TSTA3
			1013,43	0,074	R.GGNFGFGDSR.G	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			1013,50	0,182	K.GQFETYLR.D	Q13510	ASAH1_HUMAN	Acid ceramidase (AC) (ACDase) (Acid CDase) (EC 3.5.1.23) (Acylsphingosine deacylase) (N-acyl ethanolamine hydrolase ASAH1) (EC 3.5.1.-) (N-acylsphingosine amidohydrolase) (Putative 32 kDa heart protein) (PHP32) [Cleaved into: Acid ceramidase subunit alpha; Acid ceramidase subunit beta]	ASAH1
			1013,48	0,206	K.YNLDFWR.K	Q13630	FCL_HUMAN	GDP-L-fucose synthase (EC 1.1.1.271) (GDP-4-keto-6-deoxy TSTA3 D-mannose-3,5-epimerase-4-reductase) (Protein FX) (Red cell NADP(H)-binding protein) (Short-chain dehydrogenase/reductase family 4E member 1)	TSTA3
			1013,43	0,255	R.GGNFGFGDSR.G	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			1014,57	0,012	R.MLEKLGVPK.T	P55008	AIF1_HUMAN	Allograft inflammatory factor 1 (AIF-1) (Ionized calcium-binding adapter molecule 1) (Protein G1)	AIF1
			1014,57	0,012	K.AVQELWLR.L	P42126	ECI1_HUMAN	Enoyl-CoA delta isomerase 1, mitochondrial (EC 5.3.3.8) (3,2-trans-enoil-CoA isomerase) (Delta(3),Delta(2)-enoyl-CoA isomerase) (D3,D2-enoil-CoA isomerase) (Dodecenoil-CoA isomerase)	ECI1
			1014,55	0,035	K.QEILAALEK.G	P07602	SAP_HUMAN	Prosaposin (Proactivator polypeptide) [Cleaved into: Saposin-A (Protein A); Saposin-B-Val; Saposin-B (Cerebroside sulfate activator) (CSAct) (Dispersin) (Sphingolipid activator protein 1) (SAP-1) (Sulfatide/GM1 activator); Saposin-C (A1 activator) (Co-beta-glucosidase) (Glucosylceramidase activator) (Sphingolipid activator protein 2) (SAP-2); Saposin-D (Component C) (Protein C)]	PSAP
			1014,54	0,046	K.DPEAAEARR.G	P13611	CSPG2_HUMAN	Versican core protein (Chondroitin sulfate proteoglycan core protein 2) (Chondroitin sulfate proteoglycan 2) (Glial hyaluronate-binding protein) (GHAP) (Large fibroblast proteoglycan) (PG-M)	VCAN
			1014,50	0,083	R.LYDAYELK.H	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
			1014,48	0,108	R.DLTDYLMK.I	P60709	ACTB_HUMAN	Actin, cytoplasmic I (Beta-actin) [Cleaved into: Actin, cytoplasmic I, N-terminally processed]	ACTB
1014,59	1014,079	1015,094	1014,48	0,108	R.DLTDYLMK.I	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1014,48	0,108	R.DLTDYLMK.I	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1014,48	0,108	K.GKVCFEMK.V	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
			1014,48	0,108	R.DLTDYLMK.I	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			1014,48	0,108	R.DLTDYLMK.I	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1014,37	0,217	R.DYDDMSPR.R	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
			1015,61	0,014	R.IIPAIWFR.Y	Q969X5	ERG1_HUMAN	Endoplasmic reticulum-Golgi intermediate compartment protein 1 (ER-Golgi intermediate compartment 32 kDa protein) (ERGIC-32)	ERGIC1
			1015,54	0,057	K.ELLEAVDAR.T	Q8NSH7	SH2D3_HUMAN	SH2 domain-containing protein 3C (Novel SH2-containing protein 3) (SH2 domain-containing Eph receptor-binding protein 1) (SHEP1)	SH2D3C
			1015,54	0,057	R.ELLEAVDAR.Y	P29590	PML_HUMAN	Protein PML (Promyelocytic leukemia protein) (RING finger protein 71) (Tripartite motif-containing protein 19)	PML
			1015,46	0,137	R.GLDFDEYGS.K	P14625	ENPL_HUMAN	Endoplasmin (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			1015,40	0,194	R.YDDMAAAMK.N	P61981	1433G_HUMAN	14-3-3 protein gamma (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein gamma, N-terminally processed]	YWHAH
1015,60	1015,089	1016,105	1015,40	0,194	R.YDDMAAAMK.A	P31946	1433B_HUMAN	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHAH
			1016,48	0,025	R.VDFDDIHR.K	P13805	TNNT1_HUMAN	Troponin T, slow skeletal muscle (TnTs) (Slow skeletal muscle troponin T) (sTnT)	TNNT1
			1016,46	0,048	K.SYSFDEIR.K	P43490	NAMPT_HUMAN	Nicotinamide phosphoribosyltransferase (NAMPTase) (Nampt) (EC 2.4.2.12) (Pre-B-cell colony-enhancing factor 1) (Pre-B cell-enhancing factor) (Visfatin)	NAMPT
			1016,48	0,116	R.VDFDDIHR.K	P13805	TNNT1_HUMAN	Troponin T, slow skeletal muscle (TnTs) (Slow skeletal muscle troponin T) (sTnT)	TNNT1
			1016,46	0,139	K.SYSFDEIR.K	P43490	NAMPT_HUMAN	Nicotinamide phosphoribosyltransferase (NAMPTase) (Nampt) (EC 2.4.2.12) (Pre-B-cell colony-enhancing factor 1) (Pre-B cell-enhancing factor) (Visfatin)	NAMPT
			1017,54	0,067	K.SLHTLFGDK.L	P02768	ALBU_HUMAN	Serum albumin	ALB
			1017,51	0,092	R.YHFFLYK.H	Q6IBS0	TWF2_HUMAN	Twinfilin-2 (A6-related protein) (hA6RP) (Protein tyrosine kinase 9-like) (Twinfilin-1-like protein)	TWF2
			1018,47	0,217	K.EAAEQDVEK.K	P26373	RL13_HUMAN	60S ribosomal protein L13 (Breast basic conserved protein 1) (Large ribosomal subunit protein eL13)	RPL13
			1018,47	0,217	K.GDSDDKPR.K	Q9UKV3	ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus (Acinus)	ACIN1
			1018,49	0,243	R.EEATHYR.K	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1018,49	0,039	R.EEATHYR.K	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1018,53	1018,022	1019,040	1018,47	0,065	K.EAAEQDVEK.K	P26373	RL13_HUMAN	60S ribosomal protein L13 (Breast basic conserved protein 1) (Large ribosomal subunit protein eL13)	RPL13
			1018,47	0,065	K.GDSDDKPR.K	Q9UKV3	ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus (Acinus)	ACIN1
			1019,46	0,227	K.EAEDELSAR.H	P36776	LONM_HUMAN	Lon protease homolog, mitochondrial (EC 3.4.21.53) (LONHs) (Lon protease-like protein) (LONP) (Mitochondrial ATP-dependent protease Lon) (Serine protease 15)	LONP1

1019,53	1019,020	1020,039	1019,49	0,253	R.GFCFITFK.E	Q14103	HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0)	HNRNPD
			1019,51	0,272	K.GDYPLEAVR.M	P14618	KPYM_HUMAN	(AU-rich element RNA-binding protein 1) Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
			1019,51	0,021	K.GDYPLEAVR.M	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
			1019,49	0,040	R.GFCFITFK.E	Q14103	HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0)	HNRNPD
1020,55	1020,035	1021,055	1019,46	0,066	K.EAEDLSAR.H	P36776	LONM_HUMAN	(AU-rich element RNA-binding protein 1) Lon protease homolog, mitochondrial (EC 3.4.21.53) (LONHs) (Lon protease-like protein) (LONP) (Mitochondrial ATP-dependent protease Lon) (Serine protease 15)	LONP1
			1020,47	0,079	K.TLNEWDSR.H	O15371	EIF3D_HUMAN	Eukaryotic translation initiation factor 3 subunit D (eIF3d) (Eukaryotic translation initiation factor 3 subunit 7) (eIF-3-zeta) (eIF3 p66)	EIF3D
			1021,55	0,009	K.NILTEYR.I	Q15907	RB11B_HUMAN	Ras-related protein Rab-11B (GTP-binding protein YPT3)	RAB11B
			1021,53	0,021	R.ETLLQDFR.V	P02760	AMBP_HUMAN	Protein AMBP [Cleaved into: Alpha-1-microglobulin (Protein HC) (Alpha-1 microglycoprotein) (Complex-forming glycoprotein heterogeneous in charge); Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (EDC1) (HI-30) (Uronic-acid-rich protein); Trypstatin]	AMBP
1022,55	1022,043	1023,066	1021,50	0,050	R.TEMDWVLK.H	P52597	HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein F, N-terminally processed]	HNRNPF
			1022,53	0,026	K.GWNYILEK.Y	P43490	NAMPT_HUMAN	Nicotinamide phosphoribosyltransferase (NamPRTase) (Nampt) (EC 2.4.2.12) (Pre-B-cell colony-enhancing factor 1) (Pre-B cell-enhancing factor) (Visfatin)	NAMPT
			1022,59	0,034	R.LLHIEELR.E	Q9Y224	RTRAF_HUMAN	RNA transcription, translation and transport factor protein (CLE7 homolog, CLE, hCLE)	RTRAF
			1022,43	0,121	R.VDNEFDQRL.L	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
1023,56	1023,043	1024,067	1023,51	0,043	R.LSEDYGLVK.T	P32119	PRDX2_HUMAN	Peroxisiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
			1023,51	0,047	K.NIYSEELR.E	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin (Renal carcinoma antigen NY-REN-32)]	LMNA
			1023,47	0,089	R.DEAAYGELR.A	Q9UL46	PSME2_HUMAN	Proteasome activator complex subunit 2 (11S regulator complex subunit beta) (REG-beta) (Activator of multicatalytic protease subunit 2) (Proteasome activator 28 subunit beta) (PA28b) (PA28beta)	PSME2
			1023,46	0,099	K.EDAANNYAR.G	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
1024,53	1024,018	1025,042	1023,46	0,099	K.EDAANNYAR.G	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
			1023,46	0,099	K.EDAANNYAR.G	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			1024,55	0,023	R.FNALQYLR.L	P51884	LUM_HUMAN	Lumican (Keratan sulfate proteoglycan lumican) (KSPG lumican)	LUM
			1024,56	0,027	K.SSDIAKTFR.K	P13797	PLST_HUMAN	Plastin-3 (T-plastin)	PLS3
1025,45	1024,935	1025,960	1025,45	0,006	K.FEETADGR.K	Q01469	FABP5_HUMAN	Fatty acid-binding protein 5 (Epidermal-type fatty acid-binding protein) (E-FABP) (Fatty acid-binding protein, epidermal) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP)	FABP5
			1025,44	0,006	K.GLEDSYEGR.V	Q8NH8	PLBL2_HUMAN	Putative phospholipase B-like 2 (EC 3.1.1.-) (76 kDa protein) (p76) (LAMA-like protein 2) (Lamina ancestor homolog 2) (Phospholipase B domain-containing protein 2) [Cleaved into: Putative phospholipase B-like 2 32 kDa form; Putative phospholipase B-like 2 45 kDa form]	PLBD2
			1025,49	0,044	K.EAFQLFDR.T	P60660	MYL6_HUMAN	Myosin light polypeptide 6 (17 kDa myosin light chain) (LC17) (Myosin light chain 3) (MLC-3) (Myosin light chain alkali 3) (Myosin light chain A3) (Smooth muscle and nonmuscle myosin light chain alkali 6)	MYL6
			1025,53	0,085	R.DFVNLYVR.I	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A (EC 3.6.4.13) (DEAH box protein 9) (DEXH-box helicase 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II) (RNA helicase A)	DHX9
1025,58	1025,065	1026,091	1025,60	0,153	K.IGGIGTPVGR.V	P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1
			1025,60	0,023	K.IGGIGTPVGR.V	P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1
			1025,53	0,045	R.DFVNLYVR.I	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A (EC 3.6.4.13) (DEAH box protein 9) (DEXH-box helicase 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II) (RNA helicase A)	DHX9
			1025,49	0,087	K.EAFQLFDR.T	P60660	MYL6_HUMAN	Myosin light polypeptide 6 (17 kDa myosin light chain) (LC17) (Myosin light chain 3) (MLC-3) (Myosin light chain alkali 3) (Myosin light chain A3) (Smooth muscle and nonmuscle myosin light chain alkali 6)	MYL6
			1025,45	0,124	K.FEETADGR.K	Q01469	FABP5_HUMAN	Fatty acid-binding protein 5 (Epidermal-type fatty acid-binding protein) (E-FABP) (Fatty acid-binding protein, epidermal) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP)	FABP5
			1025,44	0,137	K.GLEDSYEGR.V	Q8NH8	PLBL2_HUMAN	Putative phospholipase B-like 2 (EC 3.1.1.-) (76 kDa protein) (p76) (LAMA-like protein 2) (Lamina ancestor homolog 2) (Phospholipase B domain-containing protein 2) [Cleaved into: Putative phospholipase B-like 2 32 kDa form; Putative phospholipase B-like 2 45 kDa form]	PLBD2

1026,47	1025,960	1026,987	1026,47	0,003	K.QACTPMFR.E	P34897	GLYM_HUMAN	Serine hydroxymethyltransferase, mitochondrial (SHMT) (EC 2.1.2.1) (Glycine hydroxymethyltransferase) (Serine methylase)	SHMT2
			1026,48	0,009	K.WWTCFVK.R	O15145	ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3 (Arp2/3 complex 21 kDa subunit) (p21-ARC)	ARPC3
			1026,53	0,059	R.LVFDEYLK.T	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6
1026,59	1026,075	1027,101	1026,53	0,056	R.LVFDEYLK.T	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6
			1026,48	0,105	K.WWTCFVK.R	O15145	ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3 (Arp2/3 complex 21 kDa subunit) (p21-ARC)	ARPC3
			1026,47	0,117	K.QACTPMFR.E	P34897	GLYM_HUMAN	Serine hydroxymethyltransferase, mitochondrial (SHMT) (EC 2.1.2.1) (Glycine hydroxymethyltransferase) (Serine methylase)	SHMT2
1027,48	1026,965	1027,992	1027,54	0,059	R.SIFDFSALK.E	P36871	PGM1_HUMAN	Phosphoglucomutase-1 (PGM 1) (EC 5.4.2.2) (Glucose phosphomutase 1)	PGM1
1027,57	1027,054	1028,082	1027,54	0,030	R.SIFDFSALK.E	P36871	PGM1_HUMAN	Phosphoglucomutase-1 (PGM 1) (EC 5.4.2.2) (Glucose phosphomutase 1)	PGM1
1028,57	1028,058	1029,087	1028,50	0,069	R.YFESVLR.E	Q07507	DERM_HUMAN	Dermatopontin (Tyrosine-rich acidic matrix protein) (TRAMP)	DPT
			1028,49	0,087	K.EAFMLFDR.T	P08590	MYL3_HUMAN	Myosin light chain 3 (Cardiac myosin light chain 1) (CMLC1) (Myosin light chain 1, slow-twitch muscle B/ventricular isoform) (MLC1S8) (Ventricular myosin alkali light chain) (Ventricular myosin light chain 1) (VLCI) (Ventricular/slow twitch myosin alkali light chain) (MLC-IV/sb)	MYL3
			1028,48	0,095	K.MDILSYMR.R	P22352	GPX3_HUMAN	Glutathione peroxidase 3 (GPx-3) (GSHPx-3) (EC 1.11.1.9) (Extracellular glutathione peroxidase) (Plasma glutathione peroxidase) (GPx-P) (GSHPx-P)	GPX3
1029,56	1029,044	1030,073	1029,58	0,019	K.VSGGPSLEQR.F	Q9Y262	EIF3L_HUMAN	Eukaryotic translation initiation factor 3 subunit L (eIF3L) (Eukaryotic translation initiation factor 3 subunit 6-interacting protein) (Eukaryotic translation initiation factor 3 subunit E-interacting protein)	EIF3L
			1029,59	0,031	R.VDELTLAR.T	P08779	K1C16_HUMAN	Keratin, type I cytoskeletal 16 (Cytokeratin-16) (CK-16) (Keratin-16) (K16)	KRT16
			1029,59	0,031	R.VDELTLAR.T	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1029,61	0,049	R.IIETLALK.F	O15144	ARPC2_HUMAN	Actin-related protein 2/3 complex subunit 2 (Arp2/3 complex 34 kDa subunit) (p34-ARC)	ARPC2
1030,55	1030,039	1031,070	1031,49	0,021	K.VLEEEEQRR.R	Q05682	CALD1_HUMAN	Caldesmon (CDM)	CALD1
1031,51	1030,998	1032,030	1031,55	0,037	K.VLEGMEVVR.K	P23284	PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) (CYP-51) (Cyclophilin B) (Rotamase B) (S-cyclophilin) (SCYLP)	PPIB
1031,54	1031,028	1032,060	1031,55	0,007	K.VLEGMEVVR.K	P23284	PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) (CYP-51) (Cyclophilin B) (Rotamase B) (S-cyclophilin) (SCYLP)	PPIB
			1031,49	0,050	K.VLEEEEQRR.R	Q05682	CALD1_HUMAN	Caldesmon (CDM)	CALD1
1032,57	1032,058	1033,090	1032,58	0,009	R.LFEGNALLR.R	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RP59
			1032,59	0,014	R.YRPGTVALR.E	P84243	H33_HUMAN	Histone H3.3	H3F3A; H3F3B
1033,58	1033,068	1034,101	1033,65	0,064	R.IIRPFFLK.H	Q00765	REEP5_HUMAN	Receptor expression-enhancing protein 5 (Polyposis locus protein 1) (Protein TB2)	REEP5
			1033,51	0,076	R.TLLEGESR.M	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
			1033,47	0,119	K.CEAQQLR.T	Q5M775	CYTSB_HUMAN	Cytospin-B (Nuclear structure protein 5) (NSP5) (Sperm antigen HCMOGT-1) (Sperm antigen with calponin homology and coiled-coil domains 1)	SPECC1
1034,59	1034,075	1035,110	1034,44	0,156	R.DHFEAMR.F	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (155 Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
1035,55	1035,033	1036,068	1035,55	0,004	K.DILIQYDR.T	P62249	RS16_HUMAN	40S ribosomal protein S16 (Small ribosomal subunit protein uS9)	RP516
			1035,53	0,021	K.WISIMTER.S	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1035,49	0,056	K.MLEQLDMR.R	Q13838	DX39B_HUMAN	Spliceosome RNA helicase DDX39B (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	DDX39B
			1035,48	0,068	R.GSGGFQRRGGGR.G	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A (EC 3.6.4.13) (DEAH box protein 9) (DEXH-box helicase 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II) (RNA helicase A)	DHX9
1036,55	1036,028	1037,065	1036,50	0,042	K.FGFYEVFK.V	Q00325	MPCP_HUMAN	Phosphate carrier protein, mitochondrial (Phosphate transport protein) (PTP) (Solute carrier family 25 member 3)	SLC25A3
1037,56	1037,041	1038,079	1037,54	0,016	K.GFLIDGYPR.E	P00568	KAD1_HUMAN	Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP-AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	AK1
			1037,54	0,021	R.GFTIPEAFR.G	O00299	CLIC1_HUMAN	Chloride intracellular channel protein 1 (Chloride channel ABP) (Nuclear chloride ion channel 27) (NCC27) (Regulatory nuclear chloride ion channel protein) (hRNCC)	CLIC1
			1037,52	0,039	R.YLDGLTAER.T	P35908	K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (CK-2e) (Epithelial keratin-2e) (Keratin-2 epidermis) (Keratin-2e) (K2e) (Type-II keratin Kb2)	KRT2
			1037,48	0,076	R.NWQDYGVR.E	Q8WU39	MZB1_HUMAN	Marginal zone B- and B1-cell-specific protein (Mesenteric estrogen-dependent adipose 7) (MEDA-7) (Plasma cell-induced resident endoplasmic reticulum protein) (Plasma cell-induced resident ER protein) (pERp1) (Proapoptotic caspase adapter protein)	MZB1

1038,54	1038,020	1039,058	1038,55	0,008	R.EHIEELL.R.N	P61201	CSN2_HUMAN	COP9 signalosome complex subunit 2 (SGN2) (Signalosome COP52 subunit 2) (Alien homolog) (JAB1-containing signalosome subunit 2) (Thyroid receptor-interacting protein 15) (TR-interacting protein 15) (TRIP-15)	
1039,56	1039,035	1040,075	1039,58	0,026	R.YLTVAAVF.R.G	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB
			1039,58	0,026	R.YLTVAAVF.R.G	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	EC11
			1039,51	0,040	K.SLQMYLER.L	P42126	EC11_HUMAN	Enoyl-CoA delta isomerase 1, mitochondrial (EC 5.3.3.8) (3,2-trans-enoyl-CoA isomerase) (Delta(3),Delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase) (Dodecenoyl-CoA isomerase)	
			1039,50	0,053	R.YESLTDPSK.L	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
1040,54	1040,017	1041,057	1040,44	0,098	K.EVEEDEYK.A	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			1041,56	0,068	R.HDLDLICR.A	P62140	PP1B_HUMAN	Serine/threonine-protein phosphatase PP1-beta catalytic subunit (PP-1B) (PPP1CD) (EC 3.1.3.16) (EC 3.1.3.53)	PPP1CB
			1041,56	0,068	R.IVLQIDNAR.L	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
			1041,56	0,068	R.IVLQIDNAR.L	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
1041,49	1040,972	1042,013	1041,60	0,109	R.AQQQAIALAK.E	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1041,63	0,134	K.VLQSAIAIR.H	Q12905	ILF2_HUMAN	Interleukin enhancer-binding factor 2 (Nuclear factor of activated T-cells 45 kDa)	ILF2
			1041,56	0,018	R.HDLDLICR.A	P62140	PP1B_HUMAN	Serine/threonine-protein phosphatase PP1-beta catalytic subunit (PP-1B) (PPP1CD) (EC 3.1.3.16) (EC 3.1.3.53)	PPP1CB
			1041,56	0,018	R.IVLQIDNAR.L	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
1041,58	1041,058	1042,100	1041,56	0,018	R.IVLQIDNAR.L	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1041,60	0,023	R.AQQQAIALAK.E	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1041,63	0,048	K.VLQSAIAIR.H	Q12905	ILF2_HUMAN	Interleukin enhancer-binding factor 2 (Nuclear factor of activated T-cells 45 kDa)	ILF2
			1042,52	0,049	R.LFPDFFR.V	P24158	PRTN3_HUMAN	Myeloblastin (EC 3.4.21.76) (AGP7) (C-ANCA antigen) (Leukocyte proteinase 3) (PR-3) (PR3) (Neutrophil proteinase 4) (NP-4) (P29) (Wegener autoantigen)	PRTN3
1042,57	1042,050	1043,092	1042,52	0,055	K.LLESDFYR.Y	Q96HE7	ERO1A_HUMAN	ERO1-like protein alpha (ERO1-L) (ERO1-L-alpha) (EC 1.8.4.-) (Endoplasmic oxidoreductin-1-like protein) (Endoplasmic reticulum oxidoreductase alpha) (Oxidoreductin-1-L-alpha)	
			1042,50	0,070	K.DVIEEYFK.C	P25398	RS12_HUMAN	40S ribosomal protein S12 (Small ribosomal subunit protein eS12)	RPS12
			1043,53	0,014	R.AFGYGYPLR.S	P84103	SRSF3_HUMAN	Serine/arginine-rich splicing factor 3 (Pre-mRNA-splicing factor SRP20) (Splicing factor, arginine/serine-rich 3)	SRSF3
			1043,52	0,023	K.NFAFLEFR.S	P26368	U2AF2_HUMAN	Splicing factor U2AF 65 kDa subunit (U2 auxiliary factor 65 kDa subunit) (hU2AF(65)) (hU2AF65) (U2 snRNP auxiliary factor large subunit)	U2AF2
1043,55	1043,025	1044,069	1043,46	0,091	R.ENPYDSR.V	Q00610	CLH1_HUMAN	Clathrin heavy chain 1 (Clathrin heavy chain on chromosome 17) (CLH-17)	CLTC
			1044,57	0,018	R.QLLLTADDR.V	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
			1044,52	0,029	R.WINDNNR.I	P51888	PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	PRELP
			1044,58	0,037	K.LLCGLLAER.L	P14174	MIF_HUMAN	Macrophage migration inhibitory factor (MIF) (EC 5.3.2.1) (Glycosylation-inhibiting factor) (GIF) (L-dopachrome isomerase) (L-dopachrome tautomerase) (EC 5.3.3.12) (Phenylpyruvate tautomerase)	MIF
1044,55	1044,025	1045,069	1044,57	0,018	R.QLLLTADDR.V	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
1045,55	1045,027	1046,073	1045,49	0,057	R.VEDVEALDR.K	P11216	PYGB_HUMAN	Glycogen phosphorylase, brain form (EC 2.4.1.1)	PYGB
1046,54	1046,020	1047,067	1046,52	0,024	K.LQEEMLQR.E	P08670	VIME_HUMAN	Vimentin	VIM
			1046,50	0,045	K.HPFFLDDR.R	Q13510	ASAH1_HUMAN	Acid ceramidase (AC) (ACDase) (Acid CDase) (EC 3.5.1.23) (Acylsphingosine deacylase) (N-acyl ethanolamine hydrolase ASAH1) (EC 3.5.1.-) (N-acylsphingosine amidohydrolase) (Putative 32 kDa heart protein) (PHP32) [Cleaved into: Acid ceramidase subunit alpha; Acid ceramidase subunit beta]	ASAH1
			1046,59	0,047	R.VPSYQALLR.G	P12109	CO6A1_HUMAN	Collagen alpha-1(VI) chain	COL6A1
			1046,47	0,072	K.ECADLWPR.I	P62829	RL23_HUMAN	60S ribosomal protein L23 (60S ribosomal protein L17) (Large ribosomal subunit protein uL14)	RPL23
1047,57	1047,049	1048,097	1047,55	0,024	K.EGLVMVEVR.K	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
			1047,49	0,087	R.FFTNFESR.K	Q9NV59	PNPO_HUMAN	Pyridoxine-5'-phosphate oxidase (EC 1.4.3.5) (Pyridoxamine-phosphate oxidase)	PNPO
			1049,46	0,092	R.DYFEQYKG.I	Q32P51	RA1L2_HUMAN	Heterogeneous nuclear ribonucleoprotein A1-like 2 (hnRNP A1-like 2) (hnRNP core protein A1-like 2)	HNRNPA1L2
			1049,46	0,092	R.DYFEQYKG.I	P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3
1049,62	1049,090	1050,140	1049,46	0,159	R.DYFEQYKG.I	Q32P51	RA1L2_HUMAN	Heterogeneous nuclear ribonucleoprotein A1-like 2 (hnRNP A1-like 2) (hnRNP core protein A1-like 2)	HNRNPA1L2
			1049,46	0,159	R.DYFEQYKG.I	P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3
			1050,52	0,069	R.DWVLNEFK.H	P17844	DDX5_HUMAN	Probable ATP-dependent RNA helicase DDX5 (EC 3.6.4.13) (DEAD box protein 5) (RNA helicase p68)	DDX5
			1050,51	0,080	K.GYLQEDGR.S	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
1050,59	1050,063	1051,114	1050,49	0,100	R.TCEKVEER.N	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1

1051,57	1051,047	1052,099	1050,48	0,104	K.NQDLEFER.N	P21399	ACOC_HUMAN	Cytoplasmic aconitate hydratase (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase) (Ferritin repressor protein) (Iron regulatory protein 1) (IRP1) (Iron-responsive element-binding protein 1) (IRE-BP 1)	ACO1
			1050,48	0,109	K.ETHVMDYR.A	Q9UL46	PSME2_HUMAN	Proteasome activator complex subunit 2 (11S regulator complex subunit beta) (REG-beta) (Activator of multicatalytic protease subunit 2) (Proteasome activator 28 subunit beta) (PA28b) (PA28beta)	PSME2
			1050,44	0,152	R.DYFEEYKG.I	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			1051,54	0,035	K.QFYPDLR.E	Q13228	SBP1_HUMAN	Methanethiol oxidase (MTO) (EC 1.8.3.4) (56 kDa selenium-binding protein) (SBP56) (SP56) (Selenium-binding protein 1)	SELENBP1
			1051,53	0,042	R.SIGEYDVL.R.G	P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	PRKDC
			1051,53	0,047	K.WISIMTER.S	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1051,52	0,053	K.MDELQLFR.G	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			1051,52	0,053	-MATGQKLMR.A	Q08257	QOR_HUMAN	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-crystallin)	CRYZ
			1051,50	0,073	K.FTTDLDSPR.D	P24821	TENA_HUMAN	Tenascin (TN) (Cytotactin) (GMEM) (GP 150-225) (Glioma-associated-extracellular matrix antigen) (Hexabrachion) (II) (Myotendinous antigen) (Neuronectin) (Tenascin-C) (TN-C)	TNC
			1051,48	0,091	R.ELLTTMGDR.F	Q14950	ML12B_HUMAN	Myosin regulatory light chain 12B (MLC-2A) (MLC-2) (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2) (SHUJUN-1)	MYL12B
1052,55	1052,024	1053,077	1051,48	0,091	R.ELLTTMGDR.F	P24844	MYL9_HUMAN	Myosin regulatory light polypeptide 9 (20 kDa myosin light chain) (LC20) (MLC-2C) (Myosin RLC) (Myosin regulatory light chain 2, smooth muscle isoform) (Myosin regulatory light chain 9) (Myosin regulatory light chain MRLC1)	MYL9
			1051,48	0,098	R.YLEDGGLER.K	P07099	HYEP_HUMAN	Epoxide hydrolase 1 (EC 3.3.2.9) (Epoxide hydratase) (Microsomal epoxide hydrolase) (mEH)	EPHX1
			1052,46	0,088	K.YIDENQDR.Y	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
			1052,45	0,104	R.GLQDEGDYR.M	POC0L5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and P2P-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
			1053,57	0,000	R.VIFLENYR.V	P11217	PYGM_HUMAN	Glycogen phosphorylase, muscle form (EC 2.4.1.1) (Myophosphorylase)	PYGM
			1053,57	0,000	K.VIFLENYR.V	P11216	PYGB_HUMAN	Glycogen phosphorylase, brain form (EC 2.4.1.1)	PYGB
			1053,56	0,010	R.YQDILVFR.S	P19623	SPEE_HUMAN	Spermidine synthase (SPDSY) (EC 2.5.1.16) (Putrescine aminopropyltransferase)	SRM
			1053,50	0,070	R.YLLGDMEGR.L	Q16531	DDB1_HUMAN	DNA damage-binding protein 1 (DDB p127 subunit) (DNA damage-binding protein a) (DDBa) (Damage-specific DNA-binding protein 1) (HBV X-associated protein 1) (XAP-1) (UV-damaged DNA-binding factor) (UV-damaged DNA-binding protein 1) (UV-DDB 1) (XPE-binding factor) (XPE-BF) (Xeroderma pigmentosum group E-complementing protein) (XPCE)	DDB1
			1053,45	0,125	K.YPEGSSEER.E	P21980	TGM2_HUMAN	Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (Transglutaminase C) (TG(C)) (TGC) (TGase C) (Transglutaminase H) (TGase H) (Transglutaminase-2) (TGase-2)	TGM2
			1055,54	0,057	K.ALEAFETFK.K	Q00796	DHSO_HUMAN	Sorbitol dehydrogenase (SDH) (EC 1.1.1.1-) ((R,R)-butanediol dehydrogenase) (EC 1.1.1.14) (L-iditol 2-dehydrogenase) (EC 1.1.1.14) (Polyol dehydrogenase) (Ribitol dehydrogenase) (RDH) (EC 1.1.1.56) (Xylitol dehydrogenase) (XDH) (EC 1.1.1.9)	SORD
1056,58	1056,056	1057,113	1055,54	0,059	R.VSELFADK.V	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
			1056,51	0,070	K.FINDQYK.Y	Q9UHD8	SEPT9_HUMAN	Septin-9 (MLL septin-like fusion protein MSF-A) (MLL septin-like fusion protein) (Ovarian/Breast septin) (Ov/Br septin) (Septin D1)	SEPT9
			1059,55	0,015	K.EELLEGIR.Q	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-I (eIF-4A-I) (eIF4A-I) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
			1059,49	0,076	K.KPAEDEWGK.T	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
			1059,42	0,147	R.SGYEFADDR.H	Q14112	NID2_HUMAN	Nidogen-2 (NID-2) (Osteonidogen)	NID2
			1060,55	0,004	K.IPDWFLNR.Q	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
			1060,55	0,009	R.KLLEGEESR.L	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7)	KRT7
			1060,55	0,009	R.KLLEGEESR.I	P08670	VIME_HUMAN	Vimentin	VIM
			1060,55	0,009	R.KLLEGEESR.L	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
			1060,50	0,055	R.FFFDVGSNK.Y	Q00577	PURA_HUMAN	Transcriptional activator protein Pur-alpha (Purine-rich single-stranded DNA-binding protein alpha)	PURA
1061,58	1061,044	1062,106	1061,59	0,010	R.EIGELYLPK.F	P01011	AACT_HUMAN	Alpha-1-antichymotrypsin (ACT) (Cell growth-inhibiting gene 24/25 protein) (Serpina A3) [Cleaved into: Alpha-1-antichymotrypsin His-Pro-less]	SERPINA3
			1061,59	0,020	R.GTSLGSWLK.A	P27824	CALX_HUMAN	Calnexin (IP90) (Major histocompatibility complex class I antigen-binding protein p88) (p90)	CANX
			1061,54	0,036	K.LGEVWGCLK.I	P25398	RS12_HUMAN	40S ribosomal protein S12 (Small ribosomal subunit protein eS12)	RPS12
			1061,53	0,041	R.SETDLLDIR.S	P50995	ANX11_HUMAN	Annexin A11 (56 kDa autoantigen) (Annexin XI) (Annexin-11) (Calcyclin-associated annexin 50) (CAP-50)	ANXA11

1062,56	1062,033	1063,096	1061,53	0,048	K.IDPEAFITR.H	Q92616	GCN1_HUMAN	eIF-2-alpha kinase activator GCN1 (GCN1 eIF-2-alpha kinase activator homolog) (GCN1-like protein 1) (General control of amino-acid synthesis 1-like protein 1) (Translational activator GCN1) (HsGCN1)	GCN1		
			1061,49	0,088	K.SSDNRETPR.N	Q5FWF5	ESCO1_HUMAN	N-acetyltransferase ESCO1 (EC 2.3.1.-) (CTF7 homolog 1) (Establishment factor-like protein 1) (EFO1) (EFO1p) (hEFO1) (Establishment of cohesion 1 homolog 1) (ECO1 homolog 1) (ESO1 homolog 1)	ESCO1		
			1061,47	0,102	K.WDAWNELK.G	P07108	ACBP_HUMAN	Acyl-CoA-binding protein (ACBP) (Diazepam-binding inhibitor) (DBI) (Endozepine) (EP)	DBI		
			1062,60	0,035	R.FLTWILNR.Y	Q43776	SYNC_HUMAN	Asparagine--tRNA ligase, cytoplasmic (EC 6.1.1.22) (Asparaginyl-tRNA synthetase) (AsnRS)	NARS		
			1062,51	0,054	R.QVSDDLTER.A	P35232	PHB_HUMAN	Prohibitin	PHB		
			1062,49	0,078	R.VDDNEETIK.K	P00568	KAD1_HUMAN	Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP-AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	AK1		
			1062,47	0,092	R.ASCWQPGR.T	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG		
			1062,46	0,100	R.ADAEEEAATR.I	Q13409	DC12_HUMAN	Cytoplasmic dynein 1 intermediate chain 2 (Cytoplasmic dynein intermediate chain 2) (Dynein intermediate chain 2, cytosolic) (DH IC-2)	DYNC12		
			1063,50	0,054	K.FESPEVAER.A	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM		
			1063,50	0,060	R.EKEELMLR.L	P15311	EZRI_HUMAN	Ezrin (Cyto villin) (Villin-2) (p81)	EZR		
1064,60	1064,071	1065,135	1064,59	0,016	K.SFPNALFIR.L	P51888	PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	PRELP		
			1064,48	0,121	R.SEIDMNDIK.A	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1		
			1064,48	0,121	R.SAAMDLGPMR.K	Q9NV59	PNPO_HUMAN	Pyridoxine-5'-phosphate oxidase (EC 1.4.3.5) (Pyridoxamine-phosphate oxidase)	PNPO		
			1065,54	0,054	K.LEAEIATYR.R	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cyto keratin-18) (CK-18) (Keratin-18) (K18)	KRT18		
			1065,54	0,060	K.SATTTVMNPK.F	P05107	ITB2_HUMAN	Integrin beta-2 (Cell surface adhesion glycoproteins LFA-1/CR3/p150,95 subunit beta) (Complement receptor C3 subunit beta) (CD antigen CD18)	ITGB2		
			1065,54	0,060	K.LSPEDYTLK.V	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD		
1065,54	0,060	R.ISICSSDKR.I	Q13547	HDAC1_HUMAN	Histone deacetylase 1 (HD1) (EC 3.5.1.98)	HDAC1					
1065,48	0,114	K.VESFEEVAR.E	P14920	OXDA_HUMAN	D-amino-acid oxidase (DAAO) (DAMOX) (DAO) (EC 1.4.3.3)	DAO					
1066,07	1065,539	1066,605	1066,55	0,477	K.IFSQETLTK.A	Q9UHG3	PCYOX_HUMAN	Prenylcysteine oxidase 1 (EC 1.8.3.5) (Prenylcysteine lyase)	PCYOX1		
			1065,54	0,530	K.LEAEIATYR.R	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cyto keratin-18) (CK-18) (Keratin-18) (K18)	KRT18		
			1066,17	1065,637	1066,703	1066,55	0,379	K.IFSQETLTK.A	Q9UHG3	PCYOX_HUMAN	Prenylcysteine oxidase 1 (EC 1.8.3.5) (Prenylcysteine lyase)
1066,58	1066,044	1067,111	1066,55	0,028	K.IFSQETLTK.A	Q9UHG3	PCYOX_HUMAN	Prenylcysteine oxidase 1 (EC 1.8.3.5) (Prenylcysteine lyase)	PCYOX1		
1067,13	1066,598	1067,665	1067,49	0,363	R.LGEYEDVSR.V	Q99426	TBCB_HUMAN	Tubulin-folding cofactor B (Cytoskeleton-associated protein 1) (Cytoskeleton-associated protein CKAPI) (Tubulin-specific chaperone B)	TBCB		
			1067,52	0,388	K.MDELQLFR.G	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP		
			1067,62	0,488	K.ESTLHLVLR.L	P62979	RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a (Ubiquitin carboxyl extension protein 80) [Cleaved into: Ubiquitin; 40S ribosomal protein S27a (Small ribosomal subunit protein eS31)]	RPS27A		
			1067,46	1066,923	1067,990	1067,49	0,038	R.LGEYEDVSR.V	Q99426	TBCB_HUMAN	Tubulin-folding cofactor B (Cytoskeleton-associated protein 1) (Cytoskeleton-associated protein CKAPI) (Tubulin-specific chaperone B)
			1067,52	0,063	K.MDELQLFR.G	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP		
			1067,62	0,162	K.ESTLHLVLR.L	P62979	RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a (Ubiquitin carboxyl extension protein 80) [Cleaved into: Ubiquitin; 40S ribosomal protein S27a (Small ribosomal subunit protein eS31)]	RPS27A		
			1067,59	1067,053	1068,120	1067,62	0,032	K.ESTLHLVLR.L	P62979	RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a (Ubiquitin carboxyl extension protein 80) [Cleaved into: Ubiquitin; 40S ribosomal protein S27a (Small ribosomal subunit protein eS31)]
			1067,52	0,067	K.MDELQLFR.G	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP		
			1067,49	0,092	R.LGEYEDVSR.V	Q99426	TBCB_HUMAN	Tubulin-folding cofactor B (Cytoskeleton-associated protein 1) (Cytoskeleton-associated protein CKAPI) (Tubulin-specific chaperone B)	TBCB		
			1068,60	1068,063	1069,131	1069,58	0,006	K.EIIDPVLDR.I	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)
1069,59	1069,053	1070,123	0,007	R.LEAPLEELR.A	Q16401		PSMD5_HUMAN	26S proteasome non-ATPase regulatory subunit 5 (26S protease subunit S5 basic) (26S proteasome subunit S5B)	PSMD5		
1070,79	1070,256	1071,327		1069,58	0,007		R.SQAPVLDAIR.R	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
				1069,62	0,028		K.LSPEELLR.W	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
				1069,62	0,028		K.LSPEELLR.W	P13797	PLST_HUMAN	Plastin-3 (T-plastin)	PLS3
1070,79	1070,256	1071,327	1070,54	0,248	R.QAEPDLDR.S	P20810	ICAL_HUMAN	Calpastatin (Calpain inhibitor) (Sperm BS-17 component)	CAST		
			1070,52	0,267	K.EAKYQLR.C	P27487	DPP4_HUMAN	Dipeptidyl peptidase 4 (EC 3.4.14.5) (ADABP) (Adenosine deaminase complexing protein 2) (ADCP-2) (Dipeptidyl peptidase IV) (DPP IV) (T-cell activation antigen CD26) (TP103) (CD antigen CD26) [Cleaved into: Dipeptidyl peptidase 4 membrane form (Dipeptidyl peptidase IV membrane form); Dipeptidyl peptidase 4 soluble form (Dipeptidyl peptidase IV soluble form)]	DPP4		

1071,57	1071,031	1072,103	1070,51	0,278	R.IDAYMAQSR.G	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1				
			1070,40	0,392	R.DYNDADMAR.L	Q14696	MESD_HUMAN	LRP chaperone MESD (LDLR chaperone MESD) (Mesoderm development LRP chaperone MESD) (Mesoderm development candidate 2) (Mesoderm development protein) (Renal carcinoma antigen NY-REN-61)					
			1071,55	0,018	R.MFLSFPTTK.T	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2				
			1071,49	0,079	K.FVDGEWYR.A	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1				
			1071,49	0,080	R.WHEMLDK.A	Q13510	ASAH1_HUMAN	Acid ceramidase (AC) (ACDase) (Acid CDase) (EC 3.5.1.23) (Acylsphingosine deacylase) (N-acylethanolamine hydrolase ASAH1) (EC 3.5.1.-) (N-acylsphingosine amidohydrolase) (Putative 32 kDa heart protein) (PHP32) [Cleaved into: Acid ceramidase subunit alpha; Acid ceramidase subunit beta]	ASAH1				
			1071,48	0,087	R.YFTWDPSR.F	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB				
			1071,47	0,101	R.FDSVDGEFR.A	P04440	DPB1_HUMAN	HLA class II histocompatibility antigen, DP beta 1 chain (HLA class II histocompatibility antigen, DP(W4) beta chain) (MHC class II antigen DPB1)	HLA-DPB1				
			1071,47	0,101	R.FDSVDGEFR.A	P01911	2B1F_HUMAN	HLA class II histocompatibility antigen, DRB1-15 beta chain (DW2.2/DR2.2) (MHC class II antigen DRB1*15)	HLA-DRB1				
			1071,89	1071,356	1072,427	1071,55	0,342	R.MFLSFPTTK.T	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2	
			1071,49			0,403	K.FVDGEWYR.A	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1		
1071,49	0,405	R.WHEMLDK.A	Q13510			ASAH1_HUMAN	Acid ceramidase (AC) (ACDase) (Acid CDase) (EC 3.5.1.23) (Acylsphingosine deacylase) (N-acylethanolamine hydrolase ASAH1) (EC 3.5.1.-) (N-acylsphingosine amidohydrolase) (Putative 32 kDa heart protein) (PHP32) [Cleaved into: Acid ceramidase subunit alpha; Acid ceramidase subunit beta]	ASAH1					
1071,48	0,411	R.YFTWDPSR.F	Q14697			GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB					
1071,47	0,426	R.FDSVDGEFR.A	P04440			DPB1_HUMAN	HLA class II histocompatibility antigen, DP beta 1 chain (HLA class II histocompatibility antigen, DP(W4) beta chain) (MHC class II antigen DPB1)	HLA-DPB1					
1071,47	0,426	R.FDSVDGEFR.A	P01911			2B1F_HUMAN	HLA class II histocompatibility antigen, DRB1-15 beta chain (DW2.2/DR2.2) (MHC class II antigen DRB1*15)	HLA-DRB1					
1072,61	1072,071	1073,144	1072,59			0,021	R.SEIDLLNIR.R	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6		
1072,59			0,021			K.AQASSIPVGSR.C	Q99426	TBCB_HUMAN	Tubulin-folding cofactor B (Cytoskeleton-associated protein 1) (Cytoskeleton-associated protein CKAPI) (Tubulin-specific chaperone B)	TBCB			
1072,58			0,026			R.GLVVSTANRR.L	Q9H845	ACAD9_HUMAN	Acyl-CoA dehydrogenase family member 9, mitochondrial (ACAD-9) (EC 1.3.99.-)	ACAD9			
1072,56			0,052			K.VPEWVDTVK.L	P39019	RS19_HUMAN	40S ribosomal protein S19 (Small ribosomal subunit protein eS19)	RPS19			
1072,53			0,077	K.NSTFSEIFK.K	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT					
1072,51			0,100	R.SGKYDLDFK.S	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1					
1073,59			1073,056	1074,129	1073,59	0,007	R.SEIDLLDIR.T	P12429	ANXA3_HUMAN	Annexin A3 (35-alpha calcimedlin) (Annexin III) (Annexin-3) (Inositol 1,2-cyclic phosphate 2-phosphohydrolase) (Lipocortin III) (Placental anticoagulant protein III) (PAP-III)	ANXA3		
1073,48					0,112	K.DSEGYIYAR.G	Q03154	ACY1_HUMAN	Aminoacylase-1 (ACY-1) (EC 3.5.1.14) (N-acyl-L-amino-acid amidohydrolase)	ACY1			
1074,58					1074,040	1075,115	1074,61	0,030	K.GFDWPLLVK.D	P08236	BGLR_HUMAN	Beta-glucuronidase (EC 3.2.1.31) (Beta-G1)	GUSB
1074,53							0,052	K.LDELRLDEGK.A	P02768	ALBU_HUMAN	Serum albumin	ALB	
1074,52	0,053	R.IDSLENDLR.Q					P10909	CLUS_HUMAN	Clusterin (Aging-associated gene 4 protein) (Apolipoprotein J) (Apo-J) (Complement cytotoxicity inhibitor) (CLI) (Complement-associated protein SP-40,40) (Ku70-binding protein 1) (NA1/NA2) (Sulfated glycoprotein 2) (SGP-2) (Testosterone-repressed prostate message 2) (TRPM-2) [Cleaved into: Clusterin beta chain (ApoIalpha) (Complement cytotoxicity inhibitor a chain); Clusterin alpha chain (ApoIbeta) (Complement cytotoxicity inhibitor b chain)]	CLU			
1074,43	0,151	K.HTLGSDSDNES.-					P02794	FRIH_HUMAN	Ferritin heavy chain (Ferritin H subunit) (EC 1.16.3.1) (Cell proliferation-inducing gene 15 protein) [Cleaved into: Ferritin heavy chain, N-terminally processed]	FTH1			
1075,62	1075,085	1076,161					1075,58	0,044	R.RPHFFFPK.S	P10909	CLUS_HUMAN	Clusterin (Aging-associated gene 4 protein) (Apolipoprotein J) (Apo-J) (Complement cytotoxicity inhibitor) (CLI) (Complement-associated protein SP-40,40) (Ku70-binding protein 1) (NA1/NA2) (Sulfated glycoprotein 2) (SGP-2) (Testosterone-repressed prostate message 2) (TRPM-2) [Cleaved into: Clusterin beta chain (ApoIalpha) (Complement cytotoxicity inhibitor a chain); Clusterin alpha chain (ApoIbeta) (Complement cytotoxicity inhibitor b chain)]	CLU
1075,57							0,048	K.GGFIPGSLTAR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG	
1075,54							0,088	R.AEIDMLDIR.A	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedlin) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4	
1075,53							0,095	K.MLQHIIDYR.M	P14678	RSMB_HUMAN	Small nuclear ribonucleoprotein-associated proteins B and B' (snRNP-B) (5m protein B/B') (5m-B/B') (5mB/B')	SNRNPB	

1075,84	1075,302	1076,378	1075,58	0,261	R.RPHFFPK.S	P10909	CLU5_HUMAN	Clusterin (Aging-associated gene 4 protein) (Apolipoprotein J) (Apo-J) (Complement cytolysis inhibitor) (CL) (Complement-associated protein SP-40,40) (Ku70-binding protein 1) (NA1/NA2) (Sulfated glycoprotein 2) (SGP-2) (Testosterone-repressed prostate message 2) (TRPM-2) [Cleaved into: Clusterin beta chain (ApoIalpha) (Complement cytolysis inhibitor a chain); Clusterin alpha chain (ApoIbeta) (Complement cytolysis inhibitor b chain)]	CLU
			1075,57	0,265	K.GGFIPLSTAR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1075,54	0,305	R.AEIDMLDIR.A	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedlin) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4
			1075,53	0,312	K.MLQHIIDYR.M	P14678	R5MB_HUMAN	Small nuclear ribonucleoprotein-associated proteins B and B' (snRNP-B) (Sm protein B/B') (Sm-B/B') (SmB/B')	SNRPB
1076,46	1075,919	1076,996	1076,47	0,009	K.EVHPFEYR.K	Q9BY60	GBRL3_HUMAN	Gamma-aminobutyric acid receptor-associated protein-like 3 (GABA(A) receptor-associated protein-like 3)	GABARAPL3
			1076,48	0,025	K.DGGAWGTEQR.E	P09382	LEG1_HUMAN	Galectin-1 (Gal-1) (14 kDa laminin-binding protein) (HLBP14) (14 kDa lectin) (Beta-galactoside-binding lectin L-14-I) (Galaptin) (HBL) (HPL) (Lactose-binding lectin 1) (Lectin galactoside-binding soluble 1) (Putative MAPK-activating protein PM12) (S-Lac lectin 1)	LGALS1
			1076,50	0,045	R.DNLAEDIMR.L	P08670	VIME_HUMAN	Vimentin	VIM
			1076,50	0,045	M.EGPLSVFGDR.S	P17987	TCPA_HUMAN	T-complex protein 1 subunit alpha (TCP-1-alpha) (CCT-alpha)	TCP1
			1076,53	0,076	K.NLVTEDVMR.M	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
			1076,61	0,148	R.SQLEAIFLR.D	Q8IV08	PLD3_HUMAN	Phospholipase D3 (PLD 3) (EC 3.1.4.4) (Choline phosphatase 3) (HindIII K4L homolog) (Hu-K4) (Phosphatidylcholine-hydrolyzing phospholipase D3)	PLD3
			1076,62	0,160	K.LSSWVLLMK.Y	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiprotease) (Serp A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
1076,62	1076,085	1077,162	1076,62	0,006	K.LSSWVLLMK.Y	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiprotease) (Serp A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
			1076,61	0,019	R.SQLEAIFLR.D	Q8IV08	PLD3_HUMAN	Phospholipase D3 (PLD 3) (EC 3.1.4.4) (Choline phosphatase 3) (HindIII K4L homolog) (Hu-K4) (Phosphatidylcholine-hydrolyzing phospholipase D3)	PLD3
			1076,53	0,091	K.NLVTEDVMR.M	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
			1076,50	0,121	M.EGPLSVFGDR.S	P17987	TCPA_HUMAN	T-complex protein 1 subunit alpha (TCP-1-alpha) (CCT-alpha)	TCP1
			1076,50	0,122	R.DNLAEDIMR.L	P08670	VIME_HUMAN	Vimentin	VIM
			1076,48	0,141	K.DGGAWGTEQR.E	P09382	LEG1_HUMAN	Galectin-1 (Gal-1) (14 kDa laminin-binding protein) (HLBP14) (14 kDa lectin) (Beta-galactoside-binding lectin L-14-I) (Galaptin) (HBL) (HPL) (Lactose-binding lectin 1) (Lectin galactoside-binding soluble 1) (Putative MAPK-activating protein PM12) (S-Lac lectin 1)	LGALS1
			1076,47	0,157	K.EVHPFEYR.K	Q9BY60	GBRL3_HUMAN	Gamma-aminobutyric acid receptor-associated protein-like 3 (GABA(A) receptor-associated protein-like 3)	GABARAPL3
1077,60	1077,057	1078,134	1077,54	0,052	R.IMGPNYTPGK.K	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
			1077,51	0,087	K.IREEYDPR.I	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1077,51	0,087	K.IREEYDPR.I	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1077,51	0,087	R.LDHFNFER.F	Q9UHL4	DPP2_HUMAN	Dipeptidyl peptidase 2 (EC 3.4.14.2) (Dipeptidyl aminopeptidase II) (Dipeptidyl peptidase 7) (Dipeptidyl peptidase II) (DPP II) (Quiescent cell proline dipeptidase)	DPP7
1078,59	1078,051	1079,130	1078,53	0,057	R.ENFQNWLK.D	P37802	TAGL2_HUMAN	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	TAGLN2
			1078,52	0,070	K.FLENEDRR.S	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiprotease) (Serp A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
			1078,52	0,072	R.DWVLNEFR.S	Q92841	DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.4.13) (DEAD box protein 17) (DEAD box protein p72) (DEAD box protein p82) (RNA-dependent helicase p72)	DDX17
1079,58	1079,044	1080,124	1079,62	0,039	R.GYPTLLLR.F	Q8NB59	TXND5_HUMAN	Thioredoxin domain-containing protein 5 (Endoplasmic reticulum resident protein 46) (ER protein 46) (ERp46) (Thioredoxin-like protein 46)	TXNDC5
			1079,54	0,041	R.EDAVLEYLK.I	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			1079,53	0,059	R.QLYEEIIR.E	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
			1079,50	0,088	K.KESEEDQSK.S	Q96MC2	DRC1_HUMAN	Dynein regulatory complex protein 1 (Coiled-coil domain-containing protein 164)	DRC1
1080,39	1079,846	1080,927	1080,44	0,054	K.YAYYDTER.I	O00303	EIF3F_HUMAN	Eukaryotic translation initiation factor 3 subunit F (eIF3f) (Deubiquitinating enzyme eIF3f) (EC 3.4.19.12) (Eukaryotic translation initiation factor 3 subunit 5) (eIF-3-epsilon) (eIF3 p47)	EIF3F
			1080,47	0,079	K.EMQTLMGVR.W	Q8NSH7	SH2D3_HUMAN	SH2 domain-containing protein 3C (Novel SH2-containing protein 3) (SH2 domain-containing Eph receptor-binding protein 1) (SHEP1)	SH2D3C
			1080,52	0,133	K.IISNEEGYR.H	P27487	DPP4_HUMAN	Dipeptidyl peptidase 4 (EC 3.4.14.5) (ADABP) (Adenosine deaminase complexing protein 2) (ADCP-2) (Dipeptidyl peptidase IV) (DPP IV) (T-cell activation antigen CD26) (TP103) (CD antigen CD26) [Cleaved into: Dipeptidyl peptidase 4 membrane form (Dipeptidyl peptidase IV membrane form); Dipeptidyl peptidase 4 soluble form (Dipeptidyl peptidase IV soluble form)]	DPP4
			1080,52	0,137	R.APFDLFENK.K	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
1080,60	1080,056	1081,137	1080,52	0,073	R.APFDLFENK.K	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1

1081,26 1081,60 1082,04	1080,721 1081,057 1081,498	1081,802 1082,138 1082,580	1080,52	0,076	K.IISNEEGYR.H	P27487	DPP4_HUMAN	Dipeptidyl peptidase 4 (EC 3.4.14.5) (ADA8P) (Adenosine deaminase complexing protein 2) (ADCP-2) (Dipeptidyl peptidase IV) (DPP IV) (T-cell activation antigen CD26) (TP103) (CD antigen CD26) [Cleaved into: Dipeptidyl peptidase 4 membrane form (Dipeptidyl peptidase IV membrane form); Dipeptidyl peptidase 4 soluble form (Dipeptidyl peptidase IV soluble form)]	DPP4
			1080,47	0,131	K.EMQTLMGVR.W	Q8NSH7	SH2D3_HUMAN	SH2 domain-containing protein 3C (Novel SH2-containing protein 3) (SH2 domain-containing Eph receptor-binding protein 1) (SHEP1)	SH2D3C
			1080,44	0,155	K.YAYYDTER.I	O00303	EIF3F_HUMAN	Eukaryotic translation initiation factor 3 subunit F (eIF3f) (Deubiquitinating enzyme eIF3f) (EC 3.4.19.12) (Eukaryotic translation initiation factor 3 subunit 5) (eIF-3-epsilon) (eIF3 p47)	EIF3F
1082,17	1081,628 1082,710	1082,46 1082,49	1082,46	0,417	K.YDEELEER.L	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein WS3-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
			1082,49	0,448	K.DAEAWFTSR.T	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
1082,27	1081,731 1082,813	1082,46 1082,49	1082,46	0,286	K.YDEELEER.L	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein WS3-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
			1082,49	0,318	K.DAEAWFTSR.T	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
1082,57	1082,024 1083,107	1083,51 1083,52	1082,49	0,078	K.DAEAWFTSR.T	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1082,46	0,110	K.YDEELEER.L	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein WS3-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
1083,58	1083,036	1084,119	1083,51	0,067	K.VSEEHDVLR.K	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
1084,61	1084,064	1085,149	1084,53	0,076	K.FFIEEMIR.D	Q14376	GALE_HUMAN	UDP-glucose 4-epimerase (EC 5.1.3.2) (Galactowaldenase) (UDP-N-acetylgalactosamine 4-epimerase) (UDP-GalNAc 4-epimerase) (UDP-N-acetylglucosamine 4-epimerase) (UDP-GlcNAc 4-epimerase) (EC 5.1.3.7) (UDP-galactose 4-epimerase)	GALE
1085,58	1085,037 1086,123	1086,62 1086,62 1086,62 1086,62 1086,62	1085,60	0,016	K.LPFIIDDR.N	P30041	PRDX6_HUMAN	Peroxioredoxin-6 (EC 1.11.1.15) (1-Cys peroxiredoxin) (1-Cys PRX) (24 kDa protein) (Acidic calcium-independent phospholipase A2) (aiPLA2) (EC 3.1.1.4) (Antioxidant protein 2) (Liver 2D page spot 40) (Non-selenium glutathione peroxidase) (NSGPx) (Red blood cells page spot 12)	PRDX6
			1085,62	0,036	K.EIIDLVLDR.I	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			1085,62	0,036	K.EIIDLVLDR.I	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			1085,53	0,053	K.EQIYDVYR.Y	P38919	IF4A3_HUMAN	Eukaryotic initiation factor 4A-III (eIF4A-III) (EC 3.6.4.13) (ATP-dependent RNA helicase DDX48) (ATP-dependent RNA helicase eIF4A-3) (DEAD box protein 48) (Eukaryotic initiation factor 4A-like NUK-34) (Eukaryotic translation initiation factor 4A isoform 3) (Nuclear matrix protein 265) (NMP 265) (hNMP 265) [Cleaved into: Eukaryotic initiation factor 4A-III, N-terminally processed]	EIF4A3
			1085,52	0,056	K.LEWVYGYR.G	O95834	EMAL2_HUMAN	Echinoderm microtubule-associated protein-like 2 (EMAP-2) (HuEMAP-2)	EML2
1086,59	1086,042 1087,129	1087,55 1087,55 1087,62 1087,49 1087,46	1085,52	0,064	K.IFEYETQR.R	P50402	EMD_HUMAN	Emerin	EMD
			1086,47	0,114	K.AYTNFDAER.D	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1087,55	0,020	K.QWLQEIDR.Y	P62820	RAB1A_HUMAN	Ras-related protein Rab-1A (YPT1-related protein)	RAB1A
			1087,55	0,021	R.MFLSPFTT.T	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			1087,62	0,050	K.LRVDPVNF.K	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
1087,57	1087,024 1088,112	1088,53 1088,51 1088,51 1088,51 1088,51	1087,49	0,082	R.NYYEQWGK.L	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			1087,46	0,113	R.FDSVDGEYR.A	P13760	2B14_HUMAN	HLA class II histocompatibility antigen, DRB1-4 beta chain (MHC class II antigen DRB1*4) (DR-4) (DR4)	HLA-DRB1
			1088,53	0,028	R.QDVNDASLAR.L	P08670	VIME_HUMAN	Vimentin	VIM
			1088,51	0,045	R.WELCDIPR.C	P00747	PLMN_HUMAN	Plasminogen (EC 3.4.21.7) [Cleaved into: Plasmin heavy chain A; Activation peptide; Angiostatin; Plasmin heavy chain A, short form; Plasmin light chain B]	PLG
			1088,51	0,047	K.AEDEILNR.S	P27824	CALX_HUMAN	Calnexin (IP90) (Major histocompatibility complex class I antigen-binding protein p88) (p90)	CANX
1089,57	1089,029 1090,118	1090,56 1090,56 1090,56	1089,57	0,007	K.GLFEVNPWK.R	Q9HDC9	APMAP_HUMAN	Adipocyte plasma membrane-associated protein (Protein BSCv)	APMAP
			1089,64	0,064	R.FLILPDMK.L	P62318	SMD3_HUMAN	Small nuclear ribonucleoprotein Sm D3 (Sm-D3) (snRNP core protein D3)	SNRPD3
			1089,48	0,095	K.DLEEWNRQ.Q	P09497	CLCB_HUMAN	Clathrin light chain B (Lcb)	CLTB
1090,61	1090,063 1091,154	1091,52 1091,52 1091,52	1090,56	0,048	K.WERPFEVK.D	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiprotease) (Serp1 A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
			1090,53	0,075	K.RDMPPAFIK.V	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL
			1090,53	0,075	R.DFGSFDKFK.E	P04179	SODM_HUMAN	Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1)	SOD2
1091,20	1090,650 1091,741	1091,52 1091,52 1091,52	1091,52	0,326	R.LDSSIRNMR.A	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
			1091,52	0,326	R.LCAGASEDIR.E	Q9UM54	MYO6_HUMAN	Unconventional myosin-VI (Unconventional myosin-6)	MYO6
			1091,52	0,326	R.SELDMLDIR.E	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6

1091,59	1091,043	1092,135	1091,53	0,336	K.EEERIMLR.D	O14974	MYPT1_HUMAN	Protein phosphatase 1 regulatory subunit 12A (Myosin phosphatase-targeting subunit 1) (Myosin phosphatase target subunit 1) (Protein phosphatase myosin-binding subunit)	PPP1R12A
			1091,53	0,336	R.AEIDMLDIR.A	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedin) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4
			1091,55	0,352	K.GTPWEGGLFK.L	P63279	UBC9_HUMAN	SUMO-conjugating enzyme UBC9 (EC 2.3.2.-) (RING-type E3 SUMO transferase UBC9) (SUMO-protein ligase) (Ubiquitin carrier protein 9) (Ubiquitin carrier protein I) (Ubiquitin-conjugating enzyme E2 I) (Ubiquitin-protein ligase I) (p18)	UBE2I
			1091,69	0,494	K.LILQNHILK.V	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
			1091,55	0,041	K.GTPWEGGLFK.L	P63279	UBC9_HUMAN	SUMO-conjugating enzyme UBC9 (EC 2.3.2.-) (RING-type E3 SUMO transferase UBC9) (SUMO-protein ligase) (Ubiquitin carrier protein 9) (Ubiquitin carrier protein I) (Ubiquitin-conjugating enzyme E2 I) (Ubiquitin-protein ligase I) (p18)	UBE2I
			1091,53	0,057	K.EEERIMLR.D	O14974	MYPT1_HUMAN	Protein phosphatase 1 regulatory subunit 12A (Myosin phosphatase-targeting subunit 1) (Myosin phosphatase target subunit 1) (Protein phosphatase myosin-binding subunit)	PPP1R12A
			1091,53	0,057	R.AEIDMLDIR.A	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedin) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4
			1091,52	0,068	R.LDSSIRNMR.A	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
			1091,52	0,068	R.LCAGASEDIR.E	Q9UM54	MYO6_HUMAN	Unconventional myosin-VI (Unconventional myosin-6)	MYO6
			1091,52	0,068	R.SELDMIDIR.E	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6
1092,56	1092,010	1093,103	1091,69	0,100	K.LILQNHILK.V	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
			1092,56	0,004	K.AELNEFLTR.E	P23396	RS3_HUMAN	40S ribosomal protein S3 (EC 4.2.99.18) (Small ribosomal subunit protein uS3)	RP53
			1092,56	0,007	K.NFITAEELR.R	O43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
			1092,56	0,007	M.DSTLTASEIR.Q	P49588	SYAC_HUMAN	Alanine-tRNA ligase, cytoplasmic (EC 6.1.1.7) (Alanyl-tRNA synthetase) (AlaRS) (Renal carcinoma antigen NY-REN-42)	AARS
			1092,56	0,008	R.VHIEIGPDGR.V	P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 (hnRNP H2) (FTP-3) (Heterogeneous nuclear ribonucleoprotein H') (hnRNP H') [Cleaved into: Heterogeneous nuclear ribonucleoprotein H2, N-terminally processed]	HNRNPH2
			1092,56	0,008	R.VHIEIGPDGR.V	P31943	HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H (hnRNP H) [Cleaved into: Heterogeneous nuclear ribonucleoprotein H, N-terminally processed]	HNRNPH1
			1092,56	0,008	R.VHIEIGPDGR.V	P52597	HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein F, N-terminally processed]	HNRNPF
			1092,50	0,053	R.DNLAEIDIMR.L	P08670	VIME_HUMAN	Vimentin	VIM
			1093,50	0,050	K.FADLSEAAANR.N	P08670	VIME_HUMAN	Vimentin	VIM
			1093,50	0,057	K.DFNETQLAR.I	Q9H6X2	ANTR1_HUMAN	Anthrax toxin receptor 1 (Tumor endothelial marker 8)	ANTXR1
1093,55	1093,008	1094,101	1093,48	0,078	R.LTAEEMDER.R	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
			1093,47	0,080	R.REEEMMIR.Q	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMp100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
			1093,45	0,102	K.DTDSEEEIR.E	P0DP23	CALM1_HUMAN	Calmodulin-1	CALM1
			1094,58	0,007	K.LFGPYVWGR.Y	Q9H4A4	AMPB_HUMAN	Aminopeptidase B (AP-B) (EC 3.4.11.6) (Arginine aminopeptidase) (Arginyl aminopeptidase)	RNPEP
			1094,56	0,010	K.YFDLGNLR.D	P48735	IDHP_HUMAN	Isocitrate dehydrogenase [NADP], mitochondrial (IDH) (EC 1.1.1.42) (ICD-M) (IDP) (NADP(+)-specific ICDH) (Oxalosuccinate decarboxylase)	IDH2
			1094,54	0,027	K.FLSQIESDR.L	P19367	HXK1_HUMAN	Hexokinase-1 (EC 2.7.1.1) (Brain form hexokinase) (Hexokinase type I) (HK I)	HK1
			1094,72	0,148	K.LLEPVLVLGK.E	P62249	RS16_HUMAN	40S ribosomal protein S16 (Small ribosomal subunit protein uS9)	RP516
			1095,52	0,038	R.WHFYDVTK.G	P31040	SDHA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) (Flavoprotein subunit of complex II) (Fp)	SDHA
			1095,50	0,062	K.ELEEYWAR.Q	P09496	CLCA_HUMAN	Clathrin light chain A (Lca)	CLTA
			1097,50	0,298	R.YGYTGAFR.C	P02788	TRFL_HUMAN	Lactotransferrin (Lactoferrin) (EC 3.4.21.-) (Growth-inhibiting protein 12) (Talaktoferin) [Cleaved into: Lactoferricin-H (Lfcin-H); Kalliocin-1; Lactoferronin-A; Lactoferronin-B; Lactoferronin-C]	LTF
1097,56	1097,011	1098,109	1097,50	0,060	R.YGYTGAFR.C	P02788	TRFL_HUMAN	Lactotransferrin (Lactoferrin) (EC 3.4.21.-) (Growth-inhibiting protein 12) (Talaktoferin) [Cleaved into: Lactoferricin-H (Lfcin-H); Kalliocin-1; Lactoferronin-A; Lactoferronin-B; Lactoferronin-C]	LTF
			1098,43	0,080	K.GSDFDCELR.L	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
			1098,43	0,112	K.GSDFDCELR.L	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
			1099,56	0,016	R.ELLTEFGYK.G	P49411	EFTU_HUMAN	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	TUFM
			1099,49	0,048	R.STPEYFAER.L	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6
			1099,46	0,075	R.VEFMDDTSR.S	P62857	RS28_HUMAN	40S ribosomal protein S28 (Small ribosomal subunit protein eS28)	RP528
			1100,52	0,048	R.EPEDSAAPER.Q	Q96NY7	CLIC6_HUMAN	Chloride intracellular channel protein 6 (Parchorin)	CLIC6
			1101,50	0,198	R.DETEFYLGK.R	P18077	RL35A_HUMAN	60S ribosomal protein L35a (Cell growth-inhibiting gene 33 protein) (Large ribosomal subunit protein eL33)	RPL35A

1101,50	1100,952	1102,054	1101,50	0,001	R.DETEFYLGK.R	P18077	RL35A_HUMAN	60S ribosomal protein L35a (Cell growth-inhibiting gene 33 RPL35A protein) (Large ribosomal subunit protein eL33)	
1101,65	1101,095	1102,197	1101,50	0,142	R.DETEFYLGK.R	P18077	RL35A_HUMAN	60S ribosomal protein L35a (Cell growth-inhibiting gene 33 RPL35A protein) (Large ribosomal subunit protein eL33)	
1102,30	1101,752	1102,854	1102,50	0,196	R.EDLEELQAR.Y	Q9UHQ9	NBSR1_HUMAN	NADH-cytochrome b5 reductase 1 (b5R.1) (EC 1.6.2.2) (Humb5R2) (NAD(P)H:quinone oxidoreductase type 3 polypeptide A2)	CYB5R1
			1102,57	0,263	R.EIDGGLETLR.L	P38117	ETFB_HUMAN	Electron transfer flavoprotein subunit beta (Beta-ETF)	ETFB
			1102,60	0,300	R.WDGVVPFILR.C	P11413	G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	G6PD
1102,57	1102,020	1103,122	1102,57	0,005	R.EIDGGLETLR.L	P38117	ETFB_HUMAN	Electron transfer flavoprotein subunit beta (Beta-ETF)	ETFB
			1102,60	0,032	R.WDGVVPFILR.C	P11413	G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	G6PD
			1102,50	0,071	R.EDLEELQAR.Y	Q9UHQ9	NBSR1_HUMAN	NADH-cytochrome b5 reductase 1 (b5R.1) (EC 1.6.2.2) (Humb5R2) (NAD(P)H:quinone oxidoreductase type 3 polypeptide A2)	CYB5R1
1103,56	1103,010	1104,114	1103,52	0,042	R.YGTLFTMDR.V	Q15582	BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3 (Beta ig-h3) (Kerato-epithelin) (RGD-containing collagen-associated protein) (RGD-CAP)	TGFBI
			1103,51	0,055	K.CDEPILSNR.S	P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPPP) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1
			1103,64	0,080	R.DAVLLLFANK.Q	P18085	ARF4_HUMAN	ADP-ribosylation factor 4	ARF4
1104,56	1104,004	1105,108	1104,56	0,003	K.EFSELLPNR.Q	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1104,59	0,031	K.MDAILTEAIK.A	Q555J5	HP1B3_HUMAN	Heterochromatin protein 1-binding protein 3 (Protein HP1-BP74)	HP1BP3
			1104,59	0,035	K.LTMQNLNDR.L	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1104,59	0,035	K.IGFPWSEIR.N	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			1104,59	0,035	K.IGFPWSEIR.N	P15311	EZRI_HUMAN	Ezrin (Cyto villin) (Villin-2) (p81)	EZR
			1104,62	0,067	R.VSSFLPWIR.T	P08311	CATG_HUMAN	Cathepsin G (CG) (EC 3.4.21.20)	CTSG
			1104,49	0,068	R.SQESGYDR.M	P43243	MATR3_HUMAN	Matrin-3	MATR3
			1104,49	0,068	R.QDEHGYISR.C	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	HSPB1
			1104,41	0,149	R.YDDMAACMK.S	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
1105,56	1105,007	1106,113	1105,55	0,008	K.IADTKSSIDR.N	Q86T65	DAAM2_HUMAN	Disheveled-associated activator of morphogenesis 2	DAAM2
			1105,54	0,019	R.VSPGVVPACR.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1105,54	0,023	K.GYGRIEYK.A	Q9UHX1	PUF60_HUMAN	Poly(U)-binding-splicing factor PUF60 (60 kDa poly(U)-binding-splicing factor) (FUSE-binding protein-interacting repressor) (FBP-interacting repressor) (Ro-binding protein 1) (RoBP1) (Siah-binding protein 1) (Siah-BP1)	PUF60
			1105,59	0,029	R.FLSPEFIPR.R	P49406	RM19_HUMAN	39S ribosomal protein L19, mitochondrial (L19mt) (MRP-L19) (39S ribosomal protein L15, mitochondrial) (L15mt) (MRP-L15) (Mitochondrial large ribosomal subunit protein bL19m)	MRPL19
			1105,51	0,046	R.TETLPEMR.T	P13611	CSPG2_HUMAN	Versican core protein (Chondroitin sulfate proteoglycan core protein 2) (Chondroitin sulfate proteoglycan 2) (Glial hyaluronate-binding protein) (GHAP) (Large fibroblast proteoglycan) (PG-M)	VCAN
			1105,51	0,046	R.DDTIPPEYR.H	P20810	ICAL_HUMAN	Calpastatin (Calpain inhibitor) (Sperm BS-17 component)	CAST
			1105,62	0,064	R.FULPDMLK.N	P62318	SMD3_HUMAN	Small nuclear ribonucleoprotein Sm D3 (Sm-D3) (snRNP core protein D3)	SNRPD3
1106,56	1106,010	1107,117	1106,58	0,015	K.VTEDTSSVLR.S	P05165	PCCA_HUMAN	Propionyl-CoA carboxylase alpha chain, mitochondrial (PCCase subunit alpha) (EC 6.4.1.3) (Propanoyl-CoA:carbon dioxide ligase subunit alpha)	PCCA
			1106,58	0,019	R.SEIDLFNIR.K	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
			1106,60	0,032	K.AIDLFTDAIK.L	P50502	F10A1_HUMAN	Hsc70-interacting protein (Hip) (Aging-associated protein 2) (Progesterone receptor-associated p48 protein) (Protein FAM10A1) (Putative tumor suppressor ST13) (Renal carcinoma antigen NY-REN-33) (Suppression of tumorigenicity 13 protein)	ST13
			1106,51	0,054	R.NTDEMVELR.I	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
			1106,50	0,064	K.NEGGTWSVEK.V	Q13228	SBP1_HUMAN	Methanethiol oxidase (MTO) (EC 1.8.3.4) (56 kDa selenium-binding protein) (SBP56) (SP56) (Selenium-binding protein 1)	SELENBP1
			1106,69	0,131	R.VVLPPIEPIR.M	P00403	COX2_HUMAN	Cytochrome c oxidase subunit 2 (Cytochrome c oxidase polypeptide II)	MT-CO2
1107,57	1107,012	1108,120	1107,57	0,003	R.TIAQDYGVLK.A	Q06830	PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
			1107,56	0,005	K.ELIFETAR.F	P28482	MK01_HUMAN	Mitogen-activated protein kinase 1 (MAP kinase 1) (MAPK 1) (EC 2.7.11.24) (ERT1) (Extracellular signal-regulated kinase 2) (ERK-2) (MAP kinase isoform p42) (p42-MAPK) (Mitogen-activated protein kinase 2) (MAP kinase 2) (MAPK 2)	MAPK1
			1107,56	0,010	K.ALAAGYDVEK.N	P16403	H12_HUMAN	Histone H1.2 (Histone H1c) (Histone H1d) (Histone H1s-1)	HIST1H1C
			1107,55	0,015	R.QRWDEAFR.K	P27695	APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase (EC 3.1.-.-) (EC 4.2.99.18) (APEX nuclease) (APEN) (Apyrimidinic endonuclease 1) (AP endonuclease 1) (APE-1) (REF-1) (Redox factor-1) [Cleaved into: DNA-(apurinic or apyrimidinic site) lyase, mitochondrial]	APEX1
			1107,55	0,017	R.SELDMLDIR.E	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6

			1107,52	0,042	R.GEACRVMR.T	Q96RQ3	MCCA_HUMAN	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial (MCCase subunit alpha) (EC 6.4.1.4) (3-methylcrotonyl-CoA carboxylase 1) (3-methylcrotonyl-CoA carboxylase biotin-containing subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase subunit alpha)	MCCC1
1108,57	1108,015	1109,124	1108,55	0,023	R.WRDSLEFR.E	P01011	AACT_HUMAN	Alpha-1-antichymotrypsin (ACT) (Cell growth-inhibiting gene 24/25 protein) (Serpin A3) [Cleaved into: Alpha-1-antichymotrypsin His-Pro-less]	SERPINA3
			1108,54	0,034	R.SENFEELK.V	P29373	RABP2_HUMAN	Cellular retinoic acid-binding protein 2 (Cellular retinoic acid-binding protein II) (CRABP-II)	CRABP2
			1108,54	0,034	R.APFDLFENR.K	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP 2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
			1108,50	0,071	K.DDWTPVYGR.I	Q96RQ9	OXLA_HUMAN	L-amino-acid oxidase (LAO) (LAO) (EC 1.4.3.2) (Interleukin-4-induced protein 1) (IL4-induced protein 1) (Protein Fig-1) (hFIG1)	IL4I1
			1108,50	0,072	K.DFWEQVEVR.D	Q16822	PCKGM_HUMAN	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial (PEPCK-M) (EC 4.1.1.32)	PCK2
			1108,44	0,125	K.GEELSCER.N	P31947	14335_HUMAN	14-3-3 protein sigma (Epithelial cell marker protein 1) (Stratifin)	SFN
1109,57	1109,016	1110,126	1109,57	0,004	K.LLQDFNFR.D	P0DMV8	H571A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
			1109,58	0,008	R.LLEYDTVTR.E	Q9HDC9	APMAP_HUMAN	Adipocyte plasma membrane-associated protein (Protein BScv)	APMAP
			1109,53	0,038	K.DAEAWFNEK.S	P13645	K1C10_HUMAN	Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KRT10
			1109,53	0,038	R.WIYEDVER.Q	O43852	CALU_HUMAN	Calumenin (Crocabin) (IEF SSP 9302)	CALU
			1109,53	0,041	R.LAGGDWFTSR.T	P30153	ZAAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform (Medium tumor antigen-associated 61 kDa protein) (PP2A subunit A isoform PR65-alpha) (PP2A subunit A isoform R1-alpha)	PPP2R1A
			1109,52	0,054	K.DLEALMFDR.S	P36871	PGM1_HUMAN	Phosphoglucosyltransferase-1 (PGM 1) (EC 5.4.2.2) (Glucose phosphomutase 1)	PGM1
			1109,65	0,084	R.IAIYELFK.E	P46783	RS10_HUMAN	40S ribosomal protein S10 (Small ribosomal subunit protein eS10)	RPS10
			1109,47	0,102	R.REEMMIR.Q	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
1110,55	1109,998	1111,109	1110,55	0,001	K.LFDSICNNK.W	P04899	GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2 (Adenylate cyclase-inhibiting G alpha protein)	GNAI2
			1110,55	0,003	R.EAFAEQFLR.G	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1110,56	0,010	R.FPDENFTLK.H	P30405	PPIF_HUMAN	Peptidyl-prolyl cis-trans isomerase F, mitochondrial (PPIase F) (EC 5.2.1.8) (Cyclophilin D) (CypD) (CypD) (Cyclophilin F) (Mitochondrial cyclophilin) (Cyp-M) (Rotamase F)	PPIF
			1110,46	0,088	K.QEQEEYER.E	B0I1T2	MYO1G_HUMAN	Unconventional myosin-Ig [Cleaved into: Minor histocompatibility antigen HA-2 (mHag HA-2)]	MYO1G
			1110,66	0,103	K.LLLPWLEAR.I	Q00610	CLH1_HUMAN	Clathrin heavy chain 1 (Clathrin heavy chain on chromosome 17) (CLH-17)	CLTC
1111,54	1110,983	1112,095							
1111,57	1111,017	1112,129							
1112,53	1111,972	1113,084	1112,52	0,007	K.SDVVYTDWK.K	P02763	A1AG1_HUMAN	Alpha-1-acid glycoprotein 1 (AGP 1) (Orosomucoid-1) (OMD 1)	ORM1
1112,58	1112,027	1113,140	1112,52	0,063	K.SDVVYTDWK.K	P02763	A1AG1_HUMAN	Alpha-1-acid glycoprotein 1 (AGP 1) (Orosomucoid-1) (OMD 1)	ORM1
1113,16	1112,599	1113,713							
1113,58	1113,026	1114,139							
1114,56	1114,005	1115,120	1114,60	0,035	R.GLPGTAGLPGMK.G	P02452	CO1A1_HUMAN	Collagen alpha-1(I) chain (Alpha-1 type I collagen)	COL1A1
			1114,49	0,074	R.GFEEQWYR.R	P08236	BGLR_HUMAN	Beta-glucuronidase (EC 3.2.1.31) (Beta-G1)	GUSB
1115,58	1115,018	1116,134	1115,56	0,012	K.VELOELNDR.F	P08670	VIME_HUMAN	Vimentin	VIM
			1115,56	0,016	R.RQGQELSAAR.Q	Q04323	UBXN1_HUMAN	UBX domain-containing protein 1 (SAPK substrate protein 1) (UBA/UBX 33.3 kDa protein)	UBXN1
			1115,62	0,045	K.MPLIGLTWK.S	P14550	AK1A1_HUMAN	Aldo-keto reductase family 1 member A1 (EC 1.1.1.2) (EC 1.1.1.372) (EC 1.1.1.54) (Alcohol dehydrogenase [NADP(+)] (Aldehyde reductase) (Glucuronate reductase) (EC 1.1.1.19) (Glucuronolactone reductase) (EC 1.1.1.20)	AKR1A1
			1115,51	0,068	R.YSDFEWLR.S	O60493	SNX3_HUMAN	Sorting nexin-3 (Protein SDP3)	SNX3
1116,53	1115,976	1117,093	1116,54	0,003	R.GGNIGDGGGAADR.V	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
1117,54	1116,984	1118,102							
1118,56	1117,996	1119,114	1118,55	0,001	R.GDEELDSLK.A	Q71UI9	H2AV_HUMAN	Histone H2A.V (H2A.F/Z)	H2AFV
			1118,56	0,008	R.FYFENALSK.S	Q13557	KCC2D_HUMAN	Calcium/calmodulin-dependent protein kinase type II subunit delta (CaM kinase II subunit delta) (CaMK-II subunit delta) (EC 2.7.11.17)	CAMK2D
			1118,58	0,029	K.SADTLWGIQK.E	P00338	LDHA_HUMAN	L-lactate dehydrogenase A chain (LDH-A) (EC 1.1.1.27) (Cell proliferation-inducing gene 19 protein) (LDH muscle subunit) (LDH-M) (Renal carcinoma antigen NY-REN-59)	LDHA
			1118,48	0,072	K.SCDFLSSFR.D	P35237	SPB6_HUMAN	Serpin B6 (Cytoplasmic antiproteinase) (CAP) (Peptidase inhibitor 6) (Pi-6) (Placental thrombin inhibitor)	SERPINB6
			1118,68	0,123	R.IGLLDAYLK.T	P26641	EF1G_HUMAN	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) EEF1G	EEF1G
1119,57	1119,014	1120,134	1119,53	0,044	R.GMDKLVDGR.G	Q99832	TCPH_HUMAN	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein) [Cleaved into: T-complex protein 1 subunit eta, N-terminally processed]	CCT7
			1119,50	0,078	K.DSQEDLQER.H	Q6IPX3	TCAL6_HUMAN	Transcription elongation factor A protein-like 6 (TCEA-like protein 6) (Transcription elongation factor S-II protein-like 6)	TCEAL6
1120,57	1120,006	1121,127	1120,55	0,012	K.QRIDEFEAL.-	P15311	EZRI_HUMAN	Ezrin (Cyto villin) (Villin-2) (p81)	EZR
			1120,61	0,044	R.LSSSLDNKE.E	O14974	MYPT1_HUMAN	Protein phosphatase 1 regulatory subunit 12A (Myosin phosphatase-targeting subunit 1) (Myosin phosphatase target subunit 1) (Protein phosphatase myosin-binding subunit)	PPP1R12A

			1120,51	0,059	R.DLEGSIDITR.R	P55060	XPO2_HUMAN	Exportin-2 (Exp2) (Cellular apoptosis susceptibility protein) (Chromosome segregation 1-like protein) (Importin-alpha re-exporter)	CSE1L
1121,57	1121,012	1122,134	1121,56	0,010	K.EQGVLSFWR.G	P12236	ADT3_HUMAN	ADP/ATP translocase 3 (ADP,ATP carrier protein 3) (ADP,ATP carrier protein, isoform T2) (ANT 2) (Adenine nucleotide translocator 3) (ANT 3) (Solute carrier family 25 member 6) [Cleaved into: ADP/ATP translocase 3, N-terminally processed]	SLC25A6
			1121,56	0,010	K.EQGVLSFWR.G	P05141	ADT2_HUMAN	ADP/ATP translocase 2 (ADP,ATP carrier protein 2) (ADP,ATP carrier protein, fibroblast isoform) (Adenine nucleotide translocator 2) (ANT 2) (Solute carrier family 25 member 5) [Cleaved into: ADP/ATP translocase 2, N-terminally processed]	SLC25A5
			1121,59	0,014	R.EYQDLLNVK.M	P08670	VIME_HUMAN	Vimentin	VIM
1122,59	1122,031	1123,153	1122,58	0,014	R.IDYIAGLDSR.G	P07741	APT_HUMAN	Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	APRT
			1122,56	0,027	R.LEQEIATYR.R	P08779	K1C16_HUMAN	Keratin, type I cytoskeletal 16 (Cytokeratin-16) (CK-16) (Keratin-16) (K16)	KRT16
			1122,56	0,027	R.LEQEIATYR.S	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1122,55	0,043	K.ELDGLWFSR.A	P08236	BGLR_HUMAN	Beta-glucuronidase (EC 3.2.1.31) (Beta-G1)	GUSB
			1122,53	0,061	R.NDVAWNFEK.F	P07203	GPX1_HUMAN	Glutathione peroxidase 1 (GPx-1) (GSHPx-1) (EC 1.11.1.9) (Cellular glutathione peroxidase)	GPX1
			1122,50	0,088	R.MGESDSSILR.L	P63220	RS21_HUMAN	40S ribosomal protein S21 (Small ribosomal subunit protein eS21)	RPS21
1123,42	1122,861	1123,984	1123,42	0,001	R.DGYDYGVR.L	Q07955	SRSF1_HUMAN	Serine/arginine-rich splicing factor 1 (Alternative-splicing factor 1) (ASF-1) (Splicing factor, arginine/serine-rich 1) (pre-mRNA-splicing factor SF2, P33 subunit)	SRSF1
			1123,54	0,118	K.AKHDELTYF.-	P04080	CYTB_HUMAN	Cystatin-B (CPI-B) (Liver thiol proteinase inhibitor) (Stefin-B)	CSTB
			1123,56	0,137	R.GYWGGPAFLR.K	Q9Y6N5	SQOR_HUMAN	Sulfide:quinone oxidoreductase, mitochondrial, SQOR, EC 1.8.5.- (Sulfide dehydrogenase-like) (Sulfide quinone oxidoreductase)	SQOR
			1123,60	0,174	R.DQYNETLLK.K	Q8TAG9	EXOC6_HUMAN	Exocyst complex component 6 (Exocyst complex component Sec15A) (SEC15-like protein 1)	EXOC6
			1123,60	0,174	R.TPFGAYGGLLK.D	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2
1123,59	1123,030	1124,154	1123,60	0,005	R.DQYNETLLK.K	Q8TAG9	EXOC6_HUMAN	Exocyst complex component 6 (Exocyst complex component Sec15A) (SEC15-like protein 1)	EXOC6
			1123,60	0,005	R.TPFGAYGGLLK.D	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2
			1123,56	0,032	R.GYWGGPAFLR.K	Q9Y6N5	SQOR_HUMAN	Sulfide:quinone oxidoreductase, mitochondrial, SQOR, EC 1.8.5.- (Sulfide dehydrogenase-like) (Sulfide quinone oxidoreductase)	SQOR
			1123,54	0,051	K.AKHDELTYF.-	P04080	CYTB_HUMAN	Cystatin-B (CPI-B) (Liver thiol proteinase inhibitor) (Stefin-B)	CSTB
			1123,42	0,168	R.DGYDYGVR.L	Q07955	SRSF1_HUMAN	Serine/arginine-rich splicing factor 1 (Alternative-splicing factor 1) (ASF-1) (Splicing factor, arginine/serine-rich 1) (pre-mRNA-splicing factor SF2, P33 subunit)	SRSF1
1124,54	1123,981	1125,106	1124,60	0,059	R.DGYLFQLLR.I	P04196	HRG_HUMAN	Histidine-rich glycoprotein (Histidine-proline-rich glycoprotein) (HPRG)	HRG
			1124,67	0,123	R.VDILDPAFLR.S	P17980	PR56A_HUMAN	26S proteasome regulatory subunit 6A (26S proteasome AAA-ATPase subunit RPT5) (Proteasome 26S subunit ATPase 3) (Proteasome subunit P50) (Tat-binding protein 1) (TBP-1)	PSMC3
1125,53	1124,969	1126,095	1125,56	0,026	K.HDLGHFMLR.C	P30043	BLVRB_HUMAN	Flavin reductase (NADPH) (FR) (EC 1.5.1.30) (Biliverdin reductase B) (BVR-B) (EC 1.3.1.24) (Biliverdin-IX beta-reductase) (Green heme-binding protein) (GHBp) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR)	BLVRB
			1125,49	0,041	K.NYTDNELEK.I	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			1125,64	0,108	R.IVGGWDLLPR.A	Q96RQ9	OXLA_HUMAN	L-amino-acid oxidase (LAO) (LAO) (EC 1.4.3.2) (Interleukin-4-induced protein 1) (IL4-induced protein 1) (Protein Fig-1) (hFIG1)	
1125,55	1124,987	1126,112	1125,56	0,008	K.HDLGHFMLR.C	P30043	BLVRB_HUMAN	Flavin reductase (NADPH) (FR) (EC 1.5.1.30) (Biliverdin reductase B) (BVR-B) (EC 1.3.1.24) (Biliverdin-IX beta-reductase) (Green heme-binding protein) (GHBp) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR)	BLVRB
			1125,49	0,058	K.NYTDNELEK.I	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			1125,64	0,091	R.IVGGWDLLPR.A	Q96RQ9	OXLA_HUMAN	L-amino-acid oxidase (LAO) (LAO) (EC 1.4.3.2) (Interleukin-4-induced protein 1) (IL4-induced protein 1) (Protein Fig-1) (hFIG1)	
1126,55	1125,992	1127,118	1126,55	0,006	K.LHVDPENFR.L	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			1126,55	0,006	K.LHVDPENFR.L	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
			1126,61	0,058	K.DPSLTEPVIR.G	Q16537	ZA5E_HUMAN	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform (PP2A B subunit isoform B'-epsilon) (PP2A B subunit isoform B56-epsilon) (PP2A B subunit isoform PR61-epsilon) (PP2A B subunit isoform R5-epsilon)	PPP2R5E
1127,55	1126,990	1128,117	1127,54	0,012	K.SYAKFSATPR.Y	P35998	PRS7_HUMAN	26S proteasome regulatory subunit 7 (26S proteasome AAA-ATPase subunit RPT1) (Proteasome 26S subunit ATPase 2) (Protein MSS1)	PSMC2
			1127,53	0,026	K.DLFPYEEK.E	P51858	HDGF_HUMAN	Hepatoma-derived growth factor (HDGF) (High mobility group protein 1-like 2) (HMG-112)	HDGF
1128,56	1127,995	1129,124	1128,58	0,017	R.GLLEFEHQR.A	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			1128,58	0,020	K.IGDPLLEDTR.M	P49189	AL9A1_HUMAN	4-trimethylaminobutylaldehyde dehydrogenase (TMABADH) (EC 1.2.1.47) (Aldehyde dehydrogenase E3 isozyme) (Aldehyde dehydrogenase family 9 member A1) (EC 1.2.1.3) (Gamma-aminobutylaldehyde dehydrogenase) (EC 1.2.1.19) (R-aminobutylaldehyde dehydrogenase) [Cleaved into: 4-trimethylaminobutylaldehyde dehydrogenase, N-terminally processed]	ALDH9A1

1129,56	1129,000	1130,129	1128,61	0,046	K.VADIGLAAWGR.K	P23526	SAHH_HUMAN	Adenosylhomocysteinase (AdoHcyase) (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase)	AHCY
			1128,61	0,054	K.LGGDDIDLVR.C	O15371	EIF3D_HUMAN	Eukaryotic translation initiation factor 3 subunit D (eIF3d) (Eukaryotic translation initiation factor 3 subunit 7) (eIF-3-zeta) (eIF3 p66)	EIF3D
			1128,68	0,120	K.KQTALVELVK.H	P02768	ALBU_HUMAN	Serum albumin	ALB
			1129,54	0,022	K.FFGNLM DASK.L	P36871	PGM1_HUMAN	Phosphoglucosmutase-1 (PGM 1) (EC 5.4.2.2) (Glucose phosphomutase 1)	PGM1
			1129,60	0,032	K.EDAIWNLLR.Q	P02788	TRFL_HUMAN	Lactotransferrin (Lactoferrin) (EC 3.4.21.-) (Growth-inhibiting protein 12) [Tala lactoferrin] [Cleaved into: Lactoferricin-H (Lfcin-H); Kallocin-1; Lactoferrroxin-A; Lactoferrroxin-B; Lactoferrroxin-C]	LTF
1130,57	1130,000	1131,131	1129,62	0,058	R.EAELNAKAQR.L	Q02818	NUCB1_HUMAN	Nucleobindin-1 (CALNUC)	NUCB1
			1129,62	0,058	K.LSELEAALQR.A	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
			1129,65	0,085	R.RLWWLDLK.S	P02790	HEMO_HUMAN	Hemopexin (Beta-1b-glycoprotein)	HPX
			1130,56	0,003	R.GYSFVTTAER.E	P68133	ACT5_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1130,56	0,003	R.GYSFVTTAER.E	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
1131,56	1130,999	1132,130	1130,56	0,003	R.GYSFVTTAER.E	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1130,58	0,014	R.AVGWNELEGR.D	P61457	PHS_HUMAN	Pterin-4-alpha-carbinolamine dehydratase (PHS) (EC 4.2.1.96) (4-alpha-hydroxy-tetrahydropterin dehydratase) (Dimerization cofactor of hepatocyte nuclear factor 1-alpha) (DCoH) (Dimerization cofactor of HNF1) (Phenylalanine hydroxylase-stimulating protein) (Pterin carbinolamine dehydratase) (PCD)	PCBD1
			1130,58	0,014	R.FPGQLNADLR.K	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1130,58	0,014	R.FPGQLNADLR.K	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1130,63	0,061	K.EAILDIITS.S	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6
1132,54	1131,977	1133,109	1130,48	0,083	K.FYGDEEKDK.G	P27797	CALR_HUMAN	Calreticulin (CRP55) (Calregulin) (Endoplasmic reticulum resident protein 60) (ERp60) (HACBP) (grp60)	CALR
			1131,53	0,036	K.EDLQELNDR.L	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
			1131,61	0,045	R.IMDLLGQVK.L	P21397	AOFA_HUMAN	Amine oxidase [flavin-containing] A (EC 1.4.3.4) (Monoamine oxidase type A) (MAO-A)	MAOA
			1131,51	0,050	K.AEDEVQRRER.V	P0DMV8	H571A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
			1131,51	0,052	K.GAVAEDGDDEL.T	P27695	APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase (EC 3.1.-.-) (EC 4.2.99.18) (APEX nuclease) (APEN) (Apyriminic-apyrimidinic endonuclease 1) (AP endonuclease 1) (APE-1) (REF-1) (Redox factor-1) [Cleaved into: DNA-(apurinic or apyrimidinic site) lyase, mitochondrial]	APEX1
1133,56	1132,992	1134,125	1131,48	0,083	K.EAENPEGEEK.E	P51858	HDGF_HUMAN	Hepatoma-derived growth factor (HDGF) (High mobility group protein 1-like 2) (HMG-1L2)	HDGF
			1131,47	0,097	R.YDEMVMESMK.K	P62258	1433E_HUMAN	14-3-3 protein epsilon (14-3-3E)	YWHAE
			1132,52	0,019	R.GYSFTTTAER.E	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			1132,62	0,082	R.LALQFTTNPK.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1133,54	0,023	R.VCEVDNELR.I	Q9Y323	SAMH1_HUMAN	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 (dNTPase) (EC 3.1.5.-) (Dendritic cell-derived IFNG-induced protein) (DCIP) (Monocyte protein 5) (MOP-5) (SAM domain and HD domain-containing protein 1) (hSAMHD1)	SAMHD1
1134,57	1133,999	1135,134	1134,57	0,001	K.VTLTSEEFAR.L	P00338	LDHA_HUMAN	L-lactate dehydrogenase A chain (LDH-A) (EC 1.1.1.27) (Cell proliferation-inducing gene 19 protein) (LDH muscle subunit) (LDH-M) (Renal carcinoma antigen NY-REN-59)	LDHA
			1134,55	0,021	R.DAVTYTEHAK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
			1134,54	0,028	K.DVNQQEFVR.A	P39019	RS19_HUMAN	40S ribosomal protein S19 (Small ribosomal subunit protein eS19)	RPS19
			1134,60	0,036	R.FEELTNLIR.T	Q99613	EIF3C_HUMAN	Eukaryotic translation initiation factor 3 subunit C (eIF3c) (Eukaryotic translation initiation factor 3 subunit 8) (eIF3 p110)	EIF3C
			1136,57	0,001	R.WFVLDAETR.D	Q9HC35	EMAL4_HUMAN	Echinoderm microtubule-associated protein-like 4 (EMAP-4) (Restrictedly overexpressed proliferation-associated protein) (Ropp 120)	EML4
1135,58 1136,57	1135,008 1135,997	1136,144 1137,134	1136,55	0,020	R.LEQDEYALR.S	P55084	ECHB_HUMAN	Trifunctional enzyme subunit beta, mitochondrial (TP-beta) [Includes: 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase)]	HADHB
			1136,54	0,027	R.QFEIEWER.C	Q9UM54	MYO6_HUMAN	Unconventional myosin-VI (Unconventional myosin-6)	MYO6
			1136,60	0,037	K.LTKMDGNWR.R	P17655	CAN2_HUMAN	Calpain-2 catalytic subunit (EC 3.4.22.53) (Calcium-activated neutral proteinase 2) (CANP 2) (Calpain M-type) (Calpain large polypeptide L2) (Calpain-2 large subunit) (Milimolar-calpain) (M-calpain)	CAPN2
			1137,57	0,001	K.YEELQSLAGK.H	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
			1137,54	0,030	K.ESYSVYVYK.V	O60814	H2B1K_HUMAN	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK
1138,55	1137,983	1139,122	1137,54	0,035	K.DPSPEPPSR.R.H	Q8VL6	P3H3_HUMAN	Prolyl 3-hydroxylase 3 (EC 1.14.11.7) (Leprecan-like protein 2) (Protein B)	P3H3
			1138,55	0,001	K.DGVGMVEYLR.K	Q13242	SRSF9_HUMAN	Serine/arginine-rich splicing factor 9 (Pre-mRNA-splicing factor SRp30C) (Splicing factor, arginine/serine-rich 9)	SRSF9

			1138,53	0,025	K.YEWDVAEAR.K	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2			
			1138,58	0,030	K.LQDPFSLYR.C	P21912	SDHB_HUMAN	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (EC 1.3.5.1) (Iron-sulfur subunit of complex II) (Ip)	SDHB			
			1138,50	0,050	R.MGESDSDILR.L	P63220	RS21_HUMAN	40S ribosomal protein S21 (Small ribosomal subunit protein eS21)	RPS21			
			1138,50	0,050	K.CCTESLVNR.R	P02768	ALBU_HUMAN	Serum albumin	ALB			
			1138,61	0,059	K.LKLEDFFAR.N	P11413	G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	G6PD			
			1139,56	1138,987	1140,126	1139,53	0,022	R.YYPTEDVPR.K	Q02878	RL6_HUMAN	60S ribosomal protein L6 (Large ribosomal subunit protein eL6) (Neoplasm-related protein C140) (Tax-responsive enhancer element-binding protein 107) (TaxREB107)	RPL6
			1140,56	1139,994	1141,134	1140,57	0,007	R.WESQLPQPR.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1141,58	1141,012	1142,153	1141,61	0,025	R.GDLGIEIPAEC.V	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
						1141,52	0,062	R.DYQELMNTK.L	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
						1141,48	0,099	K.TDGFIDTCR.S	P04632	CPNS1_HUMAN	Calpain small subunit 1 (CSS1) (Calcium-activated neutral proteinase small subunit) (CANP small subunit) (Calcium-dependent protease small subunit) (CDPS) (Calcium-dependent protease small subunit 1) (Calpain regulatory subunit)	CAPNS1
			1142,57	1141,996	1143,138	1142,54	0,026	R.TFDEIASGFR.Q	P11166	GTR1_HUMAN	Solute carrier family 2, facilitated glucose transporter member 1 (Glucose transporter type 1, erythrocyte/brain) (GLUT-1) (HepG2 glucose transporter)	SLC2A1
						1142,48	0,089	R.DYFMPCPR.G	P02790	HEMO_HUMAN	Hemopexin (Beta-1B-glycoprotein)	HPX
			1143,57	1142,995	1144,139	1143,62	0,058	K.LAVNMMVPPR.L	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
						1143,62	0,058	K.LAVNMMVPPR.L	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1144,58	1144,009	1145,154	1144,57	0,012	R.VFNPTYEFK.E	Q96C19	EFHD2_HUMAN	EF-hand domain-containing protein D2 (Swiprosin-1)	EFHD2
			1145,52	1144,944	1146,090	1145,55	0,036	R.YEFGIFNQK.I	P11216	PYGB_HUMAN	Glycogen phosphorylase, brain form (EC 2.4.1.1)	PYGB
						1145,55	0,036	R.YEFGIFNQK.I	P11217	PYGM_HUMAN	Glycogen phosphorylase, muscle form (EC 2.4.1.1) (Myophosphorylase)	PYGM
			1145,63	1145,062	1146,207	1145,55	0,081	R.YEFGIFNQK.I	P11216	PYGB_HUMAN	Glycogen phosphorylase, brain form (EC 2.4.1.1)	PYGB
						1145,55	0,081	R.YEFGIFNQK.I	P11217	PYGM_HUMAN	Glycogen phosphorylase, muscle form (EC 2.4.1.1) (Myophosphorylase)	PYGM
			1146,58	1146,009	1147,156	1146,58	0,002	K.YLTAEAFGK.V	Q16658	FSCN1_HUMAN	Fascin (55 kDa actin-bundling protein) (Singed-like protein) (p55)	FSCN1
			1146,59	0,004	R.DLAEITLDR.S	Q9B526	ERP44_HUMAN	Endoplasmic reticulum resident protein 44 (ER protein 44) (ERP44) (Thioredoxin domain-containing protein 4)	ERP44			
						1146,59	0,008	R.DIDEVSSLR.T	P50990	TCPQ_HUMAN	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta) (Chaperonin containing T-complex polypeptide 1 subunit 8) (Renal carcinoma antigen NY-REN-15)	CCT8
						1146,59	0,008	-MAKWGEGDPR.W	O95433	AHSA1_HUMAN	Activator of 90 kDa heat shock protein ATPase homolog 1 (AHA1) (p38)	AHSA1
			1147,51	1146,939	1148,087	1147,61	0,100	R.EQLAIAEFAR.S	P17987	TCPA_HUMAN	T-complex protein 1 subunit alpha (TCP-1-alpha) (CCT-alpha)	TCP1
			1147,61	1147,037	1148,184	1147,61	0,003	R.EQLAIAEFAR.S	P17987	TCPA_HUMAN	T-complex protein 1 subunit alpha (TCP-1-alpha) (CCT-alpha)	TCP1
			1148,52	1147,948	1149,096	1148,57	0,043	R.ITESEVVS.R.E	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
						1148,61	0,091	K.KGQGSTTTLQK.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1148,62	1148,048	1149,197	1148,61	0,009	K.KGQGSTTTLQK.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
						1148,57	0,057	R.ITESEVVS.R.E	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
			1149,57	1148,998	1150,148	1149,55	0,028	R.FDAGELITQR.E	P35232	PHB_HUMAN	Prohibitin	PHB
						1149,60	0,031	K.DRPFAGVLK.Y	P15531	NDKA_HUMAN	Nucleoside diphosphate kinase A (NDK A) (NDP kinase A) (EC 2.7.4.6) (Granzyme A-activated DNase) (GAAD) (Metastasis inhibition factor nm23) (NM23-H1) (Tumor metastatic process-associated protein)	NME1
						1149,61	0,034	K.LVNEVTEFAK.T	P02768	ALBU_HUMAN	Serum albumin	ALB
						1149,61	0,037	R.FVLSQAKDEL.-	Q8NB59	TXND5_HUMAN	Thioredoxin domain-containing protein 5 (Endoplasmic reticulum resident protein 46) (ER protein 46) (Erp46) (Thioredoxin-like protein p46)	TXNDC5
						1149,51	0,064	R.LDDCGLTEAR.C	P13489	RINI_HUMAN	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor) (Ribonuclease/angiogenin inhibitor 1) (RAI)	RNH1
						1149,67	0,093	K.VVAGVANALAHK.Y	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
						1149,67	0,093	K.VVAGVANALAHK.Y	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			1150,58	1150,010	1151,160	1150,58	0,005	K.FAEAFEIPR.A	P50990	TCPQ_HUMAN	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta) (Chaperonin containing T-complex polypeptide 1 subunit 8) (Renal carcinoma antigen NY-REN-15)	CCT8
						1150,52	0,065	K.FEAFEHENK.F	Q9UBQ0	VPS29_HUMAN	Vacuolar protein sorting-associated protein 29 (hVPS29) (PEP11 homolog) (Vesicle protein sorting 29)	VPS29
			1151,58	1151,008	1152,159	1151,56	0,022	K.ESYSIVYK.V	Q16778	H2B2E_HUMAN	Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q)	HIST2H2BE
						1151,54	0,043	R.FTNIGPDTMR.V	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
						1151,54	0,048	K.YIDQEELNK.T	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP 2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
						1151,54	0,048	K.YIDQEELNK.T	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
						1151,53	0,052	R.YEGFGLYR.G	Q9UJ50	CMC2_HUMAN	Calcium-binding mitochondrial carrier protein Aralar2 (Citrin) (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13)	SLC25A13

			1151,51	0,071	K.GESPVVDYDGG.R.T	Q15084	PDI A6_HUMAN	Protein disulfide-isomerase A6 (EC 5.3.4.1) (Endoplasmic reticulum protein 5) (ER protein 5) (ERp5) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)	PDI A6
			1151,49	0,090	K.FQEGQEER.L	P00488	F13A_HUMAN	Coagulation factor XIII A chain (Coagulation factor XIIIa) (EC 2.3.2.13) (Protein-glutamine gamma-glutamyltransferase A chain) (Transglutaminase A chain)	F13A1
1152,61	1152,029	1153,182	1152,61	0,007	R.GYPTLLWFR.D	Q8NB59	TXND5_HUMAN	Thioredoxin domain-containing protein 5 (Endoplasmic reticulum resident protein 46) (ER protein 46) (Erp46) (Thioredoxin-like protein p46)	TXNDC5
			1152,56	0,041	K.LDELYGTWR.K	P36578	RL4_HUMAN	60S ribosomal protein L4 (60S ribosomal protein L1) (Large ribosomal subunit protein uL4)	RPL4
1153,61	1153,037	1154,190	1153,58	0,037	R.EHRSELNLR.R	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
			1153,58	0,037	K.ELGDHVTNLR.K	P02794	FRIH_HUMAN	Ferritin heavy chain (Ferritin H subunit) (EC 1.16.3.1) (Cell proliferation-inducing gene 15 protein) [Cleaved into: Ferritin heavy chain, N-terminally processed]	FTTH1
			1153,56	0,058	R.EYQELMNVK.L	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
1154,59	1154,010	1155,164	1154,58	0,006	R.GMITFESIEK.A	Q9HBL7	PLRKT_HUMAN	Plasminogen receptor (KT) (Plg-R(KT))	PLGRKT
			1154,60	0,009	K.YAFVNWINK.A	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
			1154,60	0,009	K.YAFVNWINK.A	P13797	PLST_HUMAN	Plastin-3 (T-plastin)	PLS3
			1154,61	0,020	K.GPPGRAPIPHR.H	Q5IU85	IQEC2_HUMAN	IQ motif and SEC7 domain-containing protein 2	IQSEC2
			1154,61	0,020	K.DIFQEIDK.H	P48735	IDHP_HUMAN	Isocitrate dehydrogenase [NADP], mitochondrial (IDH) (EC 1.1.1.42) (ICD-M) (IDP) (NADP(+)-specific ICDH) (Oxalosuccinate decarboxylase)	IDH2
			1154,56	0,029	K.FEDENILK.H	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
			1154,55	0,036	K.NYITMDEL.R	P12814	ACTN1_HUMAN	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (F-actin cross-linking protein) (Non-muscle alpha-actinin-1)	ACTN1
			1154,53	0,056	R.KEDMEYAL.R	Q13242	SRSF9_HUMAN	Serine/arginine-rich splicing factor 9 (Pre-mRNA-splicing factor SRp30C) (Splicing factor, arginine/serine-rich 9)	SRSF9
			1154,50	0,085	K.QRIDEFESM.-	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			1154,69	0,103	R.FSVLLHIGIR.F	Q96IU4	ABHEB_HUMAN	Protein ABHD14B (EC 3.---.-) (Alpha/beta hydrolase domain-containing protein 14B) (Abhydrolase domain-containing protein 14B) (CCG1-interacting factor B)	ABHD14B
1155,60	1155,022	1156,177	1155,58	0,019	K.MLTFMLVR.L	Q86VP6	CAND1_HUMAN	Cullin-associated NEDD8-dissociated protein 1 (Cullin-associated and neddylation-dissociated protein 1) (TBP-interacting protein of 120 kDa A) (TBP-interacting protein 120A) (p120 CAND1)	CAND1
			1155,46	0,141	K.ADQCYEDVR.V	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
1156,60	1156,023	1157,180	1156,60	0,003	R.VGEVSLYGR.H	P02743	SAMP_HUMAN	Serum amyloid P-component (SAP) (9.5S alpha-1-glycoprotein) [Cleaved into: Serum amyloid P-component(1-203)]	APCS
			1156,55	0,049	R.FYTEDSPGLK.V	P60468	SC61B_HUMAN	Protein transport protein Sec61 subunit beta	SEC61B
			1156,51	0,096	K.HEAYGECYK.V	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
1157,52	1156,942	1158,099	1157,56	0,037	R.MGAGMGFGLER.M	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			1157,59	0,074	K.IMLPWDPTGK.I	P23396	RS3_HUMAN	40S ribosomal protein S3 (EC 4.2.99.18) (Small ribosomal subunit protein uS3)	RPS3
1157,66	1157,077	1158,235	1157,59	0,061	K.IMLPWDPTGK.I	P23396	RS3_HUMAN	40S ribosomal protein S3 (EC 4.2.99.18) (Small ribosomal subunit protein uS3)	RPS3
			1157,56	0,098	R.MGAGMGFGLER.M	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
1158,62	1158,039	1159,197	1158,61	0,005	K.LWEEQLAAAK.A	P14314	GLU2B_HUMAN	Glucosidase 2 subunit beta (80K-H protein) (Glucosidase II subunit beta) (Protein kinase C substrate 60.1 kDa protein heavy chain) (PKCSH)	PRKCSH
1159,63	1159,054	1160,214	1159,62	0,014	K.LAVNMVFPFR.L	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1159,62	0,014	K.LAVNMVFPFR.L	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
1160,58	1160,002	1161,163	1160,58	0,000	K.WFYIASAFR.N	P19652	A1AG2_HUMAN	Alpha-1-acid glycoprotein 2 (AGP 2) (Orosomucoid-2) (OMD 2)	ORM2
			1160,58	0,000	K.WFYIASAFR.N	P02763	A1AG1_HUMAN	Alpha-1-acid glycoprotein 1 (AGP 1) (Orosomucoid-1) (OMD 1)	ORM1
			1160,59	0,005	R.SISLYYTGEK.G	P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL
			1160,58	0,006	K.SIYITGESK.E	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			1160,60	0,016	R.LYQVEYAFK.A	P60900	PSA6_HUMAN	Proteasome subunit alpha type-6 (EC 3.4.25.1) (27 kDa prosome protein) (PROS-27) (p27K) (Macropain iota chain) (Multicatalytic endopeptidase complex iota chain) (Proteasome iota chain)	PSMA6
			1160,62	0,036	K.TEHMTRTLR.G	Q12906	ILF3_HUMAN	Interleukin enhancer-binding factor 3 (Double-stranded RNA-binding protein 76) (DRBP76) (M-phase phosphoprotein 4) (MPP4) (Nuclear factor associated with dsRNA) (NFAR) (Nuclear factor of activated T-cells 90 kDa) (NF-AT-90) (Translational control protein 80) (TCP80)	ILF3
			1160,51	0,068	R.IEELGDDEAR.F	P09104	ENO2_HUMAN	Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 2) (Neural enolase) (Neuron-specific enolase) (NSE)	ENO2
1161,62	1161,038	1162,199	1161,48	0,137	R.YHAEVEER.F	Q6NZY4	ZCHC8_HUMAN	Zinc finger CCHC domain-containing protein 8 (TRAMP-like complex RNA-binding factor ZCCHC8)	ZCCHC8
1162,64	1162,056	1163,219	1162,59	0,051	R.LATFWYYAK.V	Q75964	ATP5L_HUMAN	ATP synthase subunit g, mitochondrial (ATPase subunit g) (ATP synthase membrane subunit g)	ATP5MG
			1162,54	0,093	R.SHEGETAYIR.V	Q07955	SRSF1_HUMAN	Serine/arginine-rich splicing factor 1 (Alternative-splicing factor 1) (ASF-1) (Splicing factor, arginine/serine-rich 1) (pre-mRNA-splicing factor SF2, P33 subunit)	SRSF1

1163,48	1162,895	1164,058	1163,53	0,058	K.IAEVDCTAER.N	Q8NB59	TXND5_HUMAN	Thioredoxin domain-containing protein 5 (Endoplasmic reticulum resident protein 46) (ER protein 46) (Erp46) (Thioredoxin-like protein p46)	TXNDC5
			1163,59	0,115	R.LDGAWWFLR.R	Q9GZM7	TINAL_HUMAN	Tubulointerstitial nephritis antigen-like (Glucocorticoid-inducible protein 5) (Oxidized LDL-responsive gene 2 protein) (OLRG-2) (Tubulointerstitial nephritis antigen-related protein) (TIN Ag-related protein) (TIN-Ag-RP)	TINAGL1
			1163,62	0,140	R.LFDQAFGLPR.L	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	HSPB1
			1163,63	0,149	R.LSEFGLIQEK.F	Q9H845	ACAD9_HUMAN	Acyl-CoA dehydrogenase family member 9, mitochondrial (ACAD-9) (EC 1.3.99.-)	ACAD9
1163,60	1163,016	1164,179	1163,59	0,006	R.LDGAWWFLR.R	Q9GZM7	TINAL_HUMAN	Tubulointerstitial nephritis antigen-like (Glucocorticoid-inducible protein 5) (Oxidized LDL-responsive gene 2 protein) (OLRG-2) (Tubulointerstitial nephritis antigen-related protein) (TIN Ag-related protein) (TIN-Ag-RP)	TINAGL1
			1163,62	0,019	R.LFDQAFGLPR.L	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	HSPB1
			1163,63	0,028	R.LSEFGLIQEK.F	Q9H845	ACAD9_HUMAN	Acyl-CoA dehydrogenase family member 9, mitochondrial (ACAD-9) (EC 1.3.99.-)	ACAD9
			1163,53	0,063	K.IAEVDCTAER.N	Q8NB59	TXND5_HUMAN	Thioredoxin domain-containing protein 5 (Endoplasmic reticulum resident protein 46) (ER protein 46) (Erp46) (Thioredoxin-like protein p46)	TXNDC5
1164,58	1163,993	1165,157	1164,57	0,003	R.LTAEDLFEAR.I	Q15149	PLEC_HUMAN	Plectin (PCN) (PLTN) (Hemidesmosomal protein 1) (HD1) (Plectin-1)	PLEC
1164,58	1164,001	1165,165	1164,57	0,011	R.LTAEDLFEAR.I	Q15149	PLEC_HUMAN	Plectin (PCN) (PLTN) (Hemidesmosomal protein 1) (HD1) (Plectin-1)	PLEC
1165,59	1165,006	1166,172	1165,54	0,050	K.AAYEALGDAR.K	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin (Renal carcinoma antigen NY-REN-32)]	LMNA
			1165,52	0,067	K.EDTEEHHLR.D	Q32P51	RA1L2_HUMAN	Heterogeneous nuclear ribonucleoprotein A1-like 2 (hnRNP A1-like 2) (hnRNP core protein A1-like 2)	HNRNPA1L2
			1165,52	0,067	K.EDTEEHHLR.D	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
1166,59	1166,006	1167,172	1166,52	0,068	K.DSAYPEELSR.V	P07686	HEXB_HUMAN	Beta-hexosaminidase subunit beta (EC 3.2.1.52) (Beta-N-acetylhexosaminidase subunit beta) (Hexosaminidase subunit B) (Cervical cancer proto-oncogene 7 protein) (HCC-7) (N-acetyl-beta-glucosaminidase subunit beta) [Cleaved into: Beta-hexosaminidase subunit beta chain B; Beta-hexosaminidase subunit beta chain A]	HEXB
			1166,49	0,095	K.CYEMASHLR.R	P07737	PROF1_HUMAN	Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I)	PFN1
			1166,45	0,138	K.SCAHDWVVE.-	P22392	NDKB_HUMAN	Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (EC 2.7.4.6) (C-myc purine-binding transcription factor PUF) (Histidine protein kinase NDKB) (EC 2.7.13.3) (nm23-H2)	NME2
1167,53	1166,945	1168,112	1167,57	0,038	K.FGEVVDCTLK.L	Q14103	HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1)	HNRNPD
			1167,57	0,038	K.FGEVVDCTIK.M	Q99729	ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein A/B (hnRNP A/B) (APOBEC1-binding protein 1) (ABBP-1)	HNRNPAB
			1167,57	0,038	R.FGEVVDCTIK.T	Q14979	HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like (hnRNP D-like) (hnRNP DL) (AU-rich element RNA-binding factor) (JKT41-binding protein) (Protein laAUF1)	HNRNPDL
			1167,57	0,042	R.NLPDFTWK.M	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			1167,59	0,061	R.LQAVTDDHIR.M	P30043	BLVRB_HUMAN	Flavin reductase (NADPH) (FR) (EC 1.5.1.30) (Biliverdin reductase B) (BVR-B) (EC 1.3.1.24) (Biliverdin-IX beta-reductase) (Green heme-binding protein) (GHBp) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR)	BLVRB
			1167,59	0,041	R.LQAVTDDHIR.M	P30043	BLVRB_HUMAN	Flavin reductase (NADPH) (FR) (EC 1.5.1.30) (Biliverdin reductase B) (BVR-B) (EC 1.3.1.24) (Biliverdin-IX beta-reductase) (Green heme-binding protein) (GHBp) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR)	BLVRB
1167,63	1167,047	1168,214	1167,59	0,041	R.LQAVTDDHIR.M	P30043	BLVRB_HUMAN	Flavin reductase (NADPH) (FR) (EC 1.5.1.30) (Biliverdin reductase B) (BVR-B) (EC 1.3.1.24) (Biliverdin-IX beta-reductase) (Green heme-binding protein) (GHBp) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR)	BLVRB
			1167,57	0,060	R.NLPDFTWK.M	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			1167,57	0,064	K.FGEVVDCTLK.L	Q14103	HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1)	HNRNPD
			1167,57	0,064	K.FGEVVDCTIK.M	Q99729	ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein A/B (hnRNP A/B) (APOBEC1-binding protein 1) (ABBP-1)	HNRNPAB
			1167,57	0,064	R.FGEVVDCTIK.T	Q14979	HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like (hnRNP D-like) (hnRNP DL) (AU-rich element RNA-binding factor) (JKT41-binding protein) (Protein laAUF1)	HNRNPDL
			1167,57	0,064	R.FGEVVDCTIK.T	Q14979	HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like (hnRNP D-like) (hnRNP DL) (AU-rich element RNA-binding factor) (JKT41-binding protein) (Protein laAUF1)	HNRNPDL
1168,67	1168,081	1169,250	1168,62	0,046	K.TGPNLHGLFGR.K	P99999	CYC_HUMAN	Cytochrome c	CYC5
			1168,58	0,087	K.QVHPDTGISSK.A	O60814	H2B1K_HUMAN	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK
			1168,58	0,087	K.QVHPDTGISSK.A	Q16778	H2B2E_HUMAN	Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q)	HIST2H2BE
			1168,50	0,162	R.SYVDPSTDER.L	Q15149	PLEC_HUMAN	Plectin (PCN) (PLTN) (Hemidesmosomal protein 1) (HD1) (Plectin-1)	PLEC
			1168,50	0,167	R.FWHDTCFR.C	Q13642	FHL1_HUMAN	Four and a half LIM domains protein 1 (FHL-1) (Skeletal muscle LIM-protein 1) (SLIM) (SLIM-1)	FHL1
			1168,50	0,168	K.EDTEEYNLR.D	P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3
1169,49	1168,910	1170,079	1169,51	0,018	K.YLDESSGGWR.D	O00115	DNS2A_HUMAN	Deoxyribonuclease-2-alpha (EC 3.1.22.1) (Acid DNase) (Deoxyribonuclease II alpha) (DNase II alpha) (Lysosomal DNase II) (R31240_2)	DNASE2
			1169,54	0,040	R.EIPYTFEDR.I	P34897	GLYM_HUMAN	Serine hydroxymethyltransferase, mitochondrial (SHMT) (EC 2.1.2.1) (Glycine hydroxymethyltransferase) (Serine methylase)	SHMT2
			1169,54	0,045	K.SADFTNFDP.R	P00918	CAH2_HUMAN	Carbonic anhydrase 2 (EC 4.2.1.1) (Carbonate dehydratase II) (Carbonic anhydrase C) (CAC) (Carbonic anhydrase II) (CA-II)	CA2
			1169,57	0,076	K.EQGFLSFWR.G	P12235	ADT1_HUMAN	ADP/ATP translocase 1 (ADP,ATP carrier protein 1) (ADP,ATP carrier protein, heart/skeletal muscle isoform T1) (Adenine nucleotide translocator 1) (ANT 1) (Solute carrier family 25 member 4)	SLC25A4
			1169,71	0,212	K.ILLAELEQLK.G	P08670	VIME_HUMAN	Vimentin	VIM
			1169,71	0,052	K.ILLAELEQLK.G	P08670	VIME_HUMAN	Vimentin	VIM

1170,53	1169,944	1171,115	1169,57	0,084	K.EQGFLSFWR.G	P12235	ADT1_HUMAN	ADP/ATP translocase 1 (ADP/ATP carrier protein 1) (ADP/ATP carrier protein, heart/skeletal muscle isoform T1) (Adenine nucleotide translocator 1) (ANT 1) (Solute carrier family 25 member 4)	SLC25A4
			1169,54	0,114	K.SADFTNFDRP.R	P00918	CAH2_HUMAN	Carbonic anhydrase 2 (EC 4.2.1.1) (Carbonate dehydratase II) (Carbonic anhydrase C) (CAC) (Carbonic anhydrase II) (CA-II)	CA2
			1169,54	0,119	R.EIPYTFEDR.I	P34897	GLYM_HUMAN	Serine hydroxymethyltransferase, mitochondrial (SHMT) (EC 2.1.2.1) (Glycine hydroxymethyltransferase) (Serine methylase)	SHMT2
			1169,51	0,142	K.YLDESSGGWR.D	O00115	DNS2A_HUMAN	Deoxyribonuclease-2-alpha (EC 3.1.22.1) (Acid DNase) (Deoxyribonuclease II alpha) (DNase II alpha) (Lysosomal DNase II) (R31240_2)	DNASE2
			1170,51	0,015	K.EHEEAVSVDR.V	Q13126	MTAP_HUMAN	S-methyl-5'-thioadenosine phosphorylase (EC 2.4.2.28) (5'-methylthioadenosine phosphorylase) (MTA phosphorylase) (MTAP) (MTAPase)	MTAP
			1170,60	0,070	K.FLDGIYSEK.G	P32969	RL9_HUMAN	60S ribosomal protein L9 (Large ribosomal subunit protein uL6)	RPL9; RPL9P7; RPL9P8; RPL9P9
1170,68	1170,093	1171,264	1170,66	0,134	K.LVILEGELER.A	P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	TPM4
			1170,66	0,134	R.SLHDAIMIVR.R	Q99832	TCPH_HUMAN	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein) [Cleaved into: T-complex protein 1 subunit eta, N-terminally processed]	CCT7
			1170,68	0,153	R.IALTDNALIAR.S	P18124	RL7_HUMAN	60S ribosomal protein L7 (Large ribosomal subunit protein uL30)	RPL7
			1170,68	0,004	R.IALTDNALIAR.S	P18124	RL7_HUMAN	60S ribosomal protein L7 (Large ribosomal subunit protein uL30)	RPL7
			1170,66	0,015	K.LVILEGELER.A	P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	TPM4
			1170,66	0,015	R.SLHDAIMIVR.R	Q99832	TCPH_HUMAN	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein) [Cleaved into: T-complex protein 1 subunit eta, N-terminally processed]	CCT7
1171,54	1170,953	1172,125	1170,60	0,079	K.FLDGIYSEK.G	P32969	RL9_HUMAN	60S ribosomal protein L9 (Large ribosomal subunit protein uL6)	RPL9; RPL9P7; RPL9P8; RPL9P9
			1170,51	0,164	K.EHEEAVSVDR.V	Q13126	MTAP_HUMAN	S-methyl-5'-thioadenosine phosphorylase (EC 2.4.2.28) (5'-methylthioadenosine phosphorylase) (MTA phosphorylase) (MTAP) (MTAPase)	MTAP
			1171,56	0,020	R.HQGVMMVGMGQK.D	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			1171,56	0,020	R.HQGVMMVGMGQK.D	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1171,56	0,020	R.HQGVMMVGMGQK.D	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1171,56	0,020	R.HQGVMMVGMGQK.D	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
1171,68	1171,089	1172,261	1171,56	0,020	R.HQGVMMVGMGQK.D	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1171,59	0,055	R.STLNEYIFGK.T	P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta (CapZ beta)	CAPZB
			1171,60	0,057	K.TLEDPDNLNVR.R	Q86VP6	CAND1_HUMAN	Cullin-associated NEDD8-dissociated protein 1 (Cullin-associated and neddylation-dissociated protein 1) (TBP-interacting protein of 120 kDa A) (TBP-interacting protein 120A) (p120 CAND1)	CAND1
			1171,62	0,080	K.LAEAQIEELR.Q	Q9NR28	DBLOH_HUMAN	Diablo homolog, mitochondrial (Direct IAP-binding protein with low pI) (Second mitochondria-derived activator of caspase) (Smac)	DIABLO
			1171,62	0,057	K.LAEAQIEELR.Q	Q9NR28	DBLOH_HUMAN	Diablo homolog, mitochondrial (Direct IAP-binding protein with low pI) (Second mitochondria-derived activator of caspase) (Smac)	DIABLO
			1171,60	0,080	K.TLEDPDNLNVR.R	Q86VP6	CAND1_HUMAN	Cullin-associated NEDD8-dissociated protein 1 (Cullin-associated and neddylation-dissociated protein 1) (TBP-interacting protein of 120 kDa A) (TBP-interacting protein 120A) (p120 CAND1)	CAND1
1172,64	1172,056	1173,228	1171,59	0,081	R.STLNEYIFGK.T	P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta (CapZ beta)	CAPZB
			1171,56	0,116	R.HQGVMMVGMGQK.D	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			1171,56	0,116	R.HQGVMMVGMGQK.D	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1171,56	0,116	R.HQGVMMVGMGQK.D	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1171,56	0,116	R.HQGVMMVGMGQK.D	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			1171,56	0,116	R.HQGVMMVGMGQK.D	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
1173,59	1173,006	1174,180	1172,53	0,116	K.FVMQEFSR.D	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (Erp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (Erp60)	PDIA3
			1172,50	0,146	R.FPAMSDAYDR.T	P00491	PNPH_HUMAN	Purine nucleoside phosphorylase (PNP) (EC 2.4.2.1) (Inosine phosphorylase) (Inosine-guanosine phosphorylase)	PNP
1174,52	1173,933	1175,107	1173,60	0,009	R.DGIIDKEDLR.D	Q96A32	MLRS_HUMAN	Myosin regulatory light chain 2, skeletal muscle isoform (Fast skeletal myosin light chain 2) (MLC2B)	MYLPF
1174,63	1174,043	1175,217	1174,62	0,096	R.FRIDELEPR.R	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1175,61	1175,023	1176,199	1174,62	0,014	R.FRIDELEPR.R	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1176,60	1176,008	1177,184	1175,59	0,017	K.MSAEINEIR.V	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL
			1176,58	0,019	K.SADTLWDIQK.D	P07195	LDHB_HUMAN	L-lactate dehydrogenase B chain (LDH-B) (EC 1.1.1.27) (LDH heart subunit) (LDH-H) (Renal carcinoma antigen NY-RN-46)	LDHB
			1176,57	0,025	R.YEGFFSLWK.G	Q02978	M2OM_HUMAN	Mitochondrial 2-oxoglutarate/malate carrier protein (OGCP) (Solute carrier family 25 member 11)	SLC25A11

1177,53	1176,943	1178,121	1177,57	0,037	R.GRMTLADIER.I	Q9UJS0	CMC2_HUMAN	Calcium-binding mitochondrial carrier protein Aralar2 (Citrin) (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13)	SLC25A13
			1177,61	0,075	R.IFEGTNDILR.L	P49748	ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial (VLCAD) (EC 1.3.8.9)	ACADVL
			1177,62	0,085	R.YELGSGLAVALR.S	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
			1177,67	0,139	R.VIFFLPWQK.M	P43304	GPDM_HUMAN	Glycerol-3-phosphate dehydrogenase, mitochondrial (GPD- GPD2 M) (GPDH-M) (EC 1.1.5.3) (mtGPD)	
1177,68	1177,092	1178,270	1177,67	0,010	R.VIFFLPWQK.M	P43304	GPDM_HUMAN	Glycerol-3-phosphate dehydrogenase, mitochondrial (GPD- GPD2 M) (GPDH-M) (EC 1.1.5.3) (mtGPD)	
			1177,62	0,064	R.YELGSGLAVALR.S	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
			1177,61	0,074	R.IFEGTNDILR.L	P49748	ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial (VLCAD) (EC 1.3.8.9)	ACADVL
			1177,57	0,113	R.GRMTLADIER.I	Q9UJS0	CMC2_HUMAN	Calcium-binding mitochondrial carrier protein Aralar2 (Citrin) (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13)	SLC25A13
1178,59	1178,003	1179,181	1178,56	0,033	K.EVFEDAAEIR.L	P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL
			1178,56	0,036	K.TGYFVGISR.M	P23142	FBLN1_HUMAN	Fibulin-1 (FBL-1)	FBLN1
1179,62	1179,034	1180,214	1179,62	0,002	R.FLYIWPNAR.I	Q9HCC0	MCCB_HUMAN	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial (MCCase subunit beta) (EC 6.4.1.4) (3-methylcrotonyl-CoA carboxylase 2) (3-methylcrotonyl-CoA carboxylase non-biotin-containing subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase subunit beta)	MCCC2
			1179,58	0,042	R.SPAHYAGYWK.A	P42126	ECI1_HUMAN	Enoyl-CoA delta isomerase 1, mitochondrial (EC 5.3.3.8) (3,2-trans-enoil-CoA isomerase) (Delta(3),Delta(2)-enoil-CoA isomerase) (D3,D2-enoil-CoA isomerase) (Dodecenoyl CoA isomerase)	ECI1
1180,64	1180,051	1181,231	1180,61	0,029	R.ISGLIYEETR.G	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
1181,63	1181,036	1182,218	1181,59	0,041	K.FMQASEDLLK.E	P15531	NDKA_HUMAN	Nucleoside diphosphate kinase A (NDK A) (NDP kinase A) (EC 2.7.4.6) (Granzyme A-activated DNase) (GAAD) (Metastasis inhibition factor nm23) (NM23-H1) (Tumor metastatic process-associated protein)	NME1
1182,61	1182,022	1183,204	1182,61	0,007	R.TLEGELHDLR.G	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
			1182,58	0,028	K.APDFVIFYAPR.L	P15311	EZR1_HUMAN	Ezrin (Cyto villin) (Villin-2) (p81)	EZR
			1182,58	0,028	K.APDFVIFYAPR.L	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			1182,57	0,048	R.YLSEVASGDNK.Q	P31946	1433B_HUMAN	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHA8
			1182,49	0,127	K.CYEMASHLR.R	P07737	PROF1_HUMAN	Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I)	PFN1
1183,60	1183,008	1184,192	1183,51	0,093	R.NYYGYQGYR.-	Q1KMD3	HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 2 (Scaffold-attachment factor A2) (SAF-A2)	HNRNPUL2
1184,32	1183,727	1184,911							
1184,57	1183,976	1185,160							
1185,39	1184,793	1185,979							
1185,62	1185,028	1186,213							
1186,41	1185,816	1187,003	1186,54	0,127	K.DIVENYFMR.D	Q13263	TIF1B_HUMAN	Transcription intermediary factor 1-beta (TIF1-beta) (E3 SUMO-protein ligase TRIM28) (EC 2.3.2.27) (KRAB-associated protein 1) (KAP-1) (KRAB-interacting protein 1) (KRIP-1) (Nuclear corepressor KAP-1) (RING finger protein 96) (RING-type E3 ubiquitin transferase TIF1-beta) (Tripartite motif-containing protein 28)	TRIM28
			1186,60	0,191	K.QEELEAALQR.G	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7)	KRT7
1186,62	1186,029	1187,216	1186,60	0,023	K.QEELEAALQR.G	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7)	KRT7
			1186,54	0,086	K.DIVENYFMR.D	Q13263	TIF1B_HUMAN	Transcription intermediary factor 1-beta (TIF1-beta) (E3 SUMO-protein ligase TRIM28) (EC 2.3.2.27) (KRAB-associated protein 1) (KAP-1) (KRAB-interacting protein 1) (KRIP-1) (Nuclear corepressor KAP-1) (RING finger protein 96) (RING-type E3 ubiquitin transferase TIF1-beta) (Tripartite motif-containing protein 28)	TRIM28
1187,52	1186,928	1188,115	1187,67	0,153	K.SILFVPTSAPR.G	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
1187,66	1187,062	1188,249	1187,67	0,019	K.SILFVPTSAPR.G	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
1188,54	1187,947	1189,135	1188,53	0,012	K.FVMQEEFSR.D	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (Erp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (Erp60)	PDIA3
			1188,64	0,100	R.DLTLEENQVK.K	Q14683	SMC1A_HUMAN	Structural maintenance of chromosomes protein 1A (SMC protein 1A) (SMC-1-alpha) (SMC-1A) (Sb1.8)	SMC1A
			1188,64	0,100	K.IDTIEIHDR.Q	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNP2B1
1188,67	1188,071	1189,260	1188,64	0,025	R.DLTLEENQVK.K	Q14683	SMC1A_HUMAN	Structural maintenance of chromosomes protein 1A (SMC protein 1A) (SMC-1-alpha) (SMC-1A) (Sb1.8)	SMC1A
			1188,64	0,025	K.IDTIEIHDR.Q	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNP2B1

			1188,53	0,136	K.FVMQEEFSR.D	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	
1189,63	1189,033	1190,223	1189,65	0,026	K.DSTLIMQLLR.D	P31947	14335_HUMAN	14-3-3 protein sigma (Epithelial cell marker protein 1) (Stratfin)	SFN
			1189,65	0,026	K.DSTLIMQLLR.D	P62258	1433E_HUMAN	14-3-3 protein epsilon (14-3-3E)	YWHAE
			1189,65	0,026	K.DSTLIMQLLR.D	P61981	1433G_HUMAN	14-3-3 protein gamma (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein gamma, N-terminally processed]	YWHAH
			1189,65	0,026	K.DSTLIMQLLR.D	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
			1189,65	0,026	K.DSTLIMQLLR.D	P31946	1433B_HUMAN	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHA8
			1189,65	0,026	K.DSTLIMQLLR.D	P27348	1433T_HUMAN	14-3-3 protein theta (14-3-3 protein T-cell) (14-3-3 protein tau) (Protein HS1)	YWHAQ
			1189,65	0,026	R.EDIQRFILR.S	Q8IVL6	P3H3_HUMAN	Prolyl 3-hydroxylase 3 (EC 1.14.11.7) (Leprecan-like protein 2) (Protein B)	P3H3
			1189,65	0,026	K.DSTLIMQLLR.D	Q04917	1433F_HUMAN	14-3-3 protein eta (Protein AS1)	YWHAH
			1189,60	0,032	R.FWPAIDGRL.R	Q8IV08	PLD3_HUMAN	Phospholipase D3 (PLD 3) (EC 3.1.4.4) (Choline phosphatase 3) (HindIII K4L homolog) (Hu-K4) (Phosphatidylcholine-hydrolyzing phospholipase D3)	PLD3
1190,64	1190,040	1191,231	1190,63	0,009	K.NYPTLANIER.K	Q9UHK0	NUFP1_HUMAN	Nuclear fragile X mental retardation-interacting protein 1 (Nuclear FMRP-interacting protein 1)	NUFP1
			1190,61	0,026	K.DFDVFPVVR.W	P01024	CO3_HUMAN	Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
			1190,53	0,102	R.RDHFEAMR.F	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			1190,50	0,138	R.GDYDAFFEAR.E	O75368	SH3L1_HUMAN	SH3 domain-binding glutamic acid-rich-like protein	SH3BGR1
1191,63	1191,039	1192,230	1192,64	0,001	K.FEVDIMLIR.D	P00491	PNPH_HUMAN	Purine nucleoside phosphorylase (PNP) (EC 2.4.2.1) (Inosine phosphorylase) (Inosine-guanosine phosphorylase)	PNP
1192,64	1192,042	1193,235	1192,64	0,001	R.QINWTVLYR.R	P83731	RL24_HUMAN	60S ribosomal protein L24 (60S ribosomal protein L30) (Large ribosomal subunit protein eL24)	RPL24
1193,55	1192,958	1194,151	1193,56	0,007	K.TLADAEADVFR.G	Q02252	MMSA_HUMAN	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial (MMSDH) (Malonate-semialdehyde dehydrogenase [acylating]) (EC 1.2.1.18) (EC 1.2.1.27) (Aldehyde dehydrogenase family 6 member A1)	ALDH6A1
			1193,57	0,018	K.MGDHLTNLHR.L	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
1193,64	1193,045	1194,238	1193,57	0,069	K.MGDHLTNLHR.L	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
			1193,56	0,080	K.TLADAEADVFR.G	Q02252	MMSA_HUMAN	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial (MMSDH) (Malonate-semialdehyde dehydrogenase [acylating]) (EC 1.2.1.18) (EC 1.2.1.27) (Aldehyde dehydrogenase family 6 member A1)	ALDH6A1
1194,55	1193,954	1195,148							
1194,68	1194,086	1195,281							
1195,47	1194,871	1196,066							
1195,56	1194,963	1196,159							
1195,68	1195,082	1196,278							
1196,57	1195,969	1197,166	1196,55	0,015	R.AEAIAWYQTK.F	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolelectin) (Type-II keratin Kb7)	KRT7
			1196,59	0,022	K.SVLYFTQFK.A	Q969H8	MYDGF_HUMAN	Myeloid-derived growth factor (MYDGF)	MYDGF
			1196,63	0,064	R.LVQAQFTDK.H	Q06830	PRDX1_HUMAN	Peroxioredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
1196,67	1196,073	1197,270	1196,63	0,040	R.LVQAQFTDK.H	Q06830	PRDX1_HUMAN	Peroxioredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
			1196,59	0,082	K.SVLYFTQFK.A	Q969H8	MYDGF_HUMAN	Myeloid-derived growth factor (MYDGF)	MYDGF
			1196,55	0,119	R.AEAIAWYQTK.F	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolelectin) (Type-II keratin Kb7)	KRT7
1197,63	1197,028	1198,226	1197,57	0,056	K.EATDAIGHLDR.Q	Q12906	ILF3_HUMAN	Interleukin enhancer-binding factor 3 (Double-stranded RNA-binding protein 76) (DRBP76) (M-phase phosphoprotein 4) (MPP4) (Nuclear factor associated with dsRNA) (NFAR) (Nuclear factor of activated T-cells 90 kDa) (NF-AT-90) (Translational control protein 80) (TCP80)	ILF3
			1197,56	0,066	R.MVYVTDVAGR.T	Q14112	NID2_HUMAN	Nidogen-2 [NID-2] (Osteonidogen)	NID2
			1197,56	0,071	R.SMQDVVEDFK.N	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolelectin) (Type-II keratin Kb7)	KRT7
			1197,51	0,118	R.DAPQDFHPRD.V	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
1198,49	1197,895	1199,093	1198,51	0,015	K.DSVVGDEAQSK.R	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1198,51	0,015	K.DSVVGDEAQSK.R	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1198,51	0,015	K.DSVVGDEAQSK.R	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1198,51	0,015	K.DSVVGDEAQSK.R	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			1198,61	0,114	R.ALVSAGNPGAWR.G	O43837	IDH3B_HUMAN	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial (Isocitric dehydrogenase subunit beta) (NAD(+)-specific IDH subunit beta)	IDH3B
			1198,71	0,213	R.AVFPISVIGPRP.H	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB

1198,71	1198,110	1199,309	1198,71	0,213	R.AVFPSIVGRPR.H	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1198,71	0,213	R.AVFPSIVGRPR.H	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1198,71	0,213	R.AVFPSIVGRPR.H	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1198,71	0,213	R.AVFPSIVGRPR.Q	Q658J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			1198,71	0,003	R.AVFPSIVGRPR.H	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			1198,71	0,003	R.AVFPSIVGRPR.H	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1198,71	0,003	R.AVFPSIVGRPR.H	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1198,71	0,003	R.AVFPSIVGRPR.H	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1198,71	0,003	R.AVFPSIVGRPR.Q	Q658J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			1198,61	0,101	R.ALVSAGNPGAWR.G	O43837	IDH3B_HUMAN	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial (Isocitric dehydrogenase subunit beta) (NAD(+)-specific IDH subunit beta)	IDH3B
			1198,51	0,201	K.DSYVGDEAQSK.R	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1198,51	0,201	K.DSYVGDEAQSK.R	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
1198,91	1198,314	1199,513	1198,51	0,201	K.DSYVGDEAQSK.R	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1198,51	0,201	K.DSYVGDEAQSK.R	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			1198,71	0,207	R.AVFPSIVGRPR.H	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			1198,71	0,207	R.AVFPSIVGRPR.H	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1198,71	0,207	R.AVFPSIVGRPR.H	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1198,71	0,207	R.AVFPSIVGRPR.H	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1198,71	0,207	R.AVFPSIVGRPR.Q	Q658J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			1198,61	0,306	R.ALVSAGNPGAWR.G	O43837	IDH3B_HUMAN	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial (Isocitric dehydrogenase subunit beta) (NAD(+)-specific IDH subunit beta)	IDH3B
			1198,51	0,405	K.DSYVGDEAQSK.R	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1198,51	0,405	K.DSYVGDEAQSK.R	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1198,51	0,405	K.DSYVGDEAQSK.R	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1198,51	0,405	K.DSYVGDEAQSK.R	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
1199,52	1198,924	1200,124	1199,62	0,095	R.DLLDPAWEK.Q	P12814	ACTN1_HUMAN	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (F-actin cross-linking protein) (Non-muscle alpha-actinin-1)	ACTN1
			1199,62	0,095	R.DLLDPAWEK.Q	O43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
			1199,62	0,095	R.DLLDPAWEK.Q	P35609	ACTN2_HUMAN	Alpha-actinin-2 (Alpha-actinin skeletal muscle isoform 2) (F-actin cross-linking protein)	ACTN2
1199,71	1199,110	1200,310	1199,62	0,091	R.DLLDPAWEK.Q	P12814	ACTN1_HUMAN	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (F-actin cross-linking protein) (Non-muscle alpha-actinin-1)	ACTN1
			1199,62	0,091	R.DLLDPAWEK.Q	O43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
			1199,62	0,091	R.DLLDPAWEK.Q	P35609	ACTN2_HUMAN	Alpha-actinin-2 (Alpha-actinin skeletal muscle isoform 2) (F-actin cross-linking protein)	ACTN2
1200,71	1200,105	1201,306	1200,53	0,175	R.EAADKEEPPSK.K	Q10570	CPSF1_HUMAN	Cleavage and polyadenylation specificity factor subunit 1 (Cleavage and polyadenylation specificity factor 160 kDa subunit) (CPSF 160 kDa subunit)	CPSF1
1200,71	1200,108	1201,308	1200,53	0,177	R.EAADKEEPPSK.K	Q10570	CPSF1_HUMAN	Cleavage and polyadenylation specificity factor subunit 1 (Cleavage and polyadenylation specificity factor 160 kDa subunit) (CPSF 160 kDa subunit)	CPSF1
1201,63	1201,032	1202,234	1201,65	0,014	K.AGLLGLLEEMR.D	P12882	MYH1_HUMAN	Myosin-1 (Myosin heavy chain 1) (Myosin heavy chain 2x) (MyHC-2x) (Myosin heavy chain IIX/d) (MyHC-IIX/d) (Myosin heavy chain, skeletal muscle, adult 1)	MYH1
			1201,60	0,038	K.LEAIAEAEER.G	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcoleictin) (Type-II keratin Kb7)	KRT7
			1201,54	0,096	R.FLDNFDSEK.D	Q13938	CAYP1_HUMAN	Calcyphosin (Calcyphosine)	CAPS
1201,70	1201,099	1202,300	1201,65	0,052	K.AGLLGLLEEMR.D	P12882	MYH1_HUMAN	Myosin-1 (Myosin heavy chain 1) (Myosin heavy chain 2x) (MyHC-2x) (Myosin heavy chain IIX/d) (MyHC-IIX/d) (Myosin heavy chain, skeletal muscle, adult 1)	MYH1
			1201,60	0,104	K.LEAIAEAEER.G	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcoleictin) (Type-II keratin Kb7)	KRT7
			1201,54	0,162	R.FLDNFDSEK.D	Q13938	CAYP1_HUMAN	Calcyphosin (Calcyphosine)	CAPS
1202,65	1202,052	1203,254	1203,54	0,119	R.VAVEEVDEEGK.F	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
1203,65	1203,053	1204,256							
1204,64	1204,035	1205,240	1204,61	0,026	K.ELFDPIISDR.H	P06732	KCRM_HUMAN	Creatine kinase M-type (EC 2.7.3.2) (Creatine kinase M chain) (Creatine phosphokinase M-type) (CPK-M) (M-CK)	CKM
1205,63	1205,025	1206,231							

1206,33	1205,730	1206,937	1206,56	0,223	K.AVDTWSWGER.A	Q08380	LG3BP_HUMAN	Galectin-3-binding protein (Basement membrane autoantigen p105) (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (MAC2BP) (Mac-2 BP) (Tumor-associated antigen 90K)	LGALS3BP
1206,50	1205,896	1207,102	1206,56	0,058	K.AVDTWSWGER.A	Q08380	LG3BP_HUMAN	Galectin-3-binding protein (Basement membrane autoantigen p105) (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (MAC2BP) (Mac-2 BP) (Tumor-associated antigen 90K)	LGALS3BP
1206,65	1206,050	1207,257	1206,56	0,097	K.AVDTWSWGER.A	Q08380	LG3BP_HUMAN	Galectin-3-binding protein (Basement membrane autoantigen p105) (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (MAC2BP) (Mac-2 BP) (Tumor-associated antigen 90K)	LGALS3BP
1207,62	1207,020	1208,228	1207,67	0,046	R.FPLGESFLVAK.G	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1208,65	1208,047	1209,255	1208,64	0,015	K.FEVGDI MLIR.D	P00491	PNPH_HUMAN	Purine nucleoside phosphorylase (PNP) (EC 2.4.2.1) (Inosine phosphorylase) (Inosine-guanosine phosphorylase)	PNP
			1208,60	0,051	R.VEVTEFEDIK.S	Q01105	SET_HUMAN	Protein SET (HLA-DR-associated protein II) (Inhibitor of granzyme A-activated DNase) (IGAAD) (PHAPII) (Phosphatase 2A inhibitor I2PP2A) (I-2PP2A) (Template-activating factor I) (TAF-I)	SET
1209,63	1209,021	1210,230	1209,57	0,055	K.MGDHLTNLHR.L	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
			1209,54	0,089	R.LTNSMMMHGR.N	P46782	R55_HUMAN	40S ribosomal protein S5 (Small ribosomal subunit protein u57) [Cleaved into: 40S ribosomal protein S5, N-terminally processed]	RPS5
1210,56	1209,953	1211,164	1210,55	0,005	K.KYDEELEER.L	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein WS3-10) TAGLN (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
			1210,59	0,031	R.KDAEAWFTSR.T	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1210,74	0,185	R.VLPSIVNEVLK.S	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
1210,68	1210,078	1211,289	1210,74	0,060	R.VLPSIVNEVLK.S	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
			1210,59	0,094	R.KDAEAWFTSR.T	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1210,55	0,130	K.KYDEELEER.L	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein WS3-10) TAGLN (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
1211,38	1210,774	1211,985	1211,67	0,287	R.QITVNDLPVGR.S	P32119	PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
			1211,67	0,287	R.QITVNDLPVGR.S	Q06830	PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
1211,53	1210,924	1212,136	1211,67	0,136	R.QITVNDLPVGR.S	P32119	PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
			1211,67	0,136	R.QITVNDLPVGR.S	Q06830	PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
1211,68	1211,075	1212,286	1211,67	0,015	R.QITVNDLPVGR.S	P32119	PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
			1211,67	0,015	R.QITVNDLPVGR.S	Q06830	PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
1212,38	1211,775	1212,988	1212,47	0,091	K.YCDPDSYHR.R	P26368	U2AF2_HUMAN	Splicing factor U2AF 65 kDa subunit (U2 auxiliary factor 65 kDa subunit) (hU2AF(65)) (hU2AF65) (U2 snRNP auxiliary factor large subunit)	U2AF2
			1212,55	0,166	K.DKDNFMWTR.Q	P61160	ARP2_HUMAN	Actin-related protein 2 (Actin-like protein 2)	ACTR2
			1212,57	0,190	R.VEEVGPYTYR.E	Q14108	SCR2_HUMAN	Lysosome membrane protein 2 (85 kDa lysosomal membrane sialoglycoprotein) (LGP85) (CD36 antigen-like 2) (Lysosome membrane protein II) (LIMP II) (Scavenger receptor class B member 2) (CD antigen CD36)	SCARB2
1212,65	1212,045	1213,258	1212,57	0,080	R.VEEVGPYTYR.E	Q14108	SCR2_HUMAN	Lysosome membrane protein 2 (85 kDa lysosomal membrane sialoglycoprotein) (LGP85) (CD36 antigen-like 2) (Lysosome membrane protein II) (LIMP II) (Scavenger receptor class B member 2) (CD antigen CD36)	SCARB2
			1212,55	0,104	K.DKDNFMWTR.Q	P61160	ARP2_HUMAN	Actin-related protein 2 (Actin-like protein 2)	ACTR2
			1212,47	0,179	K.YCDPDSYHR.R	P26368	U2AF2_HUMAN	Splicing factor U2AF 65 kDa subunit (U2 auxiliary factor 65 kDa subunit) (hU2AF(65)) (hU2AF65) (U2 snRNP auxiliary factor large subunit)	U2AF2
1213,64	1213,032	1214,246	1213,63	0,009	R.WLQGSQELPR.E	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
			1213,66	0,018	R.ALPSEEWLR.L	P26640	SYVC_HUMAN	Valine--tRNA ligase (EC 6.1.1.9) (Protein G7a) (Valyl-tRNA synthetase) (ValRS)	VAR5
			1213,68	0,038	K.LVPGGKATLVMK.K	Q9UQE7	SMC3_HUMAN	Structural maintenance of chromosomes protein 3 (SMC protein 3) (SMC-3) (Basement membrane-associated chondroitin proteoglycan) (Bamacan) (Chondroitin sulfate proteoglycan 6) (Chromosome-associated polypeptide) (hCAP)	SMC3
			1213,52	0,116	K.DITSDTSGDFR.N	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin II) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
1214,58	1213,974	1215,189	1214,57	0,013	K.EFSIDVGYER.F	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
			1214,60	0,017	K.NLQYYDISAK.S	P62826	RAN_HUMAN	GTP-binding nuclear protein Ran (Androgen receptor-associated protein 24) (GTPase Ran) (Ras-like protein TC4) (Ras-related nuclear protein)	RAN
			1214,56	0,025	K.ASIHEAWTDGK.E	P12814	ACTN1_HUMAN	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (F-actin cross-linking protein) (Non-muscle alpha-actinin-1)	ACTN1
			1214,56	0,025	K.ASIHEAWTDGK.E	Q43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4

1214,63	1214,018	1215,233	1214,60	0,027	K.NLQYYDISAK.S	P62826	RAN_HUMAN	GTP-binding nuclear protein Ran (Androgen receptor-associated protein 24) (GTPase Ran) (Ras-like protein TC4) (Ras-related nuclear protein)	RAN
			1214,57	0,057	K.EFSIDVGYER.F	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
			1214,56	0,069	K.ASIHEAWTDGK.E	P12814	ACTN1_HUMAN	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (F-actin cross-linking protein) (Non-muscle alpha-actinin-1)	ACTN1
			1214,56	0,069	K.ASIHEAWTDGK.E	O43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
1215,49	1214,878	1216,093	1215,67	0,186	K.LASDLLEWIR.R	O43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
			1215,67	0,186	K.LASDLLEWIR.R	P12814	ACTN1_HUMAN	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (F-actin cross-linking protein) (Non-muscle alpha-actinin-1)	ACTN1
1215,64	1215,033	1216,249	1215,67	0,031	K.LASDLLEWIR.R	O43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
			1215,67	0,031	K.LASDLLEWIR.R	P12814	ACTN1_HUMAN	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (F-actin cross-linking protein) (Non-muscle alpha-actinin-1)	ACTN1
1216,65	1216,041	1217,257	1216,64	0,005	K.ELAPFEELR.Q	Q9UHA4	LTOR3_HUMAN	Regulator complex protein LAMTOR3 (Late endosomal/lysosomal adaptor and MAPK and MTOR activator 3) (MEK-binding partner 1) (Mpl1) (Mitogen-activated protein kinase kinase 1-interacting protein 1) (Mitogen-activated protein kinase scaffold protein 1)	LAMTOR3
			1216,61	0,040	R.VVESLDVGQDR.V	P12111	COL6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1217,43	1216,822	1218,039	1217,53	0,096	R.NSWGEPWGER.G	Q9UBR2	CATZ_HUMAN	Cathepsin Z (EC 3.4.18.1) (Cathepsin P) (Cathepsin X)	CTS2
			1217,65	0,220	K.IIQLDDYPK.C	P05388	RLA0_HUMAN	60S acidic ribosomal protein P0 (60S ribosomal protein L10E) (Large ribosomal subunit protein uL10)	RPLP0
1217,64	1217,035	1218,252	1217,65	0,007	K.IIQLDDYPK.C	P05388	RLA0_HUMAN	60S acidic ribosomal protein P0 (60S ribosomal protein L10E) (Large ribosomal subunit protein uL10)	RPLP0
			1217,53	0,117	R.NSWGEPWGER.G	Q9UBR2	CATZ_HUMAN	Cathepsin Z (EC 3.4.18.1) (Cathepsin P) (Cathepsin X)	CTS2
1218,65	1218,037	1219,256	1218,67	0,023	R.VAQLEQVYIR.G	P62318	SMD3_HUMAN	Small nuclear ribonucleoprotein Sm D3 (Sm-D3) (snRNP core protein D3)	SNRPD3
1219,40	1218,786	1220,005	1219,56	0,165	R.ERLELCDER.V	P07919	QCR6_HUMAN	Cytochrome b-c1 complex subunit 6, mitochondrial (Complex III subunit 6) (Complex III subunit VIII) (Cytochrome c1 non-heme 11 kDa protein) (Mitochondrial hinge protein) (Ubiquinol-cytochrome c reductase complex 11 kDa protein)	UQCRH
			1219,59	0,194	K.SLEDQVEMLR.T	P14314	GLU2B_HUMAN	Glucosidase 2 subunit beta (80K-H protein) (Glucosidase II subunit beta) (Protein kinase C substrate 60.1 kDa protein heavy chain) (PKCSH)	PRKCSH
1219,67	1219,056	1220,276	1219,59	0,076	K.SLEDQVEMLR.T	P14314	GLU2B_HUMAN	Glucosidase 2 subunit beta (80K-H protein) (Glucosidase II subunit beta) (Protein kinase C substrate 60.1 kDa protein heavy chain) (PKCSH)	PRKCSH
			1219,56	0,106	R.ERLELCDER.V	P07919	QCR6_HUMAN	Cytochrome b-c1 complex subunit 6, mitochondrial (Complex III subunit 6) (Complex III subunit VIII) (Cytochrome c1 non-heme 11 kDa protein) (Mitochondrial hinge protein) (Ubiquinol-cytochrome c reductase complex 11 kDa protein)	UQCRH
1220,49	1219,880	1221,100	1220,51	0,021	K.HEQEYMEVR.E	Q15363	TMED2_HUMAN	Transmembrane emp24 domain-containing protein 2 (Membrane protein p24A) (p24) (p24 family protein beta-1) (p24beta1)	TMED2
			1220,61	0,116	K.NFSPVDAAFR.Q	P02790	HEMO_HUMAN	Hemopexin (Beta-1B-glycoprotein)	HPX
			1220,65	0,156	K.VSTVMDTVGRR.L	Q9H845	ACAD9_HUMAN	Acyl-CoA dehydrogenase family member 9, mitochondrial (ACAD-9) (EC 1.3.99.-)	ACAD9
			1220,65	0,156	R.TAAENEFVLK.K	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cyokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7)	KRT7
1220,68	1220,069	1221,290	1220,65	0,033	K.VSTVMDTVGRR.L	Q9H845	ACAD9_HUMAN	Acyl-CoA dehydrogenase family member 9, mitochondrial (ACAD-9) (EC 1.3.99.-)	ACAD9
			1220,65	0,033	R.TAAENEFVLK.K	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cyokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7)	KRT7
			1220,61	0,074	K.NFSPVDAAFR.Q	P02790	HEMO_HUMAN	Hemopexin (Beta-1B-glycoprotein)	HPX
			1220,51	0,169	K.HEQEYMEVR.E	Q15363	TMED2_HUMAN	Transmembrane emp24 domain-containing protein 2 (Membrane protein p24A) (p24) (p24 family protein beta-1) (p24beta1)	TMED2
1221,67	1221,060	1222,282	1221,63	0,038	R.VFEFGGPEVLK.L	Q08257	QOR_HUMAN	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-crystallin)	CRYZ
			1221,63	0,040	K.QMEQVAQFLK.A	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein W53-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
			1221,60	0,068	K.DYIALNEDLR.S	P30508	1C12_HUMAN	HLA class I histocompatibility antigen, Cw-12 alpha chain (MHC class I antigen Cw*12)	HLA-C
			1221,60	0,068	K.DYIALNEDLR.S	P16190	1A33_HUMAN	HLA class I histocompatibility antigen, A-33 alpha chain (Aw-19) (Aw-33) (MHC class I antigen A*33)	HLA-A
			1221,58	0,092	K.FYSVNVDSK.L	O00483	NDUA4_HUMAN	Cytochrome c oxidase subunit NDUF4A (Complex I-MLRQ) (CI-MLRQ) (NADH-ubiquinone oxidoreductase MLRQ subunit)	NDUF4A
1221,67	1221,060	1222,282	1221,63	0,038	R.VFEFGGPEVLK.L	Q08257	QOR_HUMAN	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-crystallin)	CRYZ
			1221,63	0,040	K.QMEQVAQFLK.A	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein W53-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
			1221,60	0,069	K.DYIALNEDLR.S	P30508	1C12_HUMAN	HLA class I histocompatibility antigen, Cw-12 alpha chain (MHC class I antigen Cw*12)	HLA-C
			1221,60	0,069	K.DYIALNEDLR.S	P16190	1A33_HUMAN	HLA class I histocompatibility antigen, A-33 alpha chain (Aw-19) (Aw-33) (MHC class I antigen A*33)	HLA-A
			1221,58	0,092	K.FYSVNVDSK.L	O00483	NDUA4_HUMAN	Cytochrome c oxidase subunit NDUF4A (Complex I-MLRQ) (CI-MLRQ) (NADH-ubiquinone oxidoreductase MLRQ subunit)	NDUF4A
1222,63	1222,016	1223,238	1222,60	0,029	K.GIGTDEFTLNR.I	P12429	ANXA3_HUMAN	Annexin A3 (35-alpha calcimedin) (Annexin III) (Annexin-3) (Inositol 1,2-cyclic phosphate 2-phosphohydrolase) (Lipocortin III) (Placental anticoagulant protein III) (PAP-III)	ANXA3
			1222,59	0,032	K.TPAQDYASELK.A	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1222,59	0,035	R.SSSGLEWESK.S	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
1222,66	1222,052	1223,275	1222,60	0,065	K.GIGTDEFTLNR.I	P12429	ANXA3_HUMAN	Annexin A3 (35-alpha calcimedin) (Annexin III) (Annexin-3) (Inositol 1,2-cyclic phosphate 2-phosphohydrolase) (Lipocortin III) (Placental anticoagulant protein III) (PAP-III)	ANXA3

1223,64	1223,026	1224,249	1222,59	0,069	K.TPAQYDASELK.A	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1222,59	0,072	R.SSSGLEWESK.S	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
			1223,64	0,003	R.AGVLAHLEER.D	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle Ila) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain Ila) (NMMHC II-a) (NMMHC-IIA)	MYH9
1224,65	1224,034	1225,259	1223,74	0,104	K.TPASQGVLPK.S	O95813	CER1_HUMAN	Cerberus (Cerberus-related protein) (DAN domain family member 4)	CER1
			1224,62	0,030	R.ETYLAILMDR.S	Q96199	SUCB2_HUMAN	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial (EC 6.2.1.4) (GTP-specific succinyl-CoA synthetase subunit beta) (G-SCS) (GTPSCS) (Succinyl-CoA synthetase beta-G chain) (SCS-betaG)	SUCLG2
			1224,45	0,194	R.NMSACWQDGR.F	P35442	TSP2_HUMAN	Thrombospondin-2	THBS2
1225,65	1225,039	1226,265	1225,61	0,044	K.ISNIPDEYFK.R	P51884	LUM_HUMAN	Lumican (Keratan sulfate proteoglycan lumican) (KSPG lumican)	LUM
			1225,57	0,086	K.DIISDTSGDFR.K	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1225,56	0,095	R.EATTEFSVDAR.A	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
1226,66	1226,044	1227,271	1226,60	0,058	R.FKDLGEENFK.A	P02768	ALBU_HUMAN	Serum albumin	ALB
			1226,56	0,095	K.VIMDYESLEK.A	P00491	PNPH_HUMAN	Purine nucleoside phosphorylase (PNP) (EC 2.4.2.1) (Inosine phosphorylase) (Inosine-guanosine phosphorylase)	PNP
			1226,77	0,112	R.LIALLEVLSQL.K	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
1227,64	1227,025	1228,253	1226,77	0,112	R.LIALLEVLSQL.R	O75369	FLNB_HUMAN	Filamin-B (FLN-B) (ABP-278) (ABP-280 homolog) (Actin-binding-like protein) (Beta-filamin) (Filamin homolog 1) (Fh1) (Filamin-3) (Thyroid autoantigen) (Truncated actin-binding protein) (Truncated ABP)	FLNB
			1227,59	0,047	K.NHEEEISTLR.G	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1227,55	0,088	R.EVCGFAPYER.R	Q9Y3U8	RL36_HUMAN	60S ribosomal protein L36 (Large ribosomal subunit protein eL36)	RPL36
1228,67 1229,56	1228,055 1228,948	1229,283 1230,178	1229,56	0,007	R.DFMVYSQDPK.D	P55084	ECHB_HUMAN	Trifunctional enzyme subunit beta, mitochondrial (TP-beta) [Includes: 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase)]	HADHB
			1229,60	0,034	R.ISEQFTAMFR.R	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1229,60	0,034	R.ISEQFTAMFR.R	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
1229,69	1229,073	1230,302	1229,60	0,090	R.ISEQFTAMFR.R	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1229,60	0,090	R.ISEQFTAMFR.R	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1229,56	0,131	R.DFMVYSQDPK.D	P55084	ECHB_HUMAN	Trifunctional enzyme subunit beta, mitochondrial (TP-beta) [Includes: 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase)]	HADHB
1230,65	1230,032	1231,263	1230,60	0,052	R.VAEFHTELER.L	P48556	PSMD8_HUMAN	26S proteasome non-ATPase regulatory subunit 8 (26S proteasome regulatory subunit RPN12) (26S proteasome regulatory subunit S14) (p31)	PSMD8
			1230,59	0,056	K.DIWVQEPESK.D	P21397	AOFA_HUMAN	Amine oxidase [flavin-containing] A (EC 1.4.3.4) (Monoamine oxidase type A) (MAO-A)	MAOA
			1230,72	0,072	R.QGLLPVLESFK.V	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
1231,63	1231,010	1232,242	1231,59	0,032	R.SLGTADVHFER.K	Q86V81	THOC4_HUMAN	THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Aly/REF export factor) (Transcriptional coactivator Aly/REF) (bZIP-enhancing factor BEF)	ALYREF
			1231,52	0,108	K.DYLLCDYNR.D	P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta (CapZ beta)	CAPZB
			1232,60	0,010	R.SGDGVTVDDL.R.G	Q13938	CAYP1_HUMAN	Calcyphosin (Calcyphosine)	CAPS
1232,59	1231,974	1233,207	1232,61	0,022	R.EELSNVLAAMR.K	Q9Y3U8	RL36_HUMAN	60S ribosomal protein L36 (Large ribosomal subunit protein eL36)	RPL36
			1232,63	0,036	R.TEAWVLETAGR.L	Q96FV2	SCRN2_HUMAN	Secernin-2	SCRN2
			1232,63	0,044	R.TEAWVLETAGR.L	Q96FV2	SCRN2_HUMAN	Secernin-2	SCRN2
1232,67	1232,053	1233,286	1232,61	0,057	R.EELSNVLAAMR.K	Q9Y3U8	RL36_HUMAN	60S ribosomal protein L36 (Large ribosomal subunit protein eL36)	RPL36
			1232,60	0,070	R.SGDGVTVDDL.R.G	Q13938	CAYP1_HUMAN	Calcyphosin (Calcyphosine)	CAPS
			1233,63	0,000	K.TVFGVEPDLTR.E	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
1233,63	1233,018	1234,251	1233,63	0,005	R.DLYLENPEIK.I	P21980	TGM2_HUMAN	Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (Transglutaminase C) (TG(C)) (TGC) (TGase C) (Transglutaminase H) (TGase H) (Transglutaminase-2) (TGase-2)	TGM2
			1233,62	0,016	R.IQVWHEHR.G	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			1233,65	0,018	R.IYVVVGSEPR.A	Q13228	SBP1_HUMAN	Methanethiol oxidase (MTO) (EC 1.8.3.4) (56 kDa selenium-binding protein) (SBP56) (SP56) (Selenium-binding protein 1)	SELENBP1
1234,66	1234,047	1235,281	1233,70	0,068	K.IFGVTTLDIVR.A	P40926	MDHM_HUMAN	Malate dehydrogenase, mitochondrial (EC 1.1.1.37)	MDH2
			1233,56	0,077	K.ESEAVEWQQA.A	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			1234,64	0,024	K.YQELIINDIAR.D	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
1235,61	1234,988	1236,224	1234,70	0,032	R.EHVAHLFLR.D	P19652	A1AG2_HUMAN	Alpha-1-acid glycoprotein 2 (AGP 2) (Orosomucoid-2) (OMD 2)	ORM2
			1234,59	0,076	K.IETIEVMEDR.Q	P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3
			1235,59	0,013	R.GEAGAAGPAGPAGR.G	P08123	CO1A2_HUMAN	Collagen alpha-2(I) chain (Alpha-2 type I collagen)	COL1A2

1236,62	1235,998	1237,234	1236,49	0,122	R.DGEEAGAYDGPR.T	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose PDIA3 regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	
1237,62	1237,006	1238,243	1237,64	0,014	R.FVTWIEGVMR.N	P00747	PLMN_HUMAN	Plasminogen (EC 3.4.21.7) [Cleaved into: Plasmin heavy chain A; Activation peptide; Angiostatin; Plasmin heavy chain A, short form; Plasmin light chain B]	PLG
1238,63	1238,011	1239,250	1238,59	0,040	K.FFEHFIEGGR.T	Q96FW1	OTUB1_HUMAN	Ubiquitin thioesterase OTUB1 (EC 3.4.19.12) (Deubiquitinating enzyme OTUB1) (OTU domain-containing ubiquitin aldehyde-binding protein 1) (Otubain-1) (hOTU1) (Ubiquitin-specific-processing protease OTUB1)	OTUB1
			1238,58	0,049	-MVNFTVDQIR.A	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
1239,61	1238,988	1240,228	1239,61	0,005	K.FDGILGMAYPR.I	P07339	CATD_HUMAN	Cathepsin D [EC 3.4.23.5] [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
			1239,52	0,086	K.EDGGGWVYNR.C	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
1240,45	1239,834	1241,075	1240,54	0,088	K.INFDDNAEFR.Q	Q96I99	SUCB2_HUMAN	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial (EC 6.2.1.4) (GTP-specific succinyl-CoA synthetase subunit beta) (G-SCS) (GTPSCS) (Succinyl-CoA synthetase beta-G chain) (SCS-betaG)	SUCLG2
1240,52	1239,905	1241,145	1240,54	0,018	K.INFDDNAEFR.Q	Q96I99	SUCB2_HUMAN	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial (EC 6.2.1.4) (GTP-specific succinyl-CoA synthetase subunit beta) (G-SCS) (GTPSCS) (Succinyl-CoA synthetase beta-G chain) (SCS-betaG)	SUCLG2
1240,64	1240,021	1241,261	1240,54	0,098	K.INFDDNAEFR.Q	Q96I99	SUCB2_HUMAN	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial (EC 6.2.1.4) (GTP-specific succinyl-CoA synthetase subunit beta) (G-SCS) (GTPSCS) (Succinyl-CoA synthetase beta-G chain) (SCS-betaG)	SUCLG2
1241,53	1240,910	1242,152	1241,58	0,048	R.YSTDVSVDEVK.A	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
1241,68	1241,060	1242,301	1241,58	0,102	R.YSTDVSVDEVK.A	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
1242,52	1241,897	1243,139	1242,62	0,102	R.EVDIGIPDATGR.L	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			1242,64	0,119	R.GQLEALQVDGGR.L	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7)	KRT7
1242,68	1242,056	1243,298	1242,64	0,039	R.GQLEALQVDGGR.L	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7)	KRT7
			1242,62	0,057	R.EVDIGIPDATGR.L	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
1243,53	1242,912	1244,156	1243,65	0,115	R.IQLVEEELDR.A	P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	TPM4
1243,65	1243,033	1244,276	1243,65	0,006	R.IQLVEEELDR.A	P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	TPM4
1244,62	1243,996	1245,241	1244,64	0,017	R.GWPLELLCEK.S	Q12906	ILF3_HUMAN	Interleukin enhancer-binding factor 3 (Double-stranded RNA-binding protein 76) (DRBP76) (M-phase phosphoprotein 4) (MPP4) (Nuclear factor associated with dsRNA) (NFAr) (Nuclear factor of activated T-cells 90 kDa) (NF-AT-90) (Translational control protein 80) (TCP80)	ILF3
			1244,60	0,021	R.DAAEFELFFR.R	Q6XQN6	PNCB_HUMAN	Nicotinate phosphoribosyltransferase (NAPRTase) (EC 6.3.4.21) (FHA-HIT-interacting protein) (Nicotinate phosphoribosyltransferase domain-containing protein 1)	NAPRT
			1244,60	0,023	R.CLEPEGAAELR.L	Q9H4A4	AMPB_HUMAN	Aminopeptidase B (AP-B) (EC 3.4.11.6) (Arginine aminopeptidase) (Arginyl aminopeptidase)	RNPEP
1244,65	1244,026	1245,270	1244,64	0,012	R.GWPLELLCEK.S	Q12906	ILF3_HUMAN	Interleukin enhancer-binding factor 3 (Double-stranded RNA-binding protein 76) (DRBP76) (M-phase phosphoprotein 4) (MPP4) (Nuclear factor associated with dsRNA) (NFAr) (Nuclear factor of activated T-cells 90 kDa) (NF-AT-90) (Translational control protein 80) (TCP80)	ILF3
			1244,60	0,051	R.DAAEFELFFR.R	Q6XQN6	PNCB_HUMAN	Nicotinate phosphoribosyltransferase (NAPRTase) (EC 6.3.4.21) (FHA-HIT-interacting protein) (Nicotinate phosphoribosyltransferase domain-containing protein 1)	NAPRT
			1244,60	0,053	R.CLEPEGAAELR.L	Q9H4A4	AMPB_HUMAN	Aminopeptidase B (AP-B) (EC 3.4.11.6) (Arginine aminopeptidase) (Arginyl aminopeptidase)	RNPEP
1245,51	1244,887	1246,133	1245,51	0,004	R.ADDADEFGYSR.-	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
			1245,56	0,048	K.TDYMVGSGYGR.A	P52565	GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)	ARHGDI1
			1245,59	0,081	R.ISEQFTAMFR.R	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1245,59	0,081	R.ISEQFTAMFR.R	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
1245,66	1245,038	1246,283	1245,59	0,070	R.ISEQFTAMFR.R	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1245,59	0,070	R.ISEQFTAMFR.R	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1245,56	0,102	K.TDYMVGSGYGR.A	P52565	GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)	ARHGDI1
			1245,51	0,147	R.ADDADEFGYSR.-	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
1246,65	1246,024	1247,271	1246,59	0,058	R.LVEDMENKIR.S	P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta (CapZ beta)	CAPZB
			1246,56	0,090	R.IEQYFFEDR.H	Q9NYU2	UGGT1_HUMAN	UDP-glucose:glycoprotein glucosyltransferase 1 (UGT1) (hUGT1) (EC 2.4.1.-) (UDP--Glc:glycoprotein glucosyltransferase) (UDP-glucose ceramide glucosyltransferase-like 1)	UGGT1

1247,65	1247,029	1248,277	1247,68	0,031	K.YSLEPVAVELK.S	P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1
			1247,61	0,042	K.KITIADCGQLE.-	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
			1247,60 1247,56	0,052 0,090	K.SLDVNDQSELK.F R.AGELTEDEVER.V	Q99584 P62269	S10AD_HUMAN RS18_HUMAN	Protein S100-A13 (S100 calcium-binding protein A13) 40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	S100A13 RPS18
1248,64	1248,017	1249,266	1248,48	0,159	R.EWQFYCCR.Y	Q07507	DERM_HUMAN	Dermatopontin (Tyrosine-rich acidic matrix protein) (TRAMP)	DPT
1249,65	1249,025	1250,275	1249,60	0,048	K.SASDLTWDNLK.G	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
1250,65	1250,023	1251,273	1250,60 1250,56	0,043 0,092	K.YDYVLTGYTR.D R.AENYDIPSADR.H	O00764 P22314	PDXK_HUMAN UBA1_HUMAN	Pyridoxal kinase (EC 2.7.1.35) (Pyridoxine kinase) Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A1S9) (Ubiquitin-activating enzyme E1)	PDXK UBA1
			1250,54	0,104	R.EVQQGEEFER.R	P00568	KAD1_HUMAN	Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	AK1
1251,64 1252,58	1251,011 1251,949	1252,263 1253,202	1252,61	0,034	K.VQPYLDDFQK.K	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I-(1-242))]	APOA1
1252,69	1252,065	1253,318	1252,70	0,127	K.FLASVSTVLSK.Y	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			1252,70	0,011	K.FLASVSTVLSK.Y	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			1252,61	0,082	K.VQPYLDDFQK.K	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I-(1-242))]	APOA1
1253,62	1252,992	1254,245	1253,61	0,004	R.FEELNADLFR.G	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
			1253,61	0,012	K.YLEEIATQMR.T	Q01813	PFKAP_HUMAN	ATP-dependent 6-phosphofructokinase, platelet type (ATP- PFKP (PFK-P) (EC 2.7.1.11) (6-phosphofructokinase type C) (Phosphofructo-1-kinase isozyme C) (PFK-C) (Phosphohexokinase)	
1253,67	1253,044	1254,298	1253,61	0,056	R.FEELNADLFR.G	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
			1253,61	0,065	K.YLEEIATQMR.T	Q01813	PFKAP_HUMAN	ATP-dependent 6-phosphofructokinase, platelet type (ATP- PFKP (PFK-P) (EC 2.7.1.11) (6-phosphofructokinase type C) (Phosphofructo-1-kinase isozyme C) (PFK-C) (Phosphohexokinase)	
1254,55	1253,923	1255,178	1254,56 1254,56	0,009 0,009	R.LGDLYEEEMR.E R.FDDAVVQSDMK.H	P08670 P11142	VIME_HUMAN HSP7C_HUMAN	Vimentin Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	VIM HSPA8
1254,70	1254,072	1255,327	1254,56	0,140	R.FDDAVVQSDMK.H	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
			1254,56	0,140	R.LGDLYEEEMR.E	P08670	VIME_HUMAN	Vimentin	VIM
1255,57	1254,938	1256,194	1255,61	0,043	K.FDGILGMAYPR.I	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
1255,71	1255,079	1256,334	1255,61	0,098	K.FDGILGMAYPR.I	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
1256,58	1255,950	1257,207	1256,59 1256,61	0,010 0,031	R.YLAEFATGNDR.K K.SLAEGYFDAAGR.L	P62258 O43813	1433E_HUMAN LANC1_HUMAN	14-3-3 protein epsilon (14-3-3E) Glutathione S-transferase LANC1 (EC 2.5.1.18) (40 kDa erythrocyte membrane protein) (p40) (LanC-like protein 1)	YWHAE LANC1
1256,70	1256,072	1257,329	1256,61	0,090	K.SLAEGYFDAAGR.L	O43813	LANC1_HUMAN	Glutathione S-transferase LANC1 (EC 2.5.1.18) (40 kDa erythrocyte membrane protein) (p40) (LanC-like protein 1)	LANC1
			1256,59	0,112	R.YLAEFATGNDR.K	P62258	1433E_HUMAN	14-3-3 protein epsilon (14-3-3E)	YWHAE
1257,63 1258,64	1257,006 1258,014	1258,263 1259,273	1258,60	0,045	K.FNFLEQAFDK.L	Q96CX2	KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 (Pftin) (Predominantly fetal expressed T1 domain)	KCTD12
			1258,59 1258,56	0,052 0,087	R.VTGQPACESPR.C K.YDPTIEDSYR.K	P01266 P61224	THYG_HUMAN RAP1B_HUMAN	Thyroglobulin (Tg) Ras-related protein Rap-1b (GTP-binding protein smg p21B)	TG RAP1B
1259,66	1259,025	1260,285	1259,64 1259,62	0,016 0,040	K.LAIWDTAGQER.F R.LDQETAQWLR.W	Q9NP72 Q96G03	RAB18_HUMAN PGM2_HUMAN	Ras-related protein Rab-18 Phosphoglucomutase-2 (PGM 2) (EC 5.4.2.2) (Glucose phosphomutase 2) (Phosphodeoxyribomutase) (Phosphopentomutase) (EC 5.4.2.7)	RAB18 PGM2
1260,61	1259,977	1261,238	1260,60	0,006	K.GNFNYIEFTR.I	O14950	ML12B_HUMAN	Myosin regulatory light chain 12B (MLC-2A) (MLC-2) (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2) (SHUJUN-1)	MYL12B
1260,67	1260,035	1261,296	1260,60	0,064	K.GNFNYIEFTR.I	O14950	ML12B_HUMAN	Myosin regulatory light chain 12B (MLC-2A) (MLC-2) (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2) (SHUJUN-1)	MYL12B
1261,65	1261,019	1262,281	1261,65	0,004	R.LVNHFVEEFK.R	PODMV8	HS71A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
1262,64	1262,013	1263,275	1262,64	0,005	R.TIAMDGTGLVR.G	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP ATP5F1B synthase F1 subunit beta)	

1262,65	1262,021	1263,283	1262,64	0,013	R.TIAMDGTGTLVR.G	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP ATP5F1B synthase F1 subunit beta)	
1263,68	1263,052	1264,316	1263,55	0,134	R.WASEPEHDHR.K	P08574	CY1_HUMAN	Cytochrome c1, heme protein, mitochondrial (Complex III subunit 4) (Complex III subunit IV) (Cytochrome b-c1 complex subunit 4) (Ubiquinol-cytochrome-c reductase complex cytochrome c1 subunit) (Cytochrome c-1)	CYC1
			1263,52	0,164	K.ETNQDVQCN.R	Q5FWF5	ESCO1_HUMAN	N-acetyltransferase ESCO1 (EC 2.3.1.-) (CTF7 homolog 1) (Establishment factor-like protein 1) (EFO1) (EFO1p) (hEFO1) (Establishment of cohesion 1 homolog 1) (ECO1 homolog 1) (ESO1 homolog 1)	ESCO1
1264,63	1263,995	1265,259	1264,64	0,013	R.RAPFDLFENR.K	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP 2) (LP5-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
			1264,65	0,021	R.LWDLTTGTTTR.R	P63244	RACK1_HUMAN	Receptor of activated protein C kinase 1 (Cell proliferation-inducing gene 21 protein) (Guanine nucleotide-binding protein subunit beta-2-like 1) (Guanine nucleotide-binding protein subunit beta-like protein 12.3) (Human lung cancer oncogene 7 protein, HLC-7) (Receptor for activated C kinase) (Small ribosomal subunit protein RACK1) [Cleaved into: Receptor of activated protein C kinase 1, N-terminally processed (Guanine nucleotide-binding protein subunit beta-2-like 1, N-terminally processed)]	RACK1
			1264,58	0,049	K.FNVVDVGGQDK.I	P62330	ARF6_HUMAN	ADP-ribosylation factor 6	ARF6
1265,53	1264,894	1266,159	1265,57	0,048	R.QHFISFDTDR.S	P30626	SORCN_HUMAN	Sorcin (22 kDa protein) (CP-22) (CP22) (V19)	SRI
			1265,58	0,054	K.EDIPYYFYR.D	P09917	LOX5_HUMAN	Arachidonate 5-lipoxygenase (5-LO) (5-lipoxygenase) (EC 1.13.11.34)	ALOX5
			1265,61	0,084	R.FSWNVVWPSSR.L	Q15436	SC23A_HUMAN	Protein transport protein Sec23A (hSec23A) (SEC23-related protein A)	SEC23A
			1265,63	0,104	K.EANNFLWPFK.L	P18124	RL7_HUMAN	60S ribosomal protein L7 (Large ribosomal subunit protein uL30)	RPL7
			1265,63	0,105	R.KESYSVYVYK.V	O60814	H2B1K_HUMAN	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK
			1265,64	0,117	R.TGWISTSSIWK.K	Q9NSE4	SYIM_HUMAN	Isoleucine--tRNA ligase, mitochondrial (EC 6.1.1.5) (Isoleucyl-tRNA synthetase) (IleRS)	IARS2
1265,67	1265,040	1266,306	1265,64	0,030	R.TGWISTSSIWK.K	Q9NSE4	SYIM_HUMAN	Isoleucine--tRNA ligase, mitochondrial (EC 6.1.1.5) (Isoleucyl-tRNA synthetase) (IleRS)	IARS2
			1265,63	0,042	R.KESYSVYVYK.V	O60814	H2B1K_HUMAN	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK
			1265,63	0,043	K.EANNFLWPFK.L	P18124	RL7_HUMAN	60S ribosomal protein L7 (Large ribosomal subunit protein uL30)	RPL7
			1265,61	0,063	R.FSWNVVWPSSR.L	Q15436	SC23A_HUMAN	Protein transport protein Sec23A (hSec23A) (SEC23-related protein A)	SEC23A
			1265,58	0,093	K.EDIPYYFYR.D	P09917	LOX5_HUMAN	Arachidonate 5-lipoxygenase (5-LO) (5-lipoxygenase) (EC 1.13.11.34)	ALOX5
			1265,57	0,099	R.QHFISFDTDR.S	P30626	SORCN_HUMAN	Sorcin (22 kDa protein) (CP-22) (CP22) (V19)	SRI
1266,64	1266,009	1267,276							
1267,66	1267,028	1268,295	1267,67	0,004	K.ATEPVIAFYEK.R	P00568	KAD1_HUMAN	Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP-AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	AK1
			1267,72	0,062	R.IAAAILNTPDLR.K	P00505	AATM_HUMAN	Aspartate aminotransferase, mitochondrial (mAspAT) (EC 2.6.1.1) (EC 2.6.1.7) (Fatty acid-binding protein) (FABP-1) (Glutamate oxaloacetate transaminase 2) (Kynurenine aminotransferase 4) (Kynurenine aminotransferase IV) (Kynurenine--oxoglutarate transaminase 4) (Kynurenine--oxoglutarate transaminase IV) (Plasma membrane-associated fatty acid-binding protein) (FABPpm) (Transaminase A)	GOT2
1268,67	1268,037	1269,306	1268,67	0,006	K.TENLLGSYFPK.K	Q06323	PSME1_HUMAN	Proteasome activator complex subunit 1 (11S regulator complex subunit alpha) (REG-alpha) (Activator of multicatalytic protease subunit 1) (Interferon gamma up-regulated I-5111 protein) (IGUP I-5111) (Proteasome activator 28 subunit alpha) (PA28a) (PA28alpha)	PSME1
			1268,56	0,112	R.YLAEVACGDDR.K	P27348	1433T_HUMAN	14-3-3 protein theta (14-3-3 protein T-cell) (14-3-3 protein tau) (Protein HS1)	YWHAQ
1269,68	1269,049	1270,319	1269,56	0,120	K.SEEELAECFR.I	P02585	TNNC2_HUMAN	Troponin C, skeletal muscle	TNNC2
1270,69	1270,059	1271,330	1270,59	0,103	R.RGFEEQWYR.R	P08236	BGLR_HUMAN	Beta-glucuronidase (EC 3.2.1.31) (Beta-G1)	GUSB
1271,68	1271,042	1272,313	1271,70	0,024	K.VIFDANAPVAVR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1271,74	0,057	K.QVVNIPSFIVR.L	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RPS9
1271,69	1271,050	1272,322	1271,70	0,015	K.VIFDANAPVAVR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1271,74	0,049	K.QVVNIPSFIVR.L	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RPS9
1271,86	1271,222	1272,493	1271,74	0,122	K.QVVNIPSFIVR.L	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RPS9
			1271,70	0,156	K.VIFDANAPVAVR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1272,42	1271,785	1273,057	1272,67	0,253	R.NDEELNKLKG.V	Q96KK5	H2A1H_HUMAN	Histone H2A type 1-H (Histone H2A/s)	HIST1H2AH
			1272,69	0,268	K.AASKVTLLLEANR.A	Q8IVF7	FMNL3_HUMAN	Formin-like protein 3 (Formin homology 2 domain-containing protein 3) (WW domain-binding protein 3) (WBP-3)	FMNL3
1272,69	1272,049	1273,322	1272,69	0,003	K.AASKVTLLLEANR.A	Q8IVF7	FMNL3_HUMAN	Formin-like protein 3 (Formin homology 2 domain-containing protein 3) (WW domain-binding protein 3) (WBP-3)	FMNL3
			1272,67	0,012	R.NDEELNKLKG.V	Q96KK5	H2A1H_HUMAN	Histone H2A type 1-H (Histone H2A/s)	HIST1H2AH
1272,87	1272,229	1273,502	1272,69	0,177	K.AASKVTLLLEANR.A	Q8IVF7	FMNL3_HUMAN	Formin-like protein 3 (Formin homology 2 domain-containing protein 3) (WW domain-binding protein 3) (WBP-3)	FMNL3
			1272,67	0,191	R.NDEELNKLKG.V	Q96KK5	H2A1H_HUMAN	Histone H2A type 1-H (Histone H2A/s)	HIST1H2AH
1273,26	1272,621	1273,894	1273,60	0,343	R.GGYDFDEGIIR.D	P11413	G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	G6PD
			1273,70	0,446	K.LEDVLPLAFTR.L	Q5SSJ5	HP1B3_HUMAN	Heterochromatin protein 1-binding protein 3 (Protein HP1- BP74)	HP1BP3
			1272,69	0,569	K.AASKVTLLLEANR.A	Q8IVF7	FMNL3_HUMAN	Formin-like protein 3 (Formin homology 2 domain-containing protein 3) (WW domain-binding protein 3) (WBP-3)	FMNL3

			1272,67	0,584	R.NDEELNKLKG.V	Q96KK5	H2A1H_HUMAN	Histone H2A type 1-H (Histone H2A/s)	HIST1H2AH
1273,53	1272,894	1274,167	1273,60	0,070	R.GGYFDEFGIIR.D	P11413	G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	G6PD
			1273,70	0,173	K.LEDVLPLAFTR.L	Q5SSJ5	HP1B3_HUMAN	Heterochromatin protein 1-binding protein 3 (Protein HP1- BP74)	HP1BP3
1273,71	1273,078	1274,352	1273,70	0,011	K.LEDVLPLAFTR.L	Q5SSJ5	HP1B3_HUMAN	Heterochromatin protein 1-binding protein 3 (Protein HP1- BP74)	HP1BP3
			1273,60	0,114	R.GGYFDEFGIIR.D	P11413	G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	G6PD
1274,00	1273,364	1274,638	1273,70	0,297	K.LEDVLPLAFTR.L	Q5SSJ5	HP1B3_HUMAN	Heterochromatin protein 1-binding protein 3 (Protein HP1- BP74)	HP1BP3
			1273,60	0,400	R.GGYFDEFGIIR.D	P11413	G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	G6PD
			1274,61	0,612	K.AQIWDTAGQER.Y	Q15907	RB11B_HUMAN	Ras-related protein Rab-11B (GTP-binding protein YPT3)	RAB11B
			1274,63	0,634	K.ESDGLGIQVSGGR.G	O15018	PDZD2_HUMAN	PDZ domain-containing protein 2 (Activated in prostate cancer protein) (PDZ domain-containing protein 3) [Cleaved into: Processed PDZ domain-containing protein 2]	PDZD2
1274,72	1274,079	1275,354	1274,73	0,010	R.LLVVYPWTQR.F	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
			1274,73	0,010	R.LLVVYPWTQR.F	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			1274,73	0,010	R.LLVVYPWTQR.F	P69892	HBG2_HUMAN	Hemoglobin subunit gamma-2 (Gamma-2-globin) (Hb F Ggamma) (Hemoglobin gamma-2 chain) (Hemoglobin gamma-G chain)	HBG2
			1274,67	0,043	K.SIVVYPPWAR.I	Q9UH62	ARMX3_HUMAN	Armadillo repeat-containing X-linked protein 3 (ARM protein lost in epithelial cancers on chromosome X 3) (Protein ALEX3)	ARMCX3
			1274,67	0,043	R.RASHTLLPSHR.L	Q9UKV3	ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus (Acinus)	ACIN1
			1274,65	0,067	K.NFATSLYMIK.G	P08758	ANXA5_HUMAN	Annexin A5 (Anchoring CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
			1274,63	0,082	K.ESDGLGIQVSGGR.G	O15018	PDZD2_HUMAN	PDZ domain-containing protein 2 (Activated in prostate cancer protein) (PDZ domain-containing protein 3) [Cleaved into: Processed PDZ domain-containing protein 2]	PDZD2
			1274,61	0,104	K.AQIWDTAGQER.Y	Q15907	RB11B_HUMAN	Ras-related protein Rab-11B (GTP-binding protein YPT3)	RAB11B
1275,72	1275,081	1276,357	1275,64	0,082	R.ELISNASDALDK.I	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			1275,64	0,082	R.ELISNASDALDK.I	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			1275,61	0,110	K.TYHVGEQWQK.E	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			1275,55	0,171	R.DNDGWLTSDPR.K	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
			1275,54	0,175	K.YDHQAEEDLR.N	Q15417	CNN3_HUMAN	Calponin-3 (Calponin, acidic isoform)	CNN3
1276,54	1275,904	1277,180	1276,64	0,095	R.MLLADQGGQSWK.E	P09211	GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1)	GSTP1
1276,72	1276,083	1277,360	1276,64	0,085	R.MLLADQGGQSWK.E	P09211	GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1)	GSTP1
1277,57	1276,931	1278,209	1277,65	0,075	R.IFNTWLGDPK.N	P80404	GABT_HUMAN	4-aminobutyrate aminotransferase, mitochondrial (EC 2.6.1.19) [(S)-3-amino-2-methylpropionate transaminase] (EC 2.6.1.22) (GABA aminotransferase) (GABA-AT) (Gamma amino-N-butyrate transaminase) (GABA transaminase) (GABA-T) (L-AIBAT)	ABAT
1277,73	1277,092	1278,370	1277,65	0,086	R.IFNTWLGDPK.N	P80404	GABT_HUMAN	4-aminobutyrate aminotransferase, mitochondrial (EC 2.6.1.19) [(S)-3-amino-2-methylpropionate transaminase] (EC 2.6.1.22) (GABA aminotransferase) (GABA-AT) (Gamma amino-N-butyrate transaminase) (GABA transaminase) (GABA-T) (L-AIBAT)	ABAT
1278,57 1278,73 1279,49	1277,927 1278,089 1278,849	1279,206 1279,368 1280,129	1279,60	0,110	K.LDDFVETGDIR.T	Q14108	SCRB2_HUMAN	Lysosome membrane protein 2 (85 kDa lysosomal membrane sialoglycoprotein) (LGP85) (CD36 antigen-like 2) (Lysosome membrane protein II) (LIMP II) (Scavenger receptor class B member 2) (CD antigen CD36)	SCARB2
			1279,66	0,175	R.KESYSIYVK.V	Q16778	H2B2E_HUMAN	Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q)	HIST2H2BE
1279,58	1278,942	1280,221	1279,60	0,018	K.LDDFVETGDIR.T	Q14108	SCRB2_HUMAN	Lysosome membrane protein 2 (85 kDa lysosomal membrane sialoglycoprotein) (LGP85) (CD36 antigen-like 2) (Lysosome membrane protein II) (LIMP II) (Scavenger receptor class B member 2) (CD antigen CD36)	SCARB2
			1279,66	0,082	R.KESYSIYVK.V	Q16778	H2B2E_HUMAN	Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q)	HIST2H2BE
1279,73	1279,091	1280,370	1279,66	0,067	R.KESYSIYVK.V	Q16778	H2B2E_HUMAN	Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q)	HIST2H2BE
			1279,60	0,131	K.LDDFVETGDIR.T	Q14108	SCRB2_HUMAN	Lysosome membrane protein 2 (85 kDa lysosomal membrane sialoglycoprotein) (LGP85) (CD36 antigen-like 2) (Lysosome membrane protein II) (LIMP II) (Scavenger receptor class B member 2) (CD antigen CD36)	SCARB2
1280,66	1280,018	1281,299	1280,65	0,006	R.KLDELYGTWR.K	P36578	RL4_HUMAN	60S ribosomal protein L4 (60S ribosomal protein L1) (Large ribosomal subunit protein uL4)	RPL4
1281,67	1281,027	1282,309	1281,62	0,046	R.FVYHSLDCK.K	P01591	IGJ_HUMAN	Immunoglobulin J chain (Joining chain of multimeric IgA and IgM)	JCHAIN
1282,70 1283,57	1282,055 1282,924	1283,338 1284,208	1283,57	0,005	K.WQEEMELYR.Q	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I-1-242)]	APOA1

			1283,55	0,013	K.EGYGYGTGAFR.C	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
1283,68	1283,042	1284,326	1283,57	0,112	K.WQEEMELYR.Q	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I-{1-242})]	APOA1
			1283,55	0,130	K.EGYGYGTGAFR.C	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
1284,68	1284,036	1285,321	1284,67	0,007	K.DIPGLTDTTVPR.R	P62753	RS6_HUMAN	40S ribosomal protein S6 (Phosphoprotein NP33) (Small ribosomal subunit protein e56)	RPS6
			1284,63	0,051	K.YLNQDYEARL.N	P17655	CAN2_HUMAN	Calpain-2 catalytic subunit (EC 3.4.22.53) (Calcium-activated neutral proteinase 2) (CANP 2) (Calpain M-type) (Calpain large polypeptide L2) (Calpain-2 large subunit) (Millimolar-calpain) (M-calpain)	CAPN2
			1284,61	0,067	K.YLGQDYEQLR.V	P07384	CAN1_HUMAN	Calpain-1 catalytic subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase 1) (CANP 1) (Calpain mu-type) (Calpain-1 large subunit) (Cell proliferation-inducing gene 30 protein) (Micromolar-calpain) (muCANP)	CAPN1
1285,60	1284,952	1286,238	1285,61	0,010	R.DHGLPGYNAWR.R	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
1285,71	1285,069	1286,354	1285,61	0,106	R.DHGLPGYNAWR.R	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
1286,67	1286,026	1287,313	1286,66	0,012	R.EPQVYTLPPSR.D	P01857	IGHG1_HUMAN	Immunoglobulin heavy constant gamma 1 (Ig gamma-1 chain C region) (Ig gamma-1 chain C region EU) (Ig gamma-1 chain C region KOI) (Ig gamma-1 chain C region NIE)	IGHG1
			1286,66	0,012	R.EPQVYTLPPSR.E	P01859	IGHG2_HUMAN	Immunoglobulin heavy constant gamma 2 (Ig gamma-2 chain C region) (Ig gamma-2 chain C region DOT) (Ig gamma-2 chain C region TIL) (Ig gamma-2 chain C region ZIE)	IGHG2
			1286,62	0,047	R.EQWPQCPTIK.E	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
			1286,58	0,093	K.DFMIQGGDFTR.G	P23284	PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) PPIB (CYP-51) (Cyclophilin B) (Rotamase B) (S-cyclophilin) (SCYLP)	PPIB
1287,67	1287,025	1288,313	1287,69	0,017	K.HALIYDLSK.Q	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
			1287,69	0,020	K.TMLLLDILPSR.G	P78560	CRADD_HUMAN	Death domain-containing protein CRADD (Caspase and RIP adapter with death domain) (RIP-associated protein with a death domain)	CRADD
1288,71	1288,062	1289,350	1288,59	0,116	K.FSTWNTNTEFR.Y	P07099	HYEP_HUMAN	Epoxide hydrolase 1 (EC 3.3.2.9) (Epoxide hydratase) (Microsomal epoxide hydrolase) (mEH)	EPHX1
1289,68 1290,70	1289,040 1290,056	1290,330 1291,346	1290,70	0,000	R.LVNVVLGAHNVR.T	P24158	PRTN3_HUMAN	Myeloblastin (EC 3.4.21.76) (AGP7) (C-ANCA antigen) (Leukocyte proteinase 3) (PR-3) (PR3) (Neutrophil proteinase 4) (NP-4) (P29) (Wegener autoantigen)	PRTN3
			1290,68	0,019	K.VVQQTVDLFGFR.A	P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9
			1290,62	0,082	R.FDGILTEGEPR.R	Q96HE7	ERO1A_HUMAN	ERO1-like protein alpha (ERO1-L) (ERO1-L-alpha) (EC 1.8.4.- ERO1A) (Endoplasmic oxidoreductin-1-like protein) (Endoplasmic reticulum oxidoreductase alpha) (Oxidoreductin-1-L-alpha)	
			1290,60	0,101	K.SVEEEQVWR.A	Q9P2E9	RRBP1_HUMAN	Ribosome-binding protein 1 (180 kDa ribosome receptor homolog) (RRp) (ES/130-related protein) (Ribosome receptor protein)	RRBP1
1291,62	1290,971	1292,263	1291,59	0,031	R.GYFEYIENK.Y	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPUI
			1291,71	0,092	K.SDGIYIINKR.T	P08865	RSSA_HUMAN	40S ribosomal protein SA (37 kDa laminin receptor precursor) (37LRP) (37/67 kDa laminin receptor) (LRP/LR) (67 kDa laminin receptor) (67LR) (Colon carcinoma laminin-binding protein) (Laminin receptor 1) (LamR) (Laminin-binding protein precursor p40) (LBP/p40) (Multidrug resistance-associated protein MGR1-Ag) (NEM/1CHD4) (Small ribosomal subunit protein uS2)	RPSA
1291,73	1291,080	1292,371	1291,71	0,016	K.SDGIYIINKR.T	P08865	RSSA_HUMAN	40S ribosomal protein SA (37 kDa laminin receptor precursor) (37LRP) (37/67 kDa laminin receptor) (LRP/LR) (67 kDa laminin receptor) (67LR) (Colon carcinoma laminin-binding protein) (Laminin receptor 1) (LamR) (Laminin-binding protein precursor p40) (LBP/p40) (Multidrug resistance-associated protein MGR1-Ag) (NEM/1CHD4) (Small ribosomal subunit protein uS2)	RPSA
			1291,59	0,140	R.GYFEYIENK.Y	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPUI
1292,49	1291,841	1293,134	1292,67	0,179	R.THSDQFLVAFK.E	P36542	ATPG_HUMAN	ATP synthase subunit gamma, mitochondrial (ATP synthase F1 subunit gamma) (F-ATPase gamma subunit)	ATP5F1C
1292,67	1292,019	1293,311	1292,67	0,002	R.THSDQFLVAFK.E	P36542	ATPG_HUMAN	ATP synthase subunit gamma, mitochondrial (ATP synthase F1 subunit gamma) (F-ATPase gamma subunit)	ATP5F1C
1293,49 1293,71 1294,57	1292,839 1293,062 1293,922	1294,132 1294,355 1295,216	1294,56	0,008	K.EGMNIVEAMER.F	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
			1294,61	0,038	K.FNVWDTAGQEK.F	P62826	RAN_HUMAN	GTP-binding nuclear protein Ran (Androgen receptor-associated protein 24) (GTPase Ran) (Ras-like protein TC4) (Ras-related nuclear protein)	RAN

1294,71	1294,059	1295,354	1294,61	0,100	K.FNVVWDTAGQEK.F	P62826	RAN_HUMAN	GTP-binding nuclear protein Ran (Androgen receptor-associated protein 24) (GTPase Ran) (Ras-like protein TC4) (Ras-related nuclear protein)	RAN
			1294,56	0,145	K.EGMNIVEAMER.F	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
1295,62	1294,970	1296,266	1295,61	0,011	R.EFTESQLQEGK.H	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein W53-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
1295,64	1294,995	1296,291	1295,61	0,036	R.EFTESQLQEGK.H	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein W53-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
1295,66	1295,013	1296,308	1295,61	0,053	R.EFTESQLQEGK.H	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein W53-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
1296,65	1296,002	1297,299							
1296,73	1296,083	1297,380							
1297,63	1296,981	1298,279							
1298,63	1297,985	1299,283	1298,62	0,011	R.YQETFNVIER.C	Q13011	ECH1_HUMAN	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial (EC 5.3.3.-)	ECH1
			1298,58	0,059	R.FALSAMDMEQR.D	094925	GLSK_HUMAN	Glutaminase kidney isoform, mitochondrial (GLS) (EC 3.5.1.2) (K-glutaminase) (L-glutamine amidohydrolase) [Cleaved into: Glutaminase kidney isoform, mitochondrial 68 kDa chain; Glutaminase kidney isoform, mitochondrial 65 kDa chain]	GLS
1299,62	1298,968	1300,267	1299,63	0,016	K.HHPEDVEPALR.K	P14550	AK1A1_HUMAN	Aldo-keto reductase family 1 member A1 (EC 1.1.1.2) (EC 1.1.1.372) (EC 1.1.1.54) (Alcohol dehydrogenase [NADP(+)]]) (Aldehyde reductase) (Glucuronate reductase) (EC 1.1.1.19) (Glucuronolactone reductase) (EC 1.1.1.20)	AKR1A1
1299,65	1299,000	1300,300	1299,63	0,016	K.HHPEDVEPALR.K	P14550	AK1A1_HUMAN	Aldo-keto reductase family 1 member A1 (EC 1.1.1.2) (EC 1.1.1.372) (EC 1.1.1.54) (Alcohol dehydrogenase [NADP(+)]]) (Aldehyde reductase) (Glucuronate reductase) (EC 1.1.1.19) (Glucuronolactone reductase) (EC 1.1.1.20)	AKR1A1
1300,57	1299,921	1301,222	1300,55	0,019	K.NMQDMVEDYR.N	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
			1300,61	0,041	R.YHSLAPMYR.G	P51148	RAB5C_HUMAN	Ras-related protein Rab-5C (L1880) (RAB5L)	RAB5C
			1300,64	0,072	R.QLAEEDLAQQR.A	Q15149	PLEC_HUMAN	Plectin (PCN) (PLTN) (Hemidesmosomal protein 1) (HD1) (Plectin-1)	PLEC
1300,69	1300,044	1301,345	1300,64	0,051	R.QLAEEDLAQQR.A	Q15149	PLEC_HUMAN	Plectin (PCN) (PLTN) (Hemidesmosomal protein 1) (HD1) (Plectin-1)	PLEC
			1300,61	0,081	R.YHSLAPMYR.G	P51148	RAB5C_HUMAN	Ras-related protein Rab-5C (L1880) (RAB5L)	RAB5C
			1300,55	0,141	K.NMQDMVEDYR.N	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
1301,67	1301,017	1302,318	1301,65	0,021	K.HTNYTMEHIR.V	P12814	ACTN1_HUMAN	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (F-actin cross-linking protein) (Non-muscle alpha-actinin-1)	ACTN1
			1301,65	0,021	K.HTNYTMEHIR.V	O43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
			1301,65	0,021	K.HTNYTMEHIR.V	P35609	ACTN2_HUMAN	Alpha-actinin-2 (Alpha-actinin skeletal muscle isoform 2) (F-actin cross-linking protein)	ACTN2
			1301,65	0,022	R.THLAPYSDLR.Q	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
			1301,64	0,028	R.SHGQDSPAVYLK.K	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1301,63	0,037	R.DIASTPHELYR.N	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
			1301,62	0,050	R.GALTGGYDTRK.S	Q9UQE7	SMC3_HUMAN	Structural maintenance of chromosomes protein 3 (SMC protein 3) (SMC-3) (Basement membrane-associated chondroitin proteoglycan) (Bamacan) (Chondroitin sulfate proteoglycan 6) (Chromosome-associated polypeptide) (hCAP)	SMC3
			1301,46	0,212	R.DSYDSYATHNE.-	Q14011	CIRBP_HUMAN	Cold-inducible RNA-binding protein (A18 hnRNP) (Glycine-rich RNA-binding protein CIRP)	CIRBP
1302,66	1302,008	1303,311							
1303,60	1302,945	1304,249	1303,60	0,001	K.NSLESYAFNMK.A	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
			1303,62	0,027	R.FSGSGSGTDFTLK.I	P01615	KVD28_HUMAN	Immunoglobulin kappa variable 2D-28 (Ig kappa chain V-II region FR) (Ig kappa chain V-II region GM607) (Ig kappa chain V-II region MIL) (Ig kappa chain V-II region TEW)	IGKV2D-28
			1303,71	0,115	M.AGSGGAGVRCLLRL	P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	PRKDC
1304,62	1303,964	1305,269							
1305,65	1304,995	1306,300							
1306,61	1305,952	1307,259	1306,68	0,078	K.EFEPLLNWMK.D	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
1306,70	1306,049	1307,355	1306,68	0,019	K.EFEPLLNWMK.D	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
1307,68	1307,024	1308,331	1307,69	0,010	R.CIESIAVFQK.Y	P31949	S10AB_HUMAN	Protein S100-A11 (Calgizzarin) (Metastatic lymph node gene 70 protein) (MLN 70) (Protein S100-C) (S100 calcium-binding protein A11) [Cleaved into: Protein S100-A11, N-terminally processed]	S100A11
			1307,69	0,011	R.GLETFSQLVWK.S	P06865	HEXA_HUMAN	Beta-hexosaminidase subunit alpha (EC 3.2.1.52) (Beta-N-acetylhexosaminidase subunit alpha) (Hexosaminidase subunit A) (N-acetyl-beta-glucosaminidase subunit alpha)	HEXA
			1307,66	0,014	R.FENLGVSSLGER.K	Q9Y323	SAMH1_HUMAN	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 (dNTPase) (EC 3.1.5.-) (Dendritic cell-derived IFNG-induced protein) (DCIP) (Monocyte protein 5) (MOP-5) (SAM domain and HD domain-containing protein 1) (hSAMHD1)	SAMHD1
			1307,63	0,047	K.HFSGLEEAVYR.N	P50990	TCPQ_HUMAN	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta) (Chaperonin containing T-complex polypeptide 1 subunit 8) (Renal carcinoma antigen NY-REN-15)	CCT8
			1307,61	0,071	R.YALYDASFETK.E	P60981	DEST_HUMAN	Destrin (Actin-depolymerizing factor) (ADF)	DSTN

			1307,59	0,084	K.SSLMSDSRGVPR.N	O15018	PDZD2_HUMAN	PDZ domain-containing protein 2 (Activated in prostate cancer protein) (PDZ domain-containing protein 3) [Cleaved into: Processed PDZ domain-containing protein 2]	PDZD2
1308,63 1308,72 1309,67	1307,971 1308,070 1309,016	1309,280 1309,379 1310,326	1309,60	0,066	K.NLQEAEEWYK.S	P08670	VIME_HUMAN	Vimentin	VIM
1310,64	1309,982	1311,293	1310,69	0,051	K.TVTAMDVVYALK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
1310,68	1310,027	1311,337	1310,69	0,007	K.TVTAMDVVYALK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
1311,67	1311,013	1312,324	1311,65 1311,72 1311,61	0,019 0,051 0,057	R.TGYTLDVTTGQR.K R.HPDYSVLLLR.L R.SEDLLDYGPPR.D	O43390 P02768 P04843	HNRPR_HUMAN ALBU_HUMAN RPN1_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R) Serum albumin Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 (Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit) (Ribophorin I) (RPN-I) (Ribophorin-1)	HNRNPR ALB RPN1
			1311,57	0,096	K.EDQTEYLEER.R	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP 2) (LP5-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
			1311,57	0,096	K.EDQTEYLEER.R	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
1312,69	1312,030	1313,342	1312,75 1312,76	0,062 0,071	K.IQAIIELEDLLR.Y K.GILTVDELLAIR.I	P21810 P13473	PGS1_HUMAN LAMP2_HUMAN	Biglycan (Bone/cartilage proteoglycan I) (PG-S1) Lysosome-associated membrane glycoprotein 2 (LAMP-2) (Lysosome-associated membrane protein 2) (CD107 antigen-like family member B) (LGP-96) (CD antigen CD107b)	BGN LAMP2
			1312,61	0,079	R.HGESAWNLENR.F	P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG- dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	PGAM1
			1312,78	0,094	R.IASGLGLAWIVGR.V	O14880	MGST3_HUMAN	Microsomal glutathione S-transferase 3 (Microsomal GST-3) (Glutathione peroxidase MGST3) (EC 1.11.1.-) (LTC4 synthase MGST3) (EC 4.4.1.20) (Microsomal glutathione S-transferase III) (Microsomal GST-III)	MGST3
			1312,54	0,141	R.AWDDFFPGSDR.F	O75915	PRAF3_HUMAN	PRA1 family protein 3 (ADP-ribosylation factor-like protein 6-interacting protein 5) (ARL-6-interacting protein 5) (Aip-5) (Cytoskeleton-related vitamin A-responsive protein) (Dermal papilla-derived protein 11) (GTRAP3-18) (Glutamate transporter EAAC1-interacting protein) (JM5) (Prenylated Rab acceptor protein 2) (Protein JWa) (Putative MAPK-activating protein PM27)	ARL6IP5
1313,66	1313,006	1314,319	1313,70 1313,57	0,037 0,094	K.TSFFQALGITTK.I K.WDDPYDIAR.H	P05388 Q07960	RLA0_HUMAN RHG01_HUMAN	60S acidic ribosomal protein P0 (60S ribosomal protein L10E) (Large ribosomal subunit protein uL10) Rho GTPase-activating protein 1 (CDC42 GTPase-activating protein) (GTPase-activating protein rhoGAP) (Rho-related small GTPase protein activator) (Rho-type GTPase-activating protein 1) (p50-RhoGAP)	RPLP0 ARHGAP1
			1313,53	0,130	K.FSGDLDDQTCR.E	P05455	LA_HUMAN	Lupus La protein (La autoantigen) (La ribonucleoprotein) (Sjoegren syndrome type B antigen) (SS-B)	SSB
1314,66	1314,000	1315,315	1314,67 1314,67 1314,70 1314,71	0,010 0,010 0,047 0,050	K.VNVDEVGGEALGR.L K.VQSLEGEKSPK.S K.FLVGPDGIPMR.W K.LGELPSWILMR.D	P68871 P46821 P22352 P56134	HBB_HUMAN MAP1B_HUMAN GPX3_HUMAN ATPK_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin] Microtubule-associated protein 1B (MAP-1B) [Cleaved into: MAP1B heavy chain; MAP1 light chain LC1] Glutathione peroxidase 3 (GPx-3) (GSHPx-3) (EC 1.11.1.9) (Extracellular glutathione peroxidase) (Plasma glutathione peroxidase) (GPx-P) (GSHPx-P) ATP synthase subunit f, mitochondrial (ATP synthase membrane subunit f)	HBB MAP1B GPX3 ATP5MF
1315,66	1315,006	1316,322	1315,66 1315,60	0,007 0,065	R.EDLLSLQEPGSK.T R.FEELCSDLFR.S	P01266 P0DMV8	THYG_HUMAN HS71A_HUMAN	Thyroglobulin (Tg) Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	TG HSPA1A
1316,67	1316,010	1317,327	1316,66 1316,66 1316,66 1316,66 1316,74 1316,60 1316,80	0,013 0,013 0,013 0,013 0,072 0,072 0,132	R.LQLWDTAGQER.F K.LQIWDTAGQER.F K.LQIWDTAGQER.F K.LQIWDTAGQER.F K.KSAEFLHMLK.N R.DHSGLTPEEFK.A R.VFIGNLNTLVVK.K	Q9NRW1 P62820 P61106 P61026 P18621 P12814 P07910	RAB6B_HUMAN RAB1A_HUMAN RAB14_HUMAN RAB10_HUMAN RL17_HUMAN ACTN1_HUMAN HNRPC_HUMAN	Ras-related protein Rab-6B Ras-related protein Rab-1A (YPT1-related protein) Ras-related protein Rab-14 Ras-related protein Rab-10 60S ribosomal protein L17 (60S ribosomal protein L23) (Large ribosomal subunit protein uL22) (PD-1) Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (F-actin cross-linking protein) (Non-muscle alpha-actinin-1) Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1/C2)	RAB6B RAB1A RAB14 RAB10 RPL17 ACTN1 HNRNPC
1317,68 1318,64	1317,025 1317,976	1318,342 1319,294	1318,57	0,069	R.AEDTAVYYCAR.G	P01763	HV348_HUMAN	Immunoglobulin heavy variable 3-48 (Ig heavy chain V-III region WEA)	IGHV3-48

1318,67	1318,012	1319,331	1318,57	0,105	R.AEDTAVYYCAR.G	P01763	HV348_HUMAN	Immunoglobulin heavy variable 3-48 (Ig heavy chain V-III region WEA)	IGHV3-48
1319,67	1319,006	1320,326	1319,58	0,083	K.EAFDEVMAHR.F	Q9NX46	ARHL2_HUMAN	ADP-ribose glycohydrolase ARH3 (ADP-ribosylhydrolase 3) (O-acetyl-ADP-ribose deacetylase ARH3) (EC 3.5.1.-) (Poly(ADP-ribose) glycohydrolase ARH3) (EC 3.2.1.143) ([Protein ADP-ribosylarginine] hydrolase-like protein 2) ([Protein ADP-ribosylserine] hydrolase) (EC 3.2.2.-)	ADPRHL2
1320,65	1319,988	1321,309	1320,67	0,025	R.SLDMSIIAEVK.A	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8)	KRT8
			1320,62	0,030	K.SEDCFILDHGK.D	P06396	GELS_HUMAN	Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF) (Brevin)	GSN
			1320,62	0,030	K.LEHEVIQNF.K	Q15691	MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1) (End-binding protein 1) (EB1)	MAPRE1
			1320,60	0,046	R.SGEWTEDEVLR.R	Q13938	CAYP1_HUMAN	Calcyphosin (Calcyphosine)	CAPS
1321,65	1320,994	1322,315	1321,67	0,012	K.VEEVYDLSIR.G	Q15631	TSN_HUMAN	Translin (EC 3.1.-.-) (Component 3 of promoter of RISC) (C3PO)	TSN
1322,67	1322,005	1323,328	1322,63	0,036	K.SLAMEMVLTGDR.I	P30084	ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial (EC 4.2.1.17) (Enoyl-CoA hydratase 1) (Short-chain enoyl-CoA hydratase) (SCEH)	ECHS1
			1322,60	0,063	R.EFVAVTGAEEDR.A	Q9UN22	NSF1C_HUMAN	NSF1 cofactor p47 (UBX domain-containing protein 2C) (p97 cofactor p47)	NSFL1C
1323,67	1323,004	1324,328	1323,62	0,051	R.EEAENTLQSF.R	P08670	VIME_HUMAN	Vimentin	VIM
			1323,61	0,057	K.SAGVDVTLAFDGR.T	O00468	AGRIN_HUMAN	Agrin [Cleaved into: Agrin N-terminal 110 kDa subunit; Agrin C-terminal 110 kDa subunit; Agrin C-terminal 90 kDa fragment (C90); Agrin C-terminal 22 kDa fragment (C22)]	AGRN
1324,63	1323,972	1325,296	1324,59	0,043	R.GNLYWTDWNR.D	P14543	NID1_HUMAN	Nidogen-1 (NID-1) (Entactin)	NID1
			1324,59	0,043	R.GNLYWTDWNR.E	Q14112	NID2_HUMAN	Nidogen-2 (NID-2) (Osteonidogen)	NID2
			1324,58	0,052	K.GDKEEVAYEER.A	Q9NRV9	HEBP1_HUMAN	Heme-binding protein 1 (p22HBP)	HEBP1
			1324,72	0,088	K.IQVLVEPDHFK.V	P17931	LEG3_HUMAN	Galectin-3 (Gal-3) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Galactose-specific lectin 3) (Galactoside-binding protein) (GALBP) (IgE-binding protein) (L-31) (Laminin-binding protein) (Lectin L-29) (Mac 2 antigen)	LGALS3
1325,56	1324,893	1326,219	1325,68	0,125	R.ISHGEVLEWQK.T	Q9BXP5	SRRT_HUMAN	Serrate RNA effector molecule homolog (Arsenite-resistance protein 2)	SRRT
			1325,74	0,181	R.DNIQGITKPAIR.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
1325,57	1324,909	1326,234	1325,68	0,109	R.ISHGEVLEWQK.T	Q9BXP5	SRRT_HUMAN	Serrate RNA effector molecule homolog (Arsenite-resistance protein 2)	SRRT
			1325,74	0,165	R.DNIQGITKPAIR.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
1325,73	1325,062	1326,388	1325,74	0,011	R.DNIQGITKPAIR.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
			1325,68	0,044	R.ISHGEVLEWQK.T	Q9BXP5	SRRT_HUMAN	Serrate RNA effector molecule homolog (Arsenite-resistance protein 2)	SRRT
1326,58	1325,916	1327,243	1326,69	0,108	K.TVTAMDVVYALK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4

1326,73	1326,071	1327,398	1326,69	0,047	K.TVTAMDMVYALK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
1327,59	1326,921	1328,249	1327,66	0,075	K.VPLEVQEADEAK.L	P26640	SYVC_HUMAN	Valine--tRNA ligase (EC 6.1.1.9) (Protein G7a) (Valyl-tRNA synthetase) (ValRS)	VARS
1327,74	1327,076	1328,404	1327,66	0,080	K.VPLEVQEADEAK.L	P26640	SYVC_HUMAN	Valine--tRNA ligase (EC 6.1.1.9) (Protein G7a) (Valyl-tRNA synthetase) (ValRS)	VARS
1328,71	1328,048	1329,377	1328,70	0,016	R.ELLTDEKDPR.R	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RPS9
			1328,63	0,081	R.INVYYNEATGGK.Y	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1328,60	0,113	K.YWEMQPATFR.C	Q9BXN1	ASPN_HUMAN	Asporin (Periodontal ligament-associated protein 1) (PLAP-1)	ASPN
1329,64	1328,977	1330,306	1329,63	0,008	R.CLVTGFGGYDK.V	Q99536	VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog (EC 1.-.- VAT1 -.)	VAT1
			1329,65	0,012	K.GFAFQVYVNER.N	P07910	HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1/C2)	HNRNPC
			1329,67	0,031	K.NVQDAIADAQR.G	P35908	K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (CK-2e) (Epithelial keratin-2e) (Keratin-2 epidermis) (Keratin-2e) (K2e) (Type-II keratin Kb2)	KRT2
1329,72	1329,060	1330,389	1329,77	0,125	K.VMVQPINLIFR.Y	P62304	RUXE_HUMAN	Small nuclear ribonucleoprotein E (snRNP-E) (Sm protein E) (Sm-E) (SmE)	SNRPE
			1329,77	0,042	K.VMVQPINLIFR.Y	P62304	RUXE_HUMAN	Small nuclear ribonucleoprotein E (snRNP-E) (Sm protein E) (Sm-E) (SmE)	SNRPE
			1329,67	0,052	K.NVQDAIADAQR.G	P35908	K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (CK-2e) (Epithelial keratin-2e) (Keratin-2 epidermis) (Keratin-2e) (K2e) (Type-II keratin Kb2)	KRT2
1330,45	1329,789	1331,119	1329,65	0,071	K.GFAFQVYVNER.N	P07910	HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1/C2)	HNRNPC
			1329,63	0,091	R.CLVTGFGGYDK.V	Q99536	VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog (EC 1.-.- VAT1 -.)	VAT1
			1330,61	0,154	R.NPWGEVEWTGR.W	P17655	CAN2_HUMAN	Calpain-2 catalytic subunit (EC 3.4.22.53) (Calcium-activated neutral proteinase 2) (CANP 2) (Calpain M-type) (Calpain large polypeptide L2) (Calpain-2 large subunit) (Millimolar-calpain) (M-calpain)	CAPN2
1330,62	1330,63	1330,63	1330,62	0,167	R.GATQQILDEAER.S	P78371	TCPB_HUMAN	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	CCT2
			1330,63	0,176	R.GFAYVQFEDVR.D	O75494	SRS10_HUMAN	Serine/arginine-rich splicing factor 10 (40 kDa SR-repressor protein) (SRp40) (FUS-interacting serine-arginine-rich protein 1) (Splicing factor SRp38) (Splicing factor, arginine/serine-rich 13A) (TLS-associated protein with Ser-Arg repeats) (TASR) (TLS-associated protein with SR repeats) (TLS-associated serine-arginine protein) (TLS-associated SR protein)	SRSF10
			1330,63	0,178	R.VVDLMAHMASKE.-	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
1330,70	1330,037	1331,368	1330,72	0,266	K.FLVGPDGIPIMR.W	P22352	GPX3_HUMAN	Glutathione peroxidase 3 (GPx-3) (GSHPx-3) (EC 1.11.1.9) (Extracellular glutathione peroxidase) (Plasma glutathione peroxidase) (GPx-P) (GSHPx-P)	GPX3
			1330,72	0,018	K.FLVGPDGIPIMR.W	P22352	GPX3_HUMAN	Glutathione peroxidase 3 (GPx-3) (GSHPx-3) (EC 1.11.1.9) (Extracellular glutathione peroxidase) (Plasma glutathione peroxidase) (GPx-P) (GSHPx-P)	GPX3
			1330,63	0,070	R.VVDLMAHMASKE.-	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
1330,63	1330,63	1330,63	1330,63	0,073	R.GFAYVQFEDVR.D	O75494	SRS10_HUMAN	Serine/arginine-rich splicing factor 10 (40 kDa SR-repressor protein) (SRp40) (FUS-interacting serine-arginine-rich protein 1) (Splicing factor SRp38) (Splicing factor, arginine/serine-rich 13A) (TLS-associated protein with Ser-Arg repeats) (TASR) (TLS-associated protein with SR repeats) (TLS-associated serine-arginine protein) (TLS-associated SR protein)	SRSF10
			1330,62	0,082	R.GATQQILDEAER.S	P78371	TCPB_HUMAN	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	CCT2
			1330,61	0,094	R.NPWGEVEWTGR.W	P17655	CAN2_HUMAN	Calpain-2 catalytic subunit (EC 3.4.22.53) (Calcium-activated neutral proteinase 2) (CANP 2) (Calpain M-type) (Calpain large polypeptide L2) (Calpain-2 large subunit) (Millimolar-calpain) (M-calpain)	CAPN2
1331,42	1330,758	1332,089	1331,59	0,162	R.QLEEAEEEAQR.A	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
			1331,60	0,179	R.HLEFSHDQYR.E	Q9NR45	SIAS_HUMAN	Sialic acid synthase (N-acetylneuraminate synthase) (EC 2.5.1.56) (N-acetylneuraminate-9-phosphate synthase) (EC 2.5.1.57) (N-acetylneuraminic acid phosphate synthase) (N-acetylneuraminic acid synthase)	NANS
			1331,60	0,071	R.HLEFSHDQYR.E	Q9NR45	SIAS_HUMAN	Sialic acid synthase (N-acetylneuraminate synthase) (EC 2.5.1.56) (N-acetylneuraminate-9-phosphate synthase) (EC 2.5.1.57) (N-acetylneuraminic acid phosphate synthase) (N-acetylneuraminic acid synthase)	NANS
1331,67	1331,007	1332,339	1331,59	0,087	R.QLEEAEEEAQR.A	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9

1331,72	1331,051	1332,383	1331,60	0,114	R.HLEFSHQYR.E	Q9NR45	SIA5_HUMAN	Sialic acid synthase (N-acetylneuraminase synthase) (EC 2.5.1.56) (N-acetylneuraminase-9-phosphate synthase) (EC 2.5.1.57) (N-acetylneuraminic acid phosphate synthase) (N-acetylneuraminic acid synthase)	NANS
			1331,59	0,131	R.QLEAEAEQA.R	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
1332,72	1332,053	1333,386	1332,77	0,047	R.RFLAVQSVISGR.F	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1332,61	0,105	R.EFDDLPLAEQR.E	O14983	AT2A1_HUMAN	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 (SERCA1) (SR Ca(2+)-ATPase 1) (EC 7.2.2.10) (Calcium pump 1) (Calcium-transporting ATPase sarcoplasmic reticulum type, fast twitch skeletal muscle isoform) (Endoplasmic reticulum class 1/2 Ca(2+) ATPase)	ATP2A1
			1332,60	0,122	R.HQEGEIFDTEK.E	Q02878	RL6_HUMAN	60S ribosomal protein L6 (Large ribosomal subunit protein eL6) (Neoplasm-related protein C140) (Tax-responsive enhancer element-binding protein 107) (TaxREB107)	RPL6
1333,33	1332,664	1333,997	1333,55	0,224	R.MGPSGEGMEPER.R	Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 (LASP-1) (Metastatic lymph node gene 50 protein) (MLN 50)	LASP1
			1332,77	0,564	R.RFLAVQSVISGR.F	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1333,72	1333,055	1334,389	1333,55	0,167	R.MGPSGEGMEPER.R	Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 (LASP-1) (Metastatic lymph node gene 50 protein) (MLN 50)	LASP1
1334,69	1334,025	1335,360	1334,61	0,081	K.DLMVGDEASELR.S	P61160	ARP2_HUMAN	Actin-related protein 2 (Actin-like protein 2)	ACTR2
			1334,61	0,082	R.YFYNQEESVR.F	P01911	2B1F_HUMAN	HLA class II histocompatibility antigen, DRB1-15 beta chain (DW2.2/DR2.2) (MHC class II antigen DRB1*15)	HLA-DRB1
1335,69	1335,018	1336,354	1335,60	0,089	K.EGVECEVINMR.T	P11177	ODPB_HUMAN	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial (PDHE1-B) (EC 1.2.4.1)	PDHB
			1335,57	0,113	R.AECFKEGEPR.K	Q13217	DNJC3_HUMAN	DnaJ homolog subfamily C member 3 (Endoplasmic reticulum DNA J domain-containing protein 6) (ER-resident protein ERdj6) (ERdj6) (Interferon-induced, double-stranded RNA-activated protein kinase inhibitor) (Protein kinase inhibitor of 58 kDa) (Protein kinase inhibitor p58)	DNJC3
1336,70	1336,028	1337,365	1336,67	0,029	K.RISGLIYEETR.G	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
			1336,65	0,050	K.IYAMHWGTD.SR.L	P62879	GBB2_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 (G protein subunit beta-2) (Transducin beta chain 2)	GNB2
			1336,63	0,066	K.FYEEVHDLER.K	P55209	NP1L1_HUMAN	Nucleosome assembly protein 1-like 1 (NAP-1-related protein) (hNRP)	NAP1L1
			1336,62	0,071	R.MLDMGFEPQIR.K	Q92841	DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.4.13) (DEAD box protein 17) (DEAD box protein p72) (DEAD box protein p82) (RNA-dependent helicase p72)	DDX17
			1336,62	0,071	R.MLDMGFEPQIR.K	P17844	DDX5_HUMAN	Probable ATP-dependent RNA helicase DDX5 (EC 3.6.4.13) (DEAD box protein 5) (RNA helicase p68)	DDX5
			1336,62	0,075	K.VDESQPPAPSKPR.R	Q29R7	PDSSA_HUMAN	Sister chromatid cohesion protein PDSS homolog A (Cell proliferation-inducing gene 54 protein) (Sister chromatid cohesion protein 112) (SCC-112)	PDSSA
			1336,62	0,079	R.DAQELYAAGENR.L	P50995	ANX11_HUMAN	Annexin A11 (56 kDa autoantigen) (Annexin XI) (Annexin-11) (Calcyclin-associated annexin 50) (CAP-50)	ANXA11
			1336,58	0,114	K.NYDIQYFSMR.D	P78540	ARGI2_HUMAN	Arginase-2, mitochondrial (EC 3.5.3.1) (Arginase II) (Kidney-type arginase) (Non-hepatic arginase) (Type II arginase)	ARG2
			1337,64	0,032	K.WGTLTCVVMR.D	P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNP A3
			1337,72	0,046	M.PPYTVVYFVR.G	P09211	GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1)	GSTP1
1338,69	1338,024	1339,362	1337,62	0,055	R.YALYDATYETK.E	P23528	COF1_HUMAN	Cofilin-1 (18 kDa phosphoprotein) (p18) (Cofilin, non-muscle isoform)	CFL1
			1338,66	0,032	R.LFEAEAQDLFR.D	Q9H223	EHD4_HUMAN	EH domain-containing protein 4 (Hepatocellular carcinoma-associated protein 10/11) (PAST homolog 4)	EHD4
			1338,65	0,045	R.ACGLNFADLMAR.Q	Q99536	VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog (EC 1.-.-)	VAT1
			1338,64	0,057	R.DYIWNTLNSGR.V	O75390	CISY_HUMAN	Citrate synthase, mitochondrial (EC 2.3.3.1) (Citrate (Si)-synthase)	CS
			1339,68	0,021	R.DYFFALAHTRV.D	P11216	PYGB_HUMAN	Glycogen phosphorylase, brain form (EC 2.4.1.1)	PYGB
			1339,61	0,095	R.MFADYLAHESR.R	O14579	COPE_HUMAN	Coatomer subunit epsilon (Epsilon-coat protein) (Epsilon-COP)	COPE
1340,66	1339,992	1341,333	1340,66	0,002	K.TSDQIHFFAK.L	P01008	ANT3_HUMAN	Antithrombin-III (ATIII) (Serpin C1)	SERPINC1
			1340,67	0,006	K.YSFLQDFPAPR.R	P62714	PP2AB_HUMAN	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform (PP2A-beta) (EC 3.1.3.16)	PPP2CB
			1340,61	0,052	R.GTVDTPGPFDER.A	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
			1340,57	0,088	R.DYSDPSGGSYR.D	Q96E39	RMXL1_HUMAN	RNA binding motif protein, X-linked-like-1 (Heterogeneous nuclear ribonucleoprotein G-like 1)	RBMXL1
			1340,79	0,129	K.IILDLSIESPIK.G	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
			1340,49	0,172	K.NCMDICEDQR.D	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
1341,66	1340,984	1342,326	1341,65	0,006	K.YITDWQNVFR.T	O75340	PDCD6_HUMAN	Programmed cell death protein 6 (Apoptosis-linked gene 2 protein homolog) (ALG-2)	PDCD6
			1341,67	0,016	K.IMQYFSHFIR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG

1342,67	1341,999	1343,342	1341,67	0,019	R.FWPIFDTFIR.D	Q96M86	DNHD1_HUMAN	Dynein heavy chain domain-containing protein 1 (Dynein heavy chain domain 1-like protein) (Protein CCDC35)	DNHD1
			1341,70	0,041	R.EDLRLEPGLGK.E	P63241	IFSA1_HUMAN	Eukaryotic translation initiation factor 5A-1 (eIF-5A-1) (eIF-5A1) (Eukaryotic initiation factor 5A isoform 1) (eIF-5A) (Rev-binding factor) (eIF-4D)	EIF5A
			1341,72	0,061	K.QESGSEIHVEVK.A	P46013	KI67_HUMAN	Proliferation marker protein Ki-67 (Antigen identified by monoclonal antibody Ki-67) (Antigen Ki-67) (Antigen Ki67)	MKI67
			1341,78	0,123	K.TSDLIVLGLPWK.T	Q13148	TADBP_HUMAN	TAR DNA-binding protein 43 (TDP-43)	TARDBP
1343,67	1343,003	1344,347	1342,63	0,044	K.AVMDDFAAFVEK.C	P02768	ALBU_HUMAN	Serum albumin	ALB
1343,67	1343,003	1344,347	1343,70	0,028	R.DNTINLIHTFR.D	Q15144	ARPC2_HUMAN	Actin-related protein 2/3 complex subunit 2 (Arp2/3 complex 34 kDa subunit) (p34-ARPC)	ARPC2
			1343,64	0,038	R.WYVYQNTYDR.W	Q13510	ASAH1_HUMAN	Acid ceramidase (AC) (ACDase) (Acid CDase) (EC 3.5.1.23) (Acylsphingosine deacylase) (N-acyl ethanolamine hydrolase ASAH1) (EC 3.5.1.-) (N-acylsphingosine amidohydrolase) (Putative 32 kDa heart protein) (PHP32) [Cleaved into: Acid ceramidase subunit alpha; Acid ceramidase subunit beta]	ASAH1
			1344,71	0,017	R.TVIIEQSWGSPK.V	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
			1344,66	0,030	R.GTPLDTEVPMER.V	P11498	PYC_HUMAN	Pyruvate carboxylase, mitochondrial (EC 6.4.1.1) (Pyruvic carboxylase) (PCB)	PC
1344,69	1344,018	1345,363	1344,66	0,030	K.SSQEIQLRILVR.A	Q9NZT2	OGFR_HUMAN	Opioid growth factor receptor (OGFr) (Protein 7-60) (Zeta-type opioid receptor)	OGFR
			1344,66	0,030	R.ASLEAAIADEAQR.G	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
			1344,74	0,047	R.TFIAIKPDGVQR.G	P15531	NDKA_HUMAN	Nucleoside diphosphate kinase A (NDK A) (NDP kinase A) (EC 2.7.4.6) (Granzyme A-activated DNase) (GAAD) (Metastasis inhibition factor nm23) (NM23-H1) (Tumor metastatic process-associated protein)	NME1
			1344,74	0,047	R.TFIAIKPDGVQR.G	P22392	NDKB_HUMAN	Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (EC 2.7.4.6) [C-myc purine-binding transcription factor PUF] (Histidine protein kinase NDKB) (EC 2.7.13.3) (nm23-H2)	NME2
1345,69	1345,022	1346,367	1345,76	0,064	K.VMVQPINLIIFR.Y	P62304	RUXE_HUMAN	Small nuclear ribonucleoprotein E (snRNP-E) (Sm protein E) (Sm-E) (SmE)	SNRPE
			1345,63	0,067	K.YFLHQSHZER.E	P02794	FRIH_HUMAN	Ferritin heavy chain (Ferritin H subunit) (EC 1.16.3.1) (Cell proliferation-inducing gene 15 protein) [Cleaved into: Ferritin heavy chain, N-terminally processed]	FTH1
1346,67	1346,001	1347,348	1346,56	0,114	R.YTCGEAPDYDR.S	P21266	GSTM3_HUMAN	Glutathione S-transferase Mu 3 (EC 2.5.1.18) (GST class-mu 3) (GSTM3-3) (hGSTM3-3)	GSTM3
1347,71	1347,031	1348,379	1347,70	0,004	R.EPNVLICFDK.F	P01903	DRA_HUMAN	HLA class II histocompatibility antigen, DR alpha chain (MHC class II antigen DRA)	HLA-DRA
			1347,70	0,008	R.NIRDDGFIIR.H	Q9UM54	MYO6_HUMAN	Unconventional myosin-VI (Unconventional myosin-6)	MYO6
1348,71	1348,035	1349,384	1348,74	0,035	K.LKELIFEETAR.F	P28482	MK01_HUMAN	Mitogen-activated protein kinase 1 (MAP kinase 1) (MAPK 1) (EC 2.7.11.24) (ERT1) (Extracellular signal-regulated kinase 2) (ERK-2) (MAP kinase isoform p42) (p42-MAPK) (Mitogen-activated protein kinase 2) (MAP kinase 2) (MAPK 2)	MAPK1
			1348,65	0,055	K.HFSVEGQLFRA	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			1348,65	0,055	K.HFSVEGQLFRA	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP 2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
			1348,64	0,067	K.VVTDTDTELAR.Q	P05198	IF2A_HUMAN	Eukaryotic translation initiation factor 2 subunit 1 (Eukaryotic translation initiation factor 2 subunit alpha) (eIF-2-alpha) (eIF-2A) (eIF-2alpha)	EIF2S1
1348,71	1348,035	1349,384	1348,63	0,084	K.QIQDFANEVER.L	Q9BUT1	BDH2_HUMAN	3-hydroxybutyrate dehydrogenase type 2 (EC 1.1.1.-) (EC 1.1.1.30) (Dehydrogenase/reductase SDR family member 6) (Oxidoreductase UCPA) (R-beta-hydroxybutyrate dehydrogenase) (Short chain dehydrogenase/reductase family 15C member 1)	BDH2
			1348,60	0,111	K.LPTCPGSCCEAK.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1349,71	0,014	R.LQYAIIEAWR.L	Q9Y252	CRYL1_HUMAN	Lambda-crystallin homolog (EC 1.1.1.45) (L-gulonate 3-dehydrogenase) (Gul3DH)	CRYL1
			1350,65	0,045	K.SNNVEMDWVLK.H	P31943	HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H (hnRNP H) [Cleaved into: Heterogeneous nuclear ribonucleoprotein H, N-terminally processed]	HNRNP1
1351,71	1351,031	1352,383	1350,77	0,071	K.GLEQLLVGGSHLK.E	P12109	CO6A1_HUMAN	Collagen alpha-1(VI) chain	COL6A1
			1350,80	0,107	K.HGATVLTLGGLK.K	P02144	MYG_HUMAN	Myoglobin	MB
			1351,69	0,015	R.FPFLSEWQIGK.I	P30046	DOPD_HUMAN	D-dopachrome decarboxylase (EC 4.1.1.84) (D-dopachrome tautomerase) (Phenylpyruvate tautomerase II)	DDT
			1351,67	0,039	R.VLDASWYSPGTR.E	Q16762	THTR_HUMAN	Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese)	TST
1352,71	1352,033	1353,386	1351,64	0,070	K.SSPELEDATSSK.R	P46013	KI67_HUMAN	Proliferation marker protein Ki-67 (Antigen identified by monoclonal antibody Ki-67) (Antigen Ki-67) (Antigen Ki67)	MKI67
			1351,62	0,085	K.YQEGGVSAFHK.T	P40121	CAPG_HUMAN	Macrophage-capping protein (Actin regulatory protein CAP-G)	CAPG
			1351,60	0,107	K.FEIWDTAGQER.Y	P51148	RAB5C_HUMAN	Ras-related protein Rab-5C (L1880) (RAB5L)	RAB5C
			1352,69	0,022	K.DYFNVYPYLPK.I	P55786	PSA_HUMAN	Puromycin-sensitive aminopeptidase (PSA) (EC 3.4.11.14) (Cytosol alanyl aminopeptidase) (AAP-S)	NPEPPS
1352,71	1352,033	1353,386	1352,66	0,052	R.TEMENEFVLIK.K	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
			1352,64	0,067	R.MLDMGFEPQIR.K	P17844	DDX5_HUMAN	Probable ATP-dependent RNA helicase DDX5 (EC 3.6.4.13) (DEAD box protein 5) (RNA helicase p68)	DDX5
			1352,64	0,067	R.MLDMGFEPQIR.K	Q92841	DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.4.13) (DEAD box protein 17) (DEAD box protein p72) (DEAD box protein p82) (RNA-dependent helicase p72)	DDX17
			1352,63	0,080	K.GISQEQMQEFR.A	Q43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
1352,71	1352,033	1353,386	1352,60	0,111	K.IYAMHWGTDGSR.L	P62879	GBB2_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 (G protein subunit beta-2) (Transducin beta chain 2)	GNB2
			1352,58	0,126	K.MKDTDSEIEI.E	P0DP23	CALM1_HUMAN	Calmodulin-1	CALM1

			1352,55	0,159	K.GQGSMEGTADER.A	Q14108	SCRB2_HUMAN	Lysosome membrane protein 2 (85 kDa lysosomal membrane sialoglycoprotein) (LGP85) (CD36 antigen-like 2) (Lysosome membrane protein II) (LIMP II) (Scavenger receptor class B member 2) (CD antigen CD36)	SCARB2
1353,21	1352,533	1353,886	1353,68	0,468	K.LIIWDSYTTNK.V	P62879	GBB2_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 (G protein subunit beta-2) (Transducin beta chain 2)	GNB2
			1353,68	0,471	R.SLFSSIGEVESAK.L	Q15717	ELAV1_HUMAN	ELAV-like protein 1 (Hu-antigen R) (HuR)	ELAVL1
			1352,69	0,522	K.DYFNVVPYPLPK.I	P55786	PSA_HUMAN	Puromycin-sensitive aminopeptidase (PSA) (EC 3.4.11.14) (Cytosol alanyl aminopeptidase) (AAP-S)	NPEPPS
			1352,66	0,552	R.TEMENEFVLIK.K	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
			1352,64	0,567	R.MLDMGFEPQIR.K	P17844	DDX5_HUMAN	Probable ATP-dependent RNA helicase DDX5 (EC 3.6.4.13) (DEAD box protein 5) (RNA helicase p68)	DDX5
			1352,64	0,567	R.MLDMGFEPQIR.K	Q92841	DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.4.13) (DEAD box protein 17) (DEAD box protein p72) (DEAD box protein p82) (RNA-dependent helicase p72)	DDX17
			1352,63	0,580	K.GISQEQMQEFR.A	Q43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
			1352,60	0,611	K.IYAMHWGTDSR.L	P62879	GBB2_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 (G protein subunit beta-2) (Transducin beta chain 2)	GNB2
			1352,58	0,626	K.MKDTDSEEEI.E	P0DP23	CALM1_HUMAN	Calmodulin-1	CALM1
			1352,55	0,659	K.GQGSMEGTADER.A	Q14108	SCRB2_HUMAN	Lysosome membrane protein 2 (85 kDa lysosomal membrane sialoglycoprotein) (LGP85) (CD36 antigen-like 2) (Lysosome membrane protein II) (LIMP II) (Scavenger receptor class B member 2) (CD antigen CD36)	SCARB2
1353,66	1352,984	1354,337	1353,68	0,017	K.LIIWDSYTTNK.V	P62879	GBB2_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 (G protein subunit beta-2) (Transducin beta chain 2)	GNB2
			1353,68	0,020	R.SLFSSIGEVESAK.L	Q15717	ELAV1_HUMAN	ELAV-like protein 1 (Hu-antigen R) (HuR)	ELAVL1
1353,75	1353,075	1354,429	1353,68	0,071	R.SLFSSIGEVESAK.L	Q15717	ELAV1_HUMAN	ELAV-like protein 1 (Hu-antigen R) (HuR)	ELAVL1
			1353,68	0,074	K.LIIWDSYTTNK.V	P62879	GBB2_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 (G protein subunit beta-2) (Transducin beta chain 2)	GNB2
1354,22	1353,546	1354,900	1354,60	0,375	R.SQYEVMAEQNR.K	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1354,63	0,403	K.DYELLCLDGTR.K	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1354,64	0,413	K.DSYVGDEAQSKR.G	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1354,64	0,413	K.DSYVGDEAQSKR.G	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1354,64	0,413	K.DSYVGDEAQSKR.G	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			1354,64	0,413	K.DSYVGDEAQSKR.G	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1353,68	0,542	R.SLFSSIGEVESAK.L	Q15717	ELAV1_HUMAN	ELAV-like protein 1 (Hu-antigen R) (HuR)	ELAVL1
			1353,68	0,545	K.LIIWDSYTTNK.V	P62879	GBB2_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 (G protein subunit beta-2) (Transducin beta chain 2)	GNB2
1354,37	1353,688	1355,042	1354,60	0,233	R.SQYEVMAEQNR.K	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1354,63	0,261	K.DYELLCLDGTR.K	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1354,64	0,271	K.DSYVGDEAQSKR.G	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1354,64	0,271	K.DSYVGDEAQSKR.G	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1354,64	0,271	K.DSYVGDEAQSKR.G	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			1354,64	0,271	K.DSYVGDEAQSKR.G	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
1354,66	1353,986	1355,340	1354,64	0,027	K.DSYVGDEAQSKR.G	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1354,64	0,027	K.DSYVGDEAQSKR.G	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1354,64	0,027	K.DSYVGDEAQSKR.G	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			1354,64	0,027	K.DSYVGDEAQSKR.G	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1354,63	0,037	K.DYELLCLDGTR.K	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1354,60	0,065	R.SQYEVMAEQNR.K	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
1354,71	1354,032	1355,387	1354,64	0,073	K.DSYVGDEAQSKR.G	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1354,64	0,073	K.DSYVGDEAQSKR.G	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1354,64	0,073	K.DSYVGDEAQSKR.G	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			1354,64	0,073	K.DSYVGDEAQSKR.G	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1354,63	0,083	K.DYELLCLDGTR.K	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1354,60	0,111	R.SQYEVMAEQNR.K	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
1355,65	1354,969	1356,324	1355,69	0,045	K.IYLYTLNDNAR.S	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			1355,58	0,066	K.DAQHYGGWEHR.D	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1355,75	1355,073	1356,429	1355,69	0,060	K.IYLYTLNDNAR.S	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			1355,58	0,171	K.DAQHYGGWEHR.D	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB

1356,72	1356,040	1357,396	1356,71	0,003	R.LSDQFHDIUR.K	O75340	PDCD6_HUMAN	Programmed cell death protein 6 (Apoptosis-linked gene 2 protein homolog) (ALG-2)	PDCD6
			1356,66	0,063	K.NVGQFSGFPEK.G	P35659	DEK_HUMAN	Protein DEK	DEK
1357,73	1357,052	1358,410	1357,76	0,025	K.APLVCLPVFVSR.D	Q9HOW9	CK054_HUMAN	Ester hydrolase C11orf54 (EC 3.1.-.-)	C11orf54
			1357,67	0,065	K.IMQYFSHFIR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1358,71	1358,029	1359,388	1358,76	0,048	R.SLETENAGLR.LR.I	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
			1358,79	0,079	R.IITLAGPTNAIFK.A	Q15366	PCBP2_HUMAN	Poly(rC)-binding protein 2 (Alpha-CP2) (Heterogeneous nuclear ribonucleoprotein E2) (hnRNP E2)	PCBP2
1359,35	1358,674	1360,033	1358,61	0,095	K.AVMDDFAAFVEK.C	P02768	ALBU_HUMAN	Serum albumin	ALB
			1359,60	0,243	R.AAEEDEADPKR.Q	P20962	PTMS_HUMAN	Parathymosin	PTMS
			1359,63	0,275	R.FLQDYFDGNL.K.R	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	PDIA3
			1359,63	0,275	K.ADQDR.LDLEER.K	Q14683	SMC1A_HUMAN	Structural maintenance of chromosomes protein 1A (SMC protein 1A) (SMC-1-alpha) (SMC-1A) (Sb1.8)	SMC1A
			1358,79	0,566	R.IITLAGPTNAIFK.A	Q15366	PCBP2_HUMAN	Poly(rC)-binding protein 2 (Alpha-CP2) (Heterogeneous nuclear ribonucleoprotein E2) (hnRNP E2)	PCBP2
			1358,76	0,597	R.SLETENAGLR.LR.I	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
1359,70	1359,023	1360,383	1359,63	0,074	R.FLQDYFDGNL.K.R	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	PDIA3
			1359,63	0,074	K.ADQDR.LDLEER.K	Q14683	SMC1A_HUMAN	Structural maintenance of chromosomes protein 1A (SMC protein 1A) (SMC-1-alpha) (SMC-1A) (Sb1.8)	SMC1A
			1359,60	0,106	R.AAEEDEADPKR.Q	P20962	PTMS_HUMAN	Parathymosin	PTMS
1360,73	1360,046	1361,407	1360,67	0,057	R.EGDV.LTLLSER.E	P62857	RS28_HUMAN	40S ribosomal protein S28 (Small ribosomal subunit protein eS28)	RPS28
			1360,65	0,078	R.VEDTALYYCAR.G	AAOAC4DH32	HV320_HUMAN	Immunoglobulin heavy variable 3-20	IGHV3-20
1361,64	1360,957	1362,319	1361,67	0,030	R.FLQGDHFGTSPR.T	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1361,73	0,092	R.DLAEITTLDRSK.R	Q9B526	ERP44_HUMAN	Endoplasmic reticulum resident protein 44 (ER protein 44) (ERp44) (Thioredoxin domain-containing protein 4)	ERP44
			1361,73	0,092	R.AQFEGIVTDLIR.R	P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9
1361,67	1360,986	1362,348	1361,67	0,001	R.FLQGDHFGTSPR.T	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1361,73	0,063	R.DLAEITTLDRSK.R	Q9B526	ERP44_HUMAN	Endoplasmic reticulum resident protein 44 (ER protein 44) (ERp44) (Thioredoxin domain-containing protein 4)	ERP44
			1361,73	0,063	R.AQFEGIVTDLIR.R	P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9
1361,80	1361,123	1362,485	1361,73	0,074	R.DLAEITTLDRSK.R	Q9B526	ERP44_HUMAN	Endoplasmic reticulum resident protein 44 (ER protein 44) (ERp44) (Thioredoxin domain-containing protein 4)	ERP44
			1361,73	0,074	R.AQFEGIVTDLIR.R	P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9
			1361,67	0,136	R.FLQGDHFGTSPR.T	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1362,67	1361,992	1363,354	1362,69	0,015	K.EFKEEGEIPR.V	Q9UKV3	ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus (Acinus)	ACIN1
1362,81	1362,125	1363,488	1362,69	0,119	K.EFKEEGEIPR.V	Q9UKV3	ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus (Acinus)	ACIN1
1363,10	1362,416	1363,779	1362,69	0,410	K.EFKEEGEIPR.V	Q9UKV3	ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus (Acinus)	ACIN1
			1363,62	0,525	K.SWEEQMIEVGR.K	Q00059	TFAM_HUMAN	Transcription factor A, mitochondrial (mtTFA) (Mitochondrial transcription factor 1) (MtTF1) (Transcription factor 6) (TCF-6) (Transcription factor 6-like 2)	TFAM
1363,70	1363,016	1364,380	1363,62	0,076	K.SWEEQMIEVGR.K	Q00059	TFAM_HUMAN	Transcription factor A, mitochondrial (mtTFA) (Mitochondrial transcription factor 1) (MtTF1) (Transcription factor 6) (TCF-6) (Transcription factor 6-like 2)	TFAM
1363,82	1363,140	1364,503	1363,62	0,199	K.SWEEQMIEVGR.K	Q00059	TFAM_HUMAN	Transcription factor A, mitochondrial (mtTFA) (Mitochondrial transcription factor 1) (MtTF1) (Transcription factor 6) (TCF-6) (Transcription factor 6-like 2)	TFAM
1364,72	1364,041	1365,406	1364,69	0,032	K.TVDNFVALATGEK.G	P23284	PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) (CYP-51) (Cyclophilin B) (Rotamase B) (S-cyclophilin) (SCYLP)	PPIB
			1364,61	0,118	K.EAYPDHTQFEK.N	Q9P016	THYN1_HUMAN	Thymocyte nuclear protein 1 (Thymocyte protein Thy28)	THYN1
			1364,59	0,129	K.YEIDNAPEER.A	P49411	EFTU_HUMAN	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	TUFM
1365,73	1365,048	1366,414	1365,71	0,025	K.SRLEQEIATYR.S	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1365,62	0,114	K.EEAQAEIEQYR.L	Q75348	VATG1_HUMAN	V-type proton ATPase subunit G 1 (V-ATPase subunit G 1) (V-ATPase 13 kDa subunit 1) (Vacuolar proton pump subunit G 1) (Vacuolar proton pump subunit M16)	ATP6V1G1
			1365,51	0,222	R.FDHDEGDQCSR.L	Q76074	PDE5A_HUMAN	cGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.35) (cGMP-binding cGMP-specific phosphodiesterase) (cGB-PDE)	PDE5A
1366,69	1366,011	1367,378	1366,64	0,058	K.YHLGAYTGDDVR.I	Q15661	TRYB1_HUMAN	Tryptase alpha/beta-1 (Tryptase-1) (EC 3.4.21.59) (Tryptase I) (Tryptase alpha-1)	TPSAB1

1367,69 1368,68	1367,003 1367,992	1368,371 1369,360	1368,66	0,020	R.YLLEQDFPGMR.I	Q9H223	EHD4_HUMAN	EH domain-containing protein 4 (Hepatocellular carcinoma EHD4 associated protein 10/11) (PAST homolog 4)	
			1368,58 1368,78	0,092 0,102	K.MKDTDSEEEI.R K.LDNLVAIDLNR.L	P0DP23 P29401	CALM1_HUMAN TKT_HUMAN	Calmodulin-1 Transketolase (TK) (EC 2.2.1.1)	CALM1 TKT
1369,67 1369,77 1370,75	1368,983 1369,085 1370,061	1370,353 1370,455 1371,432	1370,69	0,057	R.ELSDFISYLQR.E	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	
			1370,65	0,094	K.YGDSGEQIAGFVK.E	P10619	PPGB_HUMAN	Lysosomal protective protein (EC 3.4.16.5) (Carboxypeptidase C) (Carboxypeptidase L) (Cathepsin A) (Protective protein cathepsin A) (PPCA) (Protective protein for beta-galactosidase) [Cleaved into: Lysosomal protective protein 32 kDa chain; Lysosomal protective protein 20 kDa chain]	CTSA
			1370,60	0,150	R.SQYEVMAEQNR.K	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
1371,28	1370,592	1371,963	1370,69	0,588	R.ELSDFISYLQR.E	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	
			1370,65	0,625	K.YGDSGEQIAGFVK.E	P10619	PPGB_HUMAN	Lysosomal protective protein (EC 3.4.16.5) (Carboxypeptidase C) (Carboxypeptidase L) (Cathepsin A) (Protective protein cathepsin A) (PPCA) (Protective protein for beta-galactosidase) [Cleaved into: Lysosomal protective protein 32 kDa chain; Lysosomal protective protein 20 kDa chain]	CTSA
			1370,60	0,681	R.SQYEVMAEQNR.K	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
1371,72 1372,22 1372,71 1373,72	1371,039 1371,534 1372,023 1373,030	1372,411 1372,906 1373,396 1374,404	1373,73 1373,62 1373,62	0,012 0,093 0,093	K.KDFSSVFQFLR.E K.YTISQEAQDQR.Q R.QECYAFNGTQR.F	P31937 Q99426 P04440	3HIDH_HUMAN TBCB_HUMAN DPB1_HUMAN	3-hydroxyisobutyrate dehydrogenase, mitochondrial (HIBADH) (EC 1.1.1.31) Tubulin-folding cofactor B (Cytoskeleton-associated protein 1) (Cytoskeleton-associated protein CKAP1) (Tubulin-specific chaperone B) HLA class II histocompatibility antigen, DP beta 1 chain (HLA class II histocompatibility antigen, DP(W4) beta chain) (MHC class II antigen DPB1)	HIBADH TBCB HLA-DPB1
1374,65	1373,963	1375,338	1374,63	0,018	R.WTEYGLTFTEK.W	P21796	VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal porin) (Porin 31HL) (Porin 31HM)	VDAC1
			1374,63 1374,70	0,018 0,050	K.YGEYFPGTGDLR.D R.RPFFPHSPSR.L	Q13547 P02511	HDAC1_HUMAN CRYAB_HUMAN	Histone deacetylase 1 (HD1) (EC 3.5.1.98) Alpha-crystallin B chain (Alpha(B)-crystallin) (Heat shock protein beta-5) (HspB5) (Renal carcinoma antigen NY-REN-27) (Rosenthal fiber component)	HDAC1 CRYAB
			1374,57	0,084	K.DESANQEEPEAR.V	P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP)	VASP
1374,74	1374,056	1375,430	1374,70	0,042	R.RPFFPHSPSR.L	P02511	CRYAB_HUMAN	Alpha-crystallin B chain (Alpha(B)-crystallin) (Heat shock protein beta-5) (HspB5) (Renal carcinoma antigen NY-REN-27) (Rosenthal fiber component)	CRYAB
			1374,63	0,111	R.WTEYGLTFTEK.W	P21796	VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal porin) (Porin 31HL) (Porin 31HM)	VDAC1
			1374,63 1374,57	0,111 0,176	K.YGEYFPGTGDLR.D K.DESANQEEPEAR.V	Q13547 P50552	HDAC1_HUMAN VASP_HUMAN	Histone deacetylase 1 (HD1) (EC 3.5.1.98) Vasodilator-stimulated phosphoprotein (VASP)	HDAC1 VASP
1375,66 1375,76 1376,72 1377,68	1374,971 1375,071 1376,035 1376,986	1376,346 1376,447 1377,412 1378,364	1377,61	0,067	R.FFGNSWAETYN	Q43488	ARK72_HUMAN	Aflatoxin B1 aldehyde reductase member 2 (EC 1.1.1.n11) (AFB1 aldehyde reductase 1) (AFB1-AR 1) (Aldoketoreductase 7) (Succinic semialdehyde reductase) (SSA reductase)	AKR7A2
1378,68	1377,987	1379,365	1378,67	0,009	R.LWGLTEMPFER.V	Q9N569	TOM22_HUMAN	Mitochondrial import receptor subunit TOM22 homolog (hTom22) (1C9-2) (Translocase of outer membrane 22 kDa subunit homolog)	TOMM22
			1378,70	0,022	K.MLQHIIDYRM.C	P14678	RSMB_HUMAN	Small nuclear ribonucleoprotein-associated proteins B and B' (snRNP-B) (Sm protein B/B') (Sm-B/B')	SNRPB
			1378,70	0,023	K.EFTFPVQAAYQK.V	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
1379,71	1379,018	1380,398	1379,64	0,067	R.DEGNYLDDALVR.Q	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedin) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4
			1379,59	0,119	R.FDDGAGGDNEVQR.T	P35998	PRS7_HUMAN	26S proteasome regulatory subunit 7 (26S proteasome AAA-ATPase subunit RPT1) (Proteasome 26S subunit ATPase 2) (Protein MSS1)	PSMC2
1380,72	1380,025	1381,406	1380,73	0,013	R.QEIVSLFNAFGR.I	Q96HE7	ERO1A_HUMAN	ERO1-like protein alpha (ERO1-L) (ERO1-L-alpha) (EC 1.8.4.- ERO1A) (Endoplasmic oxidoreductin-1-like protein) (Endoplasmic reticulum oxidoreductase alpha) (Oxidoreductin-1-L-alpha)	
			1380,75 1380,66 1380,66	0,040 0,052 0,052	R.GGADVASIHLLTAR.A K.DIVNMLMHDR.F K.DIVNMLMHDR.F	P01266 P11216 P11217	THYG_HUMAN PYGB_HUMAN PYGM_HUMAN	Thyroglobulin (Tg) Glycogen phosphorylase, brain form (EC 2.4.1.1) Glycogen phosphorylase, muscle form (EC 2.4.1.1) (Myophosphorylase)	TG PYGB PYGM
			1380,65 1380,79	0,069 0,077	R.NIFWTDNLDR.I K.LTIIDPETLPR.L	P14543 Q86VP6	NID1_HUMAN CAND1_HUMAN	Nidogen-1 (NID-1) (Entactin) Cullin-associated NEDD8-dissociated protein 1 (Cullin-associated and neddylation-dissociated protein 1) (TBP-interacting protein of 120 kDa A) (TBP-interacting protein 120A) (p120 CAND1)	NID1 CAND1
			1380,60	0,117	K.FRPDMEEEA.K	Q99436	PSB7_HUMAN	Proteasome subunit beta type-7 (EC 3.4.25.1) (Macropain chain Z) (Multicatalytic endopeptidase complex chain Z) (Proteasome subunit Z)	PSMB7

1380,85	1380,164	1381,545	1380,79	0,062	K.LTIIDPETLPR.L	Q86VP6	CAND1_HUMAN	Cullin-associated NEDD8-dissociated protein 1 (Cullin-associated and neddylation-dissociated protein 1) (TBP-interacting protein of 120 kDa A) (TBP-interacting protein 120A) (p120 CAND1)	CAND1
			1380,75	0,100	R.GGADVASIHLLTAR.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1380,73	0,127	R.QEIVSLFNAFGR.I	Q96HE7	ERO1A_HUMAN	ERO1-like protein alpha (ERO1-L) (ERO1-L-alpha) (EC 1.8.4.-) (Endoplasmic oxidoreductin-1-like protein) (Endoplasmic reticulum oxidoreductase alpha) (Oxidoreductin-1-L-alpha)	ERO1A
			1380,66	0,191	K.DIVNMLMHDDR.F	P11216	PYGB_HUMAN	Glycogen phosphorylase, brain form (EC 2.4.1.1)	PYGB
			1380,66	0,191	K.DIVNMLMHDDR.F	P11217	PYGM_HUMAN	Glycogen phosphorylase, muscle form (EC 2.4.1.1) (Myophosphorylase)	PYGM
			1380,65	0,208	R.NIFWTDNSLDR.I	P14543	NID1_HUMAN	Nidogen-1 (NID-1) (Entactin)	NID1
			1380,60	0,257	K.FRPDMEEEEK.N	Q99436	PSB7_HUMAN	Proteasome subunit beta type-7 (EC 3.4.25.1) (Macropain chain Z) (Multicatalytic endopeptidase complex chain Z) (Proteasome subunit Z)	PSMB7
1381,66	1380,969	1382,350							
1381,81	1381,123	1382,504							
1382,63	1381,943	1383,325	1382,58	0,052	R.GSVSDEEMMELR.E	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
			1382,52	0,116	K.ESDAQTCVESK.S	Q6PGQ7	BORA_HUMAN	Protein aurora borealis (HsBora)	BORA
1382,76	1382,070	1383,453	1382,58	0,179	R.GSVSDEEMMELR.E	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
			1382,52	0,243	K.ESDAQTCVESK.S	Q6PGQ7	BORA_HUMAN	Protein aurora borealis (HsBora)	BORA
1383,65	1382,955	1384,339	1383,68	0,035	K.SLNNQFASFIDK.V	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
			1383,58	0,070	R.GGAEQFMEETER.S	Q99832	TCPH_HUMAN	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein) [Cleaved into: T-complex protein 1 subunit eta, N-terminally processed]	CCT7
1383,77	1383,073	1384,457	1383,68	0,083	K.SLNNQFASFIDK.V	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
			1383,58	0,188	R.GGAEQFMEETER.S	Q99832	TCPH_HUMAN	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein) [Cleaved into: T-complex protein 1 subunit eta, N-terminally processed]	CCT7
1384,72	1384,030	1385,415	1384,72	0,003	R.LAAQSTLSFYQR.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1384,64	0,082	R.MEELHNQEVQK.R	Q15233	NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrb)) (p54nrb)	NONO
1384,85	1384,161	1385,546	1384,72	0,134	R.LAAQSTLSFYQR.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1384,64	0,213	R.MEELHNQEVQK.R	Q15233	NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrb)) (p54nrb)	NONO
1385,76	1385,072	1386,458	1385,74	0,028	K.DLDVAIILGSMR.R	P40925	MDHC_HUMAN	Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) (Cytosolic malate dehydrogenase) (Diiodophenylpyruvate reductase) (EC 1.1.1.96)	MDH1
			1385,73	0,032	K.TPLLMLGQEDR.R	P13798	ACPH_HUMAN	Aclamino-acid-releasing enzyme (AARE) (EC 3.4.19.1) (Acyl-peptide hydrolase) (APH) (Acylaminoacyl-peptidase) (Oxidized protein hydrolase) (OPH)	APEH
			1385,81	0,048	R.MVVPVAALFTPLK.E	Q15436	SC23A_HUMAN	Protein transport protein Sec23A (hSec23A) (SEC23-related protein A)	SEC23A
			1385,72	0,048	R.IMNVIGEPIDER.G	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
1386,75	1386,061	1387,448	1386,75	0,000	R.TGEAIVDAALSALR.Q	Q15084	PDIA6_HUMAN	Protein disulfide-isomerase A6 (EC 5.3.4.1) (Endoplasmic reticulum protein 5) (ER protein 5) (ERp5) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)	PDIA6
			1386,75	0,008	R.YGFIEGHVVIPR.I	P16070	CD44_HUMAN	CD44 antigen (CDw44) (Epican) (Extracellular matrix receptor III) (ECMR-III) (GP90 lymphocyte homing/adhesion receptor) (HUTCH-I) (Heparan sulfate proteoglycan) (Hermes antigen) (Hyaluronate receptor) (Phagocytic glycoprotein 1) (PGP-1) (Phagocytic glycoprotein I) (PGP-I) (CD antigen CD44)	CD44
			1386,78	0,029	R.VGWELQLTTIAR.T	P12814	ACTN1_HUMAN	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (F-actin cross-linking protein) (Non-muscle alpha-actinin-1)	ACTN1
			1386,78	0,029	R.VGWELQLTTIAR.T	Q43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
			1386,70	0,050	K.VSFLSALEEYTK.K	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
			1386,69	0,060	K.TSYLTPDLWK.E	P15880	RS2_HUMAN	40S ribosomal protein S2 (40S ribosomal protein S4) (Protein LLRep3) (Small ribosomal subunit protein u55)	RPS2
			1386,64	0,117	K.YDPTIEDSYRK.Q	P61224	RAP1B_HUMAN	Ras-related protein Rap-1b (GTP-binding protein smg p21B)	RAP1B
1387,75	1387,059	1388,447	1387,77	0,020	K.GVDEATHIDILT.R	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
1388,73	1388,038	1389,427	1388,68	0,056	R.DIIISAEEDLR.V	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC XRCC6 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	XRCC6
			1388,79	0,062	R.IITLTGPTNAIFK.A	Q15365	PCBP1_HUMAN	Poly(rC)-binding protein 1 (Alpha-CP1) (Heterogeneous nuclear ribonucleoprotein E1) (hnRNP E1) (Nucleic acid-binding protein SUB2.3)	PCBP1
			1388,65	0,078	R.QREEEIEAQEK.A	Q75937	DNJC8_HUMAN	Dnaj homolog subfamily C member 8 (Splicing protein spf31)	DNJC8
1389,75	1389,055	1390,444	1389,75	0,001	R.QAALQVAEGFISR.M	P40121	CAPG_HUMAN	Macrophage-capping protein (Actin regulatory protein CAP-G)	CAPG

			1389,74	0,012	R.EVPLINTIIFMGR.V	P01008	ANT3_HUMAN	Antithrombin-III (ATIII) (Serpin C1)	SERPINC1
			1389,68	0,074	K.AALEDTLAETEAR.F	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1389,66	0,085	K.NFYQEHPDLAR.R	P17844	DDX5_HUMAN	Probable ATP-dependent RNA helicase DDX5 (EC 3.6.4.13) (DEAD box protein 5) [RNA helicase p68]	DDX5
			1389,61	0,137	R.SSEDPNEDIVER.N	P01591	IGJ_HUMAN	Immunoglobulin J chain (Joining chain of multimeric IgA and IgM)	JCHAIN
1390,75	1390,058	1391,449	1390,73	0,023	R.LTPYEVDELRR.K	Q92841	DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.4.13) (DEAD box protein 17) (DEAD box protein p72) (DEAD box protein p82) (RNA-dependent helicase p72)	DDX17
			1390,67	0,086	K.QSLEASLAETEGR.Y	P13645	K1C10_HUMAN	Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KRT10
1391,76	1391,063	1392,455	1391,70	0,063	R.QVETELFPCR.H	O43488	ARK72_HUMAN	Aflatoxin B1 aldehyde reductase member 2 (EC 1.1.1.1.n11) (AFB1 aldehyde reductase 1) (AFB1-AR 1) (Aldoketoreductase 7) (Succinic semialdehyde reductase) (SSA reductase)	AKR7A2
			1391,63	0,126	R.LETHMTPEMFR.T	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A (EC 3.6.4.13) (DEAH box protein 9) (DExH-box helicase 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II) (RNA helicase A)	DHX9
1392,72	1392,028	1393,421	1392,66	0,069	R.RIEQHYFEDR.G	O75431	MTX2_HUMAN	Metaxin-2 (Mitochondrial outer membrane import complex protein 2)	MTX2
1393,73	1393,032	1394,426	1393,70	0,032	K.FVEGLPINDFSR.E	P40925	MDHC_HUMAN	Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) (Cytosolic malate dehydrogenase) (Diiodophenylpyruvate reductase) (EC 1.1.1.96)	MDH1
			1393,69	0,041	R.ASSIIDELFQDR.F	P10909	CLUS_HUMAN	Clusterin (Aging-associated gene 4 protein) (Apolipoprotein J) (Apo-J) (Complement cytolysis inhibitor) (CLI) (Complement-associated protein SP-40,40) (Ku70-binding protein 1) (NA1/NA2) (Sulfated glycoprotein 2) (SGP-2) (Testosterone-repressed prostate message 2) (TRPM-2) [Cleaved into: Clusterin beta chain (Apolalpha) (Complement cytolysis inhibitor a chain); Clusterin alpha chain (Apolbeta) (Complement cytolysis inhibitor b chain)]	CLU
			1393,69	0,041	K.EALTYDGALLGDR.S	Q15056	IF4H_HUMAN	Eukaryotic translation initiation factor 4H (eIF-4H) (Williams-Beuren syndrome chromosomal region 1 protein)	EIF4H
			1394,62	0,104	K.AADDTWEPFASGK.T	P02766	TTHY_HUMAN	Transthyretin (ATTR) (Prealbumin) (TBPA)	TTR
1395,74	1395,040	1396,435	1395,66	0,079	R.DFTPVCTTELGR.A	P30041	PRDX6_HUMAN	Peroxiredoxin-6 (EC 1.11.1.15) (1-Cys peroxiredoxin) (1-Cys PRX) (24 kDa protein) (Acidic calcium-independent phospholipase A2) (aiPLA2) (EC 3.1.1.4) (Antioxidant protein 2) (Liver 2D page spot 40) (Non-selenium glutathione peroxidase) (NSGPx) (Red blood cells page spot 12)	PRDX6
1396,73	1396,033	1397,430	1396,69	0,040	K.IHVFYIDYGNR.E	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
1397,73	1397,030	1398,428	1397,70	0,033	K.DLFLQGAYDTVR.W	Q9UHL4	DPP2_HUMAN	Dipeptidyl peptidase 2 (EC 3.4.14.2) (Dipeptidyl aminopeptidase II) (Dipeptidyl peptidase 7) (Dipeptidyl peptidase II) (DPP II) (Quiescent cell proline dipeptidase)	DPP7
1397,74	1397,040	1398,438	1397,70	0,043	K.DLFLQGAYDTVR.W	Q9UHL4	DPP2_HUMAN	Dipeptidyl peptidase 2 (EC 3.4.14.2) (Dipeptidyl aminopeptidase II) (Dipeptidyl peptidase 7) (Dipeptidyl peptidase II) (DPP II) (Quiescent cell proline dipeptidase)	DPP7
1398,77	1398,072	1399,471	1398,74	0,037	K.TTPDVIVFGFR.T	P62847	RS24_HUMAN	40S ribosomal protein S24 (Small ribosomal subunit protein eS24)	RPS24
1399,64	1398,940	1400,340	1399,75	0,109	R.RIQLVEEELDR.A	P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	TPM4
			1399,84	0,202	R.KQVVNIPSFIVR.L	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RPS9
1399,77	1399,071	1400,471	1399,75	0,022	R.RIQLVEEELDR.A	P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	TPM4
			1399,84	0,071	R.KQVVNIPSFIVR.L	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RPS9
1400,67	1399,966	1401,367	1400,68	0,016	R.STDYGIFQINSR.Y	P61626	LYSC_HUMAN	Lysozyme C (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C) (Lyz)	LYZ
			1400,64	0,027	K.YGGDEIFSPYR.V	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			1400,70	0,034	R.DYVSQFEGSALGK.Q	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
			1400,72	0,057	R.AKLEAAIAEAER.G	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcoleictin) (Type-II keratin Kb7)	KRT7
			1400,77	0,105	R.AAAITSDILEALGR.D	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
			1400,81	0,145	K.LLPLVSEVFIR.D	P11216	PYGB_HUMAN	Glycogen phosphorylase, brain form (EC 2.4.1.1)	PYGB
			1400,86	0,198	R.IGLNLFNKKPEK.G	Q5JU85	IQEC2_HUMAN	IQ motif and SEC7 domain-containing protein 2	IQSEC2
			1400,86	0,024	K.LLPLVSEVFIR.D	P11216	PYGB_HUMAN	Glycogen phosphorylase, brain form (EC 2.4.1.1)	PYGB
1400,80	1400,095	1401,496	1400,77	0,024	R.AAAITSDILEALGR.D	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
			1400,86	0,069	R.IGLNLFNKKPEK.G	Q5JU85	IQEC2_HUMAN	IQ motif and SEC7 domain-containing protein 2	IQSEC2
			1400,72	0,072	R.AKLEAAIAEAER.G	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcoleictin) (Type-II keratin Kb7)	KRT7
			1400,70	0,095	R.DYVSQFEGSALGK.Q	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
			1400,68	0,113	R.STDYGIFQINSR.Y	P61626	LYSC_HUMAN	Lysozyme C (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C) (Lyz)	LYZ
			1400,64	0,156	K.YGGDEIFSPYR.V	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
1401,70	1400,997	1402,399	1401,71	0,011	R.IMNVIGEPIDER.G	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			1401,67	0,025	K.HYQINQQWER.T	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1

1402,71	1402,006	1403,408	1401,74	0,044	R.LEELENLVSSLR.E	P24821	TENA_HUMAN	Tenascin (TN) (Cytotactin) (GMEM) (GP 150-225) (Glioma-associated-extracellular matrix antigen) (Hexabrachion) (II) (Myotendinous antigen) (Neuronectin) (Tenascin-C) (TN-C)	TNC
			1401,63	0,064	K.DTPDEPWAFPAR.E	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
			1401,59	0,110	R.ENYSHHTQDDR.R	Q92804	RBP56_HUMAN	TATA-binding protein-associated factor 2N (68 kDa TATA-binding protein-associated factor) (TAF(II)68) (TAFII68) (RNA-binding protein 56)	TAF15
1403,67	1402,971	1404,375	1402,72	0,010	R.DTGIFLDMHLK.K	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC XRCC6 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	
			1402,62	0,083	K.YFQMSLEAEER.V	P07942	LAMB1_HUMAN	Laminin subunit beta-1 (Laminin B1 chain) (Laminin-1 subunit beta) (Laminin-10 subunit beta) (Laminin-12 subunit beta) (Laminin-2 subunit beta) (Laminin-6 subunit beta) (Laminin-8 subunit beta)	LAMB1
			1402,80	0,093	R.LPFQKLMGISIR.N	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1403,80	1403,097	1404,501	1403,66	0,015	K.RAGELTEDEVER.V	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
			1403,69	0,021	R.GIHVEVPPAEAEER.L	P38117	ETFB_HUMAN	Electron transfer flavoprotein subunit beta (Beta-ETF)	ETFB
			1403,73	0,059	R.KIEFSLPDLEGR.T	P35998	PRS7_HUMAN	26S proteasome regulatory subunit 7 (26S proteasome AAA-ATPase subunit RPT1) (Proteasome 26S subunit ATPase 2) (Protein MSS1)	PSMC2
1404,63	1403,925	1405,330	1403,78	0,103	K.LSDAGITPLFLTR.Q	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1403,78	0,023	K.LSDAGITPLFLTR.Q	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1403,73	0,067	R.KIEFSLPDLEGR.T	P35998	PRS7_HUMAN	26S proteasome regulatory subunit 7 (26S proteasome AAA-ATPase subunit RPT1) (Proteasome 26S subunit ATPase 2) (Protein MSS1)	PSMC2
1404,78	1404,075	1405,480	1403,69	0,105	R.GIHVEVPPAEAEER.L	P38117	ETFB_HUMAN	Electron transfer flavoprotein subunit beta (Beta-ETF)	ETFB
			1403,66	0,141	K.RAGELTEDEVER.V	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
			1404,73	0,097	K.YYVTIIDAPGHR.D	P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1
1404,78	1404,075	1405,480	1404,74	0,116	R.MDLLPLHMGHLK.L	P21980	TGM2_HUMAN	Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (Transglutaminase C) (TG(C)) (TGC) (TGase C) (Transglutaminase H) (TGase H) (Transglutaminase-2) (TGase-2)	TGM2
			1404,74	0,034	R.MDLLPLHMGHLK.L	P21980	TGM2_HUMAN	Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (Transglutaminase C) (TG(C)) (TGC) (TGase C) (Transglutaminase H) (TGase H) (Transglutaminase-2) (TGase-2)	TGM2
			1404,73	0,053	K.YYVTIIDAPGHR.D	P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1
1405,76	1405,053	1406,458	1405,76	0,003	K.EIKDILIQYDR.T	P62249	RS16_HUMAN	40S ribosomal protein S16 (Small ribosomal subunit protein uS9)	RPS16
			1405,75	0,009	K.LLDIACWIHHK.Y	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
			1405,75	0,010	K.VESLQEEIAFLK.K	P08670	VIME_HUMAN	Vimentin	VIM
1406,74	1406,040	1407,447	1405,71	0,042	K.DVVFLLDGSSEGV.R.S	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1405,65	0,106	R.FFDEESYSLLR.K	P51571	SSRD_HUMAN	Translocon-associated protein subunit delta (TRAP-delta) (Signal sequence receptor subunit delta) (SSR-delta)	SSR4
			1406,72	0,023	R.GNPTVEVDLYTAK.G	P09104	ENOG_HUMAN	Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 2) (Neural enolase) (Neuron-specific enolase) (NSE)	ENO2
1407,74	1407,034	1408,442	1406,72	0,023	R.GNPTVEVDLFTSK.G	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			1406,70	0,044	R.LSDETLIDIMTR.F	P19367	HXX1_HUMAN	Hexokinase-1 (EC 2.7.1.1) (Brain form hexokinase) (Hexokinase type I) (HK I)	HK1
			1406,68	0,066	R.FSPDDSAGASALLR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1408,74	1408,032	1409,441	1406,66	0,085	R.EVQQGEFFERR.I	P00568	KAD1_HUMAN	Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP-AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	AK1
			1407,69	0,045	K.KLDDFVETGDIR.T	Q14108	SCRB2_HUMAN	Lysosome membrane protein 2 (85 kDa lysosomal membrane sialoglycoprotein) (LGP85) (CD36 antigen-like 2) (Lysosome membrane protein II) (LIMP II) (Scavenger receptor class B member 2) (CD antigen CD36)	SCARB2
			1407,64	0,099	R.LETHMTPEMFR.T	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A (EC 3.6.4.13) (DEAH box protein 9) (DEXH-box helicase 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II) (RNA helicase A)	DHX9
1409,74	1409,035	1410,445	1407,62	0,119	R.NTPEYEELCPR.G	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			1408,67	0,067	R.AVFDETYPDPVR.V	P49588	SYAC_HUMAN	Alanine-tRNA ligase, cytoplasmic (EC 6.1.1.7) (Alanyl-tRNA synthetase) (AlaRS) (Renal carcinoma antigen NY-REN-42)	AARS
			1408,63	0,111	R.NVEAMNFADIER.T	P36957	ODO2_HUMAN	Dihydropyridyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydropyridylsuccinyltransferase component of 2-oxoglutarate dehydrogenase complex) (E2K)	DLST
1409,74	1409,035	1410,445	1409,54	0,203	R.CEDVNECEAQR.C	P98095	FBLN2_HUMAN	Fibulin-2 (FIBL-2)	FBLN2
1410,73	1410,028	1411,438	1410,78	0,049	R.QLFHPEQLITGK.E	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A

			1410,78	0,049	R.QLFHPPEQLTGK.E	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			1410,78	0,049	R.QLFHPPEQLTGK.E	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			1410,66	0,071	R.RFDDAVVQSDMK.H	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
			1410,63	0,103	K.WAEYHADIYDK.V	Q9NRX4	PHP14_HUMAN	14 kDa phosphohistidine phosphatase (EC 3.9.1.3) (Phosphohistidine phosphatase 1) (PHPT1) (Protein histidine phosphatase) (PHP) (Protein janus-A homolog)	PHPT1
			1410,63	0,104	K.QEMASASSQRGR.R	Q32P51	RA1L2_HUMAN	Heterogeneous nuclear ribonucleoprotein A1-like 2 (hnRNP A1-like 2) (hnRNP core protein A1-like 2)	HNRNPA1L2
			1410,63	0,104	K.EQFLDGDGWTSR.W	P27797	CALR_HUMAN	Calreticulin (CRP55) (Calregulin) (Endoplasmic reticulum resident protein 60) (Erp60) (HACBP) (grp60)	CALR
1411,73 1412,75	1411,027 1412,046	1412,438 1413,459	1412,66	0,089	K.ASNTAEVFFDGVR.V	P49748	ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial (VLCAD) (EC 1.3.8.9)	ACADVL
1413,66	1412,952	1414,366	1413,66	0,004	K.WGDEHIPGSPYR.V	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			1413,81 1413,85	0,156 0,193	R.VLDPFTIKPLDR.K R.EVKLLLLGAGESGK.S	P29401 P04899	TKT_HUMAN GNAI2_HUMAN	Transketolase (TK) (EC 2.2.1.1) Guanine nucleotide-binding protein G(i) subunit alpha-2 (Adenylate cyclase-inhibiting G alpha protein)	TKT GNAI2
			1413,77	1413,067 1414,480	1413,81 1413,85 1413,66	0,041 0,079 0,118	R.VLDPFTIKPLDR.K R.EVKLLLLGAGESGK.S K.WGDEHIPGSPYR.V	P29401 P04899 P21333	TKT_HUMAN GNAI2_HUMAN FLNA_HUMAN
1414,69	1413,986	1415,401	1414,73	0,036	R.FQEUFEDFAR.F	Q96TA1	NIBL1_HUMAN	Niban-like protein 1 (Meg-3) (Melanoma invasion by ERK) (MINERVA) (Protein FAM129B)	FAM129B
			1414,77	0,081	K.IVILPDYLEIAR.D	P45974	UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.4.19.12) (Deubiquitinating enzyme 5) (isopeptidase T) (Ubiquitin thioesterase 5) (Ubiquitin-specific-processing protease 5)	USP5
			1414,78	0,083	K.AYFHLNLIQAPK.G	P13797	PLST_HUMAN	Plastin-3 (T-plastin)	PLS3
1414,78	1414,075 1415,490		1414,78	0,006	K.AYFHLNLIQAPK.G	P13797	PLST_HUMAN	Plastin-3 (T-plastin)	PLS3
			1414,77	0,008	K.IVILPDYLEIAR.D	P45974	UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.4.19.12) (Deubiquitinating enzyme 5) (isopeptidase T) (Ubiquitin thioesterase 5) (Ubiquitin-specific-processing protease 5)	USP5
			1414,73	0,053	R.FQEUFEDFAR.F	Q96TA1	NIBL1_HUMAN	Niban-like protein 1 (Meg-3) (Melanoma invasion by ERK) (MINERVA) (Protein FAM129B)	FAM129B
1415,75	1415,038	1416,454	1415,74	0,002	R.IANLQDLSGLR.L	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			1415,72	0,028	R.DHYLPDLHLRL.L	O15230	LAMAS_HUMAN	Laminin subunit alpha-5 (Laminin-10 subunit alpha) (Laminin-11 subunit alpha) (Laminin-15 subunit alpha)	LAMAS
			1415,66	0,083	K.DFTATDLSEFAAK.A	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2
			1415,63	0,114	R.FTDEEVDELYR.E	O14950	ML12B_HUMAN	Myosin regulatory light chain 12B (MLC-2A) (MLC-2) (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2) (SHUJUN-1)	MYL12B
1416,75	1416,041	1417,458	1416,67	0,078	R.AQEEAERLEADR.M	P15311	EZRI_HUMAN	Ezrin (Cyto villin) (Villin-2) (p81)	EZR
			1416,65	0,100	K.GIFGFTDSDCIGK.I	P23381	SYWC_HUMAN	Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IPF53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleaved into: T1-TrpRS; T2-TrpRS]	WARS
1417,77	1417,063 1418,481		1417,68	0,088	K.SAVGHEYVAEVEK.H	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
			1417,63	0,145	K.EHEAMKDELCR.Q	Q13361	MFAP5_HUMAN	Microfibrillar-associated protein 5 (MFAP-5) (MP25) (Microfibril-associated glycoprotein 2) (MAGP-2)	MFAP5
			1417,62	0,157	K.ILDSVGIEADDDR.L	P05387	RLA2_HUMAN	60S acidic ribosomal protein P2 (Large ribosomal subunit protein P2) (Renal carcinoma antigen NY-REN-44)	RPLP2
			1417,61	0,159	R.EAGDVCYADVYR.D	Q07955	SRSF1_HUMAN	Serine/arginine-rich splicing factor 1 (Alternative-splicing factor 1) (ASF-1) (Splicing factor, arginine/serine-rich 1) (pre-mRNA-splicing factor SF2, P33 subunit)	SRSF1
			1417,61	0,165	R.TPPSEEDSAEAER.L	O43765	SGTA_HUMAN	Small glutamine-rich tetratricopeptide repeat-containing protein alpha (Alpha-SGT) (Vpu-binding protein) (UBP)	SGTA
			1417,60	0,168	K.CFSEENHEPLR.T	Q96QK1	VPS35_HUMAN	Vacuolar protein sorting-associated protein 35 (hVPS35) (Maternal-embryonic 3) (Vesicle protein sorting 35)	VPS35
1418,75	1418,046	1419,464	1418,72	0,033	K.VDALNDEINFLR.T	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7)	KRT7
			1418,72	0,040	R.DICNDVLSLEK.F	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
			1418,70	0,056	K.VTEIWQEVQMQR.R	P08294	SODE_HUMAN	Extracellular superoxide dismutase [Cu-Zn] (EC-SOD) (EC 1.15.1.1)	SOD3
			1418,65	0,108	K.YFQMSLEAEER.V	P07942	LAMB1_HUMAN	Laminin subunit beta-1 (Laminin B1 chain) (Laminin-1 subunit beta) (Laminin-10 subunit beta) (Laminin-12 subunit beta) (Laminin-2 subunit beta) (Laminin-6 subunit beta) (Laminin-8 subunit beta)	LAMB1
1419,75	1419,040	1420,460	1419,74	0,013	R.LEGLTDEINFLR.Q	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
			1419,73	0,022	R.QAQEYFALLNIK.V	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
			1419,71	0,041	R.EIEVPDQYGTIR.A	Q9HC35	EMAL4_HUMAN	Echinoderm microtubule-associated protein-like 4 (EMAP-4) (Restrictedly overexpressed proliferation-associated protein) (Ropp 120)	EML4
1420,73	1420,017	1421,437							

1421,75	1421,042	1422,464	1421,71	0,046	K.LLETCPQVIR.K	P05109	S10A8_HUMAN	Protein S100-A8 (Calgranulin-A) (Calprotectin L1L subunit (Cystic fibrosis antigen) (CFAG) (Leukocyte L1 complex light chain) (Migration inhibitory factor-related protein 8) (MRP-8) (p8) (S100 calcium-binding protein A8) (Urinary stone protein band A)	S100A8
			1421,70	0,050	K.SLYYYQQDTK.G	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1421,69	0,068	K.GMTSEEKEILIR.D	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
1422,74	1422,025	1423,448	1422,72	0,019	R.AVAYQMWQNLAK.A	Q8WU39	MZB1_HUMAN	Marginal zone B- and B1-cell-specific protein (Mesenteric estrogen-dependent adipose 7) (MEDA-7) (Plasma cell-induced resident endoplasmic reticulum protein) (Plasma cell-induced resident ER protein) (pERp1) (Proapoptotic caspase adapter protein)	MZB1
			1422,71	0,024	K.VHVGDDEDVHLR.V	P04080	CYTB_HUMAN	Cystatin-B (CPI-B) (Liver thiol proteinase inhibitor) (Stefin-B)	CSTB
			1422,67	0,071	R.FEDGVLDPDYPR.N	P04004	VTNC_HUMAN	Vitronectin (VN) (S-protein) (Serum-spreading factor) (V75) [Cleaved into: Vitronectin V65 subunit; Vitronectin V10 subunit; Somatomedin-B]	VTN
1423,74	1423,027	1424,451	1423,68	0,058	K.TGTAEMSSILEER.I	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
			1423,68	0,063	R.APASEEEFQFLR.C	P29590	PML_HUMAN	Protein PML (Promyelocytic leukemia protein) (RING finger protein 71) (Tripartite motif-containing protein 19)	PML
			1423,66	0,079	R.ELAEDGYSGVEVR.V	P23396	RS3_HUMAN	40S ribosomal protein S3 (EC 4.2.99.18) (Small ribosomal subunit protein uS3)	RPS3
1424,72	1424,008	1425,433	1424,73	0,014	K.LLSFVDDEAFIR.D	P11217	PYGM_HUMAN	Glycogen phosphorylase, muscle form (EC 2.4.1.1) (Myophosphorylase)	PYGM
			1424,63	0,086	R.NVEAMNFADIER.T	P36957	ODO2_HUMAN	Dihydropyridyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydropyridylsuccinyltransferase component of 2-oxoglutarate dehydrogenase complex) (E2K)	DLST
1425,68	1424,966	1426,392	1425,67	0,011	R.WFEENASQSTVK.V	Q12905	ILF2_HUMAN	Interleukin enhancer-binding factor 2 (Nuclear factor of activated T-cells 45 kDa)	ILF2
			1425,72	0,046	R.YISPDQLADLYK.S	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			1425,79	0,111	K.ARIVLANDPDADR.L	Q96G03	PGM2_HUMAN	Phosphoglucosyltransferase-2 (PGM 2) (EC 5.4.2.2) (Glucose phosphomutase 2) (Phosphodeoxyribomutase) (Phosphopentomutase) (EC 5.4.2.7)	PGM2
1425,75	1425,033	1426,459	1425,72	0,021	R.YISPDQLADLYK.S	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			1425,79	0,044	K.ARIVLANDPDADR.L	Q96G03	PGM2_HUMAN	Phosphoglucosyltransferase-2 (PGM 2) (EC 5.4.2.2) (Glucose phosphomutase 2) (Phosphodeoxyribomutase) (Phosphopentomutase) (EC 5.4.2.7)	PGM2
			1425,67	0,079	R.WFEENASQSTVK.V	Q12905	ILF2_HUMAN	Interleukin enhancer-binding factor 2 (Nuclear factor of activated T-cells 45 kDa)	ILF2
1426,77	1426,059	1427,486	1426,85	0,073	R.LILPQMPKALFR.K	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1427,75	1427,038	1428,466	1427,73	0,024	K.WAAVVPVSGEEQR.Y	P30508	1C12_HUMAN	HLA class I histocompatibility antigen, Cw-12 alpha chain (MHC class I antigen Cw*12)	HLA-C
			1427,73	0,024	K.WAAVVPVSGEEQR.Y	P30493	1B55_HUMAN	HLA class I histocompatibility antigen, B-55 alpha chain (Bw-55) (HLA class I histocompatibility antigen, B-12 alpha chain) (MHC class I antigen B*55)	HLA-B
1428,72	1428,007	1429,436	1428,72	0,002	K.ANDIIVNVVNR.T	P13797	PLST_HUMAN	Plastin-3 (T-plastin)	PLS3
			1428,71	0,008	R.SLYASSPGGVYATR.S	P08670	VIME_HUMAN	Vimentin	VIM
			1428,71	0,013	R.DFSPGIFGAFQR.G	P56134	ATPK_HUMAN	ATP synthase subunit f, mitochondrial (ATP synthase membrane subunit f)	ATP5MF
			1428,52	0,204	K.NCEDMDECSIR.N	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
1429,73	1429,014	1430,444	1429,74	0,010	R.FKDIFEIFDK.H	P48735	IDHP_HUMAN	Isocitrate dehydrogenase [NADP], mitochondrial (IDH) (EC 1.1.1.42) (ICD-M) (IDP) (NADP(+)-specific ICDH) (Oxalosuccinate decarboxylase)	IDH2
			1429,71	0,023	R.IEDVTPIPSDSTR.R	P62263	RS14_HUMAN	40S ribosomal protein S14 (Small ribosomal subunit protein uS11)	RPS14
			1429,69	0,038	R.LIEDTEDWRPR.T	Q96HC4	PDLI5_HUMAN	PDZ and LIM domain protein 5 (Enigma homolog) (Enigma-like PDZ and LIM domains protein)	PDLIM5
			1429,68	0,048	R.SEAUVVEYFSGSR.L	Q7KZF4	SNB1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SNB1
1430,74	1430,022	1431,453	1430,70	0,038	K.ITGWGEETLPDGR.T	Q9GZM7	TINAL_HUMAN	Tubulointerstitial nephritis antigen-like (Glucocorticoid-inducible protein 5) (Oxidized LDL-responsive gene 2 protein) (OLRG-2) (Tubulointerstitial nephritis antigen-related protein) (TIN Ag-related protein) (TIN-Ag-RP)	TINAGL1
			1430,70	0,039	R.TWNDSVQKQDI.F	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP, EC 3.6.4.10 (78 kDa glucose-regulated protein, GRP-78) (Binding-immunoglobulin protein, BiP) (Heat shock protein 70 family protein 5, HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			1430,64	0,094	R.SGNPNYPYEFSR.K	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1430,63	0,105	K.SEDFSLPAYMDR.R	P13073	COX41_HUMAN	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial (Cytochrome c oxidase polypeptide IV) (Cytochrome c oxidase subunit IV isoform 1) (COX IV-1)	COX41
1431,74	1431,027	1432,458	1431,76	0,021	K.AYYHLLQEVAPK.G	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
			1431,70	0,044	K.EQWDTIEELIR.K	Q16698	DECR_HUMAN	2,4-dienoyl-CoA reductase, mitochondrial (EC 1.3.1.34) (2,4-dienoyl-CoA reductase [NADPH]) (4-enoyl-CoA reductase [NADPH]) (Short chain dehydrogenase/reductase family 18C member 1)	DECR1
1432,75	1432,032	1433,465	1432,74	0,008	R.FFLDRDGLFR.Y	Q96CX2	KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 (Pftin) (Predominantly fetal expressed T1 domain)	KCTD12
			1432,74	0,011	R.LNVDEAFEQLVR.A	P10301	RRAS_HUMAN	Ras-related protein R-Ras (p23)	RRAS

			1432,64	0,109	R.ELEGEVESEQKR.N	P12882	MYH1_HUMAN	Myosin-1 (Myosin heavy chain 1) (Myosin heavy chain 2x) (MyHC-2x) (Myosin heavy chain IIX/d) (MyHC-IIX/d) (Myosin heavy chain, skeletal muscle, adult 1)	MYH1
1433,75	1433,036	1434,470	1433,73	0,027	R.AVEYLLMGIPGR.E	P54727	RD23B_HUMAN	UV excision repair protein RAD23 homolog B (HR23B) (hHR23B) (XP-C repair-complementing complex 58 kDa protein) (p58)	RAD23B
			1433,69	0,064	K.GFGGQGAGALVHSE.-	P21291	CSR1_HUMAN	Cysteine and glycine-rich protein 1 (Cysteine-rich protein 1) (CRP) (CRP1) (Epididymis luminal protein 141) (HEL-141)	CSR1
			1433,67	0,082	K.AEMADQAAAWLTR.Q	P0C0L5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and P2P-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
			1433,65	0,101	R.YFYHQEEYVR.F	P13760	2B14_HUMAN	HLA class II histocompatibility antigen, DRB1-4 beta chain (MHC class II antigen DRB1*4) (DR-4) (DR4)	HLA-DRB1
			1433,58	0,171	R.FTDEEVDEMYR.E	P24844	MYL9_HUMAN	Myosin regulatory light polypeptide 9 (20 kDa myosin light chain) (LC20) (MLC-2C) (Myosin RLC) (Myosin regulatory light chain 2, smooth muscle isoform) (Myosin regulatory light chain 9) (Myosin regulatory light chain MRLC1)	MYL9
1434,74	1434,019	1435,454	1434,76	0,019	R.VEHWGLDQPLLK.H	P20036	DPA1_HUMAN	HLA class II histocompatibility antigen, DP alpha 1 chain (DP(W3)) (DP(W4)) (HLA-SB alpha chain) (MHC class II DP3-alpha) (MHC class II DPA1)	HLA-DPA1
			1434,70	0,037	-.MPMFIVNTNVR.A	P14174	MIF_HUMAN	Macrophage migration inhibitory factor (MIF) (EC 5.3.2.1) (Glycosylation-inhibiting factor) (GIF) (L-dopachrome isomerase) (L-dopachrome tautomerase) (EC 5.3.3.12) (Phenylpyruvate tautomerase)	MIF
			1434,57	0,167	K.KGQGGAGAGDDEED.-	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RP59
			1434,53	0,203	R.ETYGEMADCCAK.Q	P02768	ALBU_HUMAN	Serum albumin	ALB
1435,76	1435,046	1436,481	1435,75	0,009	R.FTQAGSEVSALLGR.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			1435,75	0,015	R.VEHWGLDEPLLK.H	P01903	DRA_HUMAN	HLA class II histocompatibility antigen, DR alpha chain (MHC class II antigen DRA)	HLA-DRA
			1435,63	0,131	K.TVFAEHISDECK.R	P39023	RL3_HUMAN	60S ribosomal protein L3 (HIV-1 TAR RNA-binding protein B) (TARBP-B) (Large ribosomal subunit protein uL3)	RPL3
1436,77	1436,054	1437,490	1436,76	0,016	R.QFLFRPWDVTK.L	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A1S9) (Ubiquitin-activating enzyme E1)	UBA1
			1436,70	0,077	K.IMMADEALGSLVSR.V	Q13011	ECH1_HUMAN	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial (EC 5.3.3.-)	ECH1
1437,77	1437,052	1438,489	1437,80	0,031	R.LVPGWTKPITIGR.H	P48735	IDHP_HUMAN	Isocitrate dehydrogenase [NADP], mitochondrial (IDH) (EC 1.1.1.42) (ICD-M) (IDP) (NADP(+)-specific ICDH) (Oxalosuccinate decarboxylase)	IDH2
1438,76	1438,041	1439,480	1438,78	0,019	R.KTVTAMDVVYALK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
1439,69	1438,969	1440,409	1439,68	0,014	K.TGTAEMSSILEER.I	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
			1439,63	0,060	R.AESEQEAYLRD.-	Q9NR28	DBLOH_HUMAN	Diablo homolog, mitochondrial (Direct IAP-binding protein with low pI) (Second mitochondria-derived activator of caspase) (Smac)	DIABLO
			1439,61	0,082	R.TDWHMAFTGMSR.R	Q96M27	PRRC1_HUMAN	Protein PRRC1 (Proline-rich and coiled-coil-containing protein 1)	PRRC1
			1439,80	0,106	R.VALTGLTVAEYFR.D	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			1439,81	0,121	K.IKYPENFLLR.G	P62140	PP1B_HUMAN	Serine/threonine-protein phosphatase PP1-beta catalytic subunit (PP-1B) (PPP1CD) (EC 3.1.3.16) (EC 3.1.3.53)	PPP1CB
1440,10	1439,384	1440,824	1439,81	0,294	K.IKYPENFLLR.G	P62140	PP1B_HUMAN	Serine/threonine-protein phosphatase PP1-beta catalytic subunit (PP-1B) (PPP1CD) (EC 3.1.3.16) (EC 3.1.3.53)	PPP1CB
			1439,80	0,309	R.VALTGLTVAEYFR.D	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			1439,68	0,429	K.TGTAEMSSILEER.I	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
			1439,63	0,475	R.AESEQEAYLRD.-	Q9NR28	DBLOH_HUMAN	Diablo homolog, mitochondrial (Direct IAP-binding protein with low pI) (Second mitochondria-derived activator of caspase) (Smac)	DIABLO
			1439,61	0,496	R.TDWHMAFTGMSR.R	Q96M27	PRRC1_HUMAN	Protein PRRC1 (Proline-rich and coiled-coil-containing protein 1)	PRRC1
			1440,62	0,519	R.NIDEHANEDVER.M	P61026	RAB10_HUMAN	Ras-related protein Rab-10	RAB10
1440,97	1440,251	1441,692	1440,62	0,349	R.NIDEHANEDVER.M	P61026	RAB10_HUMAN	Ras-related protein Rab-10	RAB10
			1441,67	0,696	K.QDPSVLHTEEMR.F	P50502	F10A1_HUMAN	Hsc70-interacting protein (Hip) (Aging-associated protein 2) (Progesterone receptor-associated p48 protein) (Protein FAM10A1) (Putative tumor suppressor ST13) (Renal carcinoma antigen NY-REN-33) (Suppression of tumorigenicity 13 protein)	ST13
			1441,68	0,705	K.AEAGAGSATEFQFR.G	P46783	RS10_HUMAN	40S ribosomal protein S10 (Small ribosomal subunit protein eS10)	RP510
1441,74	1441,022	1442,464	1441,70	0,041	K.AGVNFSEFTGVWK.Y	O75340	PDCD6_HUMAN	Programmed cell death protein 6 (Apoptosis-linked gene 2 protein homolog) (ALG-2)	PDCD6
			1441,68	0,067	K.AEAGAGSATEFQFR.G	P46783	RS10_HUMAN	40S ribosomal protein S10 (Small ribosomal subunit protein eS10)	RP510
			1441,67	0,076	K.QDPSVLHTEEMR.F	P50502	F10A1_HUMAN	Hsc70-interacting protein (Hip) (Aging-associated protein 2) (Progesterone receptor-associated p48 protein) (Protein FAM10A1) (Putative tumor suppressor ST13) (Renal carcinoma antigen NY-REN-33) (Suppression of tumorigenicity 13 protein)	ST13

1442,21	1441,486	1442,928	1442,64	0,432	K.QPSDKCSASPLR.R	P46013	KI67_HUMAN	Proliferation marker protein Ki-67 (Antigen identified by monoclonal antibody Ki-67) (Antigen Ki-67) (Antigen Ki67)	MKI67
			1442,71	0,503	R.YAAVTQFEATDAR.R	P55786	PSA_HUMAN	Puromycin-sensitive aminopeptidase (PSA) (EC 3.4.11.14) (Cytosol alanyl aminopeptidase) (AAP-S)	NPEPPS
			1441,70	0,505	K.AGVNFSEFTGVWK.Y	O75340	PDCD6_HUMAN	Programmed cell death protein 6 (Apoptosis-linked gene 2 protein homolog) (ALG-2)	PDCD6
			1441,68	0,531	K.AEAGAGSATEFQFR.G	P46783	RS10_HUMAN	40S ribosomal protein S10 (Small ribosomal subunit protein eS10)	RPS10
			1441,67	0,540	K.QDPSVLHTEEMR.F	P50502	F10A1_HUMAN	Hsc70-interacting protein (Hip) (Aging-associated protein 2) (Progesterone receptor-associated p48 protein) (Protein FAM10A1) (Putative tumor suppressor ST13) (Renal carcinoma antigen NY-REN-33) (Suppression of tumorigenicity 13 protein)	ST13
			1442,76	0,555	R.LSAEDLVLEGAGLR.V	P11047	LAMC1_HUMAN	Laminin subunit gamma-1 (Laminin B2 chain) (Laminin-1 subunit gamma) (Laminin-10 subunit gamma) (Laminin-11 subunit gamma) (Laminin-2 subunit gamma) (Laminin-3 subunit gamma) (Laminin-4 subunit gamma) (Laminin-6 subunit gamma) (Laminin-7 subunit gamma) (Laminin-8 subunit gamma) (Laminin-9 subunit gamma) (S-laminin subunit gamma) (S-LAM gamma)	LAMC1
			1442,79	0,583	R.LPDIFEAQIAGLR.G	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7)	KRT7
1442,77	1442,051	1443,494	1442,76	0,010	R.LSAEDLVLEGAGLR.V	P11047	LAMC1_HUMAN	Laminin subunit gamma-1 (Laminin B2 chain) (Laminin-1 subunit gamma) (Laminin-10 subunit gamma) (Laminin-11 subunit gamma) (Laminin-2 subunit gamma) (Laminin-3 subunit gamma) (Laminin-4 subunit gamma) (Laminin-6 subunit gamma) (Laminin-7 subunit gamma) (Laminin-8 subunit gamma) (Laminin-9 subunit gamma) (S-laminin subunit gamma) (S-LAM gamma)	LAMC1
			1442,79	0,017	R.LPDIFEAQIAGLR.G	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7)	KRT7
			1442,71	0,063	R.YAAVTQFEATDAR.R	P55786	PSA_HUMAN	Puromycin-sensitive aminopeptidase (PSA) (EC 3.4.11.14) (Cytosol alanyl aminopeptidase) (AAP-S)	NPEPPS
			1442,64	0,134	K.QPSDKCSASPLR.R	P46013	KI67_HUMAN	Proliferation marker protein Ki-67 (Antigen identified by monoclonal antibody Ki-67) (Antigen Ki-67) (Antigen Ki67)	MKI67
1443,77	1443,051	1444,495	1443,73	0,048	K.VLQDMGLPTGAEGR.D	Q12906	ILF3_HUMAN	Interleukin enhancer-binding factor 3 (Double-stranded RNA-binding protein 76) (DRBP76) (M-phase phosphoprotein 4) (MPP4) (Nuclear factor associated with dsRNA) (NFAR) (Nuclear factor of activated T-cells 90 kDa) (NF-AT-90) (Translational control protein 80) (TCP80)	ILF3
			1443,64	0,132	K.YICENQDSISSK.L	P02768	ALBU_HUMAN	Serum albumin	ALB
			1443,58	0,195	R.CECEIGVELDR.S	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
1444,78	1444,055	1445,500	1444,75	0,030	K.EGIPALDNFLDKL.-	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
			1444,71	0,071	R.KQEVQAWDGEVVR.Q	P45974	UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.4.19.12) (Deubiquitinating enzyme 5) (Isopепtidase T) (Ubiquitin thioesterase 5) (Ubiquitin-specific-processing protease 5)	USP5
			1444,66	0,115	R.LEHQFVAVGEDSGR.N	O00754	MA2B1_HUMAN	Lysosomal alpha-mannosidase (Laman) (EC 3.2.1.24) (Lysosomal acid alpha-mannosidase) (Mannosidase alpha class 2B member 1) (Mannosidase alpha-B) [Cleaved into: Lysosomal alpha-mannosidase A peptide; Lysosomal alpha-mannosidase B peptide; Lysosomal alpha-mannosidase C peptide; Lysosomal alpha-mannosidase D peptide; Lysosomal alpha-mannosidase E peptide]	MAN2B1
			1444,65	0,131	R.IFTSIGEDYDER.V	P35232	PHB_HUMAN	Prohibitin	PHB
			1444,61	0,169	R.GFCFLEYEDHK.S	O43390	HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R)	HNRNPR
			1444,56	0,217	K.MDCQECPEGVR.V	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
1445,76	1445,038	1446,484	1445,79	0,029	R.DYLPVLVLGPTAMR.K	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
			1445,72	0,036	R.VVVCAVGEQELR.K	P02788	TRFL_HUMAN	Lactotransferrin (Lactoferrin) (EC 3.4.21.-) (Growth-inhibiting protein 12) (Tala lactoferrin) [Cleaved into: Lactoferricin-H (Lfcin-H); Kaliocin-1; Lactoferrroxin-A; Lactoferrroxin-B; Lactoferrroxin-C]	LTF
			1445,81	0,052	K.EIPAKIIFEDDR.C	P49773	HINT1_HUMAN	Histidine triad nucleotide-binding protein 1 (EC 3.-.-.-) (Adenosine 5'-monophosphoramidase) (Protein kinase C inhibitor 1) (Protein kinase C-interacting protein 1) (PKCI-1)	HINT1
			1445,69	0,071	K.DNPGVVTCLEEAR.H	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
1446,76	1446,038	1447,485	1446,75	0,011	K.SDIGEVLVGGMTR.M	P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9
			1446,75	0,016	R.LQEAEEAMGVANAR.N	Q9Y2K3	MYH15_HUMAN	Myosin-15 (Myosin heavy chain 15)	MYH15
			1446,68	0,084	R.SYLSEEMIAEFK.A	P02585	TNNC2_HUMAN	Troponin C, skeletal muscle	TNNC2
			1446,67	0,088	R.FPTDQLTPDQER.S	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
			1446,67	0,089	K.EVDEQMLNVQNK.N	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1446,67	0,089	K.EVDEQMLNVQNK.N	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1446,64	0,118	K.EFHLNESGDPSSK.S	Q01105	SET_HUMAN	Protein SET (HLA-DR-associated protein II) (Inhibitor of granzyme A-activated DNase) (IGAAD) (PHAPII) (Phosphatase 2A inhibitor I2PP2A) (I-2PP2A) (Template-activating factor I) (TAF-I)	SET
1447,76	1447,038	1448,486	1447,80	0,041	K.IEEIKDFLLTAR.R	P63173	RL38_HUMAN	60S ribosomal protein L38 (Large ribosomal subunit protein eL38)	RPL38
1448,76	1448,033	1449,482	1448,73	0,033	K.YADALQEIIQER.N	Q9Y6N5	SQOR_HUMAN	Sulfide:quinone oxidoreductase, mitochondrial, SQOR, EC 1.8.5.- (Sulfide dehydrogenase-like) (Sulfide quinone oxidoreductase)	SQOR

1449,47	1448,748	1450,197	1449,70	0,228	K.VDLVDENFTELR.G	P61086	UBE2K_HUMAN	Ubiquitin-conjugating enzyme E2 K (EC 2.3.2.23) (E2 ubiquitin-conjugating enzyme K) (Huntingtin-interacting protein 2) (HIP-2) (Ubiquitin carrier protein) (Ubiquitin-conjugating enzyme E2-25 kDa) (Ubiquitin-conjugating enzyme E2(25K)) (Ubiquitin-conjugating enzyme E2-25K) (Ubiquitin-protein ligase)	UBE2K
			1449,75	0,274	R.AVEYLLMGIPGDR.E	P54727	RD23B_HUMAN	UV excision repair protein RAD23 homolog B (HR23B) (hHR23B) (XP-C repair-complementing complex 58 kDa protein) (p58)	RAD23B
			1449,77	0,296	K.KVEEVVYDLSIR.G	Q15631	TSN_HUMAN	Translin (EC 3.1.-.-) (Component 3 of promoter of RISC) (C3PO)	TSN
			1449,80	0,327	R.FVTVQTISGTGALR.I	P00505	AATM_HUMAN	Aspartate aminotransferase, mitochondrial (mAspAT) (EC 2.6.1.1) (EC 2.6.1.7) (Fatty acid-binding protein) (FABP-1) (Glutamate oxaloacetate transaminase 2) (Kynurenine aminotransferase 4) (Kynurenine aminotransferase IV) (Kynurenine--oxoglutarate transaminase 4) (Kynurenine--oxoglutarate transaminase IV) (Plasma membrane-associated fatty acid-binding protein) (FABPpm) (Transaminase A)	GOT2
1449,75	1449,030	1450,480	1449,75	0,008	R.AVEYLLMGIPGDR.E	P54727	RD23B_HUMAN	UV excision repair protein RAD23 homolog B (HR23B) (hHR23B) (XP-C repair-complementing complex 58 kDa protein) (p58)	RAD23B
			1449,77	0,014	K.KVEEVVYDLSIR.G	Q15631	TSN_HUMAN	Translin (EC 3.1.-.-) (Component 3 of promoter of RISC) (C3PO)	TSN
			1449,80	0,044	R.FVTVQTISGTGALR.I	P00505	AATM_HUMAN	Aspartate aminotransferase, mitochondrial (mAspAT) (EC 2.6.1.1) (EC 2.6.1.7) (Fatty acid-binding protein) (FABP-1) (Glutamate oxaloacetate transaminase 2) (Kynurenine aminotransferase 4) (Kynurenine aminotransferase IV) (Kynurenine--oxoglutarate transaminase 4) (Kynurenine--oxoglutarate transaminase IV) (Plasma membrane-associated fatty acid-binding protein) (FABPpm) (Transaminase A)	GOT2
			1449,70	0,054	K.VDLVDENFTELR.G	P61086	UBE2K_HUMAN	Ubiquitin-conjugating enzyme E2 K (EC 2.3.2.23) (E2 ubiquitin-conjugating enzyme K) (Huntingtin-interacting protein 2) (HIP-2) (Ubiquitin carrier protein) (Ubiquitin-conjugating enzyme E2-25 kDa) (Ubiquitin-conjugating enzyme E2(25K)) (Ubiquitin-conjugating enzyme E2-25K) (Ubiquitin-protein ligase)	UBE2K
1450,33	1449,603	1451,053	1450,53	0,199	R.ETYGEMADCCAK.Q	P02768	ALBU_HUMAN	Serum albumin	ALB
			1450,67	0,344	R.RSENEEFVEVGR.L	P10644	KAPO_HUMAN	cAMP-dependent protein kinase type I-alpha regulatory subunit (Tissue-specific extinguisher 1) (TSE1)	PRKAR1A
			1450,72	0,392	R.SHAHFFELTK.E	P30046	DOPD_HUMAN	D-dopachrome decarboxylase (EC 4.1.1.84) (D-dopachrome tautomerase) (Phenylpyruvate tautomerase II)	DDT
			1450,73	0,398	K.GVPLVYEA FNWR.H	Q16822	PCKGM_HUMAN	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial (PEPCK-M) (EC 4.1.1.32)	PCK2
			1449,80	0,529	R.FVTVQTISGTGALR.I	P00505	AATM_HUMAN	Aspartate aminotransferase, mitochondrial (mAspAT) (EC 2.6.1.1) (EC 2.6.1.7) (Fatty acid-binding protein) (FABP-1) (Glutamate oxaloacetate transaminase 2) (Kynurenine aminotransferase 4) (Kynurenine aminotransferase IV) (Kynurenine--oxoglutarate transaminase 4) (Kynurenine--oxoglutarate transaminase IV) (Plasma membrane-associated fatty acid-binding protein) (FABPpm) (Transaminase A)	GOT2
			1449,77	0,559	K.KVEEVVYDLSIR.G	Q15631	TSN_HUMAN	Translin (EC 3.1.-.-) (Component 3 of promoter of RISC) (C3PO)	TSN
			1449,75	0,582	R.AVEYLLMGIPGDR.E	P54727	RD23B_HUMAN	UV excision repair protein RAD23 homolog B (HR23B) (hHR23B) (XP-C repair-complementing complex 58 kDa protein) (p58)	RAD23B
			1449,70	0,627	K.VDLVDENFTELR.G	P61086	UBE2K_HUMAN	Ubiquitin-conjugating enzyme E2 K (EC 2.3.2.23) (E2 ubiquitin-conjugating enzyme K) (Huntingtin-interacting protein 2) (HIP-2) (Ubiquitin carrier protein) (Ubiquitin-conjugating enzyme E2-25 kDa) (Ubiquitin-conjugating enzyme E2(25K)) (Ubiquitin-conjugating enzyme E2-25K) (Ubiquitin-protein ligase)	UBE2K
1450,49	1449,762	1451,213	1450,53	0,040	R.ETYGEMADCCAK.Q	P02768	ALBU_HUMAN	Serum albumin	ALB
			1450,67	0,185	R.RSENEEFVEVGR.L	P10644	KAPO_HUMAN	cAMP-dependent protein kinase type I-alpha regulatory subunit (Tissue-specific extinguisher 1) (TSE1)	PRKAR1A
			1450,72	0,233	R.SHAHFFELTK.E	P30046	DOPD_HUMAN	D-dopachrome decarboxylase (EC 4.1.1.84) (D-dopachrome tautomerase) (Phenylpyruvate tautomerase II)	DDT
			1450,73	0,239	K.GVPLVYEA FNWR.H	Q16822	PCKGM_HUMAN	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial (PEPCK-M) (EC 4.1.1.32)	PCK2
			1449,80	0,688	R.FVTVQTISGTGALR.I	P00505	AATM_HUMAN	Aspartate aminotransferase, mitochondrial (mAspAT) (EC 2.6.1.1) (EC 2.6.1.7) (Fatty acid-binding protein) (FABP-1) (Glutamate oxaloacetate transaminase 2) (Kynurenine aminotransferase 4) (Kynurenine aminotransferase IV) (Kynurenine--oxoglutarate transaminase 4) (Kynurenine--oxoglutarate transaminase IV) (Plasma membrane-associated fatty acid-binding protein) (FABPpm) (Transaminase A)	GOT2
			1449,77	0,718	K.KVEEVVYDLSIR.G	Q15631	TSN_HUMAN	Translin (EC 3.1.-.-) (Component 3 of promoter of RISC) (C3PO)	TSN
1450,73	1450,009	1451,460	1450,73	0,008	K.GVPLVYEA FNWR.H	Q16822	PCKGM_HUMAN	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial (PEPCK-M) (EC 4.1.1.32)	PCK2
			1450,72	0,014	R.SHAHFFELTK.E	P30046	DOPD_HUMAN	D-dopachrome decarboxylase (EC 4.1.1.84) (D-dopachrome tautomerase) (Phenylpyruvate tautomerase II)	DDT
			1450,67	0,062	R.RSENEEFVEVGR.L	P10644	KAPO_HUMAN	cAMP-dependent protein kinase type I-alpha regulatory subunit (Tissue-specific extinguisher 1) (TSE1)	PRKAR1A
			1450,53	0,207	R.ETYGEMADCCAK.Q	P02768	ALBU_HUMAN	Serum albumin	ALB
1451,31	1450,581	1452,033	1451,69	0,381	K.KYPESEELTAER.I	P07237	PDIA1_HUMAN	Protein disulfide-isomerase (PDI) (EC 5.3.4.1) (Cellular thyroid hormone-binding protein) (Prolyl 4-hydroxylase subunit beta) (p55)	P4HB
			1451,74	0,431	K.AVDIPHMDIEALK.K	P62906	RL10A_HUMAN	60S ribosomal protein L10a (CSA-19) (Large ribosomal subunit protein uL1) (Neural precursor cell expressed developmentally down-regulated protein 6) (NEDD-6)	RPL10A
			1450,73	0,580	K.GVPLVYEA FNWR.H	Q16822	PCKGM_HUMAN	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial (PEPCK-M) (EC 4.1.1.32)	PCK2
			1450,72	0,587	R.SHAHFFELTK.E	P30046	DOPD_HUMAN	D-dopachrome decarboxylase (EC 4.1.1.84) (D-dopachrome tautomerase) (Phenylpyruvate tautomerase II)	DDT
			1450,67	0,635	R.RSENEEFVEVGR.L	P10644	KAPO_HUMAN	cAMP-dependent protein kinase type I-alpha regulatory subunit (Tissue-specific extinguisher 1) (TSE1)	PRKAR1A

1451,75	1451,020	1452,471	1451,74	0,007	K.AVDIPHMDIEALK.K	P62906	RL10A_HUMAN	60S ribosomal protein L10a (CSA-19) (Large ribosomal subunit protein uL1) (Neural precursor cell expressed developmentally down-regulated protein 6) (NEDD-6)	RPL10A
			1451,69	0,058	K.YKPESEELTAER.I	P07237	PDIA1_HUMAN	Protein disulfide-isomerase (PDI) (EC 5.3.4.1) (Cellular thyroid hormone-binding protein) (Prolyl 4-hydroxylase subunit beta) (p55)	P4HB
1452,71	1451,988	1453,441	1452,64	0,075	R.DGSEASLEWSSER.Q	P11047	LAMC1_HUMAN	Laminin subunit gamma-1 (Laminin B2 chain) (Laminin-1 subunit gamma) (Laminin-10 subunit gamma) (Laminin-11 subunit gamma) (Laminin-2 subunit gamma) (Laminin-3 subunit gamma) (Laminin-4 subunit gamma) (Laminin-6 subunit gamma) (Laminin-7 subunit gamma) (Laminin-8 subunit gamma) (Laminin-9 subunit gamma) (S-laminin subunit gamma) (S-LAM gamma)	LAMC1
1453,74	1453,016	1454,470	1453,70	0,047	R.DFDPAVTEYIQR.K	P09467	F16P1_HUMAN	Fructose-1,6-bisphosphatase 1 (FBPase 1) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase 1) (Liver FBPase)	FBP1
1453,80	1453,071	1454,524	1453,70	0,101	R.DFDPAVTEYIQR.K	P09467	F16P1_HUMAN	Fructose-1,6-bisphosphatase 1 (FBPase 1) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase 1) (Liver FBPase)	FBP1
1454,68	1453,952	1455,407	1454,65	0,032	K.GKSEELAEFCR.I	P02585	TNNC2_HUMAN	Troponin C, skeletal muscle	TNNC2
			1454,73	0,053	R.EEIVYLCIYR.N	Q13228	SBP1_HUMAN	Methanethiol oxidase (MTO) (EC 1.8.3.4) (56 kDa selenium-binding protein) (SBP56) (SP56) (Selenium-binding protein 1)	SELENBP1
			1454,78	0,101	R.KTVTAMDVVYALK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
1454,88	1454,151	1455,606	1454,78	0,099	R.KTVTAMDVVYALK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
			1454,73	0,146	R.EEIVYLCIYR.N	Q13228	SBP1_HUMAN	Methanethiol oxidase (MTO) (EC 1.8.3.4) (56 kDa selenium-binding protein) (SBP56) (SP56) (Selenium-binding protein 1)	SELENBP1
			1454,65	0,231	K.GKSEELAEFCR.I	P02585	TNNC2_HUMAN	Troponin C, skeletal muscle	TNNC2
1455,40	1454,672	1456,128	1454,78	0,620	R.KTVTAMDVVYALK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
			1454,73	0,667	R.EEIVYLCIYR.N	Q13228	SBP1_HUMAN	Methanethiol oxidase (MTO) (EC 1.8.3.4) (56 kDa selenium-binding protein) (SBP56) (SP56) (Selenium-binding protein 1)	SELENBP1
1456,23	1455,506	1456,963	1456,69	0,454	K.TPELNLDQFHD.K.T	P27824	CALX_HUMAN	Calnexin (IP90) (Major histocompatibility complex class I antigen-binding protein p88) (p90)	CANX
			1456,78	0,547	R.DALSDLALHFLNK.M	P50991	TCPD_HUMAN	T-complex protein 1 subunit delta (TCP-1-delta) (CCT-delta) (Stimulator of TAR RNA-binding)	CCT4
1457,24	1456,507	1457,964	1457,58	0,342	K.NEEDEGHSNSSPR.H	Q14103	HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1)	HNRNP D0
			1457,59	0,352	R.QDYMDAMAEKQ.K.L	Q9H875	PKRI1_HUMAN	PRKR-interacting protein 1	PRKRIP1
			1456,78	0,454	R.DALSDLALHFLNK.M	P50991	TCPD_HUMAN	T-complex protein 1 subunit delta (TCP-1-delta) (CCT-delta) (Stimulator of TAR RNA-binding)	CCT4
			1457,78	0,546	R.TFFSFPAVVAPFK.C	P41250	GARS_HUMAN	GARS	GARS
			1456,69	0,547	K.TPELNLDQFHD.K.T	P27824	CALX_HUMAN	Calnexin (IP90) (Major histocompatibility complex class I antigen-binding protein p88) (p90)	CANX
			1457,82	0,585	K.TVLIMELINNAK.A	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
1457,72	1456,996	1458,453	1457,78	0,057	R.TFFSFPAVVAPFK.C	P41250	GARS_HUMAN	GARS	GARS
			1457,82	0,096	K.TVLIMELINNAK.A	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			1457,59	0,137	R.QDYMDAMAEKQ.K.L	Q9H875	PKRI1_HUMAN	PRKR-interacting protein 1	PRKRIP1
			1457,58	0,147	K.NEEDEGHSNSSPR.H	Q14103	HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1)	HNRNP D0
1458,72	1457,986	1459,445	1458,71	0,004	K.TDEKQLIIDAGQK.R	Q5FWF5	ESCO1_HUMAN	N-acetyltransferase ESCO1 (EC 2.3.1.-) (CTF7 homolog 1) (Establishment factor-like protein 1) (EFO1) (EFO1p) (hEFO1) (Establishment of cohesion 1 homolog 1) (ESCO1 homolog 1) (ESCO1 homolog 1)	ESCO1
			1458,69	0,021	R.HVFGEDELIGQK.V	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP11
			1458,64	0,073	R.TNYNDRYDEIR.R	P62424	RL7A_HUMAN	60S ribosomal protein L7a (Large ribosomal subunit protein eL8) (PLA-X polypeptide) (Surfeit locus protein 3)	RPL7A

1459,67	1458,944	1460,404	1459,85	0,176	K.IGDLHPQIVNLLK.S	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1460,17	1459,439	1460,899	1459,85	0,319	K.IGDLHPQIVNLLK.S	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1460,66	0,492	K.SYSPYDMLSESIR.K	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1460,71	0,538	R.FQLLEGPPESMGR.G	P31150	GDIA_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			1460,73	0,561	K.SDIDEIVLVGGSTR.I	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BIP, EC 3.6.4.10 (78 kDa glucose-regulated protein, GRP-78) (Binding-immunoglobulin protein, BiP) (Heat shock protein 70 family protein 5, HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			1460,79	0,616	R.NLATTVTTEEILEK.S	O43390	HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R)	HNRNPR
1460,45	1459,717	1461,177	1460,66	0,214	K.SYSPYDMLSESIR.K	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1460,71	0,260	R.FQLLEGPPESMGR.G	P31150	GDIA_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			1460,73	0,283	K.SDIDEIVLVGGSTR.I	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BIP, EC 3.6.4.10 (78 kDa glucose-regulated protein, GRP-78) (Binding-immunoglobulin protein, BiP) (Heat shock protein 70 family protein 5, HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			1460,79	0,338	R.NLATTVTTEEILEK.S	O43390	HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R)	HNRNPR
			1459,85	0,597	K.IGDLHPQIVNLLK.S	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1460,68	1459,948	1461,409	1460,66	0,017	K.SYSPYDMLSESIR.K	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1460,71	0,028	R.FQLLEGPPESMGR.G	P31150	GDIA_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			1460,73	0,051	K.SDIDEIVLVGGSTR.I	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BIP, EC 3.6.4.10 (78 kDa glucose-regulated protein, GRP-78) (Binding-immunoglobulin protein, BiP) (Heat shock protein 70 family protein 5, HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			1460,79	0,107	R.NLATTVTTEEILEK.S	O43390	HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R)	HNRNPR
1461,24	1460,507	1461,968	1461,69	0,450	R.SSHYDELLAAEAR.A	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
			1460,79	0,452	R.NLATTVTTEEILEK.S	O43390	HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R)	HNRNPR
			1460,73	0,508	K.SDIDEIVLVGGSTR.I	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BIP, EC 3.6.4.10 (78 kDa glucose-regulated protein, GRP-78) (Binding-immunoglobulin protein, BiP) (Heat shock protein 70 family protein 5, HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			1460,71	0,531	R.FQLLEGPPESMGR.G	P31150	GDIA_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			1460,66	0,576	K.SYSPYDMLSESIR.K	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
1461,72	1460,987	1462,448	1461,69	0,030	R.SSHYDELLAAEAR.A	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
1462,41	1461,683	1463,146	1462,61	0,190	K.EMNDAAMFYTNR.V	Q01518	CAP1_HUMAN	Adenylyl cyclase-associated protein 1 (CAP 1)	CAP1
			1462,67	0,260	R.YYTVFDRDNNR.V	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
			1462,78	0,368	K.LTLHGLQQYYVK.L	Q13838	DX39B_HUMAN	Spliceosome RNA helicase DDX39B (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	DDX39B
			1462,80	0,385	R.DYGVVLEGGSLALR.G	P30048	PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial (EC 1.11.1.15) (Antioxidant protein 3) (AOP-1) (HBC189) (Peroxiredoxin III) (Prx-III) (Peroxiredoxin-3) (Protein MER5 homolog)	PRDX3
			1461,69	0,728	R.SSHYDELLAAEAR.A	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
1462,71	1461,983	1463,445	1462,67	0,039	R.YYTVFDRDNNR.V	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
			1462,78	0,069	K.LTLHGLQQYYVK.L	Q13838	DX39B_HUMAN	Spliceosome RNA helicase DDX39B (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	DDX39B
			1462,80	0,086	R.DYGVVLEGGSLALR.G	P30048	PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial (EC 1.11.1.15) (Antioxidant protein 3) (AOP-1) (HBC189) (Peroxiredoxin III) (Prx-III) (Peroxiredoxin-3) (Protein MER5 homolog)	PRDX3
			1462,61	0,109	K.EMNDAAMFYTNR.V	Q01518	CAP1_HUMAN	Adenylyl cyclase-associated protein 1 (CAP 1)	CAP1
1463,33	1462,594	1464,057	1463,72	0,395	K.SPYQEFTDHLVK.T	P15880	RS2_HUMAN	40S ribosomal protein S2 (40S ribosomal protein S4) (Protein LLRep3) (Small ribosomal subunit protein u55)	RPS2
			1462,80	0,525	R.DYGVVLEGGSLALR.G	P30048	PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial (EC 1.11.1.15) (Antioxidant protein 3) (AOP-1) (HBC189) (Peroxiredoxin III) (Prx-III) (Peroxiredoxin-3) (Protein MER5 homolog)	PRDX3
			1462,78	0,542	K.LTLHGLQQYYVK.L	Q13838	DX39B_HUMAN	Spliceosome RNA helicase DDX39B (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	DDX39B
			1462,67	0,650	R.YYTVFDRDNNR.V	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD

			1462,61	0,720	K.EMNDAAMFYTN.R.V	Q01518	CAP1_HUMAN	Adenylyl cyclase-associated protein 1 (CAP 1)	CAP1
1463,68	1462,950	1464,414	1463,72	0,038	K.SPYQEFTDHLVK.T	P15880	RS2_HUMAN	40S ribosomal protein S2 (40S ribosomal protein S4) (Protein LLRep3) (Small ribosomal subunit protein u55)	RPS2
1463,71	1462,978	1464,442	1463,72	0,010	K.SPYQEFTDHLVK.T	P15880	RS2_HUMAN	40S ribosomal protein S2 (40S ribosomal protein S4) (Protein LLRep3) (Small ribosomal subunit protein u55)	RPS2
1464,75	1464,021	1465,486	1464,77 1464,81	0,022 0,056	R.NEDLGLPPLFPPR.E R.IPLLSDLTHQISK.D	P01266 Q13162	THYG_HUMAN PRDX4_HUMAN	Thyroglobulin (Tg) Peroxiredoxin-4 (EC 1.11.1.15) (Antioxidant enzyme AOE372) (AOE37-2) (Peroxiredoxin IV) (Prx-IV) (Thioredoxin peroxidase AO372) (Thioredoxin-dependent peroxide reductase A0372)	TG PRDX4
			1464,69	0,064	K.HPDASVNFSEFSK.K	P09429	HMGB1_HUMAN	High mobility group protein B1 (High mobility group protein 1) (HMG-1)	HMGB1
			1464,68	0,074	R.ASHPEDPASVVEAR.K	Q9UHL4	DPP2_HUMAN	Dipeptidyl peptidase 2 (EC 3.4.14.2) (Dipeptidyl aminopeptidase II) (Dipeptidyl peptidase 7) (Dipeptidyl peptidase II) (DPP II) (Quiescent cell proline dipeptidase)	DPP7
1465,00	1464,270	1465,735	1464,81	0,193	R.IPLLSDLTHQISK.D	Q13162	PRDX4_HUMAN	Peroxiredoxin-4 (EC 1.11.1.15) (Antioxidant enzyme AOE372) (AOE37-2) (Peroxiredoxin IV) (Prx-IV) (Thioredoxin peroxidase AO372) (Thioredoxin-dependent peroxide reductase A0372)	PRDX4
			1464,77 1464,69	0,227 0,313	R.NEDLGLPPLFPPR.E K.HPDASVNFSEFSK.K	P01266 P09429	THYG_HUMAN HMGB1_HUMAN	Thyroglobulin (Tg) High mobility group protein B1 (High mobility group protein 1) (HMG-1)	TG HMGB1
			1464,68	0,323	R.ASHPEDPASVVEAR.K	Q9UHL4	DPP2_HUMAN	Dipeptidyl peptidase 2 (EC 3.4.14.2) (Dipeptidyl aminopeptidase II) (Dipeptidyl peptidase 7) (Dipeptidyl peptidase II) (DPP II) (Quiescent cell proline dipeptidase)	DPP7
			1465,73	0,730	R.SFPDFPTPGVVFR.D	P07741	APT_HUMAN	Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	APRT
1465,68	1464,944	1466,410	1465,73	0,055	R.SFPDFPTPGVVFR.D	P07741	APT_HUMAN	Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	APRT
1466,20	1465,465	1466,931	1466,63	0,428	K.NDFTEEEEAQVR.K	P63208	SKP1_HUMAN	S-phase kinase-associated protein 1 (Cyclin-A/CDK2-associated protein p19) (p19A) (Organ of Corti protein 2) (OCP-2) (Organ of Corti protein II) (OCP-II) (RNA polymerase II elongation factor-like protein) (SIII) (Transcription elongation factor B polypeptide 1-like) (p19skp1)	SKP1
			1465,73	0,466	R.SFPDFPTPGVVFR.D	P07741	APT_HUMAN	Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	APRT
			1466,73	0,532	K.TATPQQAQEVHEK.L	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP11
			1466,80	0,605	K.TVTAMDVVYALKR.Q	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
1466,68	1465,943	1467,410	1466,63	0,050	K.NDFTEEEEAQVR.K	P63208	SKP1_HUMAN	S-phase kinase-associated protein 1 (Cyclin-A/CDK2-associated protein p19) (p19A) (Organ of Corti protein 2) (OCP-2) (Organ of Corti protein II) (OCP-II) (RNA polymerase II elongation factor-like protein) (SIII) (Transcription elongation factor B polypeptide 1-like) (p19skp1)	SKP1
			1466,73	0,053	K.TATPQQAQEVHEK.L	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP11
			1466,80	0,127	K.TVTAMDVVYALKR.Q	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
1467,01	1466,281	1467,748	1466,80	0,211	K.TVTAMDVVYALKR.Q	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
			1466,73	0,285	K.TATPQQAQEVHEK.L	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP11
			1466,63	0,388	K.NDFTEEEEAQVR.K	P63208	SKP1_HUMAN	S-phase kinase-associated protein 1 (Cyclin-A/CDK2-associated protein p19) (p19A) (Organ of Corti protein 2) (OCP-2) (Organ of Corti protein II) (OCP-II) (RNA polymerase II elongation factor-like protein) (SIII) (Transcription elongation factor B polypeptide 1-like) (p19skp1)	SKP1
1467,37	1466,635	1468,102	1467,75	0,384	K.ALNLGYALDYAQR.Y	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3

			1467,84	0,467	R.RHPDYSVLLLR.L	P02768	ALBU_HUMAN	Serum albumin	ALB
			1466,80	0,565	K.TVTAMDVVYALKR.Q	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
			1466,73	0,639	K.TATPQQAQEVHEK.L	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP11
1467,68	1466,950	1468,417	1467,75	0,069	K.ALNLGYALDYAQR.Y	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1467,84	0,152	R.RHPDYSVLLLR.L	P02768	ALBU_HUMAN	Serum albumin	ALB
1468,34	1467,606	1469,074	1467,84	0,504	R.RHPDYSVLLLR.L	P02768	ALBU_HUMAN	Serum albumin	ALB
			1467,75	0,587	K.ALNLGYALDYAQR.Y	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1468,71	1467,974	1469,442							
1469,64	1468,902	1470,372	1469,65	0,010	R.LSSQEAASSFGDDR.L	P05165	PCCA_HUMAN	Propionyl-CoA carboxylase alpha chain, mitochondrial (PCCase subunit alpha) (EC 6.4.1.3) (Propanoyl-CoA:carbon dioxide ligase subunit alpha)	PCCA
			1469,66	0,019	K.GGDISVCEWYQR.V	P14854	CX6B1_HUMAN	Cytochrome c oxidase subunit 6B1 (Cytochrome c oxidase subunit Vlb isoform 1) (COX Vlb-1)	COX6B1
			1469,72	0,087	R.DADVQNFVSFSK.D	P42126	EC11_HUMAN	Enoyl-CoA delta isomerase 1, mitochondrial (EC 5.3.3.8) (3,2-trans-enoyl-CoA isomerase) (Delta(3),Delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase) (Dodecenoyl CoA isomerase)	EC11
1469,71	1468,972	1470,442	1469,72	0,017	R.DADVQNFVSFSK.D	P42126	EC11_HUMAN	Enoyl-CoA delta isomerase 1, mitochondrial (EC 5.3.3.8) (3,2-trans-enoyl-CoA isomerase) (Delta(3),Delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase) (Dodecenoyl CoA isomerase)	EC11
			1469,66	0,051	K.GGDISVCEWYQR.V	P14854	CX6B1_HUMAN	Cytochrome c oxidase subunit 6B1 (Cytochrome c oxidase subunit Vlb isoform 1) (COX Vlb-1)	COX6B1
			1469,65	0,060	R.LSSQEAASSFGDDR.L	P05165	PCCA_HUMAN	Propionyl-CoA carboxylase alpha chain, mitochondrial (PCCase subunit alpha) (EC 6.4.1.3) (Propanoyl-CoA:carbon dioxide ligase subunit alpha)	PCCA
1470,37	1469,635	1471,106	1470,66	0,294	R.DPSASPGDAGEQAIR.Q	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL
			1470,68	0,309	R.GIFTSDHPAEQR.G	O95613	PCNT_HUMAN	Pericentrin (Kendrin) (Pericentrin-B)	PCNT
			1470,70	0,334	R.SSFYVNLTLGGQK.C	P07737	PROF1_HUMAN	Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I)	PFN1
			1469,72	0,646	R.DADVQNFVSFSK.D	P42126	EC11_HUMAN	Enoyl-CoA delta isomerase 1, mitochondrial (EC 5.3.3.8) (3,2-trans-enoyl-CoA isomerase) (Delta(3),Delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase) (Dodecenoyl CoA isomerase)	EC11
			1469,66	0,714	K.GGDISVCEWYQR.V	P14854	CX6B1_HUMAN	Cytochrome c oxidase subunit 6B1 (Cytochrome c oxidase subunit Vlb isoform 1) (COX Vlb-1)	COX6B1
			1469,65	0,723	R.LSSQEAASSFGDDR.L	P05165	PCCA_HUMAN	Propionyl-CoA carboxylase alpha chain, mitochondrial (PCCase subunit alpha) (EC 6.4.1.3) (Propanoyl-CoA:carbon dioxide ligase subunit alpha)	PCCA
1470,71	1469,971	1471,441	1470,70	0,002	R.SSFYVNLTLGGQK.C	P07737	PROF1_HUMAN	Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I)	PFN1
			1470,68	0,027	R.GIFTSDHPAEQR.G	O95613	PCNT_HUMAN	Pericentrin (Kendrin) (Pericentrin-B)	PCNT
			1470,66	0,041	R.DPSASPGDAGEQAIR.Q	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL
1470,71	1469,971	1471,442	1470,70	0,003	R.SSFYVNLTLGGQK.C	P07737	PROF1_HUMAN	Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I)	PFN1
			1470,68	0,027	R.GIFTSDHPAEQR.G	O95613	PCNT_HUMAN	Pericentrin (Kendrin) (Pericentrin-B)	PCNT
			1470,66	0,042	R.DPSASPGDAGEQAIR.Q	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL
1471,44	1470,701	1472,173	1470,70	0,733	R.SSFYVNLTLGGQK.C	P07737	PROF1_HUMAN	Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I)	PFN1
1471,71	1470,975	1472,447							
1472,40	1471,667	1473,139	1472,70	0,301	R.VWDDGIIDPADTR.L	Q9HCC0	MCCB_HUMAN	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial (MCCase subunit beta) (EC 6.4.1.4) (3-methylcrotonyl-CoA carboxylase 2) (3-methylcrotonyl-CoA carboxylase non-biotin-containing subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase subunit beta)	MCCC2
			1472,71	0,311	K.AQMHLPLSPPEPR.L	Q96M86	DNHD1_HUMAN	Dynein heavy chain domain-containing protein 1 (Dynein heavy chain domain 1-like protein) (Protein CCDC35)	DNHD1
			1472,74	0,336	K.FYGPAGPYGIFAGR.D	O15173	PGRC2_HUMAN	Membrane-associated progesterone receptor component 2 (Progesterone membrane-binding protein) (Steroid receptor protein DG6)	PGRMC2
			1472,74	0,341	R.DAESIHQYLLQR.K	P55786	PSA_HUMAN	Puromycin-sensitive aminopeptidase (PSA) (EC 3.4.11.14) (Cytosol alanyl aminopeptidase) (AAP-S)	NPEPPS
1472,75	1472,019	1473,491	1472,74	0,011	R.DAESIHQYLLQR.K	P55786	PSA_HUMAN	Puromycin-sensitive aminopeptidase (PSA) (EC 3.4.11.14) (Cytosol alanyl aminopeptidase) (AAP-S)	NPEPPS
			1472,74	0,015	K.FYGPAGPYGIFAGR.D	O15173	PGRC2_HUMAN	Membrane-associated progesterone receptor component 2 (Progesterone membrane-binding protein) (Steroid receptor protein DG6)	PGRMC2
			1472,71	0,041	K.AQMHLPLSPPEPR.L	Q96M86	DNHD1_HUMAN	Dynein heavy chain domain-containing protein 1 (Dynein heavy chain domain 1-like protein) (Protein CCDC35)	DNHD1
			1472,70	0,051	R.VWDDGIIDPADTR.L	Q9HCC0	MCCB_HUMAN	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial (MCCase subunit beta) (EC 6.4.1.4) (3-methylcrotonyl-CoA carboxylase 2) (3-methylcrotonyl-CoA carboxylase non-biotin-containing subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase subunit beta)	MCCC2
1473,25	1472,515	1473,988	1472,74	0,508	R.DAESIHQYLLQR.K	P55786	PSA_HUMAN	Puromycin-sensitive aminopeptidase (PSA) (EC 3.4.11.14) (Cytosol alanyl aminopeptidase) (AAP-S)	NPEPPS
			1472,74	0,512	K.FYGPAGPYGIFAGR.D	O15173	PGRC2_HUMAN	Membrane-associated progesterone receptor component 2 (Progesterone membrane-binding protein) (Steroid receptor protein DG6)	PGRMC2
			1472,71	0,538	K.AQMHLPLSPPEPR.L	Q96M86	DNHD1_HUMAN	Dynein heavy chain domain-containing protein 1 (Dynein heavy chain domain 1-like protein) (Protein CCDC35)	DNHD1
			1472,70	0,548	R.VWDDGIIDPADTR.L	Q9HCC0	MCCB_HUMAN	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial (MCCase subunit beta) (EC 6.4.1.4) (3-methylcrotonyl-CoA carboxylase 2) (3-methylcrotonyl-CoA carboxylase non-biotin-containing subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase subunit beta)	MCCC2

			1473,84	0,586	R.LGANSLLDLVVFG.R.A	P31040	SDHA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) (Flavoprotein subunit of complex II) (Fp)	SDHA
1473,90	1473,162	1474,636	1473,84	0,061	R.LGANSLLDLVVFG.R.A	P31040	SDHA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) (Flavoprotein subunit of complex II) (Fp)	SDHA
1474,73	1473,988	1475,463							
1475,76	1475,022	1476,498	1475,74	0,020	K.WELLQQVDTSTR.T	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
			1475,79	0,029	R.DPENFPFVLGNK.I	P51149	RAB7A_HUMAN	Ras-related protein Rab-7a	RAB7A
1476,75	1476,015	1477,492	1476,74	0,010	K.LICCDILDVLDK.H	P62258	1433E_HUMAN	14-3-3 protein epsilon (14-3-3E)	YWHAE
			1476,70	0,052	R.SGEWTEDEVLR.R.F	Q13938	CAYP1_HUMAN	Calcyphosin (Calcyphosine)	CAPS
			1476,66	0,091	K.SVSPYDMLRESIR.K	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1476,66	0,091	K.VFDFTFSPEEMK.Q	P14550	AK1A1_HUMAN	Aldo-keto reductase family 1 member A1 (EC 1.1.1.2) (EC 1.1.1.372) (EC 1.1.1.54) (Alcohol dehydrogenase [NADP(+)] (Aldehyde reductase) (Glucuronate reductase) (EC 1.1.1.19) (Glucuronolactone reductase) (EC 1.1.1.20)	AKR1A1
1477,74	1477,001	1478,478	1477,75	0,007	R.TLWIWECGITAK.G	P13489	RINI_HUMAN	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor) (Ribonuclease/angiogenin inhibitor 1) (RAI)	RNH1
			1477,77	0,028	R.APDLEYLFKPR.-	Q9NX18	SDHF2_HUMAN	Succinate dehydrogenase assembly factor 2, mitochondrial (SDH assembly factor 2) (SDHAF2)	SDHAF2
			1477,77	0,034	R.RPDLTLMVVDR.T	Q15121	PEA15_HUMAN	Astrocytic phosphoprotein PEA-15 (15 kDa phosphoprotein enriched in astrocytes) (Phosphoprotein enriched in diabetes) (PED)	PEA15
			1477,68	0,063	R.LPTEEEWEFAAR.G	Q8NBJ7	SUMF2_HUMAN	Inactive C-alpha-formylglycine-generating enzyme 2 (Paralog of formylglycine-generating enzyme) (pFGE) (Sulfatase-modifying factor 2)	SUMF2
1478,06	1477,325	1478,803	1477,77	0,291	R.RPDLTLMVVDR.T	Q15121	PEA15_HUMAN	Astrocytic phosphoprotein PEA-15 (15 kDa phosphoprotein enriched in astrocytes) (Phosphoprotein enriched in diabetes) (PED)	PEA15
			1477,77	0,297	R.APDLEYLFKPR.-	Q9NX18	SDHF2_HUMAN	Succinate dehydrogenase assembly factor 2, mitochondrial (SDH assembly factor 2) (SDHAF2)	SDHAF2
			1477,75	0,318	R.TLWIWECGITAK.G	P13489	RINI_HUMAN	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor) (Ribonuclease/angiogenin inhibitor 1) (RAI)	RNH1
			1477,68	0,388	R.LPTEEEWEFAAR.G	Q8NBJ7	SUMF2_HUMAN	Inactive C-alpha-formylglycine-generating enzyme 2 (Paralog of formylglycine-generating enzyme) (pFGE) (Sulfatase-modifying factor 2)	SUMF2
			1478,71	0,643	K.TPAFAESVTEGDVR.W	P36957	ODO2_HUMAN	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex) (EZK)	DLST
			1478,71	0,646	K.GTFATLSELHCDK.L	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			1478,73	0,666	K.MYLGVEYVTAIR.N	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
1478,75	1478,007	1479,486	1478,73	0,016	K.MYLGVEYVTAIR.N	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1478,71	0,036	K.GTFATLSELHCDK.L	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			1478,71	0,039	K.TPAFAESVTEGDVR.W	P36957	ODO2_HUMAN	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex) (EZK)	DLST
1479,11	1478,374	1479,853	1478,73	0,383	K.MYLGVEYVTAIR.N	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1478,71	0,402	K.GTFATLSELHCDK.L	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			1478,71	0,405	K.TPAFAESVTEGDVR.W	P36957	ODO2_HUMAN	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex) (EZK)	DLST
1479,75	1479,013	1480,493							
1480,76	1480,020	1481,500	1480,75	0,005	R.ARFEELNADLFR.G	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
1481,73	1480,992	1482,474	1481,71	0,019	K.MIVDPVPEPHGEMK.F	Q13263	TIF1B_HUMAN	Transcription intermediary factor 1-beta (TIF1-beta) (E3 SUMO-protein ligase TRIM28) (EC 2.3.2.27) (KRAB-associated protein 1) (KAP-1) (KRAB-interacting protein 1) (KRIP-1) (Nuclear corepressor KAP-1) (RING finger protein 96) (RING-type E3 ubiquitin transferase TIF1-beta) (Tripartite motif-containing protein 28)	TRIM28
1482,74	1481,999	1483,482							
1483,73	1482,984	1484,468	1483,72	0,007	K.GSFSEQGINEFLR.E	Q15084	PDIA6_HUMAN	Protein disulfide-isomerase A6 (EC 5.3.4.1) (Endoplasmic reticulum protein 5) (ER protein 5) (Erp5) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)	PDIA6
			1483,70	0,030	R.GEWTCIAYSQLR.D	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			1483,84	0,113	R.SANLVAATLGAILNR.L	P19367	HXK1_HUMAN	Hexokinase-1 (EC 2.7.1.1) (Brain form hexokinase) (Hexokinase type I) (HK I)	HK1
1484,67	1483,930	1485,414	1484,79	0,121	K.KYDAFLASESLIK.Q	P62906	RL10A_HUMAN	60S ribosomal protein L10a (CSA-19) (Large ribosomal subunit protein uL1) (Neural precursor cell expressed developmentally down-regulated protein 6) (NEDD-6)	RPL10A
			1484,81	0,134	R.VDQLTAQLADLAAR.G	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL

1484,76	1484,020	1485,505	1484,79	0,031	K.KYDAFLASESIK.Q	P62906	RL10A_HUMAN	60S ribosomal protein L10a (CSA-19) (Large ribosomal subunit protein uL1) (Neural precursor cell expressed developmentally down-regulated protein 6) (NEDD-6)	RPL10A
			1484,81	0,043	R.VDQLTAQLADLAAR.G	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL
1485,75	1485,007	1486,492	1485,74	0,006	K.GVVDSDDLPLNVSR.E	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			1485,72	0,031	R.NIIHGSDSVESA.E	P15531	NDKA_HUMAN	Nucleoside diphosphate kinase A (NDK A) (NDP kinase A) (EC 2.7.4.6) (Granzyme A-activated DNase) (GAAD) (Metastasis inhibition factor nm23) (NM23-H1) (Tumor metastatic process-associated protein)	NME1
1486,76	1486,017	1487,504	1486,79	0,025	R.VVAEPVELAQEFR.K	O75489	NDUS3_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial (EC 1.6.99.3) (EC 7.1.1.2) (Complex I-30kD) (CI-30kD) (NADH-ubiquinone oxidoreductase 30 kDa subunit)	NDUFS3
1487,73	1486,985	1488,473	1487,71	0,022	R.TTSPYVAFDTTER.L	P0DMV8	HS71A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
			1487,71	0,022	R.TTSPYVAFDTTER.L	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
1488,72	1487,977	1489,466	1488,75	0,025	K.IFVGGLSPDTPEEK.I	Q14103	HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1)	HNRNPD
			1488,64	0,079	R.CPTGYLLNEDTR.V	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
1489,68	1488,937	1490,427	1489,75	0,071	K.GYLGPEQLPDLCK.G	P40926	MDHM_HUMAN	Malate dehydrogenase, mitochondrial (EC 1.1.1.37)	MDH2
1489,85	1489,101	1490,591	1489,75	0,092	K.GYLGPEQLPDLCK.G	P40926	MDHM_HUMAN	Malate dehydrogenase, mitochondrial (EC 1.1.1.37)	MDH2
1490,69	1489,942	1491,432	1490,73	0,041	R.EGYSALPQLDIER.F	Q9NP81	SYSM_HUMAN	Serine--tRNA ligase, mitochondrial (EC 6.1.1.11) (SerRSmt) (Seryl-tRNA synthetase) (SerRS) (Seryl-tRNA(Ser/Sec) synthetase)	SARS2
			1490,74	0,050	R.QVQSLTCEVDALK.G	P08670	VIME_HUMAN	Vimentin	VIM
			1490,79	0,100	R.ADFLEQPVLGFRV.L	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
1490,84	1490,096	1491,587	1490,79	0,055	R.ADFLEQPVLGFRV.L	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
			1490,74	0,105	R.QVQSLTCEVDALK.G	P08670	VIME_HUMAN	Vimentin	VIM
			1490,73	0,113	R.EGYSALPQLDIER.F	Q9NP81	SYSM_HUMAN	Serine--tRNA ligase, mitochondrial (EC 6.1.1.11) (SerRSmt) (Seryl-tRNA synthetase) (SerRS) (Seryl-tRNA(Ser/Sec) synthetase)	SARS2
1491,71	1490,963	1492,455	1491,71	0,001	R.DDVALEGVSHFR.E	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
			1491,69	0,021	R.SGAMVKMAAGGGGGGR.Y	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
			1491,73	0,026	K.DIVHSGLAYTMR.S	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			1491,75	0,036	K.YEASILTHDSSIR.Y	P02679	FIBG_HUMAN	Fibrinogen gamma chain	FGG
1491,84	1491,097	1492,589	1491,75	0,098	K.YEASILTHDSSIR.Y	P02679	FIBG_HUMAN	Fibrinogen gamma chain	FGG
			1491,73	0,108	K.DIVHSGLAYTMR.S	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			1491,71	0,135	R.DDVALEGVSHFR.E	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
			1491,69	0,155	R.SGAMVKMAAGGGGGGR.Y	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
1492,78	1492,037	1493,530	1492,70	0,088	K.KYEIDNAPER.A	P49411	EFTU_HUMAN	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	TUFM
1493,74	1492,989	1494,483							
1494,73	1493,987	1495,481	1494,74	0,003	R.EAEYFELPELVR.R	Q96CX2	KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 (Pletin) (Predominantly fetal expressed T1 domain)	KCTD12
			1494,79	0,057	R.TFCQLIDPIFK.V	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
			1494,66	0,070	K.GVAFCHANNIVHR.D	Q8IZL9	CDK20_HUMAN	Cyclin-dependent kinase 20 (EC 2.7.11.22) (CDK-activating kinase p42) (CAK-kinase p42) (Cell cycle-related kinase) (Cell division protein kinase 20) (Cyclin-dependent protein kinase H) (Cyclin-kinase-activating kinase p42)	CDK20
1495,75	1494,999	1496,495	1495,75	0,008	K.YGYTHLSTGDLR.S	P00568	KAD1_HUMAN	Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	AK1
			1495,67	0,072	R.YYCFQGNQFLR.F	P02790	HEMO_HUMAN	Hemopexin (Beta-1B-glycoprotein)	HPX
			1495,83	0,083	K.DILLRPELEELR.N	P00387	NBSR3_HUMAN	NADH-cytochrome b5 reductase 3 (B5R) (Cytochrome b5 reductase) (EC 1.6.2.2) (Diaphorase-1) [Cleaved into: NADH-cytochrome b5 reductase 3 membrane-bound form; NADH-cytochrome b5 reductase 3 soluble form]	CYB5R3
1496,75	1496,006	1497,503	1496,71	0,046	R.AYLEGTCVEWLR.R	P30508	1C12_HUMAN	HLA class I histocompatibility antigen, Cw-12 alpha chain (MHC class I antigen Cw*12)	HLA-C
			1496,71	0,046	R.AYLEGTCVEWLR.R	P30493	1B55_HUMAN	HLA class I histocompatibility antigen, B-55 alpha chain (Bw-55) (HLA class I histocompatibility antigen, B-12 alpha chain) (MHC class I antigen B*55)	HLA-B
			1496,71	0,046	R.AYLEGTCVEWLR.R	P16190	1A33_HUMAN	HLA class I histocompatibility antigen, A-33 alpha chain (Aw-19) (Aw-33) (MHC class I antigen A*33)	HLA-A
			1496,66	0,091	R.APSWFDFTGLSEMR.L	P02511	CRYAB_HUMAN	Alpha-crystallin B chain (Alpha(B)-crystallin) (Heat shock protein beta-5) (HspB5) (Renal carcinoma antigen NY-REN-27) (Rosenthal fiber component)	CRYAB
			1496,66	0,099	K.MSSYAFFVQTCR.E	P09429	HMGB1_HUMAN	High mobility group protein B1 (High mobility group protein 1) (HMG-1)	HMGB1
1497,75	1496,999	1498,497	1497,75	0,001	R.AATVGSAGQPQER.A	P02649	APOE_HUMAN	Apolipoprotein E (Apo-E)	APOE
			1497,73	0,017	K.GPEEHPSVTIFR.Q	Q03154	ACY1_HUMAN	Aminoacylase-1 (ACY-1) (EC 3.5.1.14) (N-acyl-L-amino-acid amidohydrolase)	ACY1
1498,74	1497,992	1499,491	1498,74	0,004	K.QADLIYSEGLHPR.I	P40227	TCPZ_HUMAN	T-complex protein 1 subunit zeta (TCP-1-zeta) (Acute morphine dependence-related protein 2) (CCT-zeta-1) (HTR3) (Tc20)	CCT6A
			1498,80	0,058	K.NQEQLLTASILR.E	Q9Y524	HEBP2_HUMAN	Heme-binding protein 2 (Placental protein 23) (PP23) (Protein SOU1)	HEBP2
			1498,56	0,185	K.TCVADESAENCOK.S	P02768	ALBU_HUMAN	Serum albumin	ALB
1499,74	1498,987	1500,487	1499,71	0,028	R.WLHNEDQMAVEK.L	P37837	TALDO_HUMAN	Transaldolase (EC 2.2.1.2)	TALDO1
			1499,70	0,037	R.HGIVEDWLMER.F	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
			1499,78	0,038	K.GISLNPQWSQLK.E	P53999	TCP4_HUMAN	Activated RNA polymerase II transcriptional coactivator p15 (Positive cofactor 4) (PC4) (SUB1 homolog) (p14)	SUB1
			1499,63	0,106	K.ADDKETCFEAEGK.K	P02768	ALBU_HUMAN	Serum albumin	ALB

			1499,57	0,166	R.NWYSDADMPASAR.Q	P09923	PPBI_HUMAN	Intestinal-type alkaline phosphatase (IAP) (Intestinal alkaline phosphatase) (EC 3.1.3.1)	ALPI
1500,74	1499,993	1501,494	1500,79	0,043	K.WVAIQSVSAWPEK.R	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
			1500,69	0,051	K.QEYDEAGPSIVHR.K	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleared into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1500,69	0,051	K.QEYDEAGPSIVHR.K	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleared into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1500,69	0,051	K.QEYDEAGPSIVHR.K	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleared into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
1501,74	1500,990	1502,491	1501,73	0,010	K.IWHHSFYNELR.V	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleared into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1501,72	0,018	R.QLVHELDEAEYR.D	Q06323	PSME1_HUMAN	Proteasome activator complex subunit 1 (11S regulator complex subunit alpha) (REG-alpha) (Activator of multicatalytic protease subunit 1) (Interferon gamma up-regulated I-5111 protein) (IGUP I-5111) (Proteasome activator 28 subunit alpha) (PA28a) (PA28alpha)	PSME1
			1501,81	0,070	R.VNQAIVLLCTGAR.E	P46782	RS5_HUMAN	40S ribosomal protein S5 (Small ribosomal subunit protein uS7) [Cleared into: 40S ribosomal protein S5, N-terminally processed]	RPS5
1502,74	1501,991	1503,494	1502,71	0,036	K.MINLSVPDTIDER.T	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
			1502,71	0,036	K.MINLSVPDTIDER.A	P13797	PLST_HUMAN	Plastin-3 (T-plastin)	PLS3
1503,76	1503,006	1504,509	1503,74	0,022	K.LVSEDEMVELIEK.N	P54819	KAD2_HUMAN	Adenylate kinase 2, mitochondrial (AK 2) (EC 2.7.4.3) (ATP-AMP transphosphorylase 2) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) [Cleared into: Adenylate kinase 2, mitochondrial, N-terminally processed]	AK2
			1503,79	0,031	R.GISHVIVDEIHER.D	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A (EC 3.6.4.13) (DEAH box protein 9) (DEXH-box helicase 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II) (RNA helicase A)	DHX9
1504,75	1504,000	1505,505	1504,81	0,059	K.FFEVILDPFHKA	P61313	RL15_HUMAN	60S ribosomal protein L15 (Large ribosomal subunit protein eL15)	RPL15
1505,79	1505,034	1506,540	1505,74	0,046	K.VKEGMNIVEAMER.F	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleared into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
			1505,71	0,076	R.LALFNPDVCWDR.N	O00483	NDUA4_HUMAN	Cytochrome c oxidase subunit NDUFA4 (Complex I-MLRQ) (CI-MLRQ) (NADH-ubiquinone oxidoreductase MLRQ subunit)	NDUFA4
			1505,64	0,149	R.SDFGSCPPEQPR.G	Q8WZ82	OVCA2_HUMAN	Esterase OVCA2 (EC 3.1.2.-) (Ovarian cancer-associated gene 2 protein)	OVCA2
1505,84	1505,087	1506,593	1505,74	0,099	K.VKEGMNIVEAMER.F	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleared into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
			1505,71	0,129	R.LALFNPDVCWDR.N	O00483	NDUA4_HUMAN	Cytochrome c oxidase subunit NDUFA4 (Complex I-MLRQ) (CI-MLRQ) (NADH-ubiquinone oxidoreductase MLRQ subunit)	NDUFA4
			1505,64	0,202	R.SDFGSCPPEQPR.G	Q8WZ82	OVCA2_HUMAN	Esterase OVCA2 (EC 3.1.2.-) (Ovarian cancer-associated gene 2 protein)	OVCA2
1506,71	1505,959	1507,466	1506,75	0,035	R.TVQSLIEDLSMR.N	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
			1506,77	0,057	K.ISSLLEEQQQKG.L	P62241	RS8_HUMAN	40S ribosomal protein S8 (Small ribosomal subunit protein eS8)	RPS8
			1506,80	0,088	R.LVTLEEFLASTQR.K	Q02818	NUCB1_HUMAN	Nucleobindin-1 (CALNUC)	NUCB1
1506,84	1506,084	1507,591	1506,80	0,037	R.LVTLEEFLASTQR.K	Q02818	NUCB1_HUMAN	Nucleobindin-1 (CALNUC)	NUCB1
			1506,77	0,068	K.ISSLLEEQQQKG.L	P62241	RS8_HUMAN	40S ribosomal protein S8 (Small ribosomal subunit protein eS8)	RPS8
			1506,75	0,090	R.TVQSLIEDLSMR.N	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
1507,80	1507,044	1508,552	1507,70	0,103	K.GGDDLPNVYLSSR.V	P06732	KCRM_HUMAN	Creatine kinase M-type (EC 2.7.3.2) (Creatine kinase M chain) (Creatine phosphokinase M-type) (CPK-M) (M-CK)	CKM
			1507,67	0,133	R.GLPWSCSADEVMR.F	P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 (hnRNP H2) (FTP-3) (Heterogeneous nuclear ribonucleoprotein H') (hnRNP H') [Cleared into: Heterogeneous nuclear ribonucleoprotein H2, N-terminally processed]	HNRNP2
			1507,65	0,146	K.SSPELEDATSSKR.R	P46013	KI67_HUMAN	Proliferation marker protein Ki-67 (Antigen identified by monoclonal antibody Ki-67) (Antigen Ki-67) (Antigen Ki67)	MKI67
1508,70	1507,943	1509,452							
1509,71	1508,952	1510,462	1509,72	0,017	K.IEFTPEQIEEFK.E	P08590	MYL3_HUMAN	Myosin light chain 3 (Cardiac myosin light chain 1) (CMLC1) (Myosin light chain 1, slow-twitch muscle B/ventricular isoform) (MLC1S8) (Ventricular myosin alkali light chain) (Ventricular myosin light chain 1) (VLCI) (Ventricular/slow twitch myosin alkali light chain) (MLC-IV/sb)	MYL3
1510,70	1509,946	1511,457	1510,72	0,015	R.VSISEGDDKIEYR.A	P22087	FBRL_HUMAN	rRNA 2'-O-methyltransferase fibrillarin (EC 2.1.1.-) (34 kDa nucleolar scleroderma antigen) (Histone-glutamine methyltransferase)	FBL
			1510,68	0,018	K.QEYDEAGPPIVHR.K	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			1510,76	0,058	R.DEWLRPEDLPK.Y	P49591	SYSC_HUMAN	Serine-tRNA ligase, cytoplasmic (EC 6.1.1.11) (Seryl-tRNA synthetase) (SerRS) (Seryl-tRNA(Ser/Sec) synthetase)	SARS
1511,75	1510,995	1512,506	1511,73	0,018	K.FLEEHPGGEEVLR.E	P00167	CYB5_HUMAN	Cytochrome b5 (Microsomal cytochrome b5 type A) (MCB5)	CYB5A
			1511,83	0,083	K.VPQVSTPTLVEVSR.N	P02768	ALBU_HUMAN	Serum albumin	ALB

1512,76	1512,008	1513,521	1512,74	0,021	R.AKFEELNMDLFR.S	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP, EC 3.6.4.10 (78 kDa glucose-regulated protein, GRP-78) (Binding-immunoglobulin protein, BiP) (Heat shock protein 70 family protein 5, HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			1512,74	0,021	R.APSWFDFTGLSEMR.L	P02511	CRYAB_HUMAN	Alpha-crystallin B chain (Alpha(B)-crystallin) (Heat shock protein beta-5) (HspB5) (Renal carcinoma antigen NY-REN-27) (Rosenthal fiber component)	CRYAB
			1512,74	0,028	R.ASGYLMIDLNFLR.S	Q8TAG9	EXOC6_HUMAN	Exocyst complex component 6 (Exocyst complex component Sec15A) (SEC15-like protein 1)	EXOC6
			1512,87	0,102	K.TVAGQDAVIVLGLTR.N	P30043	BLVRB_HUMAN	Flavin reductase (NADPH) (FR) (EC 1.5.1.30) (Biliverdin reductase B) (BVR-B) (EC 1.3.1.24) (Biliverdin-IX beta-reductase) (Green heme-binding protein) (GHBp) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR)	BLVRB
1513,77	1513,013	1514,527	1513,78	0,013	R.GVVDSEDLPLNISR.E	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			1513,78	0,013	R.GVVDSEDLPLNISR.E	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP 2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
			1513,82	0,045	-MRSAAKPWNPAIR.A	Q5M775	CYTSB_HUMAN	Cytosin-B (Nuclear structure protein 5) (NSP5) (Sperm antigen HCMOGT-1) (Sperm antigen with calponin homology and coiled-coil domains 1)	SPECC1
			1513,72	0,049	R.VISESPPDQWEAR.C	Q92616	GCN1_HUMAN	eIF-2-alpha kinase activator GCN1 (GCN1 eIF-2-alpha kinase activator homolog) (GCN1-like protein 1) (General control of amino-acid synthesis 1-like protein 1) (Translational activator GCN1) (HsGCN1)	GCN1
			1513,68	0,091	R.EVFSPTGSESEWK.D	Q07021	C1QBP_HUMAN	Complement component 1 Q subcomponent-binding protein, mitochondrial (ASF/SF2-associated protein p32) (Glycoprotein gC1qBP) (C1qBP) (Hyaluronan-binding protein 1) (Mitochondrial matrix protein p32) (gC1q-R protein) (p33) (SF2AP32)	C1QBP
1514,75	1513,990	1515,505	1514,72	0,022	K.NLEPFWAAAASEVK.E	Q15084	PDIA6_HUMAN	Protein disulfide-isomerase A6 (EC 5.3.4.1) (Endoplasmic reticulum protein 5) (ER protein 5) (ERp5) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)	PDIA6
1515,73	1514,970	1516,485	1515,74	0,016	R.FLQDYFDGNLKR.Y	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	PDIA3
			1515,76	0,036	K.IWHHTFYNELR.V	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1515,76	0,036	K.IWHHTFYNELR.V	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1515,76	0,036	K.IWHHTFYNELR.V	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			1515,76	0,036	K.IWHHTFYNELR.V	Q658J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
1516,71	1515,950	1517,467	1516,70	0,005	K.QEYDESGPSIVHR.K	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			1516,70	0,005	K.QEYDESGPSIVHR.K	Q658J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			1516,72	0,011	K.FYGPPEGYPGVFAGR.D	O00264	PGR1_HUMAN	Membrane-associated progesterone receptor component 1 (mPR) (Dap1) (IZA)	PGRM1
1516,74	1515,979	1517,496	1516,72	0,017	K.FYGPPEGYPGVFAGR.D	O00264	PGR1_HUMAN	Membrane-associated progesterone receptor component 1 (mPR) (Dap1) (IZA)	PGRM1
			1516,70	0,033	K.QEYDESGPSIVHR.K	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			1516,70	0,033	K.QEYDESGPSIVHR.K	Q658J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
1517,75	1516,989	1518,507	1518,69	0,058	K.YDPPLEDGAMPASR.L	P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta (CapZ beta)	CAPZB
1518,75	1517,991	1519,510	1518,93	0,177	R.LIHQSLAGGIQV.K	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNP
1519,77	1519,012	1520,532	1519,71	0,066	R.IEDGNNFVAVQEK.V	Q06323	PSME1_HUMAN	Proteasome activator complex subunit 1 (11S regulator complex subunit alpha) (REG-alpha) (Activator of multicatalytic protease subunit 1) (Interferon gamma up-regulated I-5111 protein) (IGUP I-5111) (Proteasome activator 28 subunit alpha) (PA28a) (PA28alpha)	PSME1
1520,77	1520,014	1521,535	1520,76	0,017	R.DTDLGDFPDEKLR.C	P49747	COMP_HUMAN	Cartilage oligomeric matrix protein (COMP) (Thrombospondin-5) (TSP5)	COMP
			1520,76	0,017	K.SMKGLGTDNTLR.V	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedin) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4
			1520,76	0,017	R.IGEDFISDLQLR.K	P11217	PYGM_HUMAN	Glycogen phosphorylase, muscle form (EC 2.4.1.1) (Myophosphorylase)	PYGM
			1520,72	0,055	R.DFEPGLGPVCPFR.C	P07585	PGS2_HUMAN	Decorin (Bone proteoglycan II) (PG-S2) (PG40)	DCN
			1520,71	0,060	K.GLIDEVNDQFTNR.I	P02671	FIBA_HUMAN	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	FGA
			1520,71	0,069	K.DHQYQFLEDAVR.N	Q13263	TIF1B_HUMAN	Transcription intermediary factor 1-beta (TIF1-beta) (E3 SUMO-protein ligase TRIM28) (EC 2.3.2.27) (KRAB-associated protein 1) (KAP-1) (KRAB-interacting protein 1) (KRIP-1) (Nuclear corepressor KAP-1) (RING finger protein 96) (RING-type E3 ubiquitin transferase TIF1-beta) (Tripartite motif-containing protein 28)	TRIM28
			1520,67	0,106	K.YKEENDDFASFR.V	P04196	HRG_HUMAN	Histidine-rich glycoprotein (Histidine-proline-rich glycoprotein) (HPRG)	HRG
1521,76	1520,997	1522,519	1521,74	0,017	K.VKEGMNVMEAMER.F	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA

			1521,73	0,026	K.VKEGMNIVEAMER.F	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
1522,75	1521,994	1523,516	1522,81	0,050	R.LLSGPYFWSLPSR.F	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
			1522,68	0,073	R.EVHGGQEALDSPR.G	Q86Y26	NUTM1_HUMAN	NUT family member 1 (Nuclear protein in testis)	NUTM1
			1522,83	0,077	R.EAVLDPVLETAPR.D	Q95571	ETHE1_HUMAN	Persulfide dioxygenase ETHE1, mitochondrial (EC 1.13.11.18) (Ethylmalonic encephalopathy protein 1) (Hepatoma subtracted clone one protein) (Sulfur dioxygenase ETHE1)	ETHE1
1523,75	1522,989	1524,512							
1524,71	1523,952	1525,477	1524,71	0,001	K.FLEELLTTQCDR.F	Q96A32	MLRS_HUMAN	Myosin regulatory light chain 2, skeletal muscle isoform (Fast skeletal myosin light chain 2) (MLC28)	MYLPF
1525,73	1524,968	1526,493	1525,93	0,204	R.ASITPGTILILTGR.H	Q02878	RL6_HUMAN	60S ribosomal protein L6 (Large ribosomal subunit protein eL6) (Neoplasm-related protein C140) (Tax-responsive enhancer element-binding protein 107) (TaxREB107)	RPL6
1526,74	1525,979	1527,506	1526,71	0,028	K.VGVNDFCPMGFGVK.R	P21810	PGS1_HUMAN	Biglycan (Bone/cartilage proteoglycan 1) (PG-S1)	BGN
			1526,84	0,094	R.FAPPLVIKEDELR.E	P04181	OAT_HUMAN	Ornithine aminotransferase, mitochondrial (EC 2.6.1.13) (Ornithine delta-aminotransferase) (Ornithine--oxo-acid aminotransferase) [Cleaved into: Ornithine aminotransferase, hepatic form; Ornithine aminotransferase, renal form]	OAT
1527,70	1526,936	1528,464	1527,74	0,037	K.SLTNDWEDHLAVK.H	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP 2) (LP5-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
			1527,74	0,037	K.SLTNDWEDHLAVK.H	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			1527,82	0,116	R.YQEALHLGSQLLR.E	O00231	PSD11_HUMAN	26S proteasome non-ATPase regulatory subunit 11 (26S proteasome regulatory subunit RPN6) (26S proteasome regulatory subunit S9) (26S proteasome regulatory subunit p44.5)	PSMD11
1527,80	1527,038	1528,566	1527,82	0,014	R.YQEALHLGSQLLR.E	O00231	PSD11_HUMAN	26S proteasome non-ATPase regulatory subunit 11 (26S proteasome regulatory subunit RPN6) (26S proteasome regulatory subunit S9) (26S proteasome regulatory subunit p44.5)	PSMD11
			1527,74	0,066	K.SLTNDWEDHLAVK.H	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP 2) (LP5-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
			1527,74	0,066	K.SLTNDWEDHLAVK.H	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
1528,74	1527,972	1529,500	1528,81	0,072	R.DPILFPSFIHSQK.R	P04040	CATA_HUMAN	Catalase (EC 1.11.1.6)	CAT
1529,70	1528,934	1530,464	1529,73	0,035	K.VGAHAGEYGAALER.M	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			1529,79	0,087	K.VVLDDKDYFLFR.D	P61604	CH10_HUMAN	10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperonin) (Chaperonin 10) (CPN10) (Early-pregnancy factor) (EPF)	HSPA1
			1529,91	0,216	R.ALPLALVHELGAGR.S	P19971	TYPH_HUMAN	Thymidine phosphorylase (TP) (EC 2.4.2.4) (Gliostatin) (Platelet-derived endothelial cell growth factor) (PD-ECGF) (TdRPase)	TYMP
1530,70	1529,930	1531,461	1530,70	0,009	K.TDMFQTVDLFEGK.D	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein WS3-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
			1530,67	0,029	K.DYDSLAPGFFDR.F	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
			1530,74	0,040	K.ELSLAGNELGDEGAR.L	P13489	RINI_HUMAN	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor) (Ribonuclease/angiogenin inhibitor 1) (RAI)	RNH1
			1530,78	0,086	R.SQHPYVLTEDTLK.V	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1530,80	0,108	R.VPTANVSVVDLTCR.L	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
1531,70	1530,938	1532,470							
1532,67	1531,904	1533,437	1532,72	0,051	K.AVTEQGAELSNEER.N	P27348	1433T_HUMAN	14-3-3 protein theta (14-3-3 protein T-cell) (14-3-3 protein tau) (Protein HS1)	YWHAQ
			1532,72	0,052	K.IFYPETTDIYDR.K	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
1532,70	1531,930	1533,463	1532,72	0,025	K.AVTEQGAELSNEER.N	P27348	1433T_HUMAN	14-3-3 protein theta (14-3-3 protein T-cell) (14-3-3 protein tau) (Protein HS1)	YWHAQ
			1532,72	0,026	K.IFYPETTDIYDR.K	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
1533,68	1532,913	1534,446	1533,73	0,050	R.GWEEGVAQMSVGQR.A	P62942	FKB1A_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP1A (PPIase FKBP1A) (EC 5.2.1.8) (12 kDa FK506-binding protein) (12 kDa FKBP) (FKBP-12) (Calstabin-1) (FK506-binding protein 1A) (FKBP-1A) (Immunophilin FKBP12) (Rotamase)	FKBP1A
			1533,75	0,069	R.AEAGVPAEFSIWTR.E	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			1533,83	0,152	K.TQSSLPALTDVFR.S	O60888	CUTA_HUMAN	Protein CutA (Acetylcholinesterase-associated protein) (Brain acetylcholinesterase putative membrane anchor)	CUTA
			1533,85	0,165	R.KVESLQEEIAFLK.K	P08670	VIME_HUMAN	Vimentin	VIM
			1533,87	0,186	R.FPLGESFLVAKGIR.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1534,68	1533,914	1535,449	1534,80	0,115	R.YTLNILEEIGGGQK.V	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
1535,69	1534,926	1536,462	1535,61	0,082	R.CECPVGFFYNDK.L	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
1536,72	1535,952	1537,489	1536,71	0,007	K.SWFEPLVEDMQR.Q	P02649	APOE_HUMAN	Apolipoprotein E (Apo-E)	APOE
			1536,71	0,012	R.FEEIEKAEQEER.K	Q96C19	EFHD2_HUMAN	EF-hand domain-containing protein D2 (Swiprosin-1)	EFHD2
			1536,70	0,017	K.SNEDQSGMGNWQIK.R	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
			1536,79	0,066	K.SMKLGTDDNTLIR.V	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedlin) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4

1537,71	1536,943	1538,481	1536,79	0,066	K.TFAPEEISAMVLTK.M	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP, EC 3.6.4.10 (78 kDa glucose-regulated protein, GRP-78) (Binding-immunoglobulin protein, BiP) (Heat shock protein 70 family protein 5, HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			1536,90	0,182	R.ILSGRPPLGLFNRL	O14773	TPP1_HUMAN	Tripeptidyl-peptidase 1 (TPP-1) (EC 3.4.14.9) (Cell growth-inhibiting gene 1 protein) (Lysosomal pepstatin-insensitive protease) (LPI-C) (Tripeptidyl aminopeptidase) (Tripeptidyl-peptidase I) (TPP-I)	TPP1
			1537,75	0,038	R.AEWQVYKEEISRF	Q00059	TFAM_HUMAN	Transcription factor A, mitochondrial (mtTFA) (Mitochondrial transcription factor 1) (MtfTf1) (Transcription factor 6) (TCF-6) (Transcription factor 6-like 2)	TFAM
			1537,77 1537,77	0,056 0,056	R.FAIQDISVEETSAK.E R.FAIQDISVEETSAK.E	O43707 P35609	ACTN4_HUMAN ACTN2_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4) Alpha-actinin-2 (Alpha-actinin skeletal muscle isoform 2) (F-actin cross-linking protein)	ACTN4 ACTN2
1538,73	1537,961	1539,499	1537,77	0,056	R.FAIQDISVEETSAK.E	P12814	ACTN1_HUMAN	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (F-actin cross-linking protein) (Non-muscle alpha-actinin-1)	ACTN1
			1538,71	0,021	K.QAMFHYFQVPDR.L	Q9UJ70	NAGK_HUMAN	N-acetyl-D-glucosamine kinase (N-acetylglucosamine kinase) (EC 2.7.1.59) (GlcNAc kinase)	NAGK
			1538,77	0,037	R.ITEYEGTSEIQR.L	P16219	ACADS_HUMAN	Short-chain specific acyl-CoA dehydrogenase, mitochondrial (SCAD) (EC 1.3.8.1) (Butyryl-CoA dehydrogenase)	ACADS
			1539,71	0,025	R.DQYELLCLDNTR.K	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
1540,69	1539,921	1541,462	1539,81	0,071	K.THLPGFVEQAEALK.A	P30044	PRDX5_HUMAN	Peroxioredoxin-5, mitochondrial (EC 1.11.1.15) (Alu corepressor 1) (Antioxidant enzyme B166) (AOEB166) (Liver tissue 2D-page spot 718) (PLP) (Peroxioredoxin V) (Prx-V) (Peroxisomal antioxidant enzyme) (TPx type VI) (Thioredoxin peroxidase PMP20)	PRDX5
			1540,71	0,015	K.EVDGEGKPYVEVR.L	Q9NY33	DPP3_HUMAN	Dipeptidyl peptidase 3 (EC 3.4.14.4) (Dipeptidyl aminopeptidase III) (Dipeptidyl arylamidase III) (Dipeptidyl peptidase III) (DPP III) (Enkephalinase B)	DPP3
			1540,73	0,037	R.DASGVTFVTWPSSGK.S	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
			1540,79	0,094	K.VVIGMDVAASEFFR.S	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
1540,78	1540,008	1541,549	1540,79	0,007	K.VVIGMDVAASEFFR.S	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			1540,73	0,049	R.DASGVTFVTWPSSGK.S	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
			1540,71	0,071	K.EVDGEGKPYVEVR.L	Q9NY33	DPP3_HUMAN	Dipeptidyl peptidase 3 (EC 3.4.14.4) (Dipeptidyl aminopeptidase III) (Dipeptidyl arylamidase III) (Dipeptidyl peptidase III) (DPP III) (Enkephalinase B)	DPP3
			1541,68	0,014	K.WSGYMEGAVEAGER.A	P21397	AOFA_HUMAN	Amine oxidase [flavin-containing] A (EC 1.4.3.4) (Monoamine oxidase type A) (MAO-A)	MAOA
1541,69	1540,922	1542,463	1541,68	0,014	K.WSGYMEGAVEAGER.A	P21397	AOFA_HUMAN	Amine oxidase [flavin-containing] A (EC 1.4.3.4) (Monoamine oxidase type A) (MAO-A)	MAOA
1541,78	1541,013	1542,555	1541,68	0,105	K.WSGYMEGAVEAGER.A	P21397	AOFA_HUMAN	Amine oxidase [flavin-containing] A (EC 1.4.3.4) (Monoamine oxidase type A) (MAO-A)	MAOA
1542,76	1541,985	1543,528	1542,77	0,014	R.EQLWLANEGJTR.L	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
			1542,70	0,060	K.DQATYEDFVEGLR.V	P05976	MYL1_HUMAN	Myosin light chain 1/3, skeletal muscle isoform (MLC1/MLC3) (MLC1F/MLC3F) (Myosin light chain alkali 1/2) (Myosin light chain A1/A2)	MYL1
			1542,84	0,081	K.LLDAVDVTYVPAR.D	P49411	EFTU_HUMAN	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	TUFM
			1542,85	0,089	R.LEEKALINQLSR.E	Q9Y2K3	MYH15_HUMAN	Myosin-15 (Myosin heavy chain 15)	MYH15
1543,75 1544,76	1542,983 1543,992	1544,526 1545,537	1542,85	0,089	K.GVDEVTVINLNR.S	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1544,77	0,011	R.TIPIDGNFFTYTR.H	P00352	AL1A1_HUMAN	Retinal dehydrogenase 1 (RALDH 1) (RaldH1) (EC 1.2.1.-) (EC 1.2.1.36) (ALDH-E1) (ALDHII) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic)	ALDH1A1
			1544,70	0,060	K.DQGTIEDYVEGLR.V	P60660	MYL6_HUMAN	Myosin light polypeptide 6 (17 kDa myosin light chain) (LC17) (Myosin light chain 3) (MLC-3) (Myosin light chain alkali 3) (Myosin light chain A3) (Smooth muscle and nonmuscle myosin light chain alkali 6)	MYL6
			1544,70	0,068	R.NEQDAYAINSYTR.S	P24752	THIL_HUMAN	Acetyl-CoA acetyltransferase, mitochondrial (EC 2.3.1.9) (Acetoacetyl-CoA thiolase) (T2)	ACAT1
1545,75	1544,979	1546,525	1544,85	0,087	R.TIQNDIMLLQLSR.R	P08311	CATG_HUMAN	Cathepsin G (CG) (EC 3.4.21.20)	CTSG
			1544,67	0,092	K.FNADEFEDMVAEK.R	P27635	RL10_HUMAN	60S ribosomal protein L10 (Laminin receptor homolog) (Large ribosomal subunit protein uL16) (Protein QM) (Ribosomal protein L10) (Tumor suppressor QM)	RPL10
			1544,67	0,093	K.HGTDDGVVMMNWK.G	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
			1545,70	0,051	R.QNYHQDSEAINR.Q	P02794	FRIH_HUMAN	Ferritin heavy chain (Ferritin H subunit) (EC 1.16.3.1) (Cell proliferation-inducing gene 15 protein) [Cleaved into: Ferritin heavy chain, N-terminally processed]	FTH1
1546,76	1545,984	1547,531	1546,75	0,012	K.LGEKEETIPPDYR.L	P20810	ICAL_HUMAN	Calpastatin (Calpain inhibitor) (Sperm BS-17 component)	CAST
			1546,70	0,059	K.SNEEGSEKGEVPR.E	P31947	1433S_HUMAN	14-3-3 protein sigma (Epithelial cell marker protein 1) (Stratifin)	SFN
			1546,75	0,018	K.LGEKEETIPPDYR.L	P20810	ICAL_HUMAN	Calpastatin (Calpain inhibitor) (Sperm BS-17 component)	CAST
			1546,70	0,065	K.SNEEGSEKGEVPR.E	P31947	1433S_HUMAN	14-3-3 protein sigma (Epithelial cell marker protein 1) (Stratifin)	SFN
1547,33	1546,556	1548,103	1547,73	0,397	R.AEAQAQAEELSFPR.S	P11498	PYC_HUMAN	Pyruvate carboxylase, mitochondrial (EC 6.4.1.1) (Pyruvic carboxylase) (PCB)	PC
			1547,74	0,415	R.DQNTGWIGELGAMR.M	Q96RQ9	OXLA_HUMAN	L-amino-acid oxidase (LAAO) (LAO) (EC 1.4.3.2) (Interleukin 4-induced protein 1) (IL4-induced protein 1) (Protein Fig-1) (hFIG1)	IL4I1

			1546,75	0,584	K.LGEKEETIPPDYR.L	P20810	ICAL_HUMAN	Calpastatin (Calpain inhibitor) (Sperm BS-17 component)	CAST
			1546,70	0,631	K.SNEEGSEEKPEVR.E	P31947	1433S_HUMAN	14-3-3 protein sigma (Epithelial cell marker protein 1) (Stratifin)	SFN
1547,77	1546,995	1548,543	1547,74	0,024	R.DQNTGWIGELGAMR.M	Q96RQ9	OXLA_HUMAN	L-amino-acid oxidase (LAAO) (LAO) (EC 1.4.3.2) (Interleukin IL4I1 4-induced protein 1) (IL4-induced protein 1) (Protein Fig-1) (hFIG1)	
			1547,73	0,043	R.AEAEQAEELSFPR.S	P11498	PYC_HUMAN	Pyruvate carboxylase, mitochondrial (EC 6.4.1.1) (Pyruvic carboxylase) (PCB)	PC
1548,33	1547,554	1549,102	1548,72	0,392	K.SVTEQGAELSNEER.N	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
			1548,76	0,430	R.FPDAFVTFSSFQR.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1547,74	0,583	R.DQNTGWIGELGAMR.M	Q96RQ9	OXLA_HUMAN	L-amino-acid oxidase (LAAO) (LAO) (EC 1.4.3.2) (Interleukin IL4I1 4-induced protein 1) (IL4-induced protein 1) (Protein Fig-1) (hFIG1)	
			1547,73	0,601	R.AEAEQAEELSFPR.S	P11498	PYC_HUMAN	Pyruvate carboxylase, mitochondrial (EC 6.4.1.1) (Pyruvic carboxylase) (PCB)	PC
1548,77	1547,996	1549,544	1548,76	0,012	R.FPDAFVTFSSFQR.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1548,72	0,050	K.SVTEQGAELSNEER.N	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
1549,38	1548,608	1550,158	1549,74	0,353	K.LDRETEELHHDR.V	O60869	EDF1_HUMAN	Endothelial differentiation-related factor 1 (EDF-1) (Multi-protein-bridging factor 1) (MBF1)	EDF1
			1549,85	0,463	K.NLMQLNLAHNLR.K	P51888	PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	PRELP
			1548,76	0,625	R.FPDAFVTFSSFQR.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1548,72	0,663	K.SVTEQGAELSNEER.N	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
1549,61	1548,839	1550,389	1549,74	0,122	K.LDRETEELHHDR.V	O60869	EDF1_HUMAN	Endothelial differentiation-related factor 1 (EDF-1) (Multi-protein-bridging factor 1) (MBF1)	EDF1
			1549,85	0,232	K.NLMQLNLAHNLR.K	P51888	PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	PRELP
1549,77	1548,996	1550,546	1549,74	0,035	K.LDRETEELHHDR.V	O60869	EDF1_HUMAN	Endothelial differentiation-related factor 1 (EDF-1) (Multi-protein-bridging factor 1) (MBF1)	EDF1
			1549,85	0,075	K.NLMQLNLAHNLR.K	P51888	PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	PRELP
1550,65	1549,872	1551,423	1550,72	0,068	R.CECFPGLAVALDGR.V	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			1550,81	0,165	K.GTDVNVNFTILTR.S	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
1550,79	1550,016	1551,567	1550,81	0,021	K.GTDVNVNFTILTR.S	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
			1550,72	0,076	R.CECFPGLAVALDGR.V	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
1551,72	1550,948	1552,500	1551,72	0,006	R.SIEYSPQLDAGSR.E	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
			1551,74	0,020	R.ILTDYGFEGHPFR.K	O75489	NDUS3_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial (EC 1.6.99.3) (EC 7.1.1.2) (Complex I-30kD) (CI-30kD) (NADH-ubiquinone oxidoreductase 30 kDa subunit)	NDUF53
			1551,77	0,049	R.ELSELVYTDVLDR.S	Q8WU39	MZB1_HUMAN	Marginal zone B- and B1-cell-specific protein (Mesenteric estrogen-dependent adipose 7) (MEDA-7) (Plasma cell-induced resident endoplasmic reticulum protein) (Plasma cell-induced resident ER protein) (pERp1) (Proapoptotic caspase adapter protein)	MZB1
			1551,78	0,055	R.FQQAVIDAEVFLR.R	Q49A26	GLYR1_HUMAN	Putative oxidoreductase GLYR1 (EC 1.-.-.-) (3-hydroxyisobutyrate dehydrogenase-like protein) (Cytokine-like nuclear factor N-PAC) (Glyoxylate reductase 1 homolog) (Nuclear protein NP60) (Nuclear protein of 60 kDa)	GLYR1
			1551,83	0,109	K.LKEIVTNFLAGFEA.-	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
			1551,87	0,147	K.SLEEYLFSLPIK.E	P15880	RS2_HUMAN	40S ribosomal protein S2 (40S ribosomal protein S4) (Protein LLRep3) (Small ribosomal subunit protein u55)	RP52
1552,72	1551,943	1553,496	1552,70	0,022	R.YEDEECTLPAGR.H	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			1552,67	0,048	R.NCWQNYLDFHR.C	P14854	CK6B1_HUMAN	Cytochrome c oxidase subunit 6B1 (Cytochrome c oxidase subunit Vlb isoform 1) (COX Vlb-1)	COX6B1
			1552,61	0,105	K.CCAAADPHECYAK.V	P02768	ALBU_HUMAN	Serum albumin	ALB
1553,73	1552,956	1554,509	1553,75	0,015	R.EAYPGDVLYLHSR.L	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
1554,33	1553,557	1555,112	1554,84	0,506	R.FSTFLSLLEAADLK.E	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
			1553,75	0,587	R.EAYPGDVLYLHSR.L	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
1554,64	1553,866	1555,421	1554,84	0,196	R.FSTFLSLLEAADLK.E	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
1554,78	1553,998	1555,553	1554,84	0,064	R.FSTFLSLLEAADLK.E	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
1555,33	1554,549	1556,104	1555,69	0,366	K.MFVLDEADEMLSR.G	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-I (eIF4A-I) (eIF4A-I) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
			1555,72	0,393	K.FESDPATHNEPGVR.L	Q9NVA2	SEP11_HUMAN	Septin-11	SEPT11
			1554,84	0,487	R.FSTFLSLLEAADLK.E	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
1555,74	1554,961	1556,516	1555,72	0,019	K.FESDPATHNEPGVR.L	Q9NVA2	SEP11_HUMAN	Septin-11	SEPT11
			1555,69	0,045	K.MFVLDEADEMLSR.G	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-I (eIF4A-I) (eIF4A-I) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
1556,67	1555,895	1557,451	1556,71	0,034	K.CLCPEGFSLSSGR.R	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			1556,75	0,079	K.CTDDHISAAGPWIK.F	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
			1556,79	0,114	K.VVIGMDVAEEFFR.S	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			1556,82	0,147	R.LDQLVIPLDEK.S	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			1556,86	0,188	K.QLDLKVELSQLR.V	P42766	RL35_HUMAN	60S ribosomal protein L35 (Large ribosomal subunit protein uL29)	RPL35

			1556,90	0,231	R.GVMLAVDAVIAELKK.Q	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
1556,79	1556,012	1557,569	1556,79	0,004	K.VVIGMDVAASEFFR.S	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) [C-myc promoter-binding protein] (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			1556,82	0,029	R.LDQLIYIPLDEK.S	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (155 Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			1556,75	0,039	K.CTTDHISAAGPWLK.F	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
			1556,86	0,070	K.QLDDLKVELSQLR.V	P42766	RL35_HUMAN	60S ribosomal protein L35 (Large ribosomal subunit protein uL29)	RPL35
			1556,71	0,084	K.CLCPEGFSLSSSGR.R	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			1556,90	0,113	R.GVMLAVDAVIAELKK.Q	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
1557,75	1556,972	1558,530	1557,71	0,045	K.TLGTMIAGDTSGDYR.R	P20073	ANXA7_HUMAN	Annexin A7 (Annexin VII) (Annexin-7) (Synexin)	ANXA7
1558,73	1557,954	1559,512	1559,75	0,003	K.ALDIAENEMPLMR.M	P23526	SAHH_HUMAN	Adenosylhomocysteinase (AdoHcyase) (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase)	AHCY
1559,75	1558,974	1560,534	1559,80	0,050	R.APLEHELAGEPQLR.E	Q95833	CLIC3_HUMAN	Chloride intracellular channel protein 3	CLIC3
1560,76	1559,983	1561,544	1560,79	0,029	K.VDFPQDQLTALTGR.I	P40926	MDHM_HUMAN	Malate dehydrogenase, mitochondrial (EC 1.1.1.37)	MDH2
			1560,72	0,043	K.LGERDDTIPPEYR.H	P20810	ICAL_HUMAN	Calpastatin (Calpain inhibitor) (Sperm BS-17 component)	CAST
			1560,82	0,054	K.LYTLVLTDPDAPSR.K	P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPPp) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1
			1560,69	0,070	R.YQSHDYAFSSVEK.L	Q9UHG3	PCYOX_HUMAN	Prenylcysteine oxidase 1 (EC 1.8.3.5) (Prenylcysteine lyase)	PCYOX1
1561,77	1560,990	1562,552	1561,73	0,036	R.ELPPDQAEYCIAR.M	Q43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
			1561,73	0,036	R.ELPPDQAEYCIAR.M	P12814	ACTN1_HUMAN	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (F-actin cross-linking protein) (Non-muscle alpha-actinin-1)	ACTN1
			1561,72	0,055	K.TVQGPPTSDDIFER.E	P04181	OAT_HUMAN	Ornithine aminotransferase, mitochondrial (EC 2.6.1.13) (Ornithine delta-aminotransferase) (Ornithine--oxo-acid aminotransferase) [Cleaved into: Ornithine aminotransferase, hepatic form; Ornithine aminotransferase, renal form]	OAT
1562,77	1561,990	1563,553	1562,79	0,020	R.GETGPSGPGVAGAVGPR.G	P08123	CO1A2_HUMAN	Collagen alpha-2(I) chain (Alpha-2 type I collagen)	COL1A2
1563,75	1562,973	1564,536	1563,65	0,100	R.GETGDDGRDGVGSEGR.R	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1563,78	1562,994	1564,558	1563,65	0,122	R.GETGDDGRDGVGSEGR.R	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1564,78	1563,998	1565,563	1564,76	0,022	K.HIGLVYSGMGPDYR.V	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
			1564,74	0,037	R.GGPPFAFVEFEDPR.D	Q07955	SRSF1_HUMAN	Serine/arginine-rich splicing factor 1 (Alternative-splicing factor 1) (ASF-1) (Splicing factor, arginine/serine-rich 1) (pre-mRNA-splicing factor SF2, P33 subunit)	SRSF1
1565,77	1564,984	1566,549	1565,79	0,019	K.LPIGDVATQYFADR.D	Q99832	TCPH_HUMAN	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein) [Cleaved into: T-complex protein 1 subunit eta, N-terminally processed]	CCT7
			1565,72	0,048	K.TFDQLTPDESKER.L	Q15293	RCN1_HUMAN	Reticulocalbin-1	RCN1
1565,79	1565,002	1566,568	1565,79	0,000	K.LPIGDVATQYFADR.D	Q99832	TCPH_HUMAN	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein) [Cleaved into: T-complex protein 1 subunit eta, N-terminally processed]	CCT7
			1565,72	0,067	K.TFDQLTPDESKER.L	Q15293	RCN1_HUMAN	Reticulocalbin-1	RCN1
1566,78	1565,992	1567,559	1566,78	0,003	R.ITPSYVAFTPEGER.L	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP, EC 3.6.4.10 (78 kDa glucose-regulated protein, GRP-78) (Binding-immunoglobulin protein, BiP) (Heat shock protein 70 family protein 5, HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			1566,81	0,035	R.QIETLAHFHLTK.D	P19367	HXX1_HUMAN	Hexokinase-1 (EC 2.7.1.1) (Brain form hexokinase)	HK1
			1566,82	0,047	K.LLPQLTYLDGYDR.D	P39687	AN32A_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member A (Acidic nuclear phosphoprotein pp32) (pp32) (Leucine-rich acidic nuclear protein) (LANP) (Mapmodulin) (Potent heat-stable protein phosphatase 2A inhibitor 1PP2A) (Putative HLA-DR-associated protein I) (PHAPI)	ANP32A
1567,76	1566,974	1568,541	1567,86	0,107	K.IAELLSPGSDPLTR.L	P35237	SPB6_HUMAN	Serin B6 (Cytoplasmic antiproteinase) (CAP) (Peptidase inhibitor 6) (PI-6) (Placental thrombin inhibitor)	SERPINB6
			1567,89	0,128	K.SPILGLSLAHQIYR.M	P31937	3HIDH_HUMAN	3-hydroxyisobutyrate dehydrogenase, mitochondrial (HIBADH) (EC 1.1.1.31)	HIBADH
1568,49	1567,702	1569,271	1568,68	0,195	K.DPAEGDGAQPEETPR.D	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			1568,71	0,219	K.VDNDENEHQLSLR.T	P06748	NPM_HUMAN	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	NPM1
			1568,74	0,254	K.SYYAISDFAVGGR.C	P11047	LAMC1_HUMAN	Laminin subunit gamma-1 (Laminin B2 chain) (Laminin-1 subunit gamma) (Laminin-10 subunit gamma) (Laminin-11 subunit gamma) (Laminin-2 subunit gamma) (Laminin-3 subunit gamma) (Laminin-4 subunit gamma) (Laminin-6 subunit gamma) (Laminin-7 subunit gamma) (Laminin-8 subunit gamma) (Laminin-9 subunit gamma) (S-laminin subunit gamma) (S-LAM gamma)	LAMC1
			1567,89	0,600	K.SPILGLSLAHQIYR.M	P31937	3HIDH_HUMAN	3-hydroxyisobutyrate dehydrogenase, mitochondrial (HIBADH) (EC 1.1.1.31)	HIBADH

			1567,86	0,622	K.IAELLSPGSDPLTR.L	P35237	SPB6_HUMAN	Serpin B6 (Cytoplasmic antiproteinasase) (CAP) (Peptidase inhibitor 6) (PI-6) (Placental thrombin inhibitor)	SERPINB6
1568,76	1567,976	1569,544	1568,74	0,020	K.SYYAISDFAVGGR.C	P11047	LAMC1_HUMAN	Laminin subunit gamma-1 (Laminin B2 chain) (Laminin-1 subunit gamma) (Laminin-10 subunit gamma) (Laminin-11 subunit gamma) (Laminin-2 subunit gamma) (Laminin-3 subunit gamma) (Laminin-4 subunit gamma) (Laminin-6 subunit gamma) (Laminin-7 subunit gamma) (Laminin-8 subunit gamma) (Laminin-9 subunit gamma) (S-laminin subunit gamma) (S-LAM gamma)	LAMC1
			1568,71	0,055	K.VDNDENEHQLSLR.T	P06748	NPM_HUMAN	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	NPM1
			1568,68	0,079	K.DPAEGDGAQPEETPR.D	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1569,36	1568,573	1570,142	1568,74	0,617	K.SYYAISDFAVGGR.C	P11047	LAMC1_HUMAN	Laminin subunit gamma-1 (Laminin B2 chain) (Laminin-1 subunit gamma) (Laminin-10 subunit gamma) (Laminin-11 subunit gamma) (Laminin-2 subunit gamma) (Laminin-3 subunit gamma) (Laminin-4 subunit gamma) (Laminin-6 subunit gamma) (Laminin-7 subunit gamma) (Laminin-8 subunit gamma) (Laminin-9 subunit gamma) (S-laminin subunit gamma) (S-LAM gamma)	LAMC1
			1568,71	0,652	K.VDNDENEHQLSLR.T	P06748	NPM_HUMAN	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	NPM1
			1568,68	0,676	K.DPAEGDGAQPEETPR.D	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1569,54 1569,76 1570,49	1568,757 1568,980 1569,702	1570,327 1570,550 1571,273	1570,81	0,323	R.NHLLHVFDEYKR.I	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedlin) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4
			1570,90	0,410	R.ALEEANADLEVKIR.D	P08779	K1C16_HUMAN	Keratin, type I cytoskeletal 16 (Cytokeratin-16) (CK-16) (Keratin-16) (K16)	KRT16
			1570,90	0,410	R.ISLPLPNFSSLNLR.E	P08670	VIME_HUMAN	Vimentin	VIM
1570,73	1569,949	1571,519	1570,81	0,076	R.NHLLHVFDEYKR.I	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedlin) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4
			1570,90	0,163	R.ALEEANADLEVKIR.D	P08779	K1C16_HUMAN	Keratin, type I cytoskeletal 16 (Cytokeratin-16) (CK-16) (Keratin-16) (K16)	KRT16
			1570,90	0,163	R.ISLPLPNFSSLNLR.E	P08670	VIME_HUMAN	Vimentin	VIM
1570,87	1570,082	1571,653	1570,90	0,030	R.ALEEANADLEVKIR.D	P08779	K1C16_HUMAN	Keratin, type I cytoskeletal 16 (Cytokeratin-16) (CK-16) (Keratin-16) (K16)	KRT16
			1570,90	0,030	R.ISLPLPNFSSLNLR.E	P08670	VIME_HUMAN	Vimentin	VIM
			1570,81	0,057	R.NHLLHVFDEYKR.I	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedlin) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4
1571,33	1570,544	1572,116	1570,90	0,432	R.ALEEANADLEVKIR.D	P08779	K1C16_HUMAN	Keratin, type I cytoskeletal 16 (Cytokeratin-16) (CK-16) (Keratin-16) (K16)	KRT16
			1570,90	0,432	R.ISLPLPNFSSLNLR.E	P08670	VIME_HUMAN	Vimentin	VIM
			1570,81	0,520	R.NHLLHVFDEYKR.I	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedlin) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4
1571,77 1571,84 1572,70	1570,985 1571,055 1571,915	1572,556 1572,626 1573,488	1572,75	0,047	R.FGFPEGSVELYAEK.V	P23396	RS3_HUMAN	40S ribosomal protein S3 (EC 4.2.99.18) (Small ribosomal subunit protein uS3)	RPS3
1572,85	1572,063	1573,636	1572,75	0,101	R.FGFPEGSVELYAEK.V	P23396	RS3_HUMAN	40S ribosomal protein S3 (EC 4.2.99.18) (Small ribosomal subunit protein uS3)	RPS3
1573,68	1572,889	1574,463	1573,81	0,138	K.NIYVLQELDNGPAK.R	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC XRCC6 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	
1573,84	1573,052	1574,626	1573,81	0,025	K.NIYVLQELDNGPAK.R	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC XRCC6 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	
1574,77 1575,77	1573,979 1574,980	1575,554 1576,556	1575,78	0,014	R.ILGADTSVDLEETGR.V	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
1576,71	1575,919	1577,496	1576,66	0,045	R.NYDVMKDFEEMR.K	P09669	COX6C_HUMAN	Cytochrome c oxidase subunit 6C (Cytochrome c oxidase polypeptide VIc)	COX6C
1576,77	1575,981	1577,557	1576,66	0,106	R.NYDVMKDFEEMR.K	P09669	COX6C_HUMAN	Cytochrome c oxidase subunit 6C (Cytochrome c oxidase polypeptide VIc)	COX6C

1577,77	1576,984	1578,562	1577,77	0,007	R.LGTFEVEDQIEAAR.Q	P27487	DPP4_HUMAN	Dipeptidyl peptidase 4 (EC 3.4.14.5) (ADABP) (Adenosine deaminase complexing protein 2) (ADCP-2) (Dipeptidyl peptidase IV) (DPP IV) (T-cell activation antigen CD26) (TP103) (CD antigen CD26) [Cleaved into: Dipeptidyl peptidase 4 membrane form (Dipeptidyl peptidase IV membrane form); Dipeptidyl peptidase 4 soluble form (Dipeptidyl peptidase IV soluble form)]	DPP4
			1577,76	0,008	R.ELQAFENIDEIK.L	P31415	CASQ1_HUMAN	Calsequestrin-1 (Calmitine) (Calsequestrin, skeletal muscle isoform)	CASQ1
			1577,81	0,041	R.TAGWNPIMGLLYNK.I	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1577,69	0,086	R.FDEFFSEGCAPGSK.K	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
1578,78	1577,989	1579,568	1578,72	0,063	R.HEERPDEHGFVAR.E	Q14558	HSPB6_HUMAN	Heat shock protein beta-6 (HspB6) (Heat shock 20 kDa-like protein p20)	HSPB6
1579,77	1578,980	1580,560	1579,73	0,042	K.TFDQLTPEESKER.L	Q43852	CALU_HUMAN	Calumenin (Crocabin) (IEF SSP 9302)	CALU
			1579,71	0,065	K.RPAEDMEEQAFK.R	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
1580,75	1579,958	1581,539	1580,78	0,036	K.ESISVSQQLAQFR.S	P00915	CAH1_HUMAN	Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase I) (Carbonic anhydrase B) (CAB) (Carbonic anhydrase I) (CA-I)	CA1
			1580,70	0,047	R.SEQEFQEQLESAR.R	Q96RQ3	MCCA_HUMAN	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial (MCCase subunit alpha) (EC 6.4.1.4) (3-methylcrotonyl-CoA carboxylase 1) (3-methylcrotonyl-CoA carboxylase biotin-containing subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase subunit alpha)	MCCC1
			1580,85	0,100	K.VFSVAITPDHLEPR.L	P12109	CO6A1_HUMAN	Collagen alpha-1(VI) chain	COL6A1
1581,76	1580,968	1582,550	1581,74	0,023	R.RDDGSWEVIEGYR.A	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			1581,66	0,095	R.DFTVSAMHGMDMQK.E	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-1 (eIF-4A-1) (eIF4A-1) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
1582,77	1581,979	1583,562	1582,68	0,092	K.DINAYNCEEPTK.L	P30041	PRDX6_HUMAN	Peroxiredoxin-6 (EC 1.11.1.15) (1-Cys peroxiredoxin) (1-Cys PRX) (24 kDa protein) (Acidic calcium-independent phospholipase A2) (aiPLA2) (EC 3.1.1.4) (Antioxidant protein 2) [Liver 2D page spot 40] (Non-selenium glutathione peroxidase) (NSGPx) (Red blood cells page spot 12)	PRDX6
1583,77	1582,982	1584,565	1583,68	0,095	K.AAGIDEQENWHEGK.E	P28838	AMPL_HUMAN	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase 3) (LAP-3) (Leucyl aminopeptidase) (Peptidase 5) (Proline aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase)	LAP3
			1583,88	0,104	K.GQLVPLETDLMLR.D	P00568	KAD1_HUMAN	Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP-AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	AK1
1584,77	1583,976	1585,560	1584,79	0,020	R.VIGFSPEEVSVHR.I	B01T2	MYO1G_HUMAN	Unconventional myosin-Ig [Cleaved into: Minor histocompatibility antigen HA-2 (mHag HA-2)]	MYO1G
			1584,75	0,022	R.SIQFVDWCPTGFK.V	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
			1584,75	0,022	R.SIQFVDWCPTGFK.V	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detryrosinated tubulin alpha-1B chain]	TUBA1B
			1584,85	0,083	R.FYAYNPLAGLLTGK.Y	O43488	ARK72_HUMAN	Aflatoxin B1 aldehyde reductase member 2 (EC 1.1.1.n11) (AFB1 aldehyde reductase 1) (AFB1-AR 1) (Aldoketoreductase 7) (Succinic semialdehyde reductase) (SSA reductase)	AKR7A2
			1584,64	0,130	K.DSDMGSRPESMGCR.K	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1585,75	1584,958	1586,544	1585,78	0,026	R.LDSGDLQLQAQEI.R	Q6XQN6	PNCB_HUMAN	Nicotinate phosphoribosyltransferase (NAPRTase) (EC 6.3.4.21) (FHA-HIT-interacting protein) (Nicotinate phosphoribosyltransferase domain-containing protein 1)	NAPRT
			1585,78	0,029	K.GDAMIMEETGKIFK.K	Q9UQ80	PA2G4_HUMAN	Proliferation-associated protein 2G4 (Cell cycle protein p38-2G4 homolog) (hG4-1) (Erbb3-binding protein 1)	PA2G4
1586,75	1585,959	1587,546	1586,74	0,010	K.AVTLENEPLSNEDR.N	Q04917	1433F_HUMAN	14-3-3 protein eta (Protein A51)	YWHAH
			1586,74	0,010	R.QLEAEADAIQMVR.E	Q72627	HUWE1_HUMAN	E3 ubiquitin-protein ligase HUWE1 (EC 3.2.2.26) (ARF-binding protein 1) (ARF-BP1) (HECT, UBA and WWE domain-containing protein 1) (HECT-type E3 ubiquitin transferase HUWE1) (Homologous to E6AP carboxyl terminus homologous protein 9) (HectH9) (Large structure of URB1) (LASU1) (Mcl-1 ubiquitin ligase E3) (Mule) (Upstream regulatory element-binding protein 1) (URE-B1) (URE-binding protein 1)	HUWE1
			1586,73	0,020	K.DCGATVWVVLGHSER.R	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP11
			1586,67	0,082	K.WCGTTQNYDADQK.F	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
1587,76	1586,962	1588,549	1587,77	0,010	R.TNEKVELQELNDR.F	P08670	VIME_HUMAN	Vimentin	VIM
			1587,72	0,037	K.LESDVSAQMEYCR.T	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
1588,76	1587,969	1589,558	1588,76	0,005	K.MYEVVYQIGTETR.S	Q9UHG3	PCYOX_HUMAN	Prenylcysteine oxidase 1 (EC 1.8.3.5) (Prenylcysteine lyase) PCYOX1	PCYOX1
			1588,75	0,012	R.YAPSEAGLHEMDIR.Y	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			1588,85	0,089	K.KSDIDEIVLVGGSTR.I	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP, EC 3.6.4.10 (78 kDa glucose-regulated protein, GRP-78) (Binding-immunoglobulin protein, BiP) (Heat shock protein 70 family protein 5, HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
1589,74	1588,944	1590,534	1589,74	0,001	R.HQEGEIFDTEKEK.Y	Q02878	RL6_HUMAN	60S ribosomal protein L6 (Large ribosomal subunit protein eL6) (Neoplasm-related protein C140) (Tax-responsive enhancer element-binding protein 107) (TaxREB107)	RPL6
			1589,82	0,081	K.EAINVEQAFQTIAR.N	P51149	RAB7A_HUMAN	Ras-related protein Rab-7a	RAB7A
1589,83	1589,035	1590,625	1589,82	0,009	K.EAINVEQAFQTIAR.N	P51149	RAB7A_HUMAN	Ras-related protein Rab-7a	RAB7A

			1589,74	0,089	R.HQEGEIFDTEKE.Y	Q02878	RL6_HUMAN	60S ribosomal protein L6 (Large ribosomal subunit protein eL6) (Neoplasm-related protein C140) (Tax-responsive enhancer element-binding protein 107) (TaxREB107)	
1590,71	1589,915	1591,505	1590,90	0,192	K.LENLLLDLQHN.R.L	P51888	PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	PRELP
1590,83	1590,035	1591,626	1590,90	0,072	K.LENLLLDLQHN.R.L	P51888	PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	PRELP
1591,73	1590,930	1592,522	1591,89	0,165	K.LNQALLDLHALGSAR.T	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
1591,86	1591,061	1592,652	1591,89	0,034	K.LNQALLDLHALGSAR.T	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
1592,71	1591,917	1593,510	1592,78	0,064	R.ELSEALGQIFDSQR.G	Q08380	LG3BP_HUMAN	Galectin-3-binding protein (Basement membrane autoantigen p105) (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (MAC2BP) (Mac-2 BP) (Tumor-associated antigen 90K)	LGALS3BP
1592,84	1592,039	1593,632	1592,78	0,059	R.ELSEALGQIFDSQR.G	Q08380	LG3BP_HUMAN	Galectin-3-binding protein (Basement membrane autoantigen p105) (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (MAC2BP) (Mac-2 BP) (Tumor-associated antigen 90K)	LGALS3BP
1593,80	1593,005	1594,599	1593,71	0,092	R.HPDEAAFFDTASTGK.T	P02671	FIBA_HUMAN	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	FGA
1593,81	1593,013	1594,607	1593,71	0,099	R.HPDEAAFFDTASTGK.T	P02671	FIBA_HUMAN	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	FGA
1594,80	1594,007	1595,602	1594,73	0,071	K.GYAFIEFASFEDAK.E	P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL
1595,75	1594,957	1596,553							
1595,83	1595,028	1596,624							
1596,81	1596,009	1597,606							
1597,83	1597,033	1598,631							
1598,80	1598,003	1599,602	1598,83	0,027	R.VPTAIHQLYLDSNK.I	P51888	PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	PRELP
			1598,76	0,043	R.VHVLWWNESADSR.A	Q9B592	NPS3B_HUMAN	Protein NipSnap homolog 3B (NipSnap3B) (SNAP1)	NIPSNAP3B
			1598,76	0,044	R.TIQFVDWCPTGFK.V	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			1598,75	0,052	R.IIPGFMCGGDFTR.H	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
			1598,75	0,056	K.AVTEQGHELSNEER.N	P31946	1433B_HUMAN	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHA3
1599,82	1599,019	1600,619	1599,81	0,012	R.FHQLDIDDLQSI.R.A	P16152	CBR1_HUMAN	Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (15-hydroxyprostaglandin dehydrogenase [NADP(+)] (EC 1.1.1.197) (NADPH-dependent carbonyl reductase 1) (Prostaglandin 9-ketoreductase) (Prostaglandin-E(2) 9-reductase) (EC 1.1.1.189) (Short chain dehydrogenase/reductase family 21C member 1)	CBR1
			1599,89	0,069	R.VVALPEDLVEVKPK.M	P13797	PLST_HUMAN	Plastin-3 (T-plastin)	PLS3
1600,80	1600,004	1601,604							
1601,81	1601,011	1602,613	1601,81	0,002	R.AVLVDLEPGTMDSV.R.S	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1601,82	0,005	K.VALVYQGMEPPGAR.A	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP ATP5F1B synthase F1 subunit beta)	ATPB
			1601,84	0,032	K.LVDQNIFSYLSR.D	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
			1601,77	0,043	K.IDKTYDMVSGYGR.A	P52565	GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)	ARHGDI1
			1601,67	0,145	R.DLNYCFSGMSDHR.Y	P31943	HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H (hnRNP H) [Cleaved into: Heterogeneous nuclear ribonucleoprotein H, N-terminally processed]	HNRNP1
			1601,67	0,145	R.DLNYCFSGMSDHR.Y	P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 (hnRNP H2) (FTP-3) (Heterogeneous nuclear ribonucleoprotein H') (hnRNP H') [Cleaved into: Heterogeneous nuclear ribonucleoprotein H2, N-terminally processed]	HNRNP2
1602,79	1601,984	1603,587	1602,78	0,004	K.THFNTVEEVHSR.F	P30740	ILEU_HUMAN	Leukocyte elastase inhibitor (LEI) (Monocyte/neutrophil elastase inhibitor) (EI) (M/NEI) (Peptidase inhibitor 2) (PI-2) (Serpine B1)	SERPINE1
			1602,89	0,104	K.VVLAYPEVVAIGTGK.T	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP1
1603,79	1602,993	1604,597							
1604,81	1604,005	1605,610	1604,81	0,005	R.LYQHQHAGLFDVTR.G	O14773	TPP1_HUMAN	Tripeptidyl-peptidase 1 (TPP-1) (EC 3.4.14.9) (Cell growth-inhibiting gene 1 protein) (Lysosomal pepstatin-insensitive protease) (LPIC) (Tripeptidyl aminopeptidase) (Tripeptidyl-peptidase I) (TPP-I)	TPP1
			1604,84	0,028	R.DLQLVLPDYFPER.S	Q96CX2	KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 (Pftin) (Predominantly fetal expressed T1 domain)	KCTD12
1605,82	1605,012	1606,618	1605,81	0,008	R.VAVEVEDEEGKFVR.L	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-RN-32)]	LMNA
			1605,96	0,143	K.ALTGHLEEVLAALK.T	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
1606,81	1606,007	1607,614	1606,83	0,016	R.KLEAAEDIAQLSR.S	P35232	PHB_HUMAN	Prohibitin	PHB
			1606,69	0,118	R.SQECYFDEPLYR.S	P11047	LAMC1_HUMAN	Laminin subunit gamma-1 (Laminin B2 chain) (Laminin-1 subunit gamma) (Laminin-10 subunit gamma) (Laminin-11 subunit gamma) (Laminin-2 subunit gamma) (Laminin-3 subunit gamma) (Laminin-4 subunit gamma) (Laminin-6 subunit gamma) (Laminin-7 subunit gamma) (Laminin-8 subunit gamma) (Laminin-9 subunit gamma) (S-laminin subunit gamma) (S-LAM gamma)	LAMC1
			1606,69	0,120	R.MTGSEFDFEEMKR.K	P50395	GDI2_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2

1607,78	1606,974	1608,582	1607,76	0,017	R.DVSELTGFPEMLGGR.V	P31939	PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH [Cleaved into: Bifunctional purine biosynthesis protein PURH, N-terminally processed] [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (ATIC) (IMP synthase) (Inosinase)]	ATIC
			1607,80	0,019	R.LGGPEAGLGEYLFER.L	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
1608,76	1607,955	1609,564	1608,76	0,003	R.YNFPVEVEVPMER.K	P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	PRKDC
			1608,77	0,015	K.QSFTMVADTPENLR.L	Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 (LASP-1) (Metastatic lymph node gene 50 protein) (MLN 50)	LASP1
1608,80	1607,993	1609,602	1608,77	0,023	K.QSFTMVADTPENLR.L	Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 (LASP-1) (Metastatic lymph node gene 50 protein) (MLN 50)	LASP1
			1608,76	0,036	R.YNFPVEVEVPMER.K	P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	PRKDC
1609,80	1608,993	1610,602	1609,80	0,006	R.WFLTQINQPQR.A	P26641	EF1G_HUMAN	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma)	EEF1G
1610,81	1610,009	1611,619	1610,77	0,039	R.VLYAYGYTGEPSK.R	O14880	MGST3_HUMAN	Microsomal glutathione S-transferase 3 (Microsomal GST-3) (Glutathione peroxidase MGST3) (EC 1.11.1.-) (LTC4 synthase MGST3) (EC 4.4.1.20) (Microsomal glutathione S-transferase III) (Microsomal GST-III)	MGST3
			1610,85	0,040	K.YFLVGAGAGICELLK.N	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A1S9) (Ubiquitin-activating enzyme E1)	UBA1
1611,79	1610,985	1612,596	1611,80	0,009	R.NYPATFWVNQPK.I	P07384	CAN1_HUMAN	Calpain-1 catalytic subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase 1) (CANP 1) (Calpain mu-type) (Calpain-1 large subunit) (Cell proliferation-inducing gene 30 protein) (Micromolar-calpain) (muCANP)	CAPN1
			1611,73	0,062	R.SGDSEVYQIGDVSQK.T	Q04837	SSBP_HUMAN	Single-stranded DNA-binding protein, mitochondrial (Mt-SSB) (MtSSB) (PWP1-interacting protein 17)	SSBP1
			1611,68	0,115	R.DRDYSDHPGSGSYR.D	Q96E39	RMXL1_HUMAN	RNA binding motif protein, X-linked-like-1 (Heterogeneous nuclear ribonucleoprotein G-like 1)	RBMXL1
1612,82	1612,010	1613,623	1612,78	0,036	K.LLDNWDSTSTFSK.L	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
1613,82	1613,014	1614,628	1613,80	0,016	K.LQEVEVPEDFGVR.T	O95834	EMAL2_HUMAN	Echinoderm microtubule-associated protein-like 2 (EMAP-2) (HuEMAP-2)	EML2
			1613,78	0,038	R.NALWHTGDTSQVR.L	P49747	COMP_HUMAN	Cartilage oligomeric matrix protein (COMP) (Thrombospondin-5) (TSP5)	COMP
			1613,77	0,052	R.MGPLGLDHMASSIER.M	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			1613,89	0,069	R.ETSGNLEQLLAVVK.S	P08758	ANXA5_HUMAN	Annexin A5 (Anchoring CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
			1613,75	0,071	R.GYAFNHSADFETVR.M	P61160	ARP2_HUMAN	Actin-related protein 2 (Actin-like protein 2)	ACTR2
1614,78	1613,975	1615,590	1614,76	0,026	K.IQALQQQADEADR.A	P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	TPM4
			1614,83	0,048	R.RHVFGSEDELIGQK.V	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP11
			1614,72	0,066	R.IIPGFMCCGGDFTR.H	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
1614,83	1614,025	1615,639	1614,83	0,001	R.RHVFGSEDELIGQK.V	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP11
			1614,76	0,075	K.IQALQQQADEADR.A	P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	TPM4
			1614,72	0,115	R.IIPGFMCCGGDFTR.H	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
1615,82	1615,009	1616,624	1615,81	0,008	R.IMGIPEEEQMGLLR.V	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIA) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIA) (NMMHC II-a) (NMMHC-IIA)	MYH9
			1615,84	0,021	R.AILVDLEPGTMDSVR.S	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
1616,80	1615,993	1617,610	1616,81	0,005	K.SFYPEEVSSMLTK.M	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
			1616,76	0,039	R.WANFHLENSGWQK.I	P13797	PLST_HUMAN	Plastin-3 (T-plastin)	PLS3
1617,77	1616,964	1618,581	1617,77	0,000	R.AVLVDLEPGTMDSVR.S	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1617,69	0,078	R.GTFCSFDPDPSIR.N	P80404	GABT_HUMAN	4-aminobutyrate aminotransferase, mitochondrial (EC 2.6.1.19) ((S)-3-amino-2-methylpropionate transaminase) (EC 2.6.1.22) (GABA aminotransferase) (GABA-AT) (Gamma amino-N-butyrate transaminase) (GABA transaminase) (GABA-T) (L-AIBAT)	ABAT
			1617,94	0,167	R.AAPLQGMPLPGLAPLR.T	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1617,90	1617,089	1618,707	1617,94	0,041	R.AAPLQGMPLPGLAPLR.T	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1617,77	0,126	R.AVLVDLEPGTMDSVR.S	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1617,69	0,204	R.GTFCSFDPDPSIR.N	P80404	GABT_HUMAN	4-aminobutyrate aminotransferase, mitochondrial (EC 2.6.1.19) ((S)-3-amino-2-methylpropionate transaminase) (EC 2.6.1.22) (GABA aminotransferase) (GABA-AT) (Gamma amino-N-butyrate transaminase) (GABA transaminase) (GABA-T) (L-AIBAT)	ABAT
1618,77	1617,957	1619,576	1618,76	0,011	R.TCVDINECLEPR.K	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
1618,89	1618,077	1619,696	1618,76	0,131	R.TCVDINECLEPR.K	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1

1619,77	1618,958	1620,578	1619,79	0,019	R.QWYESHYALPLGR.K	P62241	RS8_HUMAN	40S ribosomal protein S8 (Small ribosomal subunit protein eS8)	RP58
1620,78	1619,968	1621,589	1620,76	0,020	R.GEEGHDPKEPQLR.K	P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3
			1620,81	0,032	K.ISATSIFFESMPYK.V	P34896	GLYC_HUMAN	Serine hydroxymethyltransferase, cytosolic (SHMT) (EC 2.1.2.1) (Glycine hydroxymethyltransferase) (Serine methylase)	SHMT1
			1620,81	0,032	R.ISATSIFFESMPYK.L	P34897	GLYM_HUMAN	Serine hydroxymethyltransferase, mitochondrial (SHMT) (EC 2.1.2.1) (Glycine hydroxymethyltransferase) (Serine methylase)	SHMT2
			1620,84	0,065	R.LHFFMPGFAPLTSR.G	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1620,84	0,065	R.LHFFMPGFAPLTSR.G	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
1621,79	1620,980	1622,602	1621,80	0,009	R.LEEEAATPEGHAVR.F	O15230	LAMA5_HUMAN	Laminin subunit alpha-5 (Laminin-10 subunit alpha) (Laminin-11 subunit alpha) (Laminin-15 subunit alpha)	LAMA5
			1621,76	0,033	R.NPPGFARVEFEDPR.D	P84103	SRSF3_HUMAN	Serine/arginine-rich splicing factor 3 (Pre-mRNA-splicing factor SRP20) (Splicing factor, arginine/serine-rich 3)	SRSF3
1622,80	1621,993	1623,616	1623,81	0,026	R.ELFSNLQEFAGPSGK.L	Q9H8H3	MET7A_HUMAN	Methyltransferase-like protein 7A (EC 2.1.1.-) (Protein AAM-B)	METTL7A
1623,78	1622,973	1624,597	1623,91	0,130	R.LAGTQPLEVLEAVQR.S	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
1624,81	1623,999	1625,624	1624,77	0,042	K.DYGVYLEDSGHTLR.G	Q13162	PRDX4_HUMAN	Peroxisiredoxin-4 (EC 1.11.1.15) (Antioxidant enzyme AOE372) (AOE37-2) (Peroxisiredoxin IV) (Prx-IV) (Thioredoxin peroxidase AO372) (Thioredoxin-dependent peroxide reductase AO372)	PRDX4
			1624,90	0,084	R.TGAIVDPVPGEELLGR.V	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
1625,80	1624,986	1626,612	1625,73	0,065	R.DSLQLDGEFSMDLR.T	P07737	PROF1_HUMAN	Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I)	PFN1
1626,78	1625,968	1627,595	1626,83	0,051	K.TVGIDDLTGEPLIQR.E	Q9UIJ7	KAD3_HUMAN	GTP:AMP phosphotransferase AK3, mitochondrial (EC 2.7.4.10) (Adenylate kinase 3) (AK 3) (Adenylate kinase 3 alpha-like 1)	AK3
1627,78	1626,964	1628,591	1627,76	0,016	K.MGAPESGLAEYLFDK.H	P02794	FRIH_HUMAN	Ferritin heavy chain (Ferritin H subunit) (EC 1.16.3.1) (Cell proliferation-inducing gene 15 protein) [Cleaved into: Ferritin heavy chain, N-terminally processed]	FTH1
1628,78	1627,968	1629,596	1628,76	0,022	R.HTLADNFPNVSEER.G	P20645	MPRD_HUMAN	Cation-dependent mannose-6-phosphate receptor (CD Man-6-P receptor) (CD-MPR) (46 kDa mannose 6-phosphate receptor) (MPR 46)	M6PR
1629,82	1629,002	1630,631	1629,82	0,000	R.FIavgYVDDTQFVR.F	P30493	1B55_HUMAN	HLA class I histocompatibility antigen, B-55 alpha chain (Bw-55) (HLA class I histocompatibility antigen, B-12 alpha chain) (MHC class I antigen B*55)	HLA-B
			1629,82	0,000	R.FIavgYVDDTQFVR.F	P16190	1A33_HUMAN	HLA class I histocompatibility antigen, A-33 alpha chain (Aw-19) (Aw-33) (MHC class I antigen A*33)	HLA-A
			1629,82	0,000	R.FIavgYVDDTQFVR.F	P30508	1C12_HUMAN	HLA class I histocompatibility antigen, Cw-12 alpha chain (MHC class I antigen Cw*12)	HLA-C
			1629,81	0,002	K.LGLVLDAQAEAGVCR.K	Q13938	CAYP1_HUMAN	Calcyphosin (Calcyphosine)	CAP5
			1629,83	0,016	K.EDPQTFYYAVAVVK.K	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1629,79	0,022	R.LQEKEDLQELNDR.L	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
			1629,78	0,038	R.MGPLGLDHMASSIER.M	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			1629,85	0,038	K.VPTFATPWPDFVPR.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1629,86	0,048	R.VDIVPVNLPGEHGQR.L	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anstellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
1630,83	1630,011	1631,642	1630,76	0,062	K.ELTVSNNDINEAGVR.V	P13489	RINI_HUMAN	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor) (Ribonuclease/angiogenin inhibitor 1) (RAI)	RNH1
1631,83	1631,014	1632,646	1631,83	0,001	K.TIAECLADELINAAK.G	P46782	RS5_HUMAN	40S ribosomal protein S5 (Small ribosomal subunit protein uS7) [Cleaved into: 40S ribosomal protein S5, N-terminally processed]	RP55
			1631,83	0,002	R.VDEYLAWQHTTLR.R	P30711	GSTT1_HUMAN	Glutathione S-transferase theta-1 (EC 2.5.1.18) (GST class-theta-1) (Glutathione transferase T1-1)	GSTT1
			1631,83	0,003	R.AILVLEPGTMDSVR.S	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1631,80	0,026	K.SVEDAQDVSLATQR.G	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1632,90	1632,080	1633,713	1632,88	0,016	K.VEADIPGHGQEVJLR.I	P02144	MYG_HUMAN	Myoglobin	MB
			1632,81	0,087	K.NRPTSISWDGLDSGK.L	P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPPp) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1
1633,85	1633,036	1634,670	1633,79	0,063	K.GEMMDLQHGSLFLR.T	P00338	LDHA_HUMAN	L-lactate dehydrogenase A chain (LDH-A) (EC 1.1.1.27) (Cell proliferation-inducing gene 19 protein) (LDH muscle subunit) (LDH-M) (Renal carcinoma antigen NY-REN-59)	LDHA
			1633,95	0,098	R.AAPLQGMPLGLLAPLR.T	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1634,86	1634,043	1635,678	1634,82	0,041	R.LTVEDPVTVEITY.Y	O14818	PSA7_HUMAN	Proteasome subunit alpha type-7 (EC 3.4.25.1) (Proteasome subunit RC6-1) (Proteasome subunit XAPC7)	PSMA7
			1634,78	0,076	K.LGDVYVNDAFGTAHR.A	P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1
			1634,70	0,163	K.HYGYNSYSVSNSEK.D	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
1635,83	1635,015	1636,651	1635,76	0,070	R.IDQYQGADAVGLEEK.I	O43396	TXNL1_HUMAN	Thioredoxin-like protein 1 (32 kDa thioredoxin-related protein)	TXNL1
1636,84	1636,024	1637,661	1636,84	0,001	R.LHFFMPGFAPLTSR.G	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1636,84	0,001	R.LHFFMPGFAPLTSR.G	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1636,70	0,141	K.IIHEDGYSEECR.Q	P04899	GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2 (Adenylate cyclase-inhibiting G alpha protein)	GNAI2
1637,83	1637,010	1638,648							

1638,83	1638,008	1639,647	1639,62	0,796	R.NVYSSRYDDYDR.Y	075494	SRS10_HUMAN	Serine/arginine-rich splicing factor 10 (40 kDa SR-repressor protein) (SRrp40) (FUS-interacting serine-arginine-rich protein 1) (Splicing factor SRp38) (Splicing factor, arginine/serine-rich 13A) (TLS-associated protein with Ser-Arg repeats) (TASR) (TLS-associated protein with SR repeats) (TLS-associated serine-arginine protein) (TLS-associated SR protein)	SRSF10
1639,85	1639,030	1640,670	1639,79 1639,78	0,062 0,069	K.DVFLGMFLYEYAR.R R.AHQVVEDGYEFAK.R	P02768 P62140	ALBU_HUMAN PP1B_HUMAN	Serum albumin Serine/threonine-protein phosphatase PP1-beta catalytic subunit (PP-1B) (PPP1CD) (EC 3.1.3.16) (EC 3.1.3.53)	ALB PPP1CB
			1639,94 1639,67	0,090 0,178	K.KVPQVSTPTLVEVSR.N K.ASADLMSYCEEHAR.S	P02768 Q9UBI6	ALBU_HUMAN GBG12_HUMAN	Serum albumin Guanine nucleotide-binding protein G(i)/G(s)/G(o) subunit gamma-12	ALB GNG12
			1639,62	0,226	R.NVYSSRYDDYDR.Y	075494	SRS10_HUMAN	Serine/arginine-rich splicing factor 10 (40 kDa SR-repressor protein) (SRrp40) (FUS-interacting serine-arginine-rich protein 1) (Splicing factor SRp38) (Splicing factor, arginine/serine-rich 13A) (TLS-associated protein with Ser-Arg repeats) (TASR) (TLS-associated protein with SR repeats) (TLS-associated serine-arginine protein) (TLS-associated SR protein)	SRSF10
1640,88	1640,055	1641,696	1641,68	0,803	K.DSMIWDOCTCIGAGR.G	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
1641,83	1641,004	1642,646	1641,77	0,056	K.AGDFLEANYMNLQR.S	P01024	CO3_HUMAN	Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
			1641,72 1641,68	0,109 0,148	R.DSLQLQGEFSMDLR.T K.DSMIWDOCTCIGAGR.G	P07737 P02751	PROF1_HUMAN FINC_HUMAN	Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I) Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	PFN1 FN1
1642,81	1641,992	1643,635	1642,76	0,051	K.DPVQEAWAEDVDLR.V	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
			1642,76	0,051	K.RTPMCAHCNQVIR.G	Q96HC4	PDLIS_HUMAN	PDZ and LIM domain protein 5 (Enigma homolog) (Enigma-like PDZ and LIM domains protein)	PDLIM5
			1642,71	0,100	R.ADPEAAWEPTAEAR.A	Q9UBT2	SAE2_HUMAN	SUMO-activating enzyme subunit 2 (EC 2.3.2.-) (Anthracycline-associated resistance ARX) (Ubiquitin-like 1-activating enzyme E1B) (Ubiquitin-like modifier-activating enzyme 2)	UBA2
1643,81	1642,984	1644,628	1643,82	0,010	K.SFLVWVNEEDHLR.V	P06732	KCRM_HUMAN	Creatine kinase M-type (EC 2.7.3.2) (Creatine kinase M chain) (Creatine phosphokinase M-type) (CPK-M) (M-CK)	CKM
			1643,78	0,028	K.NVTELEPLSNEER.N	P61981	1433G_HUMAN	14-3-3 protein gamma (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein gamma, N-terminally processed]	YWHA3
1644,83	1644,005	1645,650	1644,69	0,136	K.GADIMYTGTVDCWR.K	P12235	ADT1_HUMAN	ADP/ATP translocase 1 (ADP,ATP carrier protein 1) (ADP,ATP carrier protein, heart/skeletal muscle isoform T1) (Adenine nucleotide translocator 1) (ANT 1) (Solute carrier family 25 member 4)	SLC25A4
			1644,69	0,136	K.GADIMYTGTVDCWR.K	P12236	ADT3_HUMAN	ADP/ATP translocase 3 (ADP,ATP carrier protein 3) (ADP,ATP carrier protein, isoform T2) (ANT 2) (Adenine nucleotide translocator 3) (ANT 3) (Solute carrier family 25 member 6) [Cleaved into: ADP/ATP translocase 3, N-terminally processed]	SLC25A6
1645,77	1644,947	1646,592	1645,80	0,029	K.IFINNEWHDSVSGK.K	P00352	AL1A1_HUMAN	Retinal dehydrogenase 1 (RALDH 1) (RaldH1) (EC 1.2.1.-) (EC 1.2.1.36) (ALDH-E1) (ALDH1I) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic)	ALDH1A1
			1645,66	0,105	K.GEDFYCVTCHETK.F	Q13642	FHL1_HUMAN	Four and a half LIM domains protein 1 (FHL-1) (Skeletal muscle LIM-protein 1) (SLIM) (SLIM-1)	FHL1
1645,85	1645,027	1646,673	1645,80	0,052	K.IFINNEWHDSVSGK.K	P00352	AL1A1_HUMAN	Retinal dehydrogenase 1 (RALDH 1) (RaldH1) (EC 1.2.1.-) (EC 1.2.1.36) (ALDH-E1) (ALDH1I) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic)	ALDH1A1
			1645,66	0,185	K.GEDFYCVTCHETK.F	Q13642	FHL1_HUMAN	Four and a half LIM domains protein 1 (FHL-1) (Skeletal muscle LIM-protein 1) (SLIM) (SLIM-1)	FHL1
1646,82	1645,992	1647,639	1646,82	0,001	R.DVWGIEGPIDAAFTR.I	P04004	VTNC_HUMAN	Vitronectin (VN) (S-protein) (Serum-spreading factor) (V75) [Cleaved into: Vitronectin V65 subunit; Vitronectin V10 subunit; Somatomedin-B]	VTN
			1646,75	0,064	K.DEVLVFPDSFCR.S	Q14108	SCRB2_HUMAN	Lysosome membrane protein 2 (85 kDa lysosomal membrane sialoglycoprotein) (LGP85) (CD36 antigen-like 2) (Lysosome membrane protein II) (LIMP II) (Scavenger receptor class B member 2) (CD antigen CD36)	SCARB2
1647,86	1647,035	1648,682	1647,81 1647,73	0,045 0,127	R.LVTMQIWDTAGQER.F R.FGDRFPAMSDAYDR.T	P51149 P00491	RAB7A_HUMAN PNPH_HUMAN	Ras-related protein Rab-7a Purine nucleoside phosphorylase (PNP) (EC 2.4.2.1) (Inosine phosphorylase) (Inosine-guanosine phosphorylase)	RAB7A PNP
1648,83 1649,82	1648,009 1648,994	1649,658 1650,644	1649,79	0,030	K.GEMMDLQHGSFLR.T	P00338	LDHA_HUMAN	L-lactate dehydrogenase A chain (LDH-A) (EC 1.1.1.27) (Cell proliferation-inducing gene 19 protein) (LDH muscle subunit) (LDH-M) (Renal carcinoma antigen NY-RN-59)	LDHA
1650,83	1650,008	1651,659	1650,78 1650,89	0,053 0,055	R.STYNHLSSWLTAR.N R.LVLEVAQHLGESTVR.T	P61106 P06576	RAB14_HUMAN ATPB_HUMAN	Ras-related protein Rab-14 ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP ATP5F1B synthase F1 subunit beta)	RAB14 ATP5F1B
			1650,77	0,066	K.VPDYWPYQDLQAR.A	P30711	GSTT1_HUMAN	Glutathione S-transferase theta-1 (EC 2.5.1.18) (GST class-theta-1) (Glutathione transferase T1-1)	GSTT1
			1650,98	0,148	K.SALSGHLETIVLLGK.T	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2

1651,77	1650,946	1652,598	1651,77	0,000	R.SSFDEMLPGTHFQR.V	Q02218	ODO1_HUMAN	2-oxoglutarate dehydrogenase, mitochondrial (EC 1.2.4.2) (2-oxoglutarate dehydrogenase complex component E1) (OGDC-E1) (Alpha-ketoglutarate dehydrogenase)	OGDH
			1651,78	0,007	K.LLCQLCGFGSGHFR.C	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			1651,79	0,016	R.TVPFCSTFAAFFTR.A	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
			1650,98	0,791	K.SALSGHLETVILGLLK.T	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
1651,86	1651,037	1652,689	1651,79	0,074	R.TVPFCSTFAAFFTR.A	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
			1651,78	0,083	K.LLCQLCGFGSGHFR.C	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			1651,77	0,090	R.SSFDEMLPGTHFQR.V	Q02218	ODO1_HUMAN	2-oxoglutarate dehydrogenase, mitochondrial (EC 1.2.4.2) (2-oxoglutarate dehydrogenase complex component E1) (OGDC-E1) (Alpha-ketoglutarate dehydrogenase)	OGDH
			1652,67	0,810	K.SGEHDFGAADFQDGDOR.N	P36871	PGM1_HUMAN	Phosphoglucomutase-1 (PGM 1) (EC 5.4.2.2) (Glucose phosphomutase 1)	PGM1
1652,84	1652,010	1653,663	1652,76	0,079	K.IFRDGEAGAYDGPR.T	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	
			1652,67	0,164	K.SGEHDFGAADFQDGDOR.N	P36871	PGM1_HUMAN	Phosphoglucomutase-1 (PGM 1) (EC 5.4.2.2) (Glucose phosphomutase 1)	PGM1
1653,83	1652,998	1654,652	1653,84	0,014	R.DISEASVFDAYVLPK.L	P62854	RS26_HUMAN	40S ribosomal protein S26 (Small ribosomal subunit protein eS26)	RPS26
1654,84	1654,014	1655,669	1654,90	0,063	K.GVVTIEQIVDTLPDR.G	P09917	LOX5_HUMAN	Arachidonate 5-lipoxygenase (5-LO) (5-lipoxygenase) (EC 1.13.11.34)	ALOX5
1655,80	1654,968	1656,624							
1656,82	1655,987	1657,644							
1657,82	1656,995	1658,653	1657,74	0,086	K.QNCELFEQLGEYK.F	P02768	ALBU_HUMAN	Serum albumin	ALB
1658,82	1657,995	1659,654							
1659,81	1658,978	1660,638	1659,83	0,022	R.DVVICPDASLEDAKK.E	Q99497	PARK7_HUMAN	Protein/nucleic acid deglycase DJ-1 (EC 3.1.2.-) (EC 3.5.1.-) (EC 3.5.1.124) (Maillard deglycase) (Oncogene DJ1) (Parkinson disease protein 7) (Parkinsonism-associated deglycase) (Protein DJ-1) (DJ-1)	PARK7
			1659,89	0,086	R.ALTVPCLTQQVFDAAK.N	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
1660,83	1659,999	1661,660	1660,82	0,010	K.ICGDIGHQYTDLLR.L	P62140	PP1B_HUMAN	Serine/threonine-protein phosphatase PP1-beta catalytic subunit (PP-1B) (PPP1CD) (EC 3.1.3.16) (EC 3.1.3.53)	PPP1CB
			1660,81	0,018	R.EVWFFGLQYQDTK.G	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			1660,80	0,033	R.VLNSYVWGEDSTYK.F	P61313	RL15_HUMAN	60S ribosomal protein L15 (Large ribosomal subunit protein eL15)	RPL15
			1660,78	0,048	K.EHAVEGDCDFQLLK.L	P02765	FETUA_HUMAN	Alpha-2-HS-glycoprotein (Alpha-2-Z-globulin) (Ba-alpha-2-glycoprotein) (Fetuin-A) [Cleaved into: Alpha-2-HS-glycoprotein chain A; Alpha-2-HS-glycoprotein chain B]	AHSG
1661,85	1661,015	1662,677	1661,83	0,021	K.KVEEAPEEFVVEK.V	Q13185	CBX3_HUMAN	Chromobox protein homolog 3 (HECH) (Heterochromatin protein 1 homolog gamma) (HP1 gamma) (Modifier 2 protein)	CBX3
			1661,82	0,027	R.HLDHVAALFPGDVDR.L	P11216	PYGB_HUMAN	Glycogen phosphorylase, brain form (EC 2.4.1.1)	PYGB
			1661,81	0,036	K.GAGTDEGCLIEILAS.T	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedin) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4
			1661,81	0,038	K.VESTDVSDDLHQYR.E	P28062	PSB8_HUMAN	Proteasome subunit beta type-8 (EC 3.4.25.1) (Low molecular mass protein 7) (Macropain subunit C13) (Multicatalytic endopeptidase complex subunit C13) (Proteasome component C13) (Proteasome subunit beta-5i) (Really interesting new gene 10 protein)	PSMB8
1662,84	1662,012	1663,675	1662,89	0,042	R.IVEPYIAWGPYNLK.S	P18124	RL7_HUMAN	60S ribosomal protein L7 (Large ribosomal subunit protein uL30)	RPL7
1663,75	1662,921	1664,585	1663,82	0,070	R.QDLGSPGIAVDHLGR.N	P14543	NID1_HUMAN	Nidogen-1 (NID-1) (Entactin)	NID1
1663,86	1663,029	1664,692	1663,82	0,038	R.QDLGSPGIAVDHLGR.N	P14543	NID1_HUMAN	Nidogen-1 (NID-1) (Entactin)	NID1
1664,81	1663,975	1665,640	1664,84	0,027	R.DHINLPFGSGQNPLR.G	P00491	PNPH_HUMAN	Purine nucleoside phosphorylase (PNP) (EC 2.4.2.1) (Inosine phosphorylase) (Inosine-guanosine phosphorylase)	PNP
			1664,85	0,040	R.DGLLPENTFIVGYAR.S	P11413	G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	G6PD
			1664,74	0,068	K.MDATANDVPSPYEVR.G	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	
1665,82	1664,984	1666,650	1665,82	0,001	R.YEDFSNLGTHLLR.L	P22695	QCR2_HUMAN	Cytochrome b-c1 complex subunit 2, mitochondrial (Complex III subunit 2) (Core protein II) (Ubiquinol-cytochrome-c reductase complex core protein 2)	UQCRC2
			1665,81	0,011	R.FDEILEASDGMVAR.G	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
1666,83	1665,992	1667,659	1666,80	0,030	R.DWHGVPGQVDAAMAGR.I	P04004	VTNC_HUMAN	Vitronectin (VN) (S-protein) (Serum-spreading factor) (V75) [Cleaved into: Vitronectin V65 subunit; Vitronectin V10 subunit; Somatomedin-B]	VTN
			1666,86	0,035	K.SETSGSFEDALLAIVK.C	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedin) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4
			1666,86	0,035	R.RQTGQAYIAILLNR.G	P24043	LAMA2_HUMAN	Laminin subunit alpha-2 (Laminin M chain) (Laminin-12 subunit alpha) (Laminin-2 subunit alpha) (Laminin-4 subunit alpha) (Merosin heavy chain)	LAMA2

			1666,79	0,035	R.LYQTDPSGTYHAWK.A	Q14818	PSA7_HUMAN	Proteasome subunit alpha type-7 (EC 3.4.25.1) (Proteasome subunit RC6-1) (Proteasome subunit XAPC7)	PSMA7
1667,82	1666,990	1668,658	1667,82	0,001	R.FLYFSNWLHGDLR.Q	Q13228	SBP1_HUMAN	Methanethiol oxidase (MTO) (EC 1.8.3.4) (56 kDa selenium-binding protein) (SBP56) (SP56) (Selenium-binding protein 1)	SELENBP1
			1667,78	0,049	R.NVQAEMVFSSGLK.G	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
			1667,77	0,055	R.WVVGIDENYEGSSR.E	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
			1667,76	0,067	R.SSFDEMLPGTHFQR.V	Q02218	ODO1_HUMAN	2-oxoglutarate dehydrogenase, mitochondrial (EC 1.2.4.2) (2-oxoglutarate dehydrogenase complex component E1) (OGDC-E1) (Alpha-ketoglutarate dehydrogenase)	OGDH
			1667,71	0,119	R.SANAEDAQEFSDVER.A	Q9HCY8	S10AE_HUMAN	Protein S100-A14 (S100 calcium-binding protein A14) (S114)	S100A14
1668,80	1667,967	1669,635	1668,85	0,046	R.ETNLDLSPLVDTHSK.R	P08670	VIME_HUMAN	Vimentin	VIM
			1668,87	0,070	K.SLEYLDLSFNQIAR.L	P51884	LUM_HUMAN	Lumican (Keratan sulfate proteoglycan lumican) (KSPG lumican)	LUM
			1668,72	0,076	R.YYWGGQYTWDMAK.H	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
1669,85	1669,012	1670,682	1669,82	0,032	R.SIAQYWLGCPAPGHL.-	P04004	VTNC_HUMAN	Vitronectin (VN) (S-protein) (Serum-spreading factor) (V75) [Cleaved into: Vitronectin V65 subunit; Vitronectin V10 subunit; Somatomedin-B]	VTN
			1669,89	0,040	K.VLGAFSGLAHLNLK.G	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
			1669,89	0,040	K.VLGAFSGLAHLNLK.G	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
1670,79	1669,957	1671,627							
1671,81	1670,969	1672,641							
1672,81	1671,976	1673,649							
1673,84	1673,001	1674,675	1673,87	0,035	K.GAGTNEDALIELTTR.T	P12429	ANXA3_HUMAN	Annexin A3 (35-alpha calcimedin) (Annexin III) (Annexin-3) (Inositol 1,2-cyclic phosphate 2-phosphohydrolase) (Lipocortin III) (Placental anticoagulant protein III) (PAP-III)	ANXA3
1674,85	1674,011	1675,685	1674,78	0,069	R.DYSHYYTIQDLR.D	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1674,68	0,171	K.SQNKPEDEADEWAR.R	O75112	LDB3_HUMAN	LIM domain-binding protein 3 (Protein cypher) (Z-band alternatively spliced PDZ-motif protein)	LDB3
1675,83	1674,995	1676,671	1675,83	0,002	R.FSSETWQNLGLTHR.L	Q96IU4	ABHEB_HUMAN	Protein ABHD14B (EC 3.-.-.-) (Alpha/beta hydrolase domain-containing protein 14B) (Abhydrolase domain-containing protein 14B) (CCG1-interacting factor B)	ABHD14B
			1675,83	0,004	K.FSLVGIGGQDLNEGMR.T	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
			1675,84	0,012	K.FSHEEIAMATVTLR.R	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
			1675,82	0,013	K.GAEEMETVIPVDVMR.R	Q99497	PARK7_HUMAN	Protein/nucleic acid deglycase DJ-1 (EC 3.1.2.-) (EC 3.5.1.-) (EC 3.5.1.124) (Maillard deglycase) (Oncogene DJ1) (Parkinson disease protein 7) (Parkinsonism-associated deglycase) (Protein DJ-1) (DJ-1)	PARK7
			1675,72	0,118	K.ATAGDTHLGGEDFDNR.L	P0DMV8	H571A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
1676,84	1675,998	1677,675	1676,77	0,070	K.VAKPVVMDEGDMETR.I	P48735	IDHP_HUMAN	Isocitrate dehydrogenase [NADP], mitochondrial (IDH) (EC 1.1.1.42) (ICD-M) (IDP) (NADP(+)-specific IDH) (Oxalosuccinate decarboxylase)	IDH2
			1676,74	0,094	K.KFEEEGNPYYSSAR.V	Q9HCC0	MCCB_HUMAN	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial (MCCase subunit beta) (EC 6.4.1.4) (3-methylcrotonyl-CoA carboxylase 2) (3-methylcrotonyl-CoA carboxylase non-biotin-containing subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase subunit beta)	MCCC2
1677,82	1676,983	1678,660	1677,81	0,016	K.NQLTSPNPTVFDAR.K	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP, EC 3.6.4.10 (78 kDa glucose-regulated protein, GRP-78) (Binding-immunoglobulin protein, BiP) (Heat shock protein 70 family protein 5, HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			1677,80	0,025	K.FNWYVDGVEVHNAK.T	P01857	IGHG1_HUMAN	Immunoglobulin heavy constant gamma 1 (Ig gamma-1 chain C region) (Ig gamma-1 chain C region EU) (Ig gamma-1 chain C region KOL) (Ig gamma-1 chain C region NIE)	IGHG1
			1677,90	0,076	M.VLLESEQFLTETLR.L	P37108	SRP14_HUMAN	Signal recognition particle 14 kDa protein (SRP14) (18 kDa Alu RNA-binding protein)	SRP14
1678,85	1678,009	1679,688	1678,82	0,031	K.QMEQISQFLQAAER.Y	P37802	TAGL2_HUMAN	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	TAGLN2
			1678,80	0,051	K.EIFEQSPVSVNTMR.G	Q06210	GFPT1_HUMAN	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 (EC 2.6.1.16) (D-fructose-6-phosphate amidotransferase 1) (Glutamine:fructose-6-phosphate amidotransferase 1) (GFAT 1) (GFAT1) (Hexosephosphate aminotransferase 1)	GFPT1
			1678,92	0,067	R.KGTDVNVFNITLTTR.S	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-inhibitory protein) (p35)	ANXA1
1679,83	1678,991	1680,671							
1680,76	1679,919	1681,600							
1680,89	1680,048	1681,728							
1681,83	1680,986	1682,668	1681,79	0,038	K.TTGFGMIDSLDYAK.K	P62847	RS24_HUMAN	40S ribosomal protein S24 (Small ribosomal subunit protein eS24)	RPS24
1682,78	1681,937	1683,620	1682,88	0,104	K.IVLEDGTLHVTGSGR.Y	Q16555	DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) (Unc-33-like phosphoprotein 2) (ULIP-2)	DPYSL2
			1682,96	0,178	K.IHLISTQSAIPYALR.V	P02679	FIBG_HUMAN	Fibrinogen gamma chain	FGG
1682,91	1682,065	1683,748	1682,88	0,025	K.IVLEDGTLHVTGSGR.Y	Q16555	DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) (Unc-33-like phosphoprotein 2) (ULIP-2)	DPYSL2
			1682,96	0,049	K.IHLISTQSAIPYALR.V	P02679	FIBG_HUMAN	Fibrinogen gamma chain	FGG
1683,85	1683,012	1684,696	1683,91	0,056	R.ALFPWNEEIVPQIK.E	P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG-dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	PGAM1

1684,84	1684,002	1685,686	1684,86	0,012	K.KYPYPWHPQPIENL-	075947	ATP5H_HUMAN	ATP synthase subunit d, mitochondrial (ATPase subunit d)	ATP5PD
			1684,90	0,056	R.AAVEEGVLGGGCALLR.C	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
			1684,76	0,079	K.HTGPNSPDTANDGFVR.L	P31943	HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H (hnRNP H) [Cleaved into: Heterogeneous nuclear ribonucleoprotein H, N-terminally processed]	HNRNPH1
			1684,76	0,079	K.HTGPNSPDTANDGFVR.L	P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 (hnRNP H2) (FTP-3) (Heterogeneous nuclear ribonucleoprotein H') (hnRNP H') [Cleaved into: Heterogeneous nuclear ribonucleoprotein H2, N-terminally processed]	HNRNPH2
1685,84	1685,001	1686,687	1685,85	0,009	K.HSGNITFDEIVNIAR.Q	P30050	RL12_HUMAN	60S ribosomal protein L12 (Large ribosomal subunit protein uL11)	RPL12
			1685,74	0,101	K.SLYHDISGDTSGDYR.K	P50995	ANX11_HUMAN	Annexin A11 (56 kDa autoantigen) (Annexin XI) (Annexin-11) (Calcyclin-associated annexin 50) (CAP-50)	ANXA11
1686,83	1685,982	1687,669	1686,80	0,023	R.QNLFQEAEEFLYR.F	Q9UL46	PSME2_HUMAN	Proteasome activator complex subunit 2 (11S regulator complex subunit beta) (REG-beta) (Activator of multicatalytic protease subunit 2) (Proteasome activator 28 subunit beta) (PA28b) (PA28beta)	PSME2
			1686,87	0,049	K.TYNLPFLVSTQK.T	P30740	ILEU_HUMAN	Leukocyte elastase inhibitor (LEI) (Monocyte/neutrophil elastase inhibitor) (EI) (M/NEI) (Peptidase inhibitor 2) (PI-2) (Serpine B1)	SERPINB1
			1686,96	0,139	K.LPDGSEIPLPILLGR.L	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
1687,84	1686,995	1688,683	1687,89	0,056	R.IINEPTAAAIYGLDR.T	P0DMV8	HS71A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
1688,84	1687,995	1689,684	1688,82	0,017	R.VEVERDNLAEDIMR.L	P08670	VIME_HUMAN	Vimentin	VIM
			1688,86	0,020	R.QVLLSEPEEAALYR.G	P13798	ACPH_HUMAN	Acylamino-acid-releasing enzyme (AARE) (EC 3.4.19.1) (Acyl-peptide hydrolase) (APH) (Acylaminoacyl-peptidase) (Oxidized protein hydrolase) (OPH)	APEH
			1688,74	0,104	K.GTDIMYGTGLDCWR.K	P05141	ADT2_HUMAN	ADP/ATP translocase 2 (ADP,ATP carrier protein 2) (ADP,ATP carrier protein, fibroblast isoform) (Adenine nucleotide translocator 2) (ANT 2) (Solute carrier family 25 member 5) [Cleaved into: ADP/ATP translocase 2, N-terminally processed]	SLC25A5
1689,86	1689,017	1690,707	1690,81	0,018	K.DGEAGAQGPFGPAGPAGER.G	P02452	CO1A1_HUMAN	Collagen alpha-1(I) chain (Alpha-1 type I collagen)	COL1A1
1690,83	1689,984	1691,675	1690,85	0,019	K.GFGTDEQAIVDVVANR.S	P20073	ANXA7_HUMAN	Annexin A7 (Annexin VII) (Annexin-7) (Synexin)	ANXA7
			1690,72	0,106	K.VSYGIGDEEHQDEGR.V	P27695	APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase (EC 3.1.1.-) (EC 4.2.99.18) (APEX nuclease) (APEN) (Apurinic-apyrimidinic endonuclease 1) (AP endonuclease 1) (APE-1) (REF-1) (Redox factor-1) [Cleaved into: DNA-(apurinic or apyrimidinic site) lyase, mitochondrial]	APEX1
1691,85	1690,999	1692,691	1691,86	0,017	R.ALTVPQLTQQMFDK.N	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1691,83	0,020	K.GAEEMETVIPVDVVMR.R	Q99497	PARK7_HUMAN	Protein/nucleic acid deglycase DJ-1 (EC 3.1.2.-) (EC 3.5.1.-) (EC 3.5.1.124) (Maillard deglycase) (Oncogene DJ1) (Parkinson disease protein 7) (Parkinsonism-associated deglycase) (Protein DJ-1) (DJ-1)	PARK7
			1691,82	0,025	R.SNEFDPSYVGLAHK.L	P05107	ITB2_HUMAN	Integrin beta-2 (Cell surface adhesion glycoproteins LFA-1/CR3/p150,95 subunit beta) (Complement receptor C3 subunit beta) (CD antigen CD18)	ITGB2
			1691,88	0,036	K.ELLQTSLGSLDAQK.D	P23297	S10A1_HUMAN	Protein S100-A1 (S-100 protein alpha chain) (S-100 protein subunit alpha) (S100 calcium-binding protein A1)	S100A1
			1691,73	0,112	K.STAGDTHLGGEDFDNR.M	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
			1692,67	0,823	K.AMDSDFWFAENYMGR.K	P55084	ECHB_HUMAN	Trifunctional enzyme subunit beta, mitochondrial (TP-beta) [Includes: 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase)]	HADHB
1692,39	1691,541	1693,233	1692,67	0,281	K.AMDSDFWFAENYMGR.K	P55084	ECHB_HUMAN	Trifunctional enzyme subunit beta, mitochondrial (TP-beta) [Includes: 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase)]	HADHB
			1692,88	0,490	K.GLGTDEDAISVLAYR.N	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedin) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4
			1691,88	0,505	K.ELLQTSLGFLDAQK.D	P23297	S10A1_HUMAN	Protein S100-A1 (S-100 protein alpha chain) (S-100 protein subunit alpha) (S100 calcium-binding protein A1)	S100A1
			1691,86	0,525	R.ALTVPQLTQQMFDK.N	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1691,83	0,562	K.GAEEMETVIPVDVVMR.R	Q99497	PARK7_HUMAN	Protein/nucleic acid deglycase DJ-1 (EC 3.1.2.-) (EC 3.5.1.-) (EC 3.5.1.124) (Maillard deglycase) (Oncogene DJ1) (Parkinson disease protein 7) (Parkinsonism-associated deglycase) (Protein DJ-1) (DJ-1)	PARK7
			1691,82	0,566	R.SNEFDPSYVGLAHK.L	P05107	ITB2_HUMAN	Integrin beta-2 (Cell surface adhesion glycoproteins LFA-1/CR3/p150,95 subunit beta) (Complement receptor C3 subunit beta) (CD antigen CD18)	ITGB2
1692,85	1692,001	1693,694	1691,73	0,653	K.STAGDTHLGGEDFDNR.M	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
			1692,88	0,030	K.GLGTDEDAISVLAYR.N	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedin) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4
			1692,67	0,179	K.AMDSDFWFAENYMGR.K	P55084	ECHB_HUMAN	Trifunctional enzyme subunit beta, mitochondrial (TP-beta) [Includes: 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase)]	HADHB
			1693,86	0,393	K.GLAPDLPEDLYHLIK.K	P62277	RS13_HUMAN	40S ribosomal protein S13 (Small ribosomal subunit protein uS15)	RPS13
			1692,88	0,590	K.GLGTDEDAISVLAYR.N	P09525	ANXA4_HUMAN	Annexin A4 (35-beta calcimedin) (Annexin IV) (Annexin-4) (Carbohydrate-binding protein p33/p41) (Chromobindin-4) (Endonexin I) (Lipocortin IV) (P32.5) (PP4-X) (Placental anticoagulant protein II) (PAP-II) (Protein II)	ANXA4

			1692,67	0,799	K.AMDSDWFAENYMG.R.K	P55084	ECHB_HUMAN	Trifunctional enzyme subunit beta, mitochondrial (TP-beta) [Includes: 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase)]	HADHB
1693,85	1693,007	1694,701	1693,86	0,006	K.GLAPDLPEDLYHLIK.K	P62277	RS13_HUMAN	40S ribosomal protein S13 (Small ribosomal subunit protein uS15)	RPS13
1694,85	1694,000	1695,694	1695,76	0,062	R.GFGFVTDDHDPVDK.I	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
1695,83	1694,979	1696,675		0,070	R.FAQGSGFEYAMR.W	Q15233	NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrb)) (p54nrb)	NONO
			1695,75	0,073	K.ISGGSVVEMQGDEMTR.I	O75874	IDHC_HUMAN	Isocitrate dehydrogenase [NADP] cytoplasmic (IDH) (EC 1.1.1.42) (Cytosolic NADP-isocitrate dehydrogenase) (IDP) (NADP(+)-specific ICDH) (Oxalosuccinate decarboxylase)	IDH1
1696,84	1695,993	1697,690	1696,84	0,004	K.NSSYFVEWIPNNVK.T	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1696,84	0,004	K.NSSYFVEWIPNNVK.T	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1696,85	0,005	K.NFPNAIEHTLQWAR.D	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
			1696,83	0,013	R.KLEVEANNAFDQYR.D	P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta (CapZ beta)	CAPZB
			1696,78	0,063	K.VHTGTGGQYVDKDYR.R	O75380	NDUS6_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial (Complex I-13kD-A) (CI-13kD-A) (NADH-ubiquinone oxidoreductase 13 kDa-A subunit)	NDUF56
			1696,71	0,135	R.GSNMDFREPTTEER.A	Q15056	IF4H_HUMAN	Eukaryotic translation initiation factor 4H (eIF-4H) (Williams-Beuren syndrome chromosomal region 1 protein)	EIF4H
1697,84	1696,993	1698,691	1697,82	0,025	K.AFVDFLSDEIKER.K	Q07021	C1QBP_HUMAN	Complement component 1 Q subcomponent-binding protein, mitochondrial (ASF/SF2-associated protein p32) (Glycoprotein gC1qBP) (C1qBP) (Hyaluronan-binding protein 1) (Mitochondrial matrix protein p32) (gC1q-R protein) (p33) (SF2AP32)	C1QBP
			1697,81	0,035	K.IPEGERVDFDDIHR.K	P13805	TNNT1_HUMAN	Troponin T, slow skeletal muscle (TnTs) (Slow skeletal muscle troponin T) (sTnT)	TNNT1
			1697,76	0,081	R.GYFIEENKYSR.A	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
			1697,74	0,101	K.IDAAEEKYMEVR.V	P48788	TNNI2_HUMAN	Troponin I, fast skeletal muscle (Troponin I, fast-twitch isoform)	TNNI2
1698,83	1697,983	1699,682	1698,82	0,017	K.LDHPPEWFVNNK.V	P61457	PHS_HUMAN	Pterin-4-alpha-carbinolamine dehydratase (PHS) (EC 4.2.1.96) (4-alpha-hydroxy-tetrahydropterin dehydratase) (Dimerization cofactor of hepatocyte nuclear factor 1-alpha) (Dimerization cofactor of HNF1) (Phenylalanine hydroxylase-stimulating protein) (Pterin carbinolamine dehydratase) (PCD)	PCBD1
			1698,86	0,026	R.EAVTEILGIEPDREK.G	Q15631	TSN_HUMAN	Translin (EC 3.1.-.-) (Component 3 of promoter of RISC) (C3PO)	TSN
			1698,86	0,028	K.THVADFAPEVAWVTR.S	P07814	SYEP_HUMAN	Bifunctional glutamate/proline--tRNA ligase (Bifunctional aminoacyl-tRNA synthetase) (Cell proliferation-inducing gene 32 protein) (Glutamyl-prolyl-tRNA synthetase) [Includes: Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase) (GluRS); Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)]	EPRS
			1698,87	0,040	R.FTPGTFTNQIAAFR.E	P08865	RSSA_HUMAN	40S ribosomal protein SA (37 kDa laminin receptor precursor) (37LRP) (37/67 kDa laminin receptor) (LRP/LR) (67 kDa laminin receptor) (67LR) (Colon carcinoma laminin-binding protein) (Laminin receptor 1) (LamR) (Laminin-binding protein precursor p40) (LBP/p40) (Multidrug resistance-associated protein MGR1-Ag) (NEM/1CHD4) (Small ribosomal subunit protein uS2)	RPSA
1699,86	1699,011	1700,711	1699,83	0,029	K.DVPAVEITHTFWER.N	P21397	AOFA_HUMAN	Amine oxidase [flavin-containing] A (EC 1.4.3.4)	MAOA
			1699,75	0,110	R.GFAFVTDDHSDVDK.I	Q32P51	RA1L2_HUMAN	Heterogeneous nuclear ribonucleoprotein A1-like 2 (hnRNP A1-like 2) (hnRNP core protein A1-like 2)	HNRNPAL12
1700,85	1699,998	1701,698	1700,84	0,008	R.EGVTVTFAPTNEAFR.A	Q15582	BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3 (Beta ig-h3) (Kerato-epithelin) (RGD-containing collagen-associated protein) (RGD-CAP)	TGFB1
			1700,79	0,055	K.TPKDESANQEEPEAR.V	P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP)	VASP
			1700,76	0,086	K.HGYGEFIEDHRA.R	P62244	RS15A_HUMAN	40S ribosomal protein S15a (Small ribosomal subunit protein uS8)	RPS15A
			1700,76	0,092	K.FNADEFEDMVAEKR.L	P27635	RL10_HUMAN	60S ribosomal protein L10 (Laminin receptor homolog) (Large ribosomal subunit protein uL16) (Protein QM) (Ribosomal protein L10) (Tumor suppressor QM)	RPL10
1701,72	1700,866	1702,568	1701,89	0,175	R.AVFVDLEPTVIDEVR.T	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			1701,89	0,175	R.AVFVDLEPTVIDEVR.T	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
1701,89	1701,042	1702,744	1701,89	0,001	R.AVFVDLEPTVIDEVR.T	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			1701,89	0,001	R.AVFVDLEPTVIDEVR.T	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			1702,67	0,774	K.ESDQGGAYTCEAMNAR.G	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
1702,73	1701,874	1703,577	1702,67	0,058	K.ESDQGGAYTCEAMNAR.G	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
			1702,80	0,078	K.KPAEDEWGTPTDAMK.A	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
			1702,88	0,153	R.VLDMPTQGLGPAAYR.K	Q9NP81	SYSM_HUMAN	Serine--tRNA ligase, mitochondrial (EC 6.1.1.11) (SerRSmt) (Seryl-tRNA synthetase) (SerRS) (Seryl-tRNA(Ser/Sec) synthetase)	SARS2
			1702,89	0,166	K.GLGTDEDTLIEILASR.T	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1

1702,89	1702,035	1703,737	1702,89	0,169	K.AAGVNVFPFWPGLFAK.A	P05386	RLA1_HUMAN	60S acidic ribosomal protein P1 (Large ribosomal subunit protein P1)	RPLP1
			1701,89	0,833	R.AVFVDLEPTVIDEVR.T	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			1701,89	0,833	R.AVFVDLEPTVIDEVR.T	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			1702,89	0,005	K.GLTGDEDTLIEIASR.T	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
			1702,88	0,008	R.VLDMPTQELGLPAYR.K	Q9NP81	SYSM_HUMAN	Serine--tRNA ligase, mitochondrial (EC 6.1.1.11) (SerRSmt) (Seryl-tRNA synthetase) (SerRS) (Seryl-tRNA(Ser/Sec) synthetase)	SARS2
			1702,89	0,008	K.AAGVNVFPFWPGLFAK.A	P05386	RLA1_HUMAN	60S acidic ribosomal protein P1 (Large ribosomal subunit protein P1)	RPLP1
1702,89	1702,035	1703,737	1702,80	0,082	K.KPAEDEWGTPTDAMK.A	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
			1702,67	0,219	K.ESDQGGAYTCEAMNAR.G	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
1703,76	1702,909	1704,613	1703,78	0,020	K.ELAPYDENWFYTR.A	P39019	RS19_HUMAN	40S ribosomal protein S19 (Small ribosomal subunit protein eS19)	RPS19
			1703,83	0,064	R.SDSFENPVLQQHFR.N	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC XRCC6 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	
			1703,84	0,084	K.TQEQLALEMAELTAR.I	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			1703,95	0,190	K.ILLANFLAQTEALMR.G	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
1703,85	1702,997	1704,701	1703,84	0,005	K.TQEQLALEMAELTAR.I	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			1703,83	0,024	R.SDSFENPVLQQHFR.N	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC XRCC6 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	
			1703,78	0,068	K.ELAPYDENWFYTR.A	P39019	RS19_HUMAN	40S ribosomal protein S19 (Small ribosomal subunit protein eS19)	RPS19
			1703,95	0,102	K.ILLANFLAQTEALMR.G	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
1704,86	1704,004	1705,709	1704,85	0,003	K.ACQSIYPLHDVFVR.K	P61247	RS3A_HUMAN	40S ribosomal protein S3a (Small ribosomal subunit protein eS1) (v-fos transformation effector protein) (Fte-1)	RPS3A
			1704,91	0,058	K.GLTGDEESILTITSR.S	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
1705,86	1705,008	1706,714	1705,79	0,069	R.HVQSLEPDGTPGSEER.T	Q9NX46	ARHL2_HUMAN	ADP-ribose glycohydrolase ARH3 (ADP-ribosylhydrolase 3) (O-acetyl-ADP-ribose deacetylase ARH3) (EC 3.5.1.-) (Poly(ADP-ribose) glycohydrolase ARH3) (EC 3.2.1.143) ([Protein ADP-ribosylarginine] hydrolase-like protein 2) ([Protein ADP-ribosylserine] hydrolase) (EC 3.2.2.-)	ADPRHL2
			1706,75	0,008	K.HSGQFTDEYLPQER.S	Q14112	NID2_HUMAN	Nidogen-2 (NID-2) (Osteonidogen)	NID2
			1707,78	0,049	K.YVMLPVADQDQCIR.H	P00738	HPT_HUMAN	Haptoglobin (Zonulin) [Cleaved into: Haptoglobin alpha chain; Haptoglobin beta chain]	HP
			1708,77	0,134	R.YVWLVYEQDRPLK.C	P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPPP) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1
1709,54	1708,684	1710,394	1709,86	0,326	K.NLTQYSWLDGFPR.T	Q9UIJ7	KAD3_HUMAN	GTP:AMP phosphotransferase AK3, mitochondrial (EC 2.7.4.10) (Adenylate kinase 3) (AK 3) (Adenylate kinase 3 alpha-like 1)	AK3
			1708,91	0,632	R.YVWLVYEQDRPLK.C	P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPPP) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1
1709,80	1708,943	1710,653	1709,86	0,067	K.NLTQYSWLDGFPR.T	Q9UIJ7	KAD3_HUMAN	GTP:AMP phosphotransferase AK3, mitochondrial (EC 2.7.4.10) (Adenylate kinase 3) (AK 3) (Adenylate kinase 3 alpha-like 1)	AK3
			1710,56	0,700	K.NLTQYSWLDGFPR.T	Q9UIJ7	KAD3_HUMAN	GTP:AMP phosphotransferase AK3, mitochondrial (EC 2.7.4.10) (Adenylate kinase 3) (AK 3) (Adenylate kinase 3 alpha-like 1)	AK3
			1710,83	0,053	K.SYSCQVTHEGSTVEK.T	P0DOY3	IGLC3_HUMAN	Immunoglobulin lambda constant 3	IGLC3
			1711,83	0,013	R.DLISHDEMFSDIYK.I	P13693	TCTP_HUMAN	Translationally-controlled tumor protein (TCTP) (Fortilin) (Histamine-releasing factor) (HRF) (p23)	TPT1
1712,82	1711,961	1713,674	1712,80	0,034	K.FLVYVANFDEK DPR.T	P50395	GDI8_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2

			1712,90	0,080	K.DIILREDLEELQAR.Y	Q9UHQ9	NB5R1_HUMAN	NADH-cytochrome b5 reductase 1 (b5R.1) (EC 1.6.2.2) (Humb5R2) (NAD(P)H:quinone oxidoreductase type 3 polypeptide A2)	CY85R1
			1712,94	0,121	R.APVILGSPDDVLEFLK.V	P09467	F16P1_HUMAN	Fructose-1,6-bisphosphatase 1 (FBPase 1) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase 1) (Liver FBPase)	FBP1
1713,82	1712,962	1714,676	1713,79	0,030	R.GFAFVTFDDHDTVDK.I	P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3
1714,83	1713,974	1715,689	1714,91	0,075	K.SSGPTSFAVTVAPPGAR.Q	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
			1714,75	0,084	R.YEEVSVSGFEFHR.A	Q98RA2	TXD17_HUMAN	Thioredoxin domain-containing protein 17 (14 kDa thioredoxin-related protein) (TRP14) (Protein 42-9-9) (Thioredoxin-like protein 5)	TXNDC17
			1714,68	0,153	K.MGGMGEPFGGGMENMGR.F	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			1715,91	0,185	R.AVFVDLEPTVIDEIR.N	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
1715,73	1714,871	1716,587	1715,95	0,224	R.IEEGVPOFLVLISGK.S	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1714,91	0,822	K.SSGPTSFAVTVAPPGAR.Q	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
1715,86	1715,000	1716,716	1715,91	0,056	R.AVFVDLEPTVIDEIR.N	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
			1715,95	0,095	R.IEEGVPOFLVLISGK.S	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1716,83	1715,968	1717,685	1717,90	0,210	R.EPWLLPSQHNDIIR.D	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1717,69	1716,827	1718,545		0,246	K.AHLLADMAHISGLVAAK.V	P34897	GLYM_HUMAN	Serine hydroxymethyltransferase, mitochondrial (SHMT) (EC 2.1.2.1) (Glycine hydroxymethyltransferase) (Serine methylase)	SHMT2
1717,85	1716,989	1718,707	1717,90	0,048	R.EPWLLPSQHNDIIR.D	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			1717,93	0,084	K.AHLLADMAHISGLVAAK.V	P34897	GLYM_HUMAN	Serine hydroxymethyltransferase, mitochondrial (SHMT) (EC 2.1.2.1) (Glycine hydroxymethyltransferase) (Serine methylase)	SHMT2
1718,88	1718,018	1719,737	1718,88	0,004	R.NLDIERPTYTNLNR.L	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			1718,88	0,004	R.NLDIERPTYTNLNR.L	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			1718,88	0,004	R.NLDIERPTYTNLNR.L	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
			1718,88	0,007	R.IIDVVYNASNELVR.T	P62241	RS8_HUMAN	40S ribosomal protein S8 [Small ribosomal subunit protein eS8]	RP58
1719,49	1718,629	1720,349	1719,98	0,495	K.KLNQALLDLHALGSAR.T	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
			1718,88	0,605	R.IIDVVYNASNELVR.T	P62241	RS8_HUMAN	40S ribosomal protein S8 [Small ribosomal subunit protein eS8]	RP58
			1718,88	0,608	R.NLDIERPTYTNLNR.L	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			1718,88	0,608	R.NLDIERPTYTNLNR.L	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			1718,88	0,608	R.NLDIERPTYTNLNR.L	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
1719,85	1718,985	1720,705	1719,98	0,139	K.KLNQALLDLHALGSAR.T	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
1720,84	1719,984	1721,705	1719,98	0,860	K.KLNQALLDLHALGSAR.T	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
1721,83	1720,971	1722,693	1722,86	0,006	R.EVQGESATFLGYFK.S	P06396	GELS_HUMAN	Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF) (Brevin)	GSN
1722,85	1721,988	1723,711							
1723,76	1722,897	1724,621	1723,90	0,140	R.IPWFFQYPIIDIR.A	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
1723,90	1723,036	1724,760	1723,90	0,002	R.IPWFFQYPIIDIR.A	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
			1724,75	0,855	R.EYWMDPEGEMKPGR.K	P53999	TCP4_HUMAN	Activated RNA polymerase II transcriptional coactivator p15 (Positive cofactor 4) (PC4) (SUB1 homolog) (p14)	SUB1
1724,77	1723,905	1725,630	1724,75	0,015	R.EYWMDPEGEMKPGR.K	P53999	TCP4_HUMAN	Activated RNA polymerase II transcriptional coactivator p15 (Positive cofactor 4) (PC4) (SUB1 homolog) (p14)	SUB1
			1724,80	0,029	R.DKEVGNLYDMFHTR.N	Q9Y323	SAMH1_HUMAN	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 (dNTPase) (EC 3.1.5.-) (Dendritic cell-derived IFNG-induced protein) (DCIP) (Monocyte protein 5) (MOP-5) (SAM domain and HD domain-containing protein 1) (hSAMHD1)	SAMHD1
			1724,81	0,041	K.LNYPKEEYPDLK.H	P06732	KCRM_HUMAN	Creatine kinase M-type (EC 2.7.3.2) (Creatine kinase M chain) (Creatine phosphokinase M-type) (CPK-M) (M-CK)	CKM
			1724,87	0,105	K.EFADSLGIPFLETSAK.N	P62820	RAB1A_HUMAN	Ras-related protein Rab-1A (YPT1-related protein)	RAB1A
1724,92	1724,059	1725,784	1724,87	0,049	K.EFADSLGIPFLETSAK.N	P62820	RAB1A_HUMAN	Ras-related protein Rab-1A (YPT1-related protein)	RAB1A
			1724,81	0,113	K.LNYPKEEYPDLK.H	P06732	KCRM_HUMAN	Creatine kinase M-type (EC 2.7.3.2) (Creatine kinase M chain) (Creatine phosphokinase M-type) (CPK-M) (M-CK)	CKM
			1724,80	0,125	R.DKEVGNLYDMFHTR.N	Q9Y323	SAMH1_HUMAN	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 (dNTPase) (EC 3.1.5.-) (Dendritic cell-derived IFNG-induced protein) (DCIP) (Monocyte protein 5) (MOP-5) (SAM domain and HD domain-containing protein 1) (hSAMHD1)	SAMHD1
			1724,75	0,169	R.EYWMDPEGEMKPGR.K	P53999	TCP4_HUMAN	Activated RNA polymerase II transcriptional coactivator p15 (Positive cofactor 4) (PC4) (SUB1 homolog) (p14)	SUB1

1725,46	1724,598	1726,323	1725,81	0,352	K.MDENQFVAVTSTNAAK.V	Q16555	DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) (Unc-33-like phosphoprotein 2) (ULIP-2)	DPYSL2
			1725,81	0,352	K.MDENQFVAVTSTNAAK.I	Q14195	DPYL3_HUMAN	Dihydropyrimidinase-related protein 3 (DRP-3) (Collapsin response mediator protein 4) (CRMP-4) (Unc-33-like phosphoprotein 1) (ULIP-1)	DPYSL3
			1724,87	0,588	K.EFADSLGIPFLETSAK.N	P62820	RAB1A_HUMAN	Ras-related protein Rab-1A (YPT1-related protein)	RAB1A
			1724,81	0,651	K.LNKYPPEEYDLSK.H	P06732	KCRM_HUMAN	Creatine kinase M-type (EC 2.7.3.2) (Creatine kinase M chain) (Creatine phosphokinase M-type) (CPK-M) (M-CK)	CKM
			1724,80	0,664	R.DKEVGNLYDMFHTR.N	Q9Y323	SAMH1_HUMAN	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 (dNTPase) (EC 3.1.5.-) (Dendritic cell-derived IFNG-induced protein) (DCIP) (Monocyte protein 5) (MOP-5) (SAM domain and HD domain-containing protein 1) (hSAMHD1)	SAMHD1
1725,71	1724,851	1726,576	1725,81	0,099	K.MDENQFVAVTSTNAAK.V	Q16555	DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) (Unc-33-like phosphoprotein 2) (ULIP-2)	DPYSL2
			1725,81	0,099	K.MDENQFVAVTSTNAAK.I	Q14195	DPYL3_HUMAN	Dihydropyrimidinase-related protein 3 (DRP-3) (Collapsin response mediator protein 4) (CRMP-4) (Unc-33-like phosphoprotein 1) (ULIP-1)	DPYSL3
			1724,87	0,841	K.EFADSLGIPFLETSAK.N	P62820	RAB1A_HUMAN	Ras-related protein Rab-1A (YPT1-related protein)	RAB1A
			1725,81	0,064	K.MDENQFVAVTSTNAAK.V	Q16555	DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) (Unc-33-like phosphoprotein 2) (ULIP-2)	DPYSL2
			1725,81	0,064	K.MDENQFVAVTSTNAAK.I	Q14195	DPYL3_HUMAN	Dihydropyrimidinase-related protein 3 (DRP-3) (Collapsin response mediator protein 4) (CRMP-4) (Unc-33-like phosphoprotein 1) (ULIP-1)	DPYSL3
1726,65	1725,792	1727,518	1726,79	0,133	R.FTATSFHGHPVPSCR.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1725,81	0,842	K.MDENQFVAVTSTNAAK.V	Q16555	DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) (Unc-33-like phosphoprotein 2) (ULIP-2)	DPYSL2
			1725,81	0,842	K.MDENQFVAVTSTNAAK.I	Q14195	DPYL3_HUMAN	Dihydropyrimidinase-related protein 3 (DRP-3) (Collapsin response mediator protein 4) (CRMP-4) (Unc-33-like phosphoprotein 1) (ULIP-1)	DPYSL3
			1726,79	0,063	R.FTATSFHGHPVPSCR.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1728,87	0,125	R.ALVHERDEAAYGELR.A	Q9UL46	PSME2_HUMAN	Proteasome activator complex subunit 2 (11S regulator complex subunit beta) (REG-beta) (Activator of multicatalytic protease subunit 2) (Proteasome activator 28 subunit beta) (PA28b) (PA28beta)	PSME2
1728,82	1727,952	1729,681	1728,87	0,052	R.ALVHERDEAAYGELR.A	Q9UL46	PSME2_HUMAN	Proteasome activator complex subunit 2 (11S regulator complex subunit beta) (REG-beta) (Activator of multicatalytic protease subunit 2) (Proteasome activator 28 subunit beta) (PA28b) (PA28beta)	PSME2
			1728,87	0,494	R.ALVHERDEAAYGELR.A	Q9UL46	PSME2_HUMAN	Proteasome activator complex subunit 2 (11S regulator complex subunit beta) (REG-beta) (Activator of multicatalytic protease subunit 2) (Proteasome activator 28 subunit beta) (PA28b) (PA28beta)	PSME2
			1728,87	0,011	K.SELEEQLTVPVAETR.A	P02649	APOE_HUMAN	Apolipoprotein E (Apo-E)	APOE
			1730,92	0,066	K.TPGAMEHELVHLQLR.C	P12882	MYH1_HUMAN	Myosin-1 (Myosin heavy chain 1) (Myosin heavy chain 2x) (MyHC-2x) (Myosin heavy chain IIX/d) (MyHC-IIX/d) (Myosin heavy chain, skeletal muscle, adult 1)	MYH1
			1730,97	0,117	R.ILASDKPYILAEELR.R	P35609	ACTN2_HUMAN	Alpha-actinin-2 (Alpha-actinin skeletal muscle isoform 2) (F-ACTN2 actin cross-linking protein)	ACTN2
1731,74	1730,874	1732,605	1731,89	0,146	K.ISLSPEYVFSVSTFR.E	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1731,91	0,167	R.VKPAPDETSFSEALLK.R	Q12905	ILF2_HUMAN	Interleukin enhancer-binding factor 2 (Nuclear factor of activated T-cells 45 kDa)	ILF2
			1730,97	0,773	R.ILASDKPYILAEELR.R	P35609	ACTN2_HUMAN	Alpha-actinin-2 (Alpha-actinin skeletal muscle isoform 2) (F-ACTN2 actin cross-linking protein)	ACTN2
			1730,92	0,824	K.TPGAMEHELVHLQLR.C	P12882	MYH1_HUMAN	Myosin-1 (Myosin heavy chain 1) (Myosin heavy chain 2x) (MyHC-2x) (Myosin heavy chain IIX/d) (MyHC-IIX/d) (Myosin heavy chain, skeletal muscle, adult 1)	MYH1
			1731,91	0,022	R.VKPAPDETSFSEALLK.R	Q12905	ILF2_HUMAN	Interleukin enhancer-binding factor 2 (Nuclear factor of activated T-cells 45 kDa)	ILF2
1731,93	1731,063	1732,795	1731,89	0,043	K.ISLSPEYVFSVSTFR.E	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1732,77	0,840	R.YLTESYGTGQDIDDR.I	Q9UM54	MYO6_HUMAN	Unconventional myosin-VI (Unconventional myosin-6)	MYO6
			1732,77	0,033	R.YLTESYGTGQDIDDR.I	Q9UM54	MYO6_HUMAN	Unconventional myosin-VI (Unconventional myosin-6)	MYO6
			1731,91	0,829	R.VKPAPDETSFSEALLK.R	Q12905	ILF2_HUMAN	Interleukin enhancer-binding factor 2 (Nuclear factor of activated T-cells 45 kDa)	ILF2
			1731,89	0,850	K.ISLSPEYVFSVSTFR.E	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1732,88	1732,014	1733,747	1732,77	0,112	R.YLTESYGTGQDIDDR.I	Q9UM54	MYO6_HUMAN	Unconventional myosin-VI (Unconventional myosin-6)	MYO6
			1733,96	0,042	R.LRNEDLGLPLFPFR.E	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1733,95	0,046	R.DYLHLPPEIVPATLR.R	P46783	RS10_HUMAN	40S ribosomal protein S10 (Small ribosomal subunit protein eS10)	RPS10
			1733,86	0,139	K.EEVVTVETWQEGSLK.A	P09211	GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-p) (GSTP1-1)	GSTP1
			1734,83	0,832	R.LQDEIQNMKEEMAR.H	P08670	VIME_HUMAN	Vimentin	VIM
1734,99	1734,126	1735,861	1734,97	0,027	K.EGGLGPLNIPLLADVTR.R	P32119	PRDX2_HUMAN	Peroxisiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
			1734,83	0,160	R.LQDEIQNMKEEMAR.H	P08670	VIME_HUMAN	Vimentin	VIM
			1735,80	0,811	K.RPAEDMEEEQAFKR.S	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
			1735,80	0,021	K.RPAEDMEEEQAFKR.S	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
			1734,97	0,816	K.EGGLGPLNIPLLADVTR.R	P32119	PRDX2_HUMAN	Peroxisiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
1735,96	1735,097	1736,833	1735,80	0,161	K.RPAEDMEEEQAFKR.S	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
			1736,76	0,796	R.NPGNQAAAYEHFETMK.N	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL

1736,37	1735,501	1737,238	1736,76 1735,80	0,391 0,566	R.NPGNQAAEHFETMK.N K.RPAEDMEEQAFKR.S	P18206 P61978	VINC_HUMAN HNRPK_HUMAN	Vinculin (Metavinculin) (MV) Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	VCL HNRNPK
1736,80	1735,927	1737,663	1736,76	0,035	R.NPGNQAAEHFETMK.N	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL
1736,93	1736,060	1737,797	1736,76	0,168	R.NPGNQAAEHFETMK.N	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL
1737,83	1736,962	1738,700	1737,91	0,080	K.HGGTIPIVPTAEFQDR.I	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
1737,91	1737,039	1738,777	1737,91	0,003	K.HGGTIPIVPTAEFQDR.I	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
1738,82 1739,81	1737,947 1738,938	1739,686 1740,678	1739,86 1739,74	0,049 0,072	R.AHGLEVEPSALEQGFR.Q R.SEDFGVNDLADSDAR.A	Q98SH5 P04083	HDHD3_HUMAN ANXA1_HUMAN	Haloacid dehalogenase-like hydrolase domain-containing protein 3 Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	HDHD3 ANXA1
1740,83	1739,959	1741,700	1740,84 1740,92	0,015 0,091	K.DLFVPACLETGEYAR.L R.LSFQHDPETSVLVR.K	P01266 Q14697	THYG_HUMAN GANAB_HUMAN	Thyroglobulin (Tg) Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	TG GANAB
1741,85	1740,976	1742,717	1741,80 1741,91	0,048 0,062	R.YSDIEPSTEGEVIFR.A R.LDTVAGGLQGLREGLSR.H	P07942 Q9Y6C2	LAMB1_HUMAN EMIL1_HUMAN	Laminin subunit beta-1 (Laminin B1 chain) (Laminin-1 subunit beta) (Laminin-10 subunit beta) (Laminin-12 subunit beta) (Laminin-2 subunit beta) (Laminin-6 subunit beta) (Laminin-8 subunit beta) EMILIN-1 (Elastin microfibril interface-located protein 1) (Elastin microfibril interfacer 1)	LAMB1 EMILIN1
1742,76	1741,891	1743,634	1742,81 1742,86 1741,91	0,051 0,098 0,854	K.ITPAHDQNDYEVGQR.H R.HPYFYAPELFFAK.R R.LDTVAGGLQGLREGLSR.H	P26640 P02768 Q9Y6C2	SYVC_HUMAN ALBU_HUMAN EMIL1_HUMAN	Valine--tRNA ligase (EC 6.1.1.9) (Protein G7a) (Valyl-tRNA synthetase) (ValRS) Serum albumin EMILIN-1 (Elastin microfibril interface-located protein 1) (Elastin microfibril interfacer 1)	VARS ALB EMILIN1
1743,77	1742,899	1744,643	1743,77 1743,81 1743,81 1743,81 1743,84 1743,85 1743,85 1743,88	0,002 0,040 0,040 0,042 0,064 0,076 0,078 0,112	K.NKDTGTVEFVEGLR.V K.AMGIMNSFVNDIFER.I K.AMGIMNSFVNDIFER.I R.EPFLSCCQFAESLR.K --MAACIAAGHWAAMGLGR.S K.YAASSYLSLTPEQWK.S K.GDEEGVPAVVIDMSGRL.E K.AIWNVINWENVTER.Y	P08590 Q16778 O60814 P0C0L5 P49406 P0DOY3 P13796 P04179	MYL3_HUMAN H2B2E_HUMAN H2B1K_HUMAN CO4B_HUMAN RM19_HUMAN IGLC3_HUMAN PLSL_HUMAN SODM_HUMAN	Myosin light chain 3 (Cardiac myosin light chain 1) (CMLC1) (Myosin light chain 1, slow-twitch muscle B/ventricular isoform) (MLC1SB) (Ventricular myosin alkali light chain) (Ventricular myosin light chain 1) (VLCI) (Ventricular/slow twitch myosin alkali light chain) (MLC-IV/sb) Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q) Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1) Complement C4-B (Basic complement C4) (C3 and P2P-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain] 39S ribosomal protein L19, mitochondrial (L19mt) (MRP-L19) (39S ribosomal protein L15, mitochondrial) (L15mt) (MRP-L15) (Mitochondrial large ribosomal subunit protein bL19m) Immunoglobulin lambda constant 3 Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1) Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1)	MYL3 HIST2H2BE HIST1H2BK C4B; C4B_2 MRPL19 IGLC3 LCP1 SOD2
1743,80	1742,925	1744,669	1743,81 1743,81 1743,81 1743,77 1743,84 1743,85 1743,85 1743,88	0,014 0,014 0,016 0,024 0,038 0,050 0,052 0,086	K.AMGIMNSFVNDIFER.I K.AMGIMNSFVNDIFER.I R.EPFLSCCQFAESLR.K K.NKDTGTVEFVEGLR.V --MAACIAAGHWAAMGLGR.S K.YAASSYLSLTPEQWK.S K.GDEEGVPAVVIDMSGRL.E K.AIWNVINWENVTER.Y	Q16778 O60814 P0C0L5 P08590 P49406 P0DOY3 P13796 P04179	H2B2E_HUMAN H2B1K_HUMAN CO4B_HUMAN MYL3_HUMAN RM19_HUMAN IGLC3_HUMAN PLSL_HUMAN SODM_HUMAN	Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q) Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1) Complement C4-B (Basic complement C4) (C3 and P2P-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain] Myosin light chain 3 (Cardiac myosin light chain 1) (CMLC1) (Myosin light chain 1, slow-twitch muscle B/ventricular isoform) (MLC1SB) (Ventricular myosin alkali light chain) (Ventricular myosin light chain 1) (VLCI) (Ventricular/slow twitch myosin alkali light chain) (MLC-IV/sb) 39S ribosomal protein L19, mitochondrial (L19mt) (MRP-L19) (39S ribosomal protein L15, mitochondrial) (L15mt) (MRP-L15) (Mitochondrial large ribosomal subunit protein bL19m) Immunoglobulin lambda constant 3 Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1) Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1)	HIST2H2BE HIST1H2BK C4B; C4B_2 MYL3 MRPL19 IGLC3 LCP1 SOD2
1744,79	1743,916	1745,661	1744,81	0,023	K.FLQEHGSDSFLAEHK.L	Q00688	FKBP3_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP3 (PPIase FKBP3) (EC 5.2.1.8) (25 kDa FK506-binding protein) (25 kDa FKBP) (FKBP-25) (FK506-binding protein 3) (FKBP-3) (Immunophilin FKBP25) (Rapamycin-selective 25 kDa immunophilin) (Rotamase)	FKBP3
1745,78	1744,910	1746,656	1745,83	0,046	K.NQTAKEEFHQQK.E	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LP5-associated protein 1)	HSPA8
1745,81	1744,933	1746,678	1745,83	0,024	K.NQTAKEEFHQQK.E	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LP5-associated protein 1)	HSPA8
1746,82 1747,84	1745,948 1746,967	1747,695 1748,715	1747,85 1747,88	0,005 0,036	K.GPDGLTAFEATDNQAIK.A R.IMEGPAFNFLDAPAVR.V	P58546 P11177	MTPN_HUMAN ODPB_HUMAN	Myotrophin (Protein V-1) Pyruvate dehydrogenase E1 component subunit beta, mitochondrial (PDHE1-B) (EC 1.2.4.1)	MTPN PDHB
1748,85	1747,975	1749,724	1748,89	0,040	K.TFVVQGFQNVGLHSMR.Y	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
1749,86 1750,85	1748,983 1749,979	1750,733 1751,729	1750,81	0,046	R.LQDEIQNMKEEMAR.H	P08670	VIME_HUMAN	Vimentin	VIM

1751,83	1750,956	1752,707	1751,85	0,014	R.AEEYFLTPVEEAPK.G	P52565	GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)	ARHGDI1A
			1751,87	0,034	K.EVGVEALKDDSWLK.G	P40925	MDHC_HUMAN	Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) (Cytosolic malate dehydrogenase) (Diiodophenylpyruvate reductase) (EC 1.1.1.96)	MDH1
			1751,88	0,052	R.FASFEAQGALANIVDK.A	P01903	DRA_HUMAN	HLA class II histocompatibility antigen, DR alpha chain (MHC class II antigen DRA)	HLA-DRA
1752,34	1751,464	1753,216	1751,88	0,456	R.FASFEAQGALANIVDK.A	P01903	DRA_HUMAN	HLA class II histocompatibility antigen, DR alpha chain (MHC class II antigen DRA)	HLA-DRA
			1751,87	0,475	K.EVGVEALKDDSWLK.G	P40925	MDHC_HUMAN	Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) (Cytosolic malate dehydrogenase) (Diiodophenylpyruvate reductase) (EC 1.1.1.96)	MDH1
			1751,85	0,494	R.AEEYFLTPVEEAPK.G	P52565	GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)	ARHGDI1A
			1752,85	0,507	R.NSNLVGAAHEELQQR.I	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
			1752,87	0,533	R.DEQFYWIIALGIR.K	P07814	SYEP_HUMAN	Bifunctional glutamate/proline--tRNA ligase (Bifunctional aminoacyl-tRNA synthetase) (Cell proliferation-inducing gene 32 protein) (Glutamyl-prolyl-tRNA synthetase) [Includes: Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase) (GluRS); Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)]	EPRS
			1752,92	0,577	R.YVGGQEHFAHLILR.D	P02763	A1AG1_HUMAN	Alpha-1-acid glycoprotein 1 (AGP 1) (Orosomucoid-1) (OMD 1)	ORM1
1752,84	1751,960	1753,713	1752,85	0,010	R.NSNLVGAAHEELQQR.I	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
			1752,87	0,036	R.DEQFYWIIALGIR.K	P07814	SYEP_HUMAN	Bifunctional glutamate/proline--tRNA ligase (Bifunctional aminoacyl-tRNA synthetase) (Cell proliferation-inducing gene 32 protein) (Glutamyl-prolyl-tRNA synthetase) [Includes: Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase) (GluRS); Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)]	EPRS
			1752,92	0,081	R.YVGGQEHFAHLILR.D	P02763	A1AG1_HUMAN	Alpha-1-acid glycoprotein 1 (AGP 1) (Orosomucoid-1) (OMD 1)	ORM1
1753,36	1752,482	1754,235	1752,92	0,441	R.YVGGQEHFAHLILR.D	P02763	A1AG1_HUMAN	Alpha-1-acid glycoprotein 1 (AGP 1) (Orosomucoid-1) (OMD 1)	ORM1
			1753,82	0,463	R.ETADTDTAEQVIASFR.I	P35609	ACTN2_HUMAN	Alpha-actinin-2 (Alpha-actinin skeletal muscle isoform 2) (F-actin cross-linking protein)	ACTN2
			1753,82	0,464	R.KHEAFESDLAAHQDR.V	P35609	ACTN2_HUMAN	Alpha-actinin-2 (Alpha-actinin skeletal muscle isoform 2) (F-actin cross-linking protein)	ACTN2
			1753,82	0,464	R.KHEAFESDLAAHQDR.V	O43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
			1753,82	0,464	R.KHEAFESDLAAHQDR.V	P12814	ACTN1_HUMAN	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (F-actin cross-linking protein) (Non-muscle alpha-actinin-1)	ACTN1
			1752,87	0,486	R.DEQFYWIIALGIR.K	P07814	SYEP_HUMAN	Bifunctional glutamate/proline--tRNA ligase (Bifunctional aminoacyl-tRNA synthetase) (Cell proliferation-inducing gene 32 protein) (Glutamyl-prolyl-tRNA synthetase) [Includes: Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase) (GluRS); Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)]	EPRS
			1752,85	0,512	R.NSNLVGAAHEELQQR.I	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
			1753,82	0,032	R.KHEAFESDLAAHQDR.V	P35609	ACTN2_HUMAN	Alpha-actinin-2 (Alpha-actinin skeletal muscle isoform 2) (F-actin cross-linking protein)	ACTN2
			1753,82	0,032	R.KHEAFESDLAAHQDR.V	O43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
1753,85	1752,978	1754,731	1753,82	0,032	R.KHEAFESDLAAHQDR.V	P12814	ACTN1_HUMAN	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (F-actin cross-linking protein) (Non-muscle alpha-actinin-1)	ACTN1
			1753,82	0,033	R.ETADTDTAEQVIASFR.I	P35609	ACTN2_HUMAN	Alpha-actinin-2 (Alpha-actinin skeletal muscle isoform 2) (F-actin cross-linking protein)	ACTN2
			1754,84	0,012	R.SYQDPSNAQFLESIR.R	Q9UNZ2	NSF1C_HUMAN	NSFL1 cofactor p47 (UBX domain-containing protein 2C) (p97 cofactor p47)	NSFL1C
1754,83	1753,949	1755,704	1754,85	0,026	R.VFDKDGNGVISAELR.H	P0DP23	CALM1_HUMAN	Calmodulin-1	CALM1
			1754,85	0,007	R.VFDKDGNGVISAELR.H	P0DP23	CALM1_HUMAN	Calmodulin-1	CALM1
			1754,84	0,007	R.SYQDPSNAQFLESIR.R	Q9UNZ2	NSF1C_HUMAN	NSFL1 cofactor p47 (UBX domain-containing protein 2C) (p97 cofactor p47)	NSFL1C
1755,81	1754,933	1756,689	1755,85	0,042	R.NDSKNSLYLQMSLR.A	P01763	HV348_HUMAN	Immunoglobulin heavy variable 3-48 (Ig heavy chain V-III region WEA)	IGHV3-48
			1755,89	0,074	R.KMGAPESGLAEYFDK.H	P02794	FRIH_HUMAN	Ferritin heavy chain (Ferritin H subunit) (EC 1.16.3.1) (Cell proliferation-inducing gene 15 protein) [Cleaved into: Ferritin heavy chain, N-terminally processed]	FTH1
			1755,91	0,026	R.KMGAPESGLAEYFDK.H	P02794	FRIH_HUMAN	Ferritin heavy chain (Ferritin H subunit) (EC 1.16.3.1) (Cell proliferation-inducing gene 15 protein) [Cleaved into: Ferritin heavy chain, N-terminally processed]	FTH1
			1755,85	0,059	R.NDSKNSLYLQMSLR.A	P01763	HV348_HUMAN	Immunoglobulin heavy variable 3-48 (Ig heavy chain V-III region WEA)	IGHV3-48
			1756,78	0,175	R.IHFPLATYAPVISAELR.H	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			1756,96	0,175	R.IHFPLATYAPVISAELR.H	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			1756,96	0,175	R.IHFPLATYAPVISAELR.H	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
			1756,93	0,030	R.IHFPLATYAPVISAELR.H	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			1756,96	0,030	R.IHFPLATYAPVISAELR.H	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			1756,96	0,030	R.IHFPLATYAPVISAELR.H	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
			1757,79	0,865	R.LQCEATEHATESEER.F	Q9Y6C2	EMIL1_HUMAN	EMILIN-1 (Elastin microfibril interface-located protein 1) (Elastin microfibril interfacer 1)	EMILIN1
1757,95	1757,074	1758,832	1757,95	0,003	R.KVPTFATPWPDFVPR.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1757,82	0,134	K.TAEYDVAYGESHLFR.V	P12109	CO6A1_HUMAN	Collagen alpha-1(VI) chain	COL6A1
			1757,79	0,159	R.LQCEATEHATESEER.F	Q9Y6C2	EMIL1_HUMAN	EMILIN-1 (Elastin microfibril interface-located protein 1) (Elastin microfibril interfacer 1)	EMILIN1

			1758,78	0,822	R.STAYEDYYYYPPPR.M	O43390	HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R)	HNRNPR		
1758,91	1758,033	1759,792	1758,85	0,062	K.ICDQWDALGSLTHSR.R	O43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4		
			1758,78	0,137	R.STAYEDYYYYPPPR.M	O43390	HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R)	HNRNPR		
1758,95	1758,074	1759,833	1758,85	0,103	K.ICDQWDALGSLTHSR.R	O43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4		
			1758,78	0,178	R.STAYEDYYYYPPPR.M	O43390	HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R)	HNRNPR		
			1759,80	0,851	K.AMGIMNSFVNDIFER.I	O60814	H2B1K_HUMAN	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK		
			1759,80	0,851	K.AMGIMNSFVNDIFER.I	Q16778	H2B2E_HUMAN	Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q)	HIST2H2BE		
			1759,82	0,869	K.AMGIMNSFVNDIFER.I	Q16778	H2B2E_HUMAN	Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q)	HIST2H2BE		
			1759,82	0,869	K.AMGIMNSFVNDIFER.I	O60814	H2B1K_HUMAN	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK		
1759,94	1759,055	1760,815	1759,82	0,113	K.AMGIMNSFVNDIFER.I	Q16778	H2B2E_HUMAN	Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q)	HIST2H2BE		
			1759,82	0,113	K.AMGIMNSFVNDIFER.I	O60814	H2B1K_HUMAN	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK		
			1759,80	0,131	K.AMGIMNSFVNDIFER.I	O60814	H2B1K_HUMAN	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK		
			1759,80	0,131	K.AMGIMNSFVNDIFER.I	Q16778	H2B2E_HUMAN	Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q)	HIST2H2BE		
1760,90	1760,016	1761,777	1760,90	0,006	R.GFGEFVLNPGTWALR.V	O15230	LAMA5_HUMAN	Laminin subunit alpha-5 (Laminin-10 subunit alpha) (Laminin-11 subunit alpha) (Laminin-15 subunit alpha)	LAMA5		
1761,43	1760,545	1762,306	1760,90	0,522	R.GFGEFVLNPGTWALR.V	O15230	LAMA5_HUMAN	Laminin subunit alpha-5 (Laminin-10 subunit alpha) (Laminin-11 subunit alpha) (Laminin-15 subunit alpha)	LAMA5		
1761,85	1760,971	1762,732	1762,79	0,218	R.FAQHGTFEYESQR.W	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMp100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ		
1762,57	1761,692	1763,455			1762,86	0,288	R.SEDPDQQYLINTAR.K	Q96QK1	VPS35_HUMAN	Vacuolar protein sorting-associated protein 35 (hVPS35) (Maternal-embryonic 3) (Vesicle protein sorting 35)	VPS35
					1762,90	0,329	K.GLVYETSVLPDEGIR.F	O75390	CISY_HUMAN	Citrate synthase, mitochondrial (EC 2.3.3.1) (Citrate (Si)-synthase)	CS
1762,90	1762,019	1763,782			1762,90	0,001	K.GLVYETSVLPDEGIR.F	O75390	CISY_HUMAN	Citrate synthase, mitochondrial (EC 2.3.3.1) (Citrate (Si)-synthase)	CS
			1762,86	0,039	R.SEDPDQQYLINTAR.K	Q96QK1	VPS35_HUMAN	Vacuolar protein sorting-associated protein 35 (hVPS35) (Maternal-embryonic 3) (Vesicle protein sorting 35)	VPS35		
			1762,79	0,110	R.FAQHGTFEYESQR.W	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMp100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ		
1763,88	1762,995	1764,759	1763,88	0,006	K.AAVEQLTEEQKNEFK.A	P63316	TNNC1_HUMAN	Troponin C, slow skeletal and cardiac muscles (TN-C)	TNNC1		
			1763,88	0,008	R.DLMTDLKSEISGDLAR.L	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6		
			1763,82	0,057	K.LISWYDNEFGYSNR.V	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH		
1764,72	1763,841	1765,606	1763,88	0,839	R.DLMTDLKSEISGDLAR.L	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6		
			1763,88	0,841	K.AAVEQLTEEQKNEFK.A	P63316	TNNC1_HUMAN	Troponin C, slow skeletal and cardiac muscles (TN-C)	TNNC1		
1764,90	1764,014	1765,779	1767,80	0,018	K.IQDMSGWYLTDLPR.G	P24043	LAMA2_HUMAN	Laminin subunit alpha-2 (Laminin M chain) (Laminin-12 subunit alpha) (Laminin-2 subunit alpha) (Laminin-4 subunit alpha) (Merosin heavy chain)	LAMA2		
1765,83	1764,948	1766,714			R.LVPFDHAESTYGLYR.T	O95336	6PGL_HUMAN	6-phosphogluconolactonase (6PGL) (EC 3.1.1.31)	PGLS		
1766,81	1765,929	1767,696			K.GLGTDEDTIIDITHR.S	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6		
1767,82	1766,936	1768,704			K.ACANPAAGSVILLENR.F	P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1		
			1769,03	0,179	K.ALESERPFLAILGGAK.V	P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1		
1769,87	1768,985	1770,755	1769,03	0,842	K.ALESERPFLAILGGAK.V	P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1		
1770,89	1770,004	1771,775	1770,89	0,004	K.LFIGGLSFETDDSLR.E	P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3		
			1770,83	0,063	K.APVPTGEVYFADSFDR.G	P27824	CALX_HUMAN	Calnexin (IP90) (Major histocompatibility complex class I antigen-binding protein p88) (p90)	CANX		
			1770,78	0,109	R.HYAHTDCPGHADYVK.N	P49411	EFTU_HUMAN	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	TUFM		
			1771,77	0,883	K.ADNFEYSDPVDGSGISR.N	P36871	PGM1_HUMAN	Phosphoglucomutase-1 (PGM 1) (EC 5.4.2.2) (Glucose phosphomutase 1)	PGM1		
1771,91	1771,022	1772,794	1771,77	0,136	K.ADNFEYSDPVDGSGISR.N	P36871	PGM1_HUMAN	Phosphoglucomutase-1 (PGM 1) (EC 5.4.2.2) (Glucose phosphomutase 1)	PGM1		
1772,89	1772,007	1773,779	1772,89	0,002	K.ILDSVGIEADDDRLNK.V	P05387	RLA2_HUMAN	60S acidic ribosomal protein P2 (Large ribosomal subunit protein P2) (Renal carcinoma antigen NY-REN-44)	RPLP2		
			1773,78	0,886	K.WEMPFDPQDTHQSR.F	P01011	AACT_HUMAN	Alpha-1-antichymotrypsin (ACT) (Cell growth-inhibiting gene 24/25 protein) (Serpine A3) [Cleaved into: Alpha-1-antichymotrypsin His-Pro-less]	SERPINA3		
1773,88	1772,998	1774,771	1773,78	0,105	K.WEMPFDPQDTHQSR.F	P01011	AACT_HUMAN	Alpha-1-antichymotrypsin (ACT) (Cell growth-inhibiting gene 24/25 protein) (Serpine A3) [Cleaved into: Alpha-1-antichymotrypsin His-Pro-less]	SERPINA3		

1774,88	1773,997	1775,772	1774,88	0,008	K.LADEQLSSVIQDMAVR.Q	Q8NFV4	ABHD8_HUMAN	Protein ABHD11 (EC 3.-.-.-) (Alpha/beta hydrolase domain-containing protein 11) (Abhydrolase domain-containing protein 11) (Williams-Beuren syndrome chromosomal region 21 protein)	ABHD11
1775,86	1774,973	1776,749	1775,80	0,066	K.AMGIMNSFVNDIFER.I	Q16778	H2B2E_HUMAN	Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q)	HIST2H2BE
			1775,80	0,066	K.AMGIMNSFVNDIFER.I	O60814	H2B1K_HUMAN	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK
			1775,79	0,067	R.APWIEQEGPEYWDR.N	P16190	1A33_HUMAN	HLA class I histocompatibility antigen, A-33 alpha chain (Aw-19) (Aw-33) (MHC class I antigen A*33)	HLA-A
			1775,79	0,067	R.APWIEQEGPEYWDR.N	P30493	1B55_HUMAN	HLA class I histocompatibility antigen, B-55 alpha chain (Bw-55) (HLA class I histocompatibility antigen, B-12 alpha chain) (MHC class I antigen B*55)	HLA-B
1775,88	1774,990	1776,766	1775,80	0,083	K.AMGIMNSFVNDIFER.I	Q16778	H2B2E_HUMAN	Histone H2B type 2-E (Histone H2B-GL105) (Histone H2B.q) (H2B/q)	HIST2H2BE
			1775,80	0,083	K.AMGIMNSFVNDIFER.I	O60814	H2B1K_HUMAN	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK
			1775,79	0,084	R.APWIEQEGPEYWDR.N	P16190	1A33_HUMAN	HLA class I histocompatibility antigen, A-33 alpha chain (Aw-19) (Aw-33) (MHC class I antigen A*33)	HLA-A
			1775,79	0,084	R.APWIEQEGPEYWDR.N	P30493	1B55_HUMAN	HLA class I histocompatibility antigen, B-55 alpha chain (Bw-55) (HLA class I histocompatibility antigen, B-12 alpha chain) (MHC class I antigen B*55)	HLA-B
1776,87	1775,986	1777,763	1776,98	0,104	R.LLGNVLVCVLAHHFGK.E	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemophrin-7; Spinorhin]	HBB
1777,87	1776,978	1778,755	1777,86	0,006	K.GLTDEDSLIEIICS.R.T	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1777,80	0,066	R.THYSNIEANEESEVR.Q	P04632	CPNS1_HUMAN	Calpain small subunit 1 (CSS1) (Calcium-activated neutral proteinase small subunit) (CANP small subunit) (Calcium-dependent protease small subunit) (CDPS) (Calcium-dependent protease small subunit 1) (Calpain regulatory subunit)	CAPNS1
			1777,99	0,121	K.EIRPALELLEPIEQK.F	P50395	GDI8_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
			1776,98	0,887	R.LLGNVLVCVLAHHFGK.E	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemophrin-7; Spinorhin]	HBB
1778,93	1778,040	1779,819	1778,89	0,042	R.GAPSSNIEDFHGLLPK.G	P43243	MATR3_HUMAN	Matrin-3	MATR3
			1778,81	0,124	R.NQYDNDVTVWSPQGR.I	P25786	PSA1_HUMAN	Proteasome subunit alpha type-1 (EC 3.4.25.1) (30 kDa prosomal protein) (PROS-30) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome component C2) (Proteasome nu chain)	PSMA1
			1779,78	0,845	K.TDTSHHDDHPTFNK.I	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiprotease) (Serp1 A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
1779,94	1779,054	1780,834	1779,78	0,168	K.TDTSHHDDHPTFNK.I	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiprotease) (Serp1 A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
			1780,80	0,861	R.TDYNASVSPDSSGPER.I	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
1780,92	1780,030	1781,811	1780,84	0,084	K.VDATEESDLAQYGV.R.G	P07237	PDIA1_HUMAN	Protein disulfide-isomerase (PDI) (EC 5.3.4.1) (Cellular thyroid hormone-binding protein) (Prolyl 4-hydroxylase subunit beta) (p55)	P4HB
			1780,80	0,116	R.TDYNASVSPDSSGPER.I	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
1781,86	1780,973	1782,755	1781,89	0,027	R.NAPWTLTPEFLAHR.I	P49585	PCY1A_HUMAN	Choline-phosphate cytidyltransferase A (EC 2.7.7.15) (CCT-alpha) (CTP:phosphocholine cytidyltransferase A) (CCT A) (CT A) (Phosphorylcholine transferase A)	PCYT1A
			1781,82	0,041	R.YTEFYHVPHSDASK.K	Q96HC4	PDLIS_HUMAN	PDZ and LIM domain protein 5 (Enigma homolog) (Enigma-like PDZ and LIM domains protein)	PDLIM5
1782,86	1781,970	1783,753	1782,83	0,028	K.FDTGNLCMVTGGANLGR.I	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein eS4)	RPS4X
			1782,89	0,033	K.WGTDEAQFIYILGNR.S	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6
			1782,95	0,087	K.HLEINPDHPIVETLR.Q	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
1783,87	1782,973	1784,757	1783,90	0,033	R.VLPEFDTPGHTLSWGK.G	P07686	HEXB_HUMAN	Beta-hexosaminidase subunit beta (EC 3.2.1.52) (Beta-N-acetylhexosaminidase subunit beta) (Hexosaminidase subunit B) (Cervical cancer proto-oncogene 7 protein) (HCC-7) (N-acetyl-beta-glucosaminidase subunit beta) [Cleaved into: Beta-hexosaminidase subunit beta chain B; Beta-hexosaminidase subunit beta chain A]	HEXB
			1783,93	0,066	R.VSLDVNHFADELTVK.T	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP 27)	HSPB1
1784,90	1784,008	1785,793	1784,91	0,014	K.FIGGLSFETTTDESLR.S	Q32P51	RA1L2_HUMAN	Heterogeneous nuclear ribonucleoprotein A1-like 2 (hnRNP A1-like 2) (hnRNP core protein A1-like 2)	HNRNPA1L2
			1784,92	0,022	K.SNRYFEKPFELWLAR.K	P62826	RAN_HUMAN	GTP-binding nuclear protein Ran (Androgen receptor-associated protein 24) (GTPase Ran) (Ras-like protein TC4) (Ras-related nuclear protein)	RAN
			1784,86	0,040	R.LNLEAINYMAADGDFK.I	P09382	LEG1_HUMAN	Galectin-1 (Gal-1) (14 kDa laminin-binding protein) (HLBP14) (14 kDa lectin) (Beta-galactoside-binding lectin L-14-I) (Galaptin) (HBL) (HPL) (Lactose-binding lectin 1) (Lectin galactoside-binding soluble 1) (Putative MAPK-activating protein PM12) (S-Lac lectin 1)	LGALS1
			1784,82	0,076	K.MSASDPNSSFILTDTAQ.Q	P23381	SYWC_HUMAN	Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (iIFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleaved into: T1-TrpRS; T2-TrpRS]	WARS

1785,91	1785,013	1786,799	1785,83	0,078	R.LVAGEMGQNEPDQGGQR.G	Q99714	HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2 (EC 1.1.1.35) (17-HSD17B10 beta-hydroxysteroid dehydrogenase 10) (17-beta-HSD 10) (EC 1.1.1.51) (2-methyl-3-hydroxybutyryl-CoA dehydrogenase) (MHB8) (3-hydroxy-2-methylbutyryl-CoA dehydrogenase) (EC 1.1.1.178) (3-hydroxyacyl-CoA dehydrogenase type II) (Endoplasmic reticulum-associated amyloid beta-peptide-binding protein) (Mitochondrial ribonuclease P protein 2) (Mitochondrial RNase P protein 2) (Short chain dehydrogenase/reductase family 5C member 1) (Short-chain type dehydrogenase/reductase XH98G2) (Type II HADH)	
1786,91	1786,014	1787,801	1786,92	0,009	K.HLEINPDHSIIETLR.Q	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP 2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
			1786,84	0,063	K.NKDQGTYYDYVEGLR.V	P60660	MYL6_HUMAN	Myosin light polypeptide 6 (17 kDa myosin light chain) (LC17) (Myosin light chain 3) (MLC-3) (Myosin light chain alkali 3) (Myosin light chain A3) (Smooth muscle and nonmuscle myosin light chain alkali 6)	MYL6
1787,88	1786,989	1788,777	1787,90 1787,93	0,018 0,048	K.DLPETNELHLDHNK.I K.TITLVEPDSDTIENVK.A	P21810 P62979	PGS1_HUMAN RS27A_HUMAN	Biglycan (Bone/cartilage proteoglycan I) (PG-S1) Ubiquitin-40S ribosomal protein S27a (Ubiquitin carboxyl extension protein 80) [Cleaved into: Ubiquitin; 40S ribosomal protein S27a (Small ribosomal subunit protein eS31)]	BGN RPS27A
			1787,96	0,077	R.SGIPIVTSPIYQHFTK.T	P01024	CO3_HUMAN	Complement C3 (C3 and P2P-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
			1787,80	0,081	R.DPDAQPGGELMLGGTDSK.Y	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
1788,87 1789,86	1787,971 1788,967	1789,760 1790,756	1789,94	0,074	K.FATVEVTDKPVDEALR.E	Q9NRV9	HEBP1_HUMAN	Heme-binding protein 1 (p22HBP)	HEBP1
1790,88	1789,982	1791,773	1790,89	0,009	R.EIQAQNFSSFTLMK.L	Q9UJ70	NAGK_HUMAN	N-acetyl-D-glucosamine kinase (N-acetylglucosamine kinase) (EC 2.7.1.59) (GlcNAc kinase)	NAGK
			1790,89	0,017	K.SYELPDGQVITIGNER.F	Q658J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			1790,89	0,017	K.SYELPDGQVITIGNER.F	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1790,89	0,017	K.SYELPDGQVITIGNER.F	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1790,89	0,017	R.SYELPDGQVITIGNER.F	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			1790,89	0,017	K.SYELPDGQVITIGNER.F	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			1790,89	0,017	K.SYELPDGQVITIGNER.F	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1790,83	0,050	K.HELOQANCYEEVKDR.C	P23528	COF1_HUMAN	Cofilin-1 (18 kDa phosphoprotein) (p18) (Cofilin, non-muscle isoform)	CF1
1791,88 1792,88	1790,983 1791,986	1792,775 1793,779	1792,87	0,014	R.GDADQASNILASFGLSAR.D	P43243	MATR3_HUMAN	Matrin-3	MATR3
1793,89	1792,996	1794,790	1793,91	0,016	K.ETIPLQETSLYTQDR.L	P50897	PPT1_HUMAN	Palmitoyl-protein thioesterase 1 (PPT-1) (EC 3.1.2.22) (Palmitoyl-protein hydrolase 1)	PPT1
			1794,78	0,889	R.DWQSYYYHPQDR.D	Q1KMD3	HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 2 (Scaffold-attachment factor A2) (SAF-A2)	HNRNPUL2
1794,92	1794,026	1795,821	1794,78	0,142	R.DWQSYYYHPQDR.D	Q1KMD3	HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 2 (Scaffold-attachment factor A2) (SAF-A2)	HNRNPUL2
1795,92 1796,89	1795,021 1795,996	1796,817 1797,793	1796,87	0,023	R.LSGAQADLHIEDGDSIR.F	Q95571	ETHE1_HUMAN	Persulfide dioxygenase ETHE1, mitochondrial (EC 1.13.11.18) (Ethylmalonic encephalopathy protein 1) (Hepatooma subtracted clone one protein) (Sulfur dioxygenase ETHE1)	ETHE1
			1796,84	0,055	R.VSQTTWDSGCAVNP.K.F	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
1797,89	1796,989	1798,787	1797,89	0,000	K.SGTASVCLNNFPR.E	P01834	IGKC_HUMAN	Immunoglobulin kappa constant (Ig kappa chain C region) (Ig kappa chain C region AG) (Ig kappa chain C region CUM) (Ig kappa chain C region EU) (Ig kappa chain C region OU) (Ig kappa chain C region ROY) (Ig kappa chain C region TI)	IGKC
			1797,97	0,077	K.KVLGAFSDGLAHLNLK.G	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
			1797,97	0,077	K.KVLGAFSDGLAHLNLK.G	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
1798,89	1797,986	1799,785	1798,93	0,039	K.LFIGGLSFETTEESLR.N	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
1799,90	1798,997	1800,797	1799,88	0,017	K.WGTDEEKFITGTR.S	P08758	ANXA5_HUMAN	Annexin A5 (Anchoring CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
			1799,87	0,027	K.AYLPVNESFGFTADLR.S	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
1800,91	1800,009	1801,810	1800,85	0,062	K.IKDPDASKPEDWDER.A	P27797	CALR_HUMAN	Calreticulin (CRP55) (Calregulin) (Endoplasmic reticulum resident protein 60) (Erp60) (HACBP) (grp60)	CALR
			1801,02	0,108	K.ALIEVLQPLIAEHQAR.R	P23381	SYWC_HUMAN	Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleaved into: T1-TrpRS; T2-TrpRS]	WARS

1801,87	1800,973	1802,775	1801,82	0,054	R.LVAGEMGQNEPDQGGQR.G	Q99714	HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2 (EC 1.1.1.35) (17- HSD17B10 beta-hydroxysteroid dehydrogenase 10) (17-beta-HSD 10) (EC 1.1.1.51) (2-methyl-3-hydroxybutyryl-CoA dehydrogenase) (MHBd) (3-hydroxy-2-methylbutyryl-CoA dehydrogenase) (EC 1.1.1.178) (3-hydroxyacyl-CoA dehydrogenase type II) (Endoplasmic reticulum-associated amyloid beta-peptide-binding protein) (Mitochondrial ribonuclease P protein 2) (Mitochondrial RNase P protein 2) (Short chain dehydrogenase/reductase family 5C member 1) (Short-chain type dehydrogenase/reductase XH98G2) (Type II HADH)	
			1801,02	0,857	K.ALIEVLQPLIAEHQAR.R	P23381	SYWC_HUMAN	Tryptophan-tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleared into: T1-TrpRS; T2-TrpRS]	WARS
1801,92	1801,023	1802,825	1801,82	0,103	R.LVAGEMGQNEPDQGGQR.G	Q99714	HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2 (EC 1.1.1.35) (17- HSD17B10 beta-hydroxysteroid dehydrogenase 10) (17-beta-HSD 10) (EC 1.1.1.51) (2-methyl-3-hydroxybutyryl-CoA dehydrogenase) (MHBd) (3-hydroxy-2-methylbutyryl-CoA dehydrogenase) (EC 1.1.1.178) (3-hydroxyacyl-CoA dehydrogenase type II) (Endoplasmic reticulum-associated amyloid beta-peptide-binding protein) (Mitochondrial ribonuclease P protein 2) (Mitochondrial RNase P protein 2) (Short chain dehydrogenase/reductase family 5C member 1) (Short-chain type dehydrogenase/reductase XH98G2) (Type II HADH)	
1802,91	1802,011	1803,814	1802,88	0,032	R.QTLPEDNEEPPAPPR.T	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	
			1802,86	0,054	K.YMTISGFQJEEITDR.E	P08758	ANXA5_HUMAN	Annexin A5 (Anchoring CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
1803,89	1802,988	1804,792	1803,94	0,046	K.LQHLENELTHDITK.F	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antitrypsinase) (Serpina1) [Cleared into: Short peptide from AAT (SPAAT)]	SERPINA1
1804,75	1803,843	1805,647	1804,94	0,191	R.AAVPSGASTGIYEALRL.D	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			1804,94	0,191	R.AAVPSGASTGIYEALRL.D	P13929	ENOB_HUMAN	Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 3) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase)	ENO3
			1804,94	0,191	R.AAVPSGASTGIYEALRL.D	P09104	ENOG_HUMAN	Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 2) (Neural enolase) (Neuron-specific enolase) (NSE)	ENO2
			1803,94	0,809	K.LQHLENELTHDITK.F	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antitrypsinase) (Serpina1) [Cleared into: Short peptide from AAT (SPAAT)]	SERPINA1
1804,90	1804,000	1805,805	1804,94	0,034	R.AAVPSGASTGIYEALRL.D	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			1804,94	0,034	R.AAVPSGASTGIYEALRL.D	P13929	ENOB_HUMAN	Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 3) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase)	ENO3
			1804,94	0,034	R.AAVPSGASTGIYEALRL.D	P09104	ENOG_HUMAN	Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 2) (Neural enolase) (Neuron-specific enolase) (NSE)	ENO2
1805,76	1804,859	1806,665	1804,94	0,826	R.AAVPSGASTGIYEALRL.D	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			1804,94	0,826	R.AAVPSGASTGIYEALRL.D	P13929	ENOB_HUMAN	Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 3) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase)	ENO3
			1804,94	0,826	R.AAVPSGASTGIYEALRL.D	P09104	ENOG_HUMAN	Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 2) (Neural enolase) (Neuron-specific enolase) (NSE)	ENO2
1805,91 1806,79	1805,005 1805,883	1806,811 1807,690	1806,87	0,088	K.YLDEDTIYHLQPSGR.F	P31153	METK2_HUMAN	S-adenosylmethionine synthase isoform type-2 (AdoMet synthase 2) (EC 2.5.1.6) (Methionine adenosyltransferase 2) (MAT 2) (Methionine adenosyltransferase II) (MAT-II)	MAT2A
			1806,94	0,157	R.NIETINTFHQYSVK.L	P06702	S10A9_HUMAN	Protein S100-A9 (Calgranulin-B) (Calprotectin L1H subunit) (Leukocyte L1 complex heavy chain) (Migration inhibitory factor-related protein 14) (MRP-14) (p14) (S100 calcium-binding protein A9)	S100A9
1806,93	1806,022	1807,829	1806,94	0,017	R.NIETINTFHQYSVK.L	P06702	S10A9_HUMAN	Protein S100-A9 (Calgranulin-B) (Calprotectin L1H subunit) (Leukocyte L1 complex heavy chain) (Migration inhibitory factor-related protein 14) (MRP-14) (p14) (S100 calcium-binding protein A9)	S100A9
			1806,87	0,051	K.YLDEDTIYHLQPSGR.F	P31153	METK2_HUMAN	S-adenosylmethionine synthase isoform type-2 (AdoMet synthase 2) (EC 2.5.1.6) (Methionine adenosyltransferase 2) (MAT 2) (Methionine adenosyltransferase II) (MAT-II)	MAT2A
			1807,77	0,846	R.NSYVAGQYDDAASYQR.L	P11413	G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	G6PD
1807,90	1806,994	1808,802	1807,90	0,002	K.VTIMWTPPESAVTGYR.V	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleared into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			1807,77	0,126	R.NSYVAGQYDDAASYQR.L	P11413	G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	G6PD
1808,90	1807,992	1809,801	1808,94	0,047	R.ALPAVQQNNLEDLIR.K	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1

1809,85	1808,942	1810,752	1808,94	0,903	R.ALPAVQQNNLDEDLIR.K	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
1809,96	1809,053	1810,863	1810,83	0,873	R.DDTIYEDVDKEAIR.R	P14927	QCR7_HUMAN	Cytochrome b-c1 complex subunit 7 (Complex III subunit 7) (Complex III subunit VII) (QP-C) (Ubiquinol-cytochrome c reductase complex 14 kDa protein)	UQCRB
			1810,83	0,876	R.ISETSLPPDMYECLR.V	P51884	LUM_HUMAN	Lumican (Keratan sulfate proteoglycan lumican) (KSPG lumican)	LUM
1810,80	1809,894	1811,705	1810,83	0,031	R.DDTIYEDVDKEAIR.R	P14927	QCR7_HUMAN	Cytochrome b-c1 complex subunit 7 (Complex III subunit 7) (Complex III subunit VII) (QP-C) (Ubiquinol-cytochrome c reductase complex 14 kDa protein)	UQCRB
			1810,83	0,035	R.ISETSLPPDMYECLR.V	P51884	LUM_HUMAN	Lumican (Keratan sulfate proteoglycan lumican) (KSPG lumican)	LUM
			1810,99	0,192	K.NAPAIIFIDELDAIPK.R	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			1811,01	0,209	R.LKVPAINQFTQALDR.Q	P62424	RL7A_HUMAN	60S ribosomal protein L7a (Large ribosomal subunit protein eL8) (PLA-X polypeptide) (Surfeit locus protein 3)	RPL7A
1810,96	1810,050	1811,861	1810,99	0,037	K.NAPAIIFIDELDAIPK.R	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			1811,01	0,054	R.LKVPAINQFTQALDR.Q	P62424	RL7A_HUMAN	60S ribosomal protein L7a (Large ribosomal subunit protein eL8) (PLA-X polypeptide) (Surfeit locus protein 3)	RPL7A
			1810,83	0,120	R.ISETSLPPDMYECLR.V	P51884	LUM_HUMAN	Lumican (Keratan sulfate proteoglycan lumican) (KSPG lumican)	LUM
			1810,83	0,124	R.DDTIYEDVDKEAIR.R	P14927	QCR7_HUMAN	Cytochrome b-c1 complex subunit 7 (Complex III subunit 7) (Complex III subunit VII) (QP-C) (Ubiquinol-cytochrome c reductase complex 14 kDa protein)	UQCRB
			1811,84	0,885	R.IDEYDYSKPIQGQK.K	P31040	SDHA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) (Flavoprotein subunit of complex II) (Fp)	SDHA
1811,81	1810,907	1812,719	1811,84	0,027	R.IDEYDYSKPIQGQK.K	P31040	SDHA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) (Flavoprotein subunit of complex II) (Fp)	SDHA
			1811,87	0,058	K.TDLEKDIISDTSGDFR.K	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1811,89	0,076	K.IVLGQEQDSYGGKFDR.S	P02743	SAMP_HUMAN	Serum amyloid P-component (SAP) (9.5S alpha-1-glycoprotein) [Cleaved into: Serum amyloid P-component[1-203]]	APCS
			1811,01	0,804	R.LKVPAINQFTQALDR.Q	P62424	RL7A_HUMAN	60S ribosomal protein L7a (Large ribosomal subunit protein eL8) (PLA-X polypeptide) (Surfeit locus protein 3)	RPL7A
			1810,99	0,822	K.NAPAIIFIDELDAIPK.R	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
1811,96	1811,054	1812,865	1811,89	0,070	K.IVLGQEQDSYGGKFDR.S	P02743	SAMP_HUMAN	Serum amyloid P-component (SAP) (9.5S alpha-1-glycoprotein) [Cleaved into: Serum amyloid P-component[1-203]]	APCS
			1811,87	0,089	K.TDLEKDIISDTSGDFR.K	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1811,84	0,119	R.IDEYDYSKPIQGQK.K	P31040	SDHA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) (Flavoprotein subunit of complex II) (Fp)	SDHA
1812,90	1811,990	1813,803	1812,92	0,024	R.LGPNYLHIPVNCOPYR.A	P04040	CATA_HUMAN	Catalase (EC 1.11.1.6)	CAT
1813,87	1812,962	1814,776							
1814,86	1813,951	1815,766							
1815,89	1814,979	1816,795	1815,86	0,028	R.IMDPNIVGSEHYDVAR.G	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP ATP5F1B synthase F1 subunit beta)	
1816,85	1815,943	1817,759	1816,89	0,042	R.SNLDEIIAEENVSR.S	P01024	CO3_HUMAN	Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
1817,86	1816,948	1818,765	1817,95	0,095	R.TLQGLEIELQSQLSMK.A	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
1818,86	1817,953	1819,772							
1819,87	1818,956	1820,776	1819,78	0,081	R.GTDDSPKDSQEDLQER.H	Q6IPX3	TCAL6_HUMAN	Transcription elongation factor A protein-like 6 (TCEA-like protein 6) (Transcription elongation factor S-II protein-like 6)	TCEAL6
1820,88	1819,972	1821,793	1820,84	0,038	R.YMGLPTPEDNLDHYR.N	P27487	DPP4_HUMAN	Dipeptidyl peptidase 4 (EC 3.4.14.5) (ADABP) (Adenosine deaminase complexing protein 2) (ADCP-2) (Dipeptidyl peptidase IV) (DPP IV) (T-cell activation antigen CD26) (TP103) (CD antigen CD26) [Cleaved into: Dipeptidyl peptidase 4 membrane form (Dipeptidyl peptidase IV membrane form); Dipeptidyl peptidase 4 soluble form (Dipeptidyl peptidase IV soluble form)]	DPP4
1821,88	1820,970	1822,792	1821,93	0,044	R.RFDEILEASDGIMVAR.G	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
			1821,93	0,049	K.SDERQGVCIGLSEIMK.S	Q92616	GCN1_HUMAN	eIF-2-alpha kinase activator GCN1 (GCN1 eIF-2-alpha kinase activator homolog) (GCN1-like protein 1) (General control of amino-acid synthesis 1-like protein 1) (Translational activator GCN1) (HsGCN1)	GCN1
			1822,77	0,890	R.YFDGSGGNNHAVEHYR.E	P45974	UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.4.19.12) (Deubiquitinating enzyme 5) (Isopeptidase T) (Ubiquitin thioesterase 5) (Ubiquitin-specific-processing protease 5)	USP5

1822,87	1821,959	1823,782	1822,77	0,100	R.YFDGSGGNHAVEHYR.E	P45974	UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.4.19.12) (Deubiquitinating enzyme 5) (Isopепtidase T) (Ubiquitin thioesterase 5) (Ubiquitin-specific-processing protease 5)	USP5
1823,89	1822,979	1824,802	1823,89	0,004	R.AGGENYKEFSELLPNR.Q	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1823,88	0,013	R.GQDHCGIESEVVAGIPR.T	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
			1823,87	0,024	R.DGHFTLFAPTNEAFEK.L	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
			1823,86	0,031	K.SPLIIFSDCDMNNNAVK.G	P49189	AL9A1_HUMAN	4-trimethylaminobutyraldehyde dehydrogenase (TMABADH) (EC 1.2.1.47) (Aldehyde dehydrogenase E3 isozyme) (Aldehyde dehydrogenase family 9 member A1) (EC 1.2.1.3) (Gamma-aminobutyraldehyde dehydrogenase) (EC 1.2.1.19) (R-aminobutyraldehyde dehydrogenase) [Cleaved into: 4-trimethylaminobutyraldehyde dehydrogenase, N-terminally processed]	ALDH9A1
1824,41	1823,496	1825,321	1823,93	0,041	R.ELQELVQYPVEHPDK.F	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			1823,93	0,477	R.ELQELVQYPVEHPDK.F	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			1823,89	0,514	R.AGGENYKEFSELLPNR.Q	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1823,88	0,531	R.GQDHCGIESEVVAGIPR.T	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
1824,90	1823,986	1825,810	1825,73	0,835	K.YQCACNPGYHSTPDR.L	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			1825,37	0,360	K.YQCACNPGYHSTPDR.L	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			1825,90	0,164	K.YQCACNPGYHSTPDR.L	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			1826,70	0,803	K.MAEGSGGSDVDAGDCSGAR.Y	Q9UH62	ARMX3_HUMAN	Armadillo repeat-containing X-linked protein 3 (ARM protein lost in epithelial cancers on chromosome X 3) (Protein ALEX3)	ARMCX3
1826,87	1825,961	1827,788	1826,70	0,175	K.MAEGSGGSDVDAGDCSGAR.Y	Q9UH62	ARMX3_HUMAN	Armadillo repeat-containing X-linked protein 3 (ARM protein lost in epithelial cancers on chromosome X 3) (Protein ALEX3)	ARMCX3
1827,77	1826,852	1828,679	1827,90	0,138	K.VGDAIPAVEVFEGEPGNK.V	P30044	PRDX5_HUMAN	Peroxisomal oxidoreductase (EC 1.1.1.15) (Alu corepressor 1) (Antioxidant enzyme B166) (AOEB166) (Liver tissue 2D-page spot 718) (PLP) (Peroxisomal oxidoreductase) (TPx type VI) (Thioredoxin peroxidase PMP20)	PRDX5
			1827,96	0,195	K.TYMSGGLQPVPVIFR.G	P11177	ODPB_HUMAN	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial (PDHE1-B) (EC 1.2.4.1)	PDHB
1827,91	1826,995	1828,823	1827,90	0,005	K.VGDAIPAVEVFEGEPGNK.V	P30044	PRDX5_HUMAN	Peroxisomal oxidoreductase (EC 1.1.1.15) (Alu corepressor 1) (Antioxidant enzyme B166) (AOEB166) (Liver tissue 2D-page spot 718) (PLP) (Peroxisomal oxidoreductase) (TPx type VI) (Thioredoxin peroxidase PMP20)	PRDX5
			1827,96	0,052	K.TYMSGGLQPVPVIFR.G	P11177	ODPB_HUMAN	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial (PDHE1-B) (EC 1.2.4.1)	PDHB
1828,88	1827,963	1829,792	1829,87	0,029	R.DLAQYDAHHEEFKRY	Q02818	NUCB1_HUMAN	Nucleobindin-1 (CALNUC)	NUCB1
1829,89	1828,980	1830,810		0,053	K.QTQVSVLPGETPLFK.Q	P06396	GELS_HUMAN	Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF) (Brevin)	GSN
1830,90	1829,980	1831,811	1830,93	0,033	K.HLSAQQAANWCLSR.C	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1831,89	1830,977	1832,809	1831,91	0,022	K.SIYGKFDENFILK.H	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
			1831,86	0,036	R.IMDPNVIGSEHYDVAR.G	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP ATP5F1B synthase F1 subunit beta)	MSN
			1831,96	0,064	K.KTQEQLALEMAELTAR.I	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
1832,83	1831,916	1833,748	1831,96	0,875	K.KTQEQLALEMAELTAR.I	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
1832,85	1831,930	1833,763	1831,96	0,889	K.KTQEQLALEMAELTAR.I	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
1833,86	1832,940	1834,774	1833,90	0,042	K.TYFPHFDLSHGSQVKG	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			1833,80	0,058	R.NPDDITNEEYGEFYK.S	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP 2) (LP5-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
1834,85	1833,932	1835,766	1834,86	0,012	K.CPTPCQLQSEQAFRL.T	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1834,92	0,069	R.KKPLDIDYMGEELR.A	P13805	TNNT1_HUMAN	Troponin T, slow skeletal muscle (TnTs) (Slow skeletal muscle troponin T) (sTnT)	TNNT1
1834,86	1833,942	1835,777	1834,86	0,002	K.CPTPCQLQSEQAFRL.T	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1834,92	0,058	R.KKPLDIDYMGEELR.A	P13805	TNNT1_HUMAN	Troponin T, slow skeletal muscle (TnTs) (Slow skeletal muscle troponin T) (sTnT)	TNNT1
1835,86	1834,947	1836,783	1835,92	0,057	K.VLGSQALHPVHYEEK.N	P21397	AOFA_HUMAN	Amine oxidase [flavin-containing] A (EC 1.4.3.4)	MAOA
			1835,95	0,083	R.QEPSQGTTFVAVTSILR.V	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
1836,87	1835,951	1837,788	1836,79	0,075	R.DGQVINETSQHDDLE.-	P08670	VIME_HUMAN	Vimentin	VIM

1837,87	1836,949	1838,787	1837,89	0,022	K.TPSAAYLVWVGTGASEAEK.T	P06396	GELS_HUMAN	Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF (Brevin))	GSN
			1837,90	0,032	K.SGAQATWTELPWPHEK.V	P02790	HEMO_HUMAN	Hemopexin (Beta-1B-glycoprotein)	HPX
			1838,06	0,190	R.EFVGQLVAPLPLGTGALR.A	Q6PCB0	VWA1_HUMAN	von Willebrand factor A domain-containing protein 1	VWA1
1838,86	1837,941	1839,780	1838,84	0,018	R.TDDYLDQPCLETVNR.I	P31150	GDIA_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			1838,06	0,803	R.EFVGQLVAPLPLGTGALR.A	Q6PCB0	VWA1_HUMAN	von Willebrand factor A domain-containing protein 1	VWA1
1839,86	1838,940	1840,779	1839,90	0,044	R.VMFTEDKLPAFSDAR.E	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
			1839,95	0,087	R.WLVLCNPGLAEVIAER.I	P11217	PYGM_HUMAN	Glycogen phosphorylase, muscle form (EC 2.4.1.1) (Myophosphorylase)	PYGM
1840,44	1839,523	1841,364	1839,95	0,497	R.WLVLCNPGLAEVIAER.I	P11217	PYGM_HUMAN	Glycogen phosphorylase, muscle form (EC 2.4.1.1) (Myophosphorylase)	PYGM
			1839,90	0,540	R.VMFTEDKLPAFSDAR.E	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
1840,87	1839,949	1841,790	1841,89	0,507	K.IVYGHLDPPASQEIER.G	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
1841,38	1840,462	1842,303	1841,90	0,514	R.STGEAFVQFASQEIAEK.A	P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 (hnRNP H2) (FTP-3) (Heterogeneous nuclear ribonucleoprotein H') (hnRNP H') [Cleaved into: Heterogeneous nuclear ribonucleoprotein H2, N-terminally processed]	HNRNP2
			1841,90	0,514	R.STGEAFVQFASQEIAEK.A	P31943	HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H (hnRNP H) [Cleaved into: Heterogeneous nuclear ribonucleoprotein H, N-terminally processed]	HNRNP1
1841,88	1840,961	1842,803	1841,89	0,008	K.IVYGHLDPPASQEIER.G	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
			1841,90	0,015	R.STGEAFVQFASQEIAEK.A	P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 (hnRNP H2) (FTP-3) (Heterogeneous nuclear ribonucleoprotein H') (hnRNP H') [Cleaved into: Heterogeneous nuclear ribonucleoprotein H2, N-terminally processed]	HNRNP2
			1841,90	0,015	R.STGEAFVQFASQEIAEK.A	P31943	HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H (hnRNP H) [Cleaved into: Heterogeneous nuclear ribonucleoprotein H, N-terminally processed]	HNRNP1
1842,88	1841,961	1843,804	1842,86	0,019	K.MLDAEDIVNTPKPDER.A	P35609	ACTN2_HUMAN	Alpha-actinin-2 (Alpha-actinin skeletal muscle isoform 2) (F-ACTN2 actin cross-linking protein)	CD44
			1843,76	0,874	K.ESSETPDQFMTADETR.N	P16070	CD44_HUMAN	CD44 antigen (CDw44) (Epicam) (Extracellular matrix receptor III) (ECMR-III) (GP90 lymphocyte homing/adhesion receptor) (HUTCH-I) (Heparan sulfate proteoglycan) (Hermes antigen) (Hyaluronate receptor) (Phagocytic glycoprotein 1) (PGP-1) (Phagocytic glycoprotein I) (PGP-I) (CD antigen CD44)	CD44
1843,90	1842,978	1844,822	1843,76	0,144	K.ESSETPDQFMTADETR.N	P16070	CD44_HUMAN	CD44 antigen (CDw44) (Epicam) (Extracellular matrix receptor III) (ECMR-III) (GP90 lymphocyte homing/adhesion receptor) (HUTCH-I) (Heparan sulfate proteoglycan) (Hermes antigen) (Hyaluronate receptor) (Phagocytic glycoprotein 1) (PGP-1) (Phagocytic glycoprotein I) (PGP-I) (CD antigen CD44)	CD44
1844,77	1843,846	1845,691	1844,89	0,119	K.EAFSLFDKDGDTITTK.E	P0DP23	CALM1_HUMAN	Calmodulin-1	CALM1
1844,92	1844,002	1845,846	1844,89	0,037	K.EAFSLFDKDGDTITTK.E	P0DP23	CALM1_HUMAN	Calmodulin-1	CALM1
1845,82	1844,893	1846,738							
1845,90	1844,973	1846,819							
1846,74	1845,813	1847,659							
1846,92	1846,001	1847,848	1847,82	0,894	R.SNMDNMFESYNNLR.R	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
			1847,82	0,897	R.NPDDITQEEYGEFYK.S	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
1847,89	1846,968	1848,815	1847,96	0,066	R.QGFGEQLQAVPLADSFR.H	P27695	APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase (EC 3.1.-.-) (EC 4.2.99.18) (APEX nuclease) (APEN) (Apurinic-apyrimidinic endonuclease 1) (AP endonuclease 1) (APE-1) (REF-1) (Redox factor-1) [Cleaved into: DNA-(apurinic or apyrimidinic site) lyase, mitochondrial]	APEX1
			1847,82	0,070	R.NPDDITQEEYGEFYK.S	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			1847,82	0,073	R.SNMDNMFESYNNLR.R	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
1848,89	1847,967	1849,816							
1849,95	1849,022	1850,872	1849,90	0,050	K.TEFLSFMNTELAATK.N	P31949	S10AB_HUMAN	Protein S100-A11 (Calgizzarin) (Metastatic lymph node gene 70 protein) (MLN 70) (Protein S100-C) (S100 calcium-binding protein A11) [Cleaved into: Protein S100-A11, N-terminally processed]	S100A11
1850,90	1849,975	1851,825	1851,79	0,885	R.EQTEGEYSLEHESAR.G	O43837	IDH3B_HUMAN	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial (Isocitric dehydrogenase subunit beta) (NAD(+)-specific IDH subunit beta)	IDH3B
1851,85	1850,926	1852,778	1851,79	0,066	R.EQTEGEYSLEHESAR.G	O43837	IDH3B_HUMAN	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial (Isocitric dehydrogenase subunit beta) (NAD(+)-specific IDH subunit beta)	IDH3B
1851,92	1850,991	1852,843	1851,79	0,132	R.EQTEGEYSLEHESAR.G	O43837	IDH3B_HUMAN	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial (Isocitric dehydrogenase subunit beta) (NAD(+)-specific IDH subunit beta)	IDH3B
1852,86	1851,936	1853,789							
1853,89	1852,967	1854,821	1854,00	0,105	R.IGGVQQDTILAEGLHFR.I	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
1854,86	1853,930	1855,785	1854,98	0,122	K.NPVPQAQDEALYQQLLR.A	O95833	CLIC3_HUMAN	Chloride intracellular channel protein 3	CLIC3
			1854,00	0,858	R.IGGVQQDTILAEGLHFR.I	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
1855,87	1854,941	1856,797	1854,98	0,889	K.NPVPQAQDEALYQQLLR.A	O95833	CLIC3_HUMAN	Chloride intracellular channel protein 3	CLIC3
1856,88	1855,952	1857,809							
1857,89	1856,958	1858,816	1857,94	0,049	K.GEETPVIVGSALCALEGR.D	P49411	EFTU_HUMAN	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	TUFM
			1857,94	0,052	K.MSATFIGNSTAIQELFK.R	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B

1858,86	1857,931	1859,790	1857,94	0,922	K.MSATFIGNSTAIQELFK.R	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1857,94	0,925	K.GEETPVIVGSALCALEGR.D	P49411	EFTU_HUMAN	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	TUFM
1859,90	1858,974	1860,833	1859,91	0,011	R.LFVGNLPDITEEEMR.K	Q15233	NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrb)) (p54nrb)	NONO
			1859,87	0,037	R.CWSPGVTVAPEMCPIR.A	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
1860,89	1859,963	1861,824	1859,96	0,058	R.LDGLVETPTGYIESLPR.V	P55209	NP1L1_HUMAN	Nucleosome assembly protein 1-like 1 (NAP-1-related protein) (hNRP)	NP1L1
			1862,04	0,203	K.APIRPDIVNFVHTNLR.K	P36578	RL4_HUMAN	60S ribosomal protein L4 (60S ribosomal protein L1) (Large ribosomal subunit protein uL4)	RPL4
1861,99	1861,063	1862,925	1862,04	0,050	K.APIRPDIVNFVHTNLR.K	P36578	RL4_HUMAN	60S ribosomal protein L4 (60S ribosomal protein L1) (Large ribosomal subunit protein uL4)	RPL4
			1862,77	0,781	K.FDEYFSQSCAPGSDPR.S	P02788	TRFL_HUMAN	Lactotransferrin (Lactoferrin) (EC 3.4.21.-) (Growth-inhibiting protein 12) (Talaktoferrin) [Cleaved into: Lactoferricin-H (Lfcin-H); Kaliocin-1; Lactoferron-A; Lactoferron-B; Lactoferron-C]	LTF
1862,93	1862,000	1863,863	1863,06	0,132	R.KEGGLGPLNPLIADVTR.R	P32119	PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
			1862,77	0,157	K.FDEYFSQSCAPGSDPR.S	P02788	TRFL_HUMAN	Lactotransferrin (Lactoferrin) (EC 3.4.21.-) (Growth-inhibiting protein 12) (Talaktoferrin) [Cleaved into: Lactoferricin-H (Lfcin-H); Kaliocin-1; Lactoferron-A; Lactoferron-B; Lactoferron-C]	LTF
1863,94	1863,010	1864,873	1863,91	0,028	R.KIPNPDFFELEPFR.M	P27824	CALX_HUMAN	Calnexin (IP90) (Major histocompatibility complex class I antigen-binding protein p88) (p90)	CANX
			1863,06	0,878	R.KEGGLGPLNPLIADVTR.R	P32119	PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
1864,91	1863,978	1865,843	1864,92	0,007	R.AVCMLSNTTAAIEAWAR.L	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			1864,92	0,007	R.AVCMLSNTTAAIEAWAR.L	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
1865,95	1865,021	1866,887	1866,00	0,042	R.AVLMGGSALSPAIVISHER.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1866,91	0,198	R.AVLMGGSALSPAIVISHER.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1866,19	1865,261	1867,127	1866,91	0,713	K.SDALETGLFNHYQMK.N	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
			1866,92	0,729	K.GSDHSASLEPGELAEIVR.S	Q9NR45	SIA5_HUMAN	Sialic acid synthase (N-acetylneuraminase synthase) (EC 2.5.1.56) (N-acetylneuraminase-9-phosphate synthase) (EC 2.5.1.57) (N-acetylneuraminic acid phosphate synthase) (N-acetylneuraminic acid synthase)	NANS
1866,95	1866,021	1867,888	1866,92	0,031	K.GSDHSASLEPGELAEIVR.S	Q9NR45	SIA5_HUMAN	Sialic acid synthase (N-acetylneuraminase synthase) (EC 2.5.1.56) (N-acetylneuraminase-9-phosphate synthase) (EC 2.5.1.57) (N-acetylneuraminic acid phosphate synthase) (N-acetylneuraminic acid synthase)	NANS
			1866,91	0,047	K.SDALETGLFNHYQMK.N	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
1867,19	1866,256	1868,123	1867,80	0,841	K.ELGKMVVDCTDPDGR.A	O60733	PLP9_HUMAN	85/88 kDa calcium-independent phospholipase A2 (Cal-PLA2) (EC 3.1.1.4) (Group VI phospholipase A2) (GVI PLA2) (Intracellular membrane-associated calcium-independent phospholipase A2 beta) (iPLA2-beta) (Patatin-like phospholipase domain-containing protein 9) (PNPLA9)	PLA2G6
			1867,85	0,900	K.SKPGAAMVEMADGYAVDR.A	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
1867,19	1866,256	1868,123	1866,92	0,267	K.GSDHSASLEPGELAEIVR.S	Q9NR45	SIA5_HUMAN	Sialic acid synthase (N-acetylneuraminase synthase) (EC 2.5.1.56) (N-acetylneuraminase-9-phosphate synthase) (EC 2.5.1.57) (N-acetylneuraminic acid phosphate synthase) (N-acetylneuraminic acid synthase)	NANS
			1866,91	0,282	K.SDALETGLFNHYQMK.N	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
1868,02	1867,085	1868,953	1867,80	0,605	K.ELGKMVVDCTDPDGR.A	O60733	PLP9_HUMAN	85/88 kDa calcium-independent phospholipase A2 (Cal-PLA2) (EC 3.1.1.4) (Group VI phospholipase A2) (GVI PLA2) (Intracellular membrane-associated calcium-independent phospholipase A2 beta) (iPLA2-beta) (Patatin-like phospholipase domain-containing protein 9) (PNPLA9)	PLA2G6
			1867,85	0,665	K.SKPGAAMVEMADGYAVDR.A	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
1868,02	1867,085	1868,953	1867,95	0,759	K.ITGEAFVQFASQELAEK.A	P52597	HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein F, N-terminally processed]	HNRNPF
			1867,95	0,070	K.ITGEAFVQFASQELAEK.A	P52597	HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein F, N-terminally processed]	HNRNPF
1868,02	1867,085	1868,953	1867,85	0,165	K.SKPGAAMVEMADGYAVDR.A	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
			1867,80	0,224	K.ELGKMVVDCTDPDGR.A	O60733	PLP9_HUMAN	85/88 kDa calcium-independent phospholipase A2 (Cal-PLA2) (EC 3.1.1.4) (Group VI phospholipase A2) (GVI PLA2) (Intracellular membrane-associated calcium-independent phospholipase A2 beta) (iPLA2-beta) (Patatin-like phospholipase domain-containing protein 9) (PNPLA9)	PLA2G6
1868,02	1867,085	1868,953	1868,95	0,927	R.EQEELLAPDGTVELVR.A	P19971	TYPH_HUMAN	Thymidine phosphorylase (TP) (EC 2.4.2.4) (Gliostatin) (Platelet-derived endothelial cell growth factor) (PD-ECGF) (TDRPase)	TYMP
			1868,95	0,931	K.LAMQEFMILPVGASSFK.E	P13929	ENOB_HUMAN	Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 3) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase)	ENO3

1868,95	1868,017	1869,886	1868,95	0,001	K.LAMQEFMILPVGASSFK.E	P13929	ENOB_HUMAN	Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 3) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase)	ENO3
			1868,95	0,005	R.EQEELLAPADGTVELVR.A	P19971	TYPH_HUMAN	Thymidine phosphorylase (TP) (EC 2.4.2.4) (Gliostatin) (Platelet-derived endothelial cell growth factor) (PD-ECGF) (TdRPase)	TYMP
			1869,76	0,809	R.FPEVSGYCHCADSQGR.E	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1869,87	1868,937	1870,807	1869,76	0,112	R.FPEVSGYCHCADSQGR.E	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1868,95	0,922	K.LAMQEFMILPVGASSFK.E	P13929	ENOB_HUMAN	Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 3) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase)	ENO3
			1868,95	0,926	R.EQEELLAPADGTVELVR.A	P19971	TYPH_HUMAN	Thymidine phosphorylase (TP) (EC 2.4.2.4) (Gliostatin) (Platelet-derived endothelial cell growth factor) (PD-ECGF) (TdRPase)	TYMP
1870,86	1869,929	1871,800	1872,87	0,032	R.QQTHMLDVMQDHFISR.A	P10909	CLUS_HUMAN	Clusterin (Aging-associated gene 4 protein) (Apolipoprotein J) (Apo-J) (Complement cytotoxicity inhibitor) (CLU) (Complement-associated protein SP-40,40) (Ku70-binding protein 1) (NA1/NA2) (Sulfated glycoprotein 2) (SGP-2) (Testosterone-repressed prostate message 2) (TRPM-2) [Cleaved into: Clusterin beta chain (ApoIalpha) (Complement cytotoxicity inhibitor a chain); Clusterin alpha chain (ApoIbeta) (Complement cytotoxicity inhibitor b chain)]	CLU
1871,88	1870,946	1872,818							
1872,90	1871,964	1873,837							
1873,92	1872,981	1874,855	1873,90	0,014	K.TTPPVLDSDGSFFLYSK.L	P01857	IGHG1_HUMAN	Immunoglobulin heavy constant gamma 1 (Ig gamma-1 chain C region) (Ig gamma-1 chain C region EU) (Ig gamma-1 chain C region KOL) (Ig gamma-1 chain C region NIE)	IGHG1
			1874,00	0,083	K.LFDSDPITVTVPVEVSR.K	P10909	CLUS_HUMAN	Clusterin (Aging-associated gene 4 protein) (Apolipoprotein J) (Apo-J) (Complement cytotoxicity inhibitor) (CLU) (Complement-associated protein SP-40,40) (Ku70-binding protein 1) (NA1/NA2) (Sulfated glycoprotein 2) (SGP-2) (Testosterone-repressed prostate message 2) (TRPM-2) [Cleaved into: Clusterin beta chain (ApoIalpha) (Complement cytotoxicity inhibitor a chain); Clusterin alpha chain (ApoIbeta) (Complement cytotoxicity inhibitor b chain)]	CLU
			1874,94	0,004	K.LPGLGNFPGPFEEEMK.G	Q13510	ASAH1_HUMAN	Acid ceramidase (AC) (ACDase) (Acid CDase) (EC 3.5.1.23) (Acylsphingosine deacylase) (N-acyl ethanolamine hydrolase ASAH1) (EC 3.5.1.-) (N-acylsphingosine amidohydrolase) (Putative 32 kDa heart protein) (PHP32) [Cleaved into: Acid ceramidase subunit alpha; Acid ceramidase subunit beta]	ASAH1
1874,93	1873,994	1875,869	1874,88	0,055	K.ATEDEGSEQKIPEATNR.R	P01008	ANT3_HUMAN	Antithrombin-III (ATIII) (Serpin C1)	SERPINC1
			1874,00	0,930	K.LFDSDPITVTVPVEVSR.K	P10909	CLUS_HUMAN	Clusterin (Aging-associated gene 4 protein) (Apolipoprotein J) (Apo-J) (Complement cytotoxicity inhibitor) (CLU) (Complement-associated protein SP-40,40) (Ku70-binding protein 1) (NA1/NA2) (Sulfated glycoprotein 2) (SGP-2) (Testosterone-repressed prostate message 2) (TRPM-2) [Cleaved into: Clusterin beta chain (ApoIalpha) (Complement cytotoxicity inhibitor a chain); Clusterin alpha chain (ApoIbeta) (Complement cytotoxicity inhibitor b chain)]	CLU
			1875,93	0,015	K.VYACEVTHQGLSPVTK.S	P01834	IGKC_HUMAN	Immunoglobulin kappa constant (Ig kappa chain C region) (Ig kappa chain C region AG) (Ig kappa chain C region CUM) (Ig kappa chain C region EU) (Ig kappa chain C region OU) (Ig kappa chain C region ROY) (Ig kappa chain C region TI)	IGKC
1876,90	1875,962	1877,839	1876,83	0,889	R.SEPSKLPCTPGSCEEAK.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1876,83	0,070	R.SEPSKLPCTPGSCEEAK.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1876,99	0,088	R.AGKPVICATQMLESMIK.K	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
1877,91	1876,971	1878,849	1877,00	0,103	R.LQEAAELEAVLPVPIR.F	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
			1877,91	0,005	K.LSPPYSSPQEFQAQDVGR.M	Q13263	TIF1B_HUMAN	Transcription intermediary factor 1-beta (TIF1-beta) (E3 SUMO-protein ligase TRIM28) (EC 2.3.2.27) (KRAB-associated protein 1) (KAP-1) (KRAB-interacting protein 1) (KRIP-1) (Nuclear corepressor KAP-1) (RING finger protein 96) (RING-type E3 ubiquitin transferase TIF1-beta) (Tripartite motif-containing protein 28)	TRIM28
			1877,93	0,019	R.YPSLSLHGIEGAFSGGAK.T	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
1877,91	1876,971	1878,849	1877,87	0,038	R.EITENLMATGOLDQDGR.I	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
			1877,00	0,906	R.LQEAAELEAVLPVPIR.F	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
			1876,99	0,921	R.AGKPVICATQMLESMIK.K	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
1878,92	1877,977	1879,856	1878,94	0,019	K.GQETSTNPIASIFAWTR.G	O75874	IDHC_HUMAN	Isocitrate dehydrogenase [NADP] cytoplasmic (IDH) (EC 1.1.1.42) (Cytosolic NADP-isocitrate dehydrogenase) (IDP) (NADP(+)-specific ICDH) (Oxalosuccinate decarboxylase)	IDH1
1879,93	1878,986	1880,866	1879,97	0,043	K.IFVGGIKEDTEEHILR.D	Q32P51	RA1L2_HUMAN	Heterogeneous nuclear ribonucleoprotein A1-like 2 (hnRNP A1-like 2) (hnRNP core protein A1-like 2)	HNRNPA1L2
			1879,97	0,043	K.LFVGGIKEDTEEHILR.D	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			1879,86	0,067	K.VGEFEEQTVDGRPCK.S	P29373	RABP2_HUMAN	Cellular retinoic acid-binding protein 2 (Cellular retinoic acid-binding protein II) (CRABP-II)	CRABP2
1880,93	1879,987	1881,868	1880,91	0,018	R.AVCMLNSTTAAIEAWAR.L	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A

1881,94	1880,996	1882,878	1880,91	0,018	R.AVCMLSNTTAAIEAWAR.L	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
			1880,91	0,018	R.AVCMLSNTTAAIEAWAR.L	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			1881,89	0,043	K.ADRDQYELLCLDNTR.K	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1881,99 1881,88	0,052 0,062	R.AVLMGGSAPAAVISHER.A R.EHPWEVMPDLYFYR.D	P01266 P08865	THYG_HUMAN RSSA_HUMAN	Thyroglobulin (Tg) 40S ribosomal protein SA (37 kDa laminin receptor precursor) (37LRP) (37/67 kDa laminin receptor) (LRP/LR) (67 kDa laminin receptor) (67LR) (Colon carcinoma laminin-binding protein) (Laminin receptor 1) (LamR) (Laminin-binding protein precursor p40) (LBP/p40) (Multidrug resistance-associated protein MGR1-Ag) (NEM/1CHD4) (Small ribosomal subunit protein uS2)	TG RPSA
1882,93	1881,989	1883,872	1882,93	0,001	K.SDALETGLFNHYQMK.N	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
			1882,91	0,019	R.WGTDEDKTEILCLR.S	P12429	ANXA3_HUMAN	Annexin A3 (35-alpha calcimedin) (Annexin III) (Annexin-3) (Inositol 1,2-cyclic phosphate 2-phosphohydrolase) (Lipocortin III) (Placental anticoagulant protein III) (PAP-III)	ANXA3
			1882,97	0,036	K.IFVGKIDETEEYNLR.D	P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3
1883,95	1883,007	1884,891	1883,96	0,007	K.FQDGLTLYQSNTILR.H	P09211	GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1)	GSTP1
			1883,94	0,009	R.NEEDAAELVALAQAVNAR.A	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
			1883,91	0,034	R.LNFSHGTHEYHAETIK.N	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
1884,96	1884,015	1885,900	1884,94	0,021	R.SVPTSTVFYPSDGVATEK.A	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
			1884,98	0,027	R.ELAILLGMLDPAEKDEK.G	P30041	PRDX6_HUMAN	Peroxiredoxin-6 (EC 1.11.1.15) (1-Cys peroxiredoxin) (1-Cys PRX) (24 kDa protein) (Acidic calcium-independent phospholipase A2) (aiPLA2) (EC 3.1.1.4) (Antioxidant protein 2) (Liver 2D page spot 40) (Non-selenium glutathione peroxidase) (NSGPs) (Red blood cells page spot 12)	PRDX6
			1884,91	0,047	K.NATNVEQSFMTMAAEIK.K	P62820	RAB1A_HUMAN	Ras-related protein Rab-1A (YPT1-related protein)	RAB1A
1885,86	1884,917	1886,803	1885,93	0,068	R.TDITYPAGFMVDISIDK.T	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein eS4)	RP54X
			1884,98	0,876	R.ELAILLGMLDPAEKDEK.G	P30041	PRDX6_HUMAN	Peroxiredoxin-6 (EC 1.11.1.15) (1-Cys peroxiredoxin) (1-Cys PRX) (24 kDa protein) (Acidic calcium-independent phospholipase A2) (aiPLA2) (EC 3.1.1.4) (Antioxidant protein 2) (Liver 2D page spot 40) (Non-selenium glutathione peroxidase) (NSGPs) (Red blood cells page spot 12)	PRDX6
			1884,94	0,924	R.SVPTSTVFYPSDGVATEK.A	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
1885,98	1885,040	1886,926	1885,93	0,055	R.TDITYPAGFMVDISIDK.T	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein eS4)	RP54X
			1886,90	0,920	R.HRHPDEAAFFDTASTGK.T	P02671	FIBA_HUMAN	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	FGA
			1886,91	0,009	R.HRHPDEAAFFDTASTGK.T	P02671	FIBA_HUMAN	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	FGA
1887,96 1888,93	1887,013 1887,988	1888,901 1889,877	1888,95	0,019	R.EQHILYQDQLLPVSR.I	Q15661	TRYB1_HUMAN	Tryptase alpha/beta-1 (Tryptase-1) (EC 3.4.21.59) (Tryptase I) (Tryptase alpha-1)	TPSAB1
			1888,95	0,019	R.QQGRPVACLSFCQLQK.Q	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1889,92 1890,92	0,911	K.DTEEDFHVDQVTVTK.V	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiprotease) (Serp1 A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
1891,94	1890,991	1892,883	1891,85	0,923	R.DAINQGMDEELERDEK.V	P11177	ODPB_HUMAN	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial (PDHE1-B) (EC 1.2.4.1)	PDHB
			1891,92	0,019	K.ADEDPIMGFHMFLK.N	P61970	NTF2_HUMAN	Nuclear transport factor 2 (NTF-2) (Placental protein 15) (PP15)	NUTF2
			1891,88	0,055	R.LYGSEAFATDFQDSAAAK.K	P01011	AACT_HUMAN	Alpha-1-antichymotrypsin (ACT) (Cell growth-inhibiting gene 24/25 protein) (Serp1 A3) [Cleaved into: Alpha-1-antichymotrypsin His-Pro-less]	SERPINA3
			1891,85	0,091	R.DAINQGMDEELERDEK.V	P11177	ODPB_HUMAN	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial (PDHE1-B) (EC 1.2.4.1)	PDHB
1892,91 1893,86 1893,99	1891,964 1892,911 1893,043	1893,857 1894,805 1894,937	1891,84	0,911	K.DTEEDFHVDQVTVTK.V	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiprotease) (Serp1 A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
			1894,89	0,897	R.EQQHVMEEFQSSFR.R	P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	PRKDC
			1894,94	0,050	R.EQQHVMEEFQSSFR.R	P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	PRKDC
			1896,80	0,848	K.SEEAHAEDSVMDHHRF.K	Q8NC51	PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein (PAI1 RNA-binding protein 1) (PAI-RBP1) (SERPINE1 mRNA-binding protein 1)	SERBP1
1895,95	1895,003	1896,899	1896,80	0,850	R.GNWDEQFDKENTEER.L	P35237	SPB6_HUMAN	Serp1 B6 (Cytoplasmic antiprotease) (CAP) (Peptidase inhibitor 6) (PI-6) (Placental thrombin inhibitor)	SERPINB6
			1896,80	0,159	R.GNWDEQFDKENTEER.L	P35237	SPB6_HUMAN	Serp1 B6 (Cytoplasmic antiprotease) (CAP) (Peptidase inhibitor 6) (PI-6) (Placental thrombin inhibitor)	SERPINB6
			1896,80	0,161	K.SEEAHAEDSVMDHHRF.K	Q8NC51	PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein (PAI1 RNA-binding protein 1) (PAI-RBP1) (SERPINE1 mRNA-binding protein 1)	SERBP1

1897,96 1898,96	1897,014 1898,012	1898,912 1899,911	1899,01	0,046	R.RHPYFYAPELFFAK.R	P02768	ALBU_HUMAN	Serum albumin	ALB
1899,97 1900,95 1901,96	1899,017 1899,996 1901,007	1900,917 1901,897 1902,909	1901,91	0,044	K.TTPPVLDSDGSFFLYSR.L	P01861	IGHG4_HUMAN	Immunoglobulin heavy constant gamma 4 (Ig gamma-4 chain C region)	IGHG4
			1902,82	0,863	R.TDDYLDQPCYETINR.I	P50395	GDI8_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
			1902,86	0,902	R.GPSWDPFRDWYPHSR.L	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	HSPB1
			1902,87	0,915	K.AGSMKDPLLDHGDIFIR.M	Q9UM54	MYO6_HUMAN	Unconventional myosin-VI (Unconventional myosin-6)	MYO6
1902,96	1902,006	1903,909	1902,87	0,085	K.AGSMKDPLLDHGDIFIR.M	Q9UM54	MYO6_HUMAN	Unconventional myosin-VI (Unconventional myosin-6)	MYO6
			1902,86	0,098	R.GPSWDPFRDWYPHSR.L	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	HSPB1
			1902,82	0,137	R.TDDYLDQPCYETINR.I	P50395	GDI8_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
1903,96	1903,007	1904,911	1904,77	0,812	R.DCHEEYVYAGSHQYGR.G	Q9H3P7	GCP60_HUMAN	Golgi resident protein GCP60 (Acyl-CoA-binding domain-containing protein 3) (Golgi complex-associated protein 1) (GOCAP1) (Golgi phosphoprotein 1) (GOLPH1) (PBR- and PKA-associated protein 7) (Peripheral benzodiazepine receptor-associated protein PAP7) [Cleaved into: Golgi resident protein GCP60, N-terminally processed]	ACBD3
1904,96	1904,008	1905,913	1904,92	0,037	R.SLLEGQEDHYNNLSASK.V	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1904,77	0,190	R.DCHEEYVYAGSHQYGR.G	Q9H3P7	GCP60_HUMAN	Golgi resident protein GCP60 (Acyl-CoA-binding domain-containing protein 3) (Golgi complex-associated protein 1) (GOCAP1) (Golgi phosphoprotein 1) (GOLPH1) (PBR- and PKA-associated protein 7) (Peripheral benzodiazepine receptor-associated protein PAP7) [Cleaved into: Golgi resident protein GCP60, N-terminally processed]	ACBD3
			1905,88	0,917	K.TTPPMLDSDGSFFLYSK.L	P01859	IGHG2_HUMAN	Immunoglobulin heavy constant gamma 2 (Ig gamma-2 chain C region) (Ig gamma-2 chain C region DOT) (Ig gamma-2 chain C region TIL) (Ig gamma-2 chain C region ZIE)	IGHG2
1905,97	1905,017	1906,923	1905,99	0,022	K.LATQSNIEIPTVFESR.A	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	HSPB1
			1905,88	0,093	K.TTPPMLDSDGSFFLYSK.L	P01859	IGHG2_HUMAN	Immunoglobulin heavy constant gamma 2 (Ig gamma-2 chain C region) (Ig gamma-2 chain C region DOT) (Ig gamma-2 chain C region TIL) (Ig gamma-2 chain C region ZIE)	IGHG2
			1906,86	0,886	R.EFEEESKQPGVSEQQR.H	Q94776	MTA2_HUMAN	Metastasis-associated protein MTA2 (Metastasis-associated 1-like 1) (MTA1-L1 protein) (p53 target protein in deacetylase complex)	MTA2
			1906,87	0,897	K.GGQSAESEEELTAGSGLR.E	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1906,98	1906,025	1907,932	1906,87	0,112	K.GGQSAESEEELTAGSGLR.E	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1906,86	0,123	R.EFEEESKQPGVSEQQR.H	Q94776	MTA2_HUMAN	Metastasis-associated protein MTA2 (Metastasis-associated 1-like 1) (MTA1-L1 protein) (p53 target protein in deacetylase complex)	MTA2
			1907,91	0,932	R.FSPNSSNPIIVSCGWDK.L	P63244	RACK1_HUMAN	Receptor of activated protein C kinase 1 (Cell proliferation-inducing gene 21 protein) (Guanine nucleotide-binding protein subunit beta-2-like 1) (Guanine nucleotide-binding protein subunit beta-like protein 12.3) (Human lung cancer oncogene 7 protein, HLC-7) (Receptor for activated C kinase) (Small ribosomal subunit protein RACK1) [Cleaved into: Receptor of activated protein C kinase 1, N-terminally processed (Guanine nucleotide-binding protein subunit beta-2-like 1, N-terminally processed)]	RACK1
1907,97	1907,016	1908,924	1908,00	0,034	K.LAMQEFMILPVGAANFR.E	P06733	ENO4_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			1907,91	0,059	R.FSPNSSNPIIVSCGWDK.L	P63244	RACK1_HUMAN	Receptor of activated protein C kinase 1 (Cell proliferation-inducing gene 21 protein) (Guanine nucleotide-binding protein subunit beta-2-like 1) (Guanine nucleotide-binding protein subunit beta-like protein 12.3) (Human lung cancer oncogene 7 protein, HLC-7) (Receptor for activated C kinase) (Small ribosomal subunit protein RACK1) [Cleaved into: Receptor of activated protein C kinase 1, N-terminally processed (Guanine nucleotide-binding protein subunit beta-2-like 1, N-terminally processed)]	RACK1
			1908,87	0,902	R.AEDGSVIDYELIDQDAR.D	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
1908,97	1908,016	1909,925	1908,95	0,016	K.LPGGELNPGDEVEGLKR.L	O43809	CPSF5_HUMAN	Cleavage and polyadenylation specificity factor subunit 5 (Cleavage and polyadenylation specificity factor 25 kDa subunit) (CPSF 25 kDa subunit) (Cleavage factor Im complex 25 kDa subunit) (Cflm25) (Nucleoside diphosphate-linked moiety X motif 21) (Nudix motif 21) (Nudix hydrolase 21) (Pre-mRNA cleavage factor Im 68 kDa subunit)	NUDT21
			1908,99	0,021	K.SILVASLAEPDFVTFDAK.F	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
			1908,87	0,099	R.AEDGSVIDYELIDQDAR.D	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1909,91	0,945	K.EHNGQVTGIDWAPESNR.I	O15143	ARC1B_HUMAN	Actin-related protein 2/3 complex subunit 1B (Arp2/3 complex 41 kDa subunit) (p41-ARC)	ARPC1B

1909,96	1909,001	1910,911	1909,93	0,027	R.EGPYSISVLYGDDEVPR.S	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			1909,91	0,041	K.EHNGQVTGIDWAPESNR.I	O15143	ARC1B_HUMAN	Actin-related protein 2/3 complex subunit 1B (Arp2/3 complex 41 kDa subunit) (p41-ARC)	ARPC1B
			1910,78	0,826	R.SSGSPYGGGYGGGGGGYGSR.R	P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3
1910,89	1909,935	1911,846	1910,94	0,047	R.RPCFSALEVDETYVPK.E	P02768	ALBU_HUMAN	Serum albumin	ALB
			1910,78	0,109	R.SSGSPYGGGYGGGGGGYGSR.R	P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3
1910,98	1910,022	1911,933	1910,94	0,040	R.RPCFSALEVDETYVPK.E	P02768	ALBU_HUMAN	Serum albumin	ALB
			1910,78	0,196	R.SSGSPYGGGYGGGGGGYGSR.R	P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3
1911,96	1911,001	1912,913	1912,98	0,011	R.KLFIGGLSFETTEDSLR.S	Q32P51	RA1L2_HUMAN	Heterogeneous nuclear ribonucleoprotein A1-like 2 (hnRNP A1-like 2) (hnRNP core protein A1-like 2)	HNRNPA1L2
1912,97	1912,013	1913,926							
1913,97	1913,017	1914,931	1914,91	0,932	K.EQQDEFKEAFLLFDR.T	P05976	MYL1_HUMAN	Myosin light chain 1/3, skeletal muscle isoform (MLC1/MLC3) (MLC1F/MLC3F) (Myosin light chain alkali 1/2) (Myosin light chain A1/A2)	MYL1
			1914,92	0,948	K.LFDYFPKYPNSEAAR.A	P08574	CY1_HUMAN	Cytochrome c1, heme protein, mitochondrial (Complex III subunit 4) (Complex III subunit IV) (Cytochrome b-c1 complex subunit 4) (Ubiquinol-cytochrome-c reductase complex cytochrome c1 subunit) (Cytochrome c-1)	CYC1
1914,97	1914,016	1915,931	1914,92	0,051	K.LFDYFPKYPNSEAAR.A	P08574	CY1_HUMAN	Cytochrome c1, heme protein, mitochondrial (Complex III subunit 4) (Complex III subunit IV) (Cytochrome b-c1 complex subunit 4) (Ubiquinol-cytochrome-c reductase complex cytochrome c1 subunit) (Cytochrome c-1)	CYC1
			1914,91	0,068	K.EQQDEFKEAFLLFDR.T	P05976	MYL1_HUMAN	Myosin light chain 1/3, skeletal muscle isoform (MLC1/MLC3) (MLC1F/MLC3F) (Myosin light chain alkali 1/2) (Myosin light chain A1/A2)	MYL1
1915,99	1915,031	1916,947	1915,93	0,057	K.GFIGPGIDVPAPDMSTGER.E	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
1916,95	1915,994	1917,911	1917,82	0,863	R.TYDATHTHFETTCDDIK.N	P50395	GDI2_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
1917,96	1917,001	1918,919	1917,94	0,021	K.SIQEIQLDKDDESLR.K	P52565	GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)	ARHGDI1A
			1917,82	0,144	R.TYDATHTHFETTCDDIK.N	P50395	GDI2_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
			1918,85	0,893	R.EVQGNESDLFMSYFPR.G	P40121	CAPG_HUMAN	Macrophage-capping protein (Actin regulatory protein CAP-G)	CAPG
1918,98	1918,016	1919,935	1918,96	0,012	R.ATENDIANFFSPLNPIR.V	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNPH3
			1919,07	0,094	K.VLDSGAPIKIPVGPETLGR.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP ATP5F1B synthase F1 subunit beta)	
			1919,08	0,106	K.ISSIQSVPALEIANAHR.K	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
			1918,85	0,123	R.EVQGNESDLFMSYFPR.G	P40121	CAPG_HUMAN	Macrophage-capping protein (Actin regulatory protein CAP-G)	CAPG
			1919,95	0,035	R.GECVPGEQEPELIPILR.V	P02760	AMBP_HUMAN	Protein AMBP [Cleaved into: Alpha-1-microglobulin (Protein HC) (Alpha-1 microglycoprotein) (Complex-forming glycoprotein heterogeneous in charge); Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (EDC1) (HI-30) (Uronic-acid-rich protein); Trypsatin]	AMBP
			1920,89	0,904	R.DSNYHLLMSVQESLER.K	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			1919,08	0,907	K.ISSIQSVPALEIANAHR.K	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
			1919,07	0,919	K.VLDSGAPIKIPVGPETLGR.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP ATP5F1B synthase F1 subunit beta)	
1921,00	1920,039	1921,960	1920,89	0,107	R.DSNYHLLMSVQESLER.K	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
1921,97	1921,006	1922,928	1922,88	0,915	R.DESSPYAAMLAQDVAQR.C	P62263	RS14_HUMAN	40S ribosomal protein S14 (Small ribosomal subunit protein uS11)	RPS14
1922,95	1921,992	1923,914	1922,88	0,071	R.DESSPYAAMLAQDVAQR.C	P62263	RS14_HUMAN	40S ribosomal protein S14 (Small ribosomal subunit protein uS11)	RPS14
1923,98	1923,021	1924,945	1923,95	0,030	R.QAAPCVLFFDELDIAK.A	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (155 Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
1924,95 1926,01	1923,985 1925,045	1925,910 1926,971	1926,06	0,051	R.VTWAPPSIDLTNFLVR.Y	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
1927,02	1926,054	1927,981	1927,01	0,003	R.KLFIGGLSFETTESLR.N	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			1927,03	0,011	R.FIATTPNSLLVSWQPPR.A	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			1927,84	0,825	K.MMDYLQSGSETPQTDVR.W	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			1927,86	0,841	R.SSYVYVSGNDPAAEPSR.A	P46821	MAP1B_HUMAN	Microtubule-associated protein 1B (MAP-1B) [Cleaved into: MAP1B heavy chain; MAP1 light chain LC1]	MAP1B
			1926,06	0,959	R.VTWAPPSIDLTNFLVR.Y	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
1927,52	1926,556	1928,483	1927,84	0,324	K.MMDYLQSGSETPQTDVR.W	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			1927,86	0,339	R.SSYVYVSGNDPAAEPSR.A	P46821	MAP1B_HUMAN	Microtubule-associated protein 1B (MAP-1B) [Cleaved into: MAP1B heavy chain; MAP1 light chain LC1]	MAP1B

1928,01	1927,050	1928,978	1927,03	0,491	R.FIATTPNSLLVSWQPPR.A	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			1927,01	0,505	R.KLFIGGLSFETTEESLR.N	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			1927,86	0,156	R.SSYVYVSGNDPAEEPSR.A	P46821	MAP1B_HUMAN	Microtubule-associated protein 1B (MAP-1B) [Cleaved into: MAP1B heavy chain; MAP1 light chain LC1]	MAP1B
			1927,84	0,171	K.MMDYLQSGSETPQTDVR.W	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1928,45	1927,489	1929,417	1928,94	0,929	R.TALAEAELEYNPEHVS.R.S	Q9NSE4	SYIM_HUMAN	Isoleucine-tRNA ligase, mitochondrial (EC 6.1.1.5) (Isoleucyl-tRNA synthetase) (IleRS)	IARS2
			1928,94	0,491	R.TALAEAELEYNPEHVS.R.S	Q9NSE4	SYIM_HUMAN	Isoleucine-tRNA ligase, mitochondrial (EC 6.1.1.5) (Isoleucyl-tRNA synthetase) (IleRS)	IARS2
			1927,86	0,595	R.SSYVYVSGNDPAEEPSR.A	P46821	MAP1B_HUMAN	Microtubule-associated protein 1B (MAP-1B) [Cleaved into: MAP1B heavy chain; MAP1 light chain LC1]	MAP1B
			1927,84	0,610	K.MMDYLQSGSETPQTDVR.W	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1929,01	1928,041	1929,970	1928,94	0,062	R.TALAEAELEYNPEHVS.R.S	Q9NSE4	SYIM_HUMAN	Isoleucine-tRNA ligase, mitochondrial (EC 6.1.1.5) (Isoleucyl-tRNA synthetase) (IleRS)	IARS2
			1929,89	0,887	K.SGVYQHVVTGEMMGGAIR.I	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
1929,90	1928,931	1930,861	1929,89	0,004	K.SGVYQHVVTGEMMGGAIR.I	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
			1928,94	0,953	R.TALAEAELEYNPEHVS.R.S	Q9NSE4	SYIM_HUMAN	Isoleucine-tRNA ligase, mitochondrial (EC 6.1.1.5) (Isoleucyl-tRNA synthetase) (IleRS)	IARS2
1930,00	1929,036	1930,966	1929,89	0,108	K.SGVYQHVVTGEMMGGAIR.I	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
			1931,17	0,183	K.VTIAQGGVLPNIQAVLLPK.K	Q96KK5	H2A1H_HUMAN	Histone H2A type 1-H (Histone H2A/s)	HIST1H2AH
1930,99	1930,020	1931,951	1931,93	0,949	K.GEMMDLQHGSLFLQTPK.I	P07195	LDHB_HUMAN	L-lactate dehydrogenase B chain (LDH-B) (EC 1.1.1.27) (LDH heart subunit) (LDH-H) (Renal carcinoma antigen NY-REN-46)	LDHB
			1932,02	0,037	R.LEDIPVASLPDLHDIER.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1931,99	0,073	R.EAEAIYHLQLFEELR.R	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
			1931,93	0,126	K.GEMMDLQHGSLFLQTPK.I	P07195	LDHB_HUMAN	L-lactate dehydrogenase B chain (LDH-B) (EC 1.1.1.27) (LDH heart subunit) (LDH-H) (Renal carcinoma antigen NY-REN-46)	LDHB
1932,06	1931,094	1933,026	1931,17	0,892	K.VTIAQGGVLPNIQAVLLPK.K	Q96KK5	H2A1H_HUMAN	Histone H2A type 1-H (Histone H2A/s)	HIST1H2AH
			1932,97	0,909	R.EQLGPVTQEFWDNLEK.E	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
			1932,99	0,931	R.AAVATFLQSVQVPEFTPK.S	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
			1932,99	0,069	R.AAVATFLQSVQVPEFTPK.S	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
1933,06	1932,094	1934,027	1932,99	0,069	R.AAVATFLQSVQVPEFTPK.S	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
			1932,97	0,092	R.EQLGPVTQEFWDNLEK.E	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
1934,04	1933,077	1935,011	1934,80	0,755	R.LYHSCADPTGCGTGPDAR.A	Q9UHL4	DPP2_HUMAN	Dipeptidyl peptidase 2 (EC 3.4.14.2) (Dipeptidyl aminopeptidase II) (Dipeptidyl peptidase 7) (Dipeptidyl peptidase II) (DPP II) (Quiescent cell proline dipeptidase)	DPP7
			1934,84	0,796	R.EVQGNESDLFMSYFPR.G	P40121	CAPG_HUMAN	Macrophage-capping protein (Actin regulatory protein CAP-G)	CAPG
			1934,84	0,152	R.EVQGNESDLFMSYFPR.G	P40121	CAPG_HUMAN	Macrophage-capping protein (Actin regulatory protein CAP-G)	CAPG
			1934,80	0,193	R.LYHSCADPTGCGTGPDAR.A	Q9UHL4	DPP2_HUMAN	Dipeptidyl peptidase 2 (EC 3.4.14.2) (Dipeptidyl aminopeptidase II) (Dipeptidyl peptidase 7) (Dipeptidyl peptidase II) (DPP II) (Quiescent cell proline dipeptidase)	DPP7
1935,04	1934,075	1936,010	1935,90	0,912	K.NLDSTTVAVHGEEYCK.S	P21291	CSRP1_HUMAN	Cysteine and glycine-rich protein 1 (Cysteine-rich protein 1) (CRP) (CRP1) (Epididymis luminal protein 141) (HEL-141)	CSRP1
			1934,84	0,203	R.EVQGNESDLFMSYFPR.G	P40121	CAPG_HUMAN	Macrophage-capping protein (Actin regulatory protein CAP-G)	CAPG
			1934,80	0,244	R.LYHSCADPTGCGTGPDAR.A	Q9UHL4	DPP2_HUMAN	Dipeptidyl peptidase 2 (EC 3.4.14.2) (Dipeptidyl aminopeptidase II) (Dipeptidyl peptidase 7) (Dipeptidyl peptidase II) (DPP II) (Quiescent cell proline dipeptidase)	DPP7
			1935,90	0,862	K.NLDSTTVAVHGEEYCK.S	P21291	CSRP1_HUMAN	Cysteine and glycine-rich protein 1 (Cysteine-rich protein 1) (CRP) (CRP1) (Epididymis luminal protein 141) (HEL-141)	CSRP1
1936,03	1935,061	1936,997	1935,90	0,125	K.NLDSTTVAVHGEEYCK.S	P21291	CSRP1_HUMAN	Cysteine and glycine-rich protein 1 (Cysteine-rich protein 1) (CRP) (CRP1) (Epididymis luminal protein 141) (HEL-141)	CSRP1
			1937,02	0,905	K.EASSVSDFNQNFVEVPNR.I	P41218	MNDA_HUMAN	Myeloid cell nuclear differentiation antigen	MNDA
1938,02	1937,051	1938,989	1939,87	0,939	K.YFLHQSHEREHAEL.K	P02794	FRIH_HUMAN	Ferritin heavy chain (Ferritin H subunit) (EC 1.16.3.1) (Cell proliferation-inducing gene 15 protein) [Cleaved into: Ferritin heavy chain, N-terminally processed]	FTTH1
			1939,90	0,068	K.YFLHQSHEREHAEL.K	P02794	FRIH_HUMAN	Ferritin heavy chain (Ferritin H subunit) (EC 1.16.3.1) (Cell proliferation-inducing gene 15 protein) [Cleaved into: Ferritin heavy chain, N-terminally processed]	FTTH1
1939,97	1938,999	1940,939	1939,87	0,101	K.EASSVSDFNQNFVEVPNR.I	P41218	MNDA_HUMAN	Myeloid cell nuclear differentiation antigen	MNDA
			1942,92	0,933	K.VVWLDPNETNEIANANSR.Q	P84098	RL19_HUMAN	60S ribosomal protein L19 (Large ribosomal subunit protein eL19)	RPL19
1940,98	1941,013	1942,955	1942,92	0,937	R.TSIDAYDNFDNISLAQR.L	Q00610	CLH1_HUMAN	Clathrin heavy chain 1 (Clathrin heavy chain on chromosome 17) (CLH-17)	CLTC

1942,56	1941,584	1943,526	1942,92	0,362	K.VWLDPNETNEIANANSR.Q	P84098	RL19_HUMAN	60S ribosomal protein L19 (Large ribosomal subunit protein eL19)	RPL19
			1942,92	0,366	R.TSIDAYDNFDNISLAQR.L	Q00610	CLH1_HUMAN	Clathrin heavy chain 1 (Clathrin heavy chain on chromosome 17) (CLH-17)	CLTC
			1943,14	0,581	K.QKLPDGSEIPLPILLGR.L	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
1943,03	1942,058	1944,001	1943,14	0,107	K.QKLPDGSEIPLPILLGR.L	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
			1942,92	0,108	R.TSIDAYDNFDNISLAQR.L	Q00610	CLH1_HUMAN	Clathrin heavy chain 1 (Clathrin heavy chain on chromosome 17) (CLH-17)	CLTC
			1942,92	0,112	K.VWLDPNETNEIANANSR.Q	P84098	RL19_HUMAN	60S ribosomal protein L19 (Large ribosomal subunit protein eL19)	RPL19
1943,55	1942,577	1944,520	1943,14	0,412	K.QKLPDGSEIPLPILLGR.L	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
			1944,04	0,489	K.ENAPAIIFIDEIDAIATK.R	P43686	PR56B_HUMAN	26S proteasome regulatory subunit 6B (26S proteasome AAA-ATPase subunit RPT3) (MB67-interacting protein) (MIP224) (Proteasome 26S subunit ATPase 4) (Tat-binding protein 7) (TBP-7)	PSMC4
			1942,92	0,628	R.TSIDAYDNFDNISLAQR.L	Q00610	CLH1_HUMAN	Clathrin heavy chain 1 (Clathrin heavy chain on chromosome 17) (CLH-17)	CLTC
			1942,92	0,631	K.VWLDPNETNEIANANSR.Q	P84098	RL19_HUMAN	60S ribosomal protein L19 (Large ribosomal subunit protein eL19)	RPL19
1943,96	1942,985	1944,929	1944,04	0,080	K.ENAPAIIFIDEIDAIATK.R	P43686	PR56B_HUMAN	26S proteasome regulatory subunit 6B (26S proteasome AAA-ATPase subunit RPT3) (MB67-interacting protein) (MIP224) (Proteasome 26S subunit ATPase 4) (Tat-binding protein 7) (TBP-7)	PSMC4
			1943,14	0,821	K.QKLPDGSEIPLPILLGR.L	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
1945,00	1944,025	1945,970	1945,89	0,889	K.SGVYQHVTGEMMGHAI.R	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
			1944,04	0,960	K.ENAPAIIFIDEIDAIATK.R	P43686	PR56B_HUMAN	26S proteasome regulatory subunit 6B (26S proteasome AAA-ATPase subunit RPT3) (MB67-interacting protein) (MIP224) (Proteasome 26S subunit ATPase 4) (Tat-binding protein 7) (TBP-7)	PSMC4
1945,99	1945,018	1946,964	1946,00	0,011	M.VNPTVFFDIADVGEPLGR.V	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
			1946,03	0,038	-TVAAPSVFIFPPSDEQLK.S	P01834	IGKC_HUMAN	Immunoglobulin kappa constant (Ig kappa chain C region) (Ig kappa chain C region AG) (Ig kappa chain C region CUM) (Ig kappa chain C region EU) (Ig kappa chain C region OU) (Ig kappa chain C region ROY) (Ig kappa chain C region TI)	IGKC
			1945,89	0,104	K.SGVYQHVTGEMMGHAI.R	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
			1946,96	0,968	R.FGAVWTGDNTAEWDHLK.I	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1946,93	1945,960	1947,907	1946,96	0,025	R.FGAVWTGDNTAEWDHLK.I	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			1946,03	0,905	-TVAAPSVFIFPPSDEQLK.S	P01834	IGKC_HUMAN	Immunoglobulin kappa constant (Ig kappa chain C region) (Ig kappa chain C region AG) (Ig kappa chain C region CUM) (Ig kappa chain C region EU) (Ig kappa chain C region OU) (Ig kappa chain C region ROY) (Ig kappa chain C region TI)	IGKC
			1946,00	0,932	M.VNPTVFFDIADVGEPLGR.V	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
1946,99	1946,014	1947,961	1946,96	0,029	R.FGAVWTGDNTAEWDHLK.I	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			1946,03	0,959	-TVAAPSVFIFPPSDEQLK.S	P01834	IGKC_HUMAN	Immunoglobulin kappa constant (Ig kappa chain C region) (Ig kappa chain C region AG) (Ig kappa chain C region CUM) (Ig kappa chain C region EU) (Ig kappa chain C region OU) (Ig kappa chain C region ROY) (Ig kappa chain C region TI)	IGKC
1947,97	1946,993	1948,941	1947,99	0,027	K.LVHLWSSDSHQPLWSR.I	O95834	EMAL2_HUMAN	Echinoderm microtubule-associated protein-like 2 (EMAP-2) (HuEMAP-2)	EML2
1948,89	1947,918	1949,867	1947,99	0,898	K.LVHLWSSDSHQPLWSR.I	O95834	EMAL2_HUMAN	Echinoderm microtubule-associated protein-like 2 (EMAP-2) (HuEMAP-2)	EML2
1949,01	1948,039	1949,988	1949,94	0,923	R.HWILPQDYDHAQAEAR.H	Q15293	RCN1_HUMAN	Reticulocalbin-1	RCN1
			1949,95	0,935	K.GNDISSGTVLSDYVGSQPPK.G	P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPPp) (Neuropolyptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1
1949,99	1949,017	1950,967	1950,03	0,037	R.LENYPPEPGPNEVLRL.M	Q00796	DHSO_HUMAN	Sorbitol dehydrogenase (SDH) (EC 1.1.1.-) ((R,R)-butanediol dehydrogenase) (EC 1.1.1.14) (L-iditol 2-dehydrogenase) (EC 1.1.1.14) (Polyol dehydrogenase) (Ribitol dehydrogenase) (RDH) (EC 1.1.1.56) (Xylitol dehydrogenase) (XDH) (EC 1.1.1.9)	SORD
			1949,95	0,043	K.GNDISSGTVLSDYVGSQPPK.G	P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPPp) (Neuropolyptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1
			1949,94	0,056	R.HWILPQDYDHAQAEAR.H	Q15293	RCN1_HUMAN	Reticulocalbin-1	RCN1
1950,99	1950,014	1951,965	1950,93	0,938	K.VVIHFTDGDAGDLADLHR.A	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1950,93	0,059	K.VVIHFTDGDAGDLADLHR.A	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1951,85	0,856	K.SPPQCSAEGFMPVQCK.F	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG

1951,97	1950,996	1952,948	1951,91	0,923	K.GPELLTMWFGSEANVR.E	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			1950,03	0,960	R.LENYPIPEPGPNEVLLR.M	Q00796	DHSO_HUMAN	Sorbitol dehydrogenase (SDH) (EC 1.1.1.1-) ((R,R)-butanediol dehydrogenase) (EC 1.1.1.4) (L-iditol 2-dehydrogenase) (EC 1.1.1.14) (Polyol dehydrogenase) (Ribitol dehydrogenase) (RDH) (EC 1.1.1.56) (Xylitol dehydrogenase) (XDH) (EC 1.1.1.9)	SORD
			1951,98	0,011	R.VFEVSLADLQNDVAFR.K	P61247	RS3A_HUMAN	40S ribosomal protein S3a (Small ribosomal subunit protein eS1) (v-fos transformation effector protein) (Fte-1)	RPS3A
			1951,91	0,059	K.GPELLTMWFGSEANVR.E	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			1951,85	0,126	K.SPQCSAEGFMPVQCK.F	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1952,93	0,957	R.VLTEDEMGHPEIGDAIAR.L	P14324	FPPS_HUMAN	Farnesyl pyrophosphate synthase (FPP synthase) (FPS) (EC 2.5.1.10) ((2E,6E)-farnesyl diphosphate synthase) (Dimethylallyltransferase) (EC 2.5.1.1) (Farnesyl diphosphate synthase) (Geranyltransferase)	FDP5
			1952,94	0,971	K.NLNEKDYELLCLDGTR.K	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1952,94	0,191	K.NLNEKDYELLCLDGTR.K	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1952,93	0,205	R.VLTEDEMGHPEIGDAIAR.L	P14324	FPPS_HUMAN	Farnesyl pyrophosphate synthase (FPP synthase) (FPS) (EC 2.5.1.10) ((2E,6E)-farnesyl diphosphate synthase) (Dimethylallyltransferase) (EC 2.5.1.1) (Farnesyl diphosphate synthase) (Geranyltransferase)	FDP5
			1953,80	0,662	R.NCWCVDEAGQLEGMR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1954,11	1953,132	1955,086	1954,08	0,948	R.VAPEEHPVLLTEAPLNPK.A	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			1954,08	0,948	R.VAPDEHPILLTEAPLNPK.I	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			1954,08	0,028	R.VAPEEHPVLLTEAPLNPK.A	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			1954,08	0,028	R.VAPDEHPILLTEAPLNPK.I	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			1953,80	0,314	R.NCWCVDEAGQLEGMR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1954,87	0,757	K.EVSCPMSSSQEVVSLR.Q	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1954,91	0,798	K.AANDAGYFNDEMAPIEVK.T	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2
			1955,01	0,905	K.YVRPGGGFVPNFQLEK.G	P22352	GPX3_HUMAN	Glutathione peroxidase 3 (GPx-3) (GSHPx-3) (EC 1.11.1.9) (Extracellular glutathione peroxidase) (Plasma glutathione peroxidase) (GPx-P) (GSHPx-P)	GPX3
			1954,12	0,041	R.VAPEEHPVLLTEAPLNPK.A	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			1954,08	0,041	R.VAPDEHPILLTEAPLNPK.I	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
1955,10	1954,125	1956,080	1953,80	0,327	R.NCWCVDEAGQLEGMR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1954,87	0,744	K.EVSCPMSSSQEVVSLR.Q	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1954,91	0,785	K.AANDAGYFNDEMAPIEVK.T	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2
			1955,01	0,892	K.YVRPGGGFVPNFQLEK.G	P22352	GPX3_HUMAN	Glutathione peroxidase 3 (GPx-3) (GSHPx-3) (EC 1.11.1.9) (Extracellular glutathione peroxidase) (Plasma glutathione peroxidase) (GPx-P) (GSHPx-P)	GPX3
			1955,01	0,088	K.YVRPGGGFVPNFQLEK.G	P22352	GPX3_HUMAN	Glutathione peroxidase 3 (GPx-3) (GSHPx-3) (EC 1.11.1.9) (Extracellular glutathione peroxidase) (Plasma glutathione peroxidase) (GPx-P) (GSHPx-P)	GPX3
			1954,91	0,195	K.AANDAGYFNDEMAPIEVK.T	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2
			1954,87	0,236	K.EVSCPMSSSQEVVSLR.Q	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1956,05	0,948	R.VAPEEHPVLLTEAPLNPK.A	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1956,05	0,948	R.VAPEEHPVLLTEAPLNPK.A	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1956,05	0,948	R.VAPEEHPVLLTEAPLNPK.A	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
1956,08	1955,101	1957,057	1956,05	0,028	R.VAPEEHPVLLTEAPLNPK.A	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1956,05	0,028	R.VAPEEHPVLLTEAPLNPK.A	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1956,05	0,028	R.VAPEEHPVLLTEAPLNPK.A	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1957,96	0,908	K.TKPSDEEMLFYGHYK.Q	P07108	ACBP_HUMAN	Acyl-CoA-binding protein (ACBP) (Diazepam-binding inhibitor) (DBI) (Endozepine) (EP)	DBI
			1957,71	0,249	K.TKPSDEEMLFYGHYK.Q	P07108	ACBP_HUMAN	Acyl-CoA-binding protein (ACBP) (Diazepam-binding inhibitor) (DBI) (Endozepine) (EP)	DBI
			1957,99	0,028	K.TKPSDEEMLFYGHYK.Q	P07108	ACBP_HUMAN	Acyl-CoA-binding protein (ACBP) (Diazepam-binding inhibitor) (DBI) (Endozepine) (EP)	DBI
			1958,94	0,960	R.QKEEESQQQAVLEQER.R	Q9UM54	MYO6_HUMAN	Unconventional myosin-VI (Unconventional myosin-6)	MYO6
			1958,95	0,967	K.IFAQYLVPHNLETER.M	Q29RF7	PDSSA_HUMAN	Sister chromatid cohesion protein PDSS homolog A (Cell proliferation-inducing gene 54 protein) (Sister chromatid cohesion protein 112) (SCC-112)	PDSSA
			1958,94	0,227	R.QKEEESQQQAVLEQER.R	Q9UM54	MYO6_HUMAN	Unconventional myosin-VI (Unconventional myosin-6)	MYO6
			1958,95	0,234	K.IFAQYLVPHNLETER.M	Q29RF7	PDSSA_HUMAN	Sister chromatid cohesion protein PDSS homolog A (Cell proliferation-inducing gene 54 protein) (Sister chromatid cohesion protein 112) (SCC-112)	PDSSA
1958,72	1957,739	1959,698	1958,98	0,261	K.GHYTEGAELVDSVLDVVR.K	P68371	TBB4B_HUMAN	Tubulin beta-48 chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1958,98	0,261	K.GHYTEGAELVDSVLDVVR.K	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1959,02	0,304	R.ISVNNVLPVFDNLMQQL.L	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
			1957,96	0,761	K.TKPSDEEMLFYGHYK.Q	P07108	ACBP_HUMAN	Acyl-CoA-binding protein (ACBP) (Diazepam-binding inhibitor) (DBI) (Endozepine) (EP)	DBI
			1958,98	0,006	K.GHYTEGAELVDSVLDVVR.K	P68371	TBB4B_HUMAN	Tubulin beta-48 chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1958,98	0,006	K.GHYTEGAELVDSVLDVVR.K	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1958,95	0,022	K.IFAQYLVPHNLETER.M	Q29RF7	PDSSA_HUMAN	Sister chromatid cohesion protein PDSS homolog A (Cell proliferation-inducing gene 54 protein) (Sister chromatid cohesion protein 112) (SCC-112)	PDSSA
			1958,98	0,006	K.GHYTEGAELVDSVLDVVR.K	P68371	TBB4B_HUMAN	Tubulin beta-48 chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1958,98	0,006	K.GHYTEGAELVDSVLDVVR.K	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1958,95	0,022	K.IFAQYLVPHNLETER.M	Q29RF7	PDSSA_HUMAN	Sister chromatid cohesion protein PDSS homolog A (Cell proliferation-inducing gene 54 protein) (Sister chromatid cohesion protein 112) (SCC-112)	PDSSA

			1958,94	0,029	R.QKEEESQQQAVLEQER.R	Q9UM54	MYO6_HUMAN	Unconventional myosin-VI (Unconventional myosin-6)	MYO6
			1959,02	0,049	R.ISVNNVLPVFDNLMQQL	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
1959,99	1959,014	1960,974	1960,92	0,931	K.YPIEHGII TNWDDMEK.I	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1960,92	0,931	K.YPIEHGII TNWDDMEK.I	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1960,92	0,931	K.YPIEHGII TNWDDMEK.I	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1960,93	0,937	K.DATNVGDEGGFAPNILENK.E	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			1959,02	0,971	R.ISVNNVLPVFDNLMQQL	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
			1960,95	0,024	K.DATNVGDEGGFAPNILENK.E	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
1960,95	1959,974	1961,935	1960,93	0,030	K.YPIEHGII TNWDDMEK.I	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1960,92	0,030	K.YPIEHGII TNWDDMEK.I	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1960,92	0,030	K.YPIEHGII TNWDDMEK.I	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1961,90	0,950	K.SGVYQHVTGEMMGGHAI.R	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
			1961,97	0,018	R.GHVFEESQVAGTPMFVVK.A	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
			1961,90	0,067	K.SGVYQHVTGEMMGGHAI.R	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
1963,00	1962,021	1963,984	1963,01	0,003	K.EPVELGQPNTLICHIDK.F	P20036	DPA1_HUMAN	HLA class II histocompatibility antigen, DP alpha 1 chain (DP(W3)) (DP(W4)) (HLA-SB alpha chain) (MHC class II DP3-alpha) (MHC class II DPA1)	HLA-DPA1
			1963,96	0,952	R.AVTELRGPD AEYWN SQK.D	P13760	2B14_HUMAN	HLA class II histocompatibility antigen, DRB1-4 beta chain (MHC class II antigen DRB1*4) (DR-4) (DR4)	HLA-DRB1
			1963,96	0,952	R.AVTELRGPD AEYWN SQK.D	P01911	2B1F_HUMAN	HLA class II histocompatibility antigen, DRB1-15 beta chain (DW2.2/DR2.2) (MHC class II antigen DRB1*15)	HLA-DRB1
			1963,97	0,014	R.AVTELRGPD AEYWN SQK.D	P13760	2B14_HUMAN	HLA class II histocompatibility antigen, DRB1-4 beta chain (MHC class II antigen DRB1*4) (DR-4) (DR4)	HLA-DRB1
			1963,96	0,014	R.AVTELRGPD AEYWN SQK.D	P01911	2B1F_HUMAN	HLA class II histocompatibility antigen, DRB1-15 beta chain (DW2.2/DR2.2) (MHC class II antigen DRB1*15)	HLA-DRB1
			1964,00	0,030	R.LFVGNLPADITEDEFKR.L	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMp100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
1965,01	1964,024	1965,989	1963,01	0,963	K.EPVELGQPNTLICHIDK.F	P20036	DPA1_HUMAN	HLA class II histocompatibility antigen, DP alpha 1 chain (DP(W3)) (DP(W4)) (HLA-SB alpha chain) (MHC class II DP3-alpha) (MHC class II DPA1)	HLA-DPA1
			1965,78	0,777	K.MPCESSPPESADTPTSTR.R	P46013	KI67_HUMAN	Proliferation marker protein Ki-67 (Antigen identified by monoclonal antibody Ki-67) (Antigen Ki-67) (Antigen Ki67)	MKI67
			1965,83	0,826	K.VDCTQHYELCSGNQVR.G	Q8NB59	TXND5_HUMAN	Thioredoxin domain-containing protein 5 (Endoplasmic reticulum resident protein 46) (ER protein 46) (Erp46) (Thioredoxin-like protein p46)	TXNDC5
			1965,91	0,900	R.SHFEQWGTLTDCVVMR.D	Q32P51	RA1L2_HUMAN	Heterogeneous nuclear ribonucleoprotein A1-like 2 (hnRNP A1-like 2) (hnRNP core protein A1-like 2)	HNRNPA1L2
			1966,00	0,093	R.SHFEQWGTLTDCVVMR.D	Q32P51	RA1L2_HUMAN	Heterogeneous nuclear ribonucleoprotein A1-like 2 (hnRNP A1-like 2) (hnRNP core protein A1-like 2)	HNRNPA1L2
			1965,83	0,168	K.VDCTQHYELCSGNQVR.G	Q8NB59	TXND5_HUMAN	Thioredoxin domain-containing protein 5 (Endoplasmic reticulum resident protein 46) (ER protein 46) (Erp46) (Thioredoxin-like protein p46)	TXNDC5
1966,00	1965,017	1966,983	1965,78	0,216	K.MPCESSPPESADTPTSTR.R	P46013	KI67_HUMAN	Proliferation marker protein Ki-67 (Antigen identified by monoclonal antibody Ki-67) (Antigen Ki-67) (Antigen Ki67)	MKI67
			1966,94	0,938	K.GTVGEPTYDAEFQHFLR.G	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
			1967,02	0,080	K.GTVGEPTYDAEFQHFLR.G	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
			1967,93	0,910	K.MMDFTFLPMLQHISK.N	P08590	MYL3_HUMAN	Myosin light chain 3 (Cardiac myosin light chain 1) (CMLC1) (Myosin light chain 1, slow-twitch muscle B/ventricular isoform) (MLC1S8) (Ventricular myosin alkali light chain) (Ventricular myosin light chain 1) (VLCI) (Ventricular/slow twitch myosin alkali light chain) (MLC-IV/sb)	MYL3
			1968,02	0,069	R.VAPEEHPIILLTEAPLNPK.A	Q658J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			1967,93	0,089	K.MMDFTFLPMLQHISK.N	P08590	MYL3_HUMAN	Myosin light chain 3 (Cardiac myosin light chain 1) (CMLC1) (Myosin light chain 1, slow-twitch muscle B/ventricular isoform) (MLC1S8) (Ventricular myosin alkali light chain) (Ventricular myosin light chain 1) (VLCI) (Ventricular/slow twitch myosin alkali light chain) (MLC-IV/sb)	MYL3
1968,89	1967,901	1969,870	1969,00	0,118	R.IAPLEEGTLPFNLAEAQR.Q	Q9UJ50	CMC2_HUMAN	Calcium-binding mitochondrial carrier protein Aralar2 (Citrin) (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13)	SLC25A13
			1968,09	0,800	R.VAPEEHPIILLTEAPLNPK.A	Q658J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			1969,79	0,904	R.NCWCVDEAGQLEGMR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG

			1967,93	0,958	K.MMDFETFLPMLQHISK.N	P08590	MYL3_HUMAN	Myosin light chain 3 (Cardiac myosin light chain 1) (CMLC1) MYL3 (Myosin light chain 1, slow-twitch muscle B/ventricular isoform) (MLC1S8) (Ventricular myosin alkali light chain) (Ventricular myosin light chain 1) (VLCI) (Ventricular/slow twitch myosin alkali light chain) (MLC-IV/sb)	
1969,07	1968,088	1970,057	1969,00	0,068	R.IAPLEEGTLFPNLAEAR.Q	Q9UJS0	CMC2_HUMAN	Calcium-binding mitochondrial carrier protein Aralar2 (Citrin) (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13)	SLC25A13
			1969,79	0,717	R.NCWCVDEAGQELEGMR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1969,89	1968,905	1970,875	1969,79	0,100	R.NCWCVDEAGQELEGMR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1969,00	0,886	R.IAPLEEGTLFPNLAEAR.Q	Q9UJS0	CMC2_HUMAN	Calcium-binding mitochondrial carrier protein Aralar2 (Citrin) (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13)	SLC25A13
1970,08	1969,092	1971,062	1969,79	0,287	R.NCWCVDEAGQELEGMR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1971,02	0,941	K.QVDQFLGVPYAAPPLAER.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1971,05	0,975	K.AIEPPPLDAVIEAEHTLR.E	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A (EC 3.6.4.13) (DEAH box protein 9) (DEXH-box helicase 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II) (RNA helicase A)	DHX9
1971,07	1970,086	1972,057	1971,05	0,020	K.AIEPPPLDAVIEAEHTLR.E	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A (EC 3.6.4.13) (DEAH box protein 9) (DEXH-box helicase 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II) (RNA helicase A)	DHX9
			1971,02	0,054	K.QVDQFLGVPYAAPPLAER.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1971,86	0,790	K.IDASKNEEDEGHSSNSPR.H	Q14103	HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1)	HNRNP
1972,05	1971,068	1973,040	1971,86	0,193	K.IDASKNEEDEGHSSNSPR.H	Q14103	HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1)	HNRNP
1972,46	1971,477	1973,450	1971,86	0,602	K.IDASKNEEDEGHSSNSPR.H	Q14103	HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1)	HNRNP
1973,05	1972,067	1974,040	1973,93	0,880	R.VADGLPLAASMQEDEQSGR.D	075396	SC22B_HUMAN	Vesicle-trafficking protein SEC22b (ER-Golgi SNARE of 24 kDa) (ERS-24) (ERS24) (SEC22 vesicle-trafficking protein homolog B) (SEC22 vesicle-trafficking protein-like 1)	SEC22B
1973,48	1972,490	1974,463	1973,93	0,457	R.VADGLPLAASMQEDEQSGR.D	075396	SC22B_HUMAN	Vesicle-trafficking protein SEC22b (ER-Golgi SNARE of 24 kDa) (ERS-24) (ERS24) (SEC22 vesicle-trafficking protein homolog B) (SEC22 vesicle-trafficking protein-like 1)	SEC22B
1974,06	1973,076	1975,050	1973,93	0,130	R.VADGLPLAASMQEDEQSGR.D	075396	SC22B_HUMAN	Vesicle-trafficking protein SEC22b (ER-Golgi SNARE of 24 kDa) (ERS-24) (ERS24) (SEC22 vesicle-trafficking protein homolog B) (SEC22 vesicle-trafficking protein-like 1)	SEC22B
1974,91	1973,927	1975,902	1973,93	0,981	R.VADGLPLAASMQEDEQSGR.D	075396	SC22B_HUMAN	Vesicle-trafficking protein SEC22b (ER-Golgi SNARE of 24 kDa) (ERS-24) (ERS24) (SEC22 vesicle-trafficking protein homolog B) (SEC22 vesicle-trafficking protein-like 1)	SEC22B
1975,07	1974,080	1976,055	1976,92	0,895	K.YPIEHGIITNWDDMEK.I	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
1976,03	1975,039	1977,015		0,895	K.YPIEHGIITNWDDMEK.I	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
				0,895	K.YPIEHGIITNWDDMEK.I	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
1977,04	1976,051	1978,028	1977,04	0,001	K.LAETTVLVESYTLPDGR.I	P61160	ARP2_HUMAN	Actin-related protein 2 (Actin-like protein 2)	ACTR2
			1976,92	0,117	K.YPIEHGIITNWDDMEK.I	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1976,92	0,117	K.YPIEHGIITNWDDMEK.I	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			1976,92	0,117	K.YPIEHGIITNWDDMEK.I	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			1977,81	0,766	R.QQGEPPSCAEGQSCASER.Q	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1978,04	1977,055	1979,033	1977,81	0,238	R.QQGEPPSCAEGQSCASER.Q	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1979,01	1978,022	1980,001	1979,85	0,837	R.FSGWYDADLSPAGHEEAK.R	P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG- PGAM1 dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	
			1979,94	0,927	R.SVEFEEMDILDQGALQR.L	Q14376	GALE_HUMAN	UDP-glucose 4-epimerase (EC 5.1.3.2) (Galactowaldenase) (UDP-N-acetylgalactosamine 4-epimerase) (UDP-GalNAc 4-epimerase) (UDP-N-acetylglucosamine 4-epimerase) (UDP-GlcNAc 4-epimerase) (EC 5.1.3.7) (UDP-galactose 4-epimerase)	GALE
1980,00	1979,010	1980,990	1979,94	0,062	R.SVEFEEMDILDQGALQR.L	Q14376	GALE_HUMAN	UDP-glucose 4-epimerase (EC 5.1.3.2) (Galactowaldenase) (UDP-N-acetylgalactosamine 4-epimerase) (UDP-GalNAc 4-epimerase) (UDP-N-acetylglucosamine 4-epimerase) (UDP-GlcNAc 4-epimerase) (EC 5.1.3.7) (UDP-galactose 4-epimerase)	GALE
			1979,85	0,152	R.FSGWYDADLSPAGHEEAK.R	P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG- PGAM1 dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	
			1980,97	0,968	R.VQVVDEEGDQQHQEGKR.L	Q02447	SP3_HUMAN	Transcription factor Sp3 (SPR-2)	SP3
1980,99	1980,002	1981,983	1980,97	0,024	R.VQVVDEEGDQQHQEGKR.L	Q02447	SP3_HUMAN	Transcription factor Sp3 (SPR-2)	SP3
			1981,87	0,880	K.YTVQDESHSEWVSCVR.F	P63244	RACK1_HUMAN	Receptor of activated protein C kinase 1 (Cell proliferation-inducing gene 21 protein) (Guanine nucleotide-binding protein subunit beta-2-like 1) (Guanine nucleotide-binding protein subunit beta-like protein 12.3) (Human lung cancer oncogene 7 protein, HLC-7) (Receptor for activated C kinase) (Small ribosomal subunit protein RACK1) [Cleaved into: Receptor of activated protein C kinase 1, N-terminally processed (Guanine nucleotide-binding protein subunit beta-2-like 1, N-terminally processed)]	RACK1

1981,98	1980,988	1982,970	1981,87	0,108	K.YTVQDESHSEWVSCVR.F	P63244	RACK1_HUMAN	Receptor of activated protein C kinase 1 (Cell proliferation-inducing gene 21 protein) [Guanine nucleotide-binding protein subunit beta-2-like 1] (Guanine nucleotide-binding protein subunit beta-like protein 12.3) (Human lung cancer oncogene 7 protein, HLC-7) (Receptor for activated C kinase) (Small ribosomal subunit protein RACK1) [Cleaved into: Receptor of activated protein C kinase 1, N-terminally processed (Guanine nucleotide-binding protein subunit beta-2-like 1, N-terminally processed)]	RACK1
			1982,96	0,985	R.AYPDVAALSDGYVWVSNR.V	O14773	TPP1_HUMAN	Tripeptidyl-peptidase 1 (TPP-1) (EC 3.4.14.9) (Cell growth-inhibiting gene 1 protein) (Lysosomal pepstatin-insensitive protease) (LPIC) (Tripeptidyl aminopeptidase) (Tripeptidyl-peptidase I) (TPP-I)	TPP1
1982,98	1981,993	1983,976	1982,96	0,020	R.AYPDVAALSDGYVWVSNR.V	O14773	TPP1_HUMAN	Tripeptidyl-peptidase 1 (TPP-1) (EC 3.4.14.9) (Cell growth-inhibiting gene 1 protein) (Lysosomal pepstatin-insensitive protease) (LPIC) (Tripeptidyl aminopeptidase) (Tripeptidyl-peptidase I) (TPP-I)	TPP1
1983,97	1982,979	1984,963	1984,07	0,096	K.TLQALEFHTVPFQLLAR.Y	Q08380	LG3BP_HUMAN	Galectin-3-binding protein (Basement membrane autoantigen p105) (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (MAC2BP) (Mac-2 BP) (Tumor-associated antigen 90K)	LGALS3BP
1984,96	1983,969	1985,954	1984,07	0,895	K.TLQALEFHTVPFQLLAR.Y	Q08380	LG3BP_HUMAN	Galectin-3-binding protein (Basement membrane autoantigen p105) (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (MAC2BP) (Mac-2 BP) (Tumor-associated antigen 90K)	LGALS3BP
1984,96	1983,969	1985,954	1984,07	0,895	K.TLQALEFHTVPFQLLAR.Y	Q08380	LG3BP_HUMAN	Galectin-3-binding protein (Basement membrane autoantigen p105) (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (MAC2BP) (Mac-2 BP) (Tumor-associated antigen 90K)	LGALS3BP
1985,96 1986,96	1984,966 1985,970	1986,952 1987,957	1987,93	0,971	K.GKEDEGEAAASPMQLQIR.D	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
1987,99	1986,999	1988,987	1987,98	0,011	K.YVRPGGGFEPNFMFEK.C	P07203	GPX1_HUMAN	Glutathione peroxidase 1 (GPx-1) (GSHPx-1) (EC 1.11.1.9) (Cellular glutathione peroxidase)	GPX1
			1988,02	0,022	R.AIAELGIYPADVPDLSR.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			1987,93	0,059	K.GKEDEGEAAASPMQLQIR.D	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
			1988,89	0,896	R.DAQDVQASQAEADQQQTR.L	Q9P2E9	RRBP1_HUMAN	Ribosome-binding protein 1 (180 kDa ribosome receptor homolog) (RRp) (ES/130-related protein) (Ribosome receptor protein)	RRBP1
			1988,96	0,965	K.ICPVETLVEEAIQCAEK.I	P30084	ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial (EC 4.2.1.17) (Enoyl-CoA hydratase 1) (Short-chain enoyl-CoA hydratase) (SCEH)	ECHS1
1989,00	1988,003	1989,992	1989,02	0,027	K.AIGAVPLIQGEYMIPCEK.V	P07339	CATD_HUMAN	Cathepsin D [EC 3.4.23.5] [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
			1988,96	0,039	K.ICPVETLVEEAIQCAEK.I	P30084	ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial (EC 4.2.1.17) (Enoyl-CoA hydratase 1) (Short-chain enoyl-CoA hydratase) (SCEH)	ECHS1
			1988,89	0,108	R.DAQDVQASQAEADQQQTR.L	Q9P2E9	RRBP1_HUMAN	Ribosome-binding protein 1 (180 kDa ribosome receptor homolog) (RRp) (ES/130-related protein) (Ribosome receptor protein)	RRBP1
			1989,93	0,935	R.FFDSFGLNSSASAIMGNPK.V	P69892	HBG2_HUMAN	Hemoglobin subunit gamma-2 (Gamma-2-globin) (Hb F Ggamma) (Hemoglobin gamma-2 chain) (Hemoglobin gamma-G chain)	HBG2
			1988,02	0,982	R.AIAELGIYPADVPDLSR.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
1990,00	1989,009	1990,999	1989,93	0,071	R.FFDSFGLNSSASAIMGNPK.V	P69892	HBG2_HUMAN	Hemoglobin subunit gamma-2 (Gamma-2-globin) (Hb F Ggamma) (Hemoglobin gamma-2 chain) (Hemoglobin gamma-G chain)	HBG2
			1989,02	0,979	K.AIGAVPLIQGEYMIPCEK.V	P07339	CATD_HUMAN	Cathepsin D [EC 3.4.23.5] [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
1991,02 1992,01	1990,023 1991,016	1992,014 1993,008	1992,06	0,045	R.QATTIADNIIFLSDQTK.E	Q04837	SSBP_HUMAN	Single-stranded DNA-binding protein, mitochondrial (Mt-SSB) (MtSSB) (PWP1-interacting protein 17)	SSBP1
1993,01	1992,016	1994,009	1993,86	0,851	R.FSPATHPSEGLEENYCR.N	P00747	PLMN_HUMAN	Plasminogen (EC 3.4.21.7) [Cleaved into: Plasmin heavy chain A; Activation peptide; Angiostatin; Plasmin heavy chain A, short form; Plasmin light chain B]	PLG
			1993,96	0,950	R.THNLEPYFESFINLR.R	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
			1992,06	0,956	R.QATTIADNIIFLSDQTK.E	Q04837	SSBP_HUMAN	Single-stranded DNA-binding protein, mitochondrial (Mt-SSB) (MtSSB) (PWP1-interacting protein 17)	SSBP1
			1993,98	0,964	R.NTFAEVTGLSPGVYYFK.V	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
1994,01	1993,013	1995,007	1993,98	0,034	R.NTFAEVTGLSPGVYYFK.V	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			1993,96	0,048	R.THNLEPYFESFINLR.R	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
			1993,86	0,147	R.FSPATHPSEGLEENYCR.N	P00747	PLMN_HUMAN	Plasminogen (EC 3.4.21.7) [Cleaved into: Plasmin heavy chain A; Activation peptide; Angiostatin; Plasmin heavy chain A, short form; Plasmin light chain B]	PLG
			1994,91	0,900	R.GTGGVDTAAGVGFVDSNADR.L	P06732	KCRM_HUMAN	Creatine kinase M-type (EC 2.7.3.2) (Creatine kinase M chain) (Creatine phosphokinase M-type) (CPK-M) (M-CK)	CKM
1995,01	1994,010	1996,005	1994,91	0,097	R.GTGGVDTAAGVGFVDSNADR.L	P06732	KCRM_HUMAN	Creatine kinase M-type (EC 2.7.3.2) (Creatine kinase M chain) (Creatine phosphokinase M-type) (CPK-M) (M-CK)	CKM
1996,00	1995,004	1997,000	1996,94 1996,98	0,933 0,981	R.NECFLQHKDDNPMLR.L R.ATENDIYNFFSPLNPVR.V	P02768 P31943	ALBU_HUMAN HNRH1_HUMAN	Serum albumin Heterogeneous nuclear ribonucleoprotein H (hnRNP H) [Cleaved into: Heterogeneous nuclear ribonucleoprotein H, N-terminally processed]	ALB HNRNP1
			1996,98	0,981	K.ATENDIYNFFSPLNPVR.V	P52597	HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein F, N-terminally processed]	HNRNPF

1996,99	1995,987	1997,984	1996,98	0,003	R.ATENDIYNFFSLNPVR.V	P31943	HNRRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H (hnRNP H) [Cleared into: Heterogeneous nuclear ribonucleoprotein H, N-terminally processed]	HNRRNP.H1			
			1996,98	0,003	K.ATENDIYNFFSLNPVR.V	P52597	HNRRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) [Cleared into: Heterogeneous nuclear ribonucleoprotein F, N-terminally processed]	HNRRNP.F			
			1997,03	0,045	R.LQAYHTQTTPUEYYR.K	P54819	KAD2_HUMAN	Adenylate kinase 2, mitochondrial (AK 2) (EC 2.7.4.3) (ATP-AMP transphosphorylase 2) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) [Cleared into: Adenylate kinase 2, mitochondrial, N-terminally processed]	AK2			
			1996,94	0,050	R.NECFLQHKDDNP.NLPR.L	P02768	ALBU_HUMAN	Serum albumin	ALB			
			1997,94	0,953	K.GVNTGAVGSYYDRDPEGK.V	P52943	CRIP2_HUMAN	Cysteine-rich protein 2 (CRP-2) (Protein ESP1)	CRIP2			
			1998,06	0,055	K.GVNTGAVGSYYDRDPEGK.V	P52943	CRIP2_HUMAN	Cysteine-rich protein 2 (CRP-2) (Protein ESP1)	CRIP2			
			1998,06	0,064	K.AELIANSLATAGDGJLIER.K	P35232	PHB_HUMAN	Prohibitin	PHB			
			1997,03	0,963	R.LQAYHTQTTPUEYYR.K	P54819	KAD2_HUMAN	Adenylate kinase 2, mitochondrial (AK 2) (EC 2.7.4.3) (ATP-AMP transphosphorylase 2) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) [Cleared into: Adenylate kinase 2, mitochondrial, N-terminally processed]	AK2			
1999,00	1997,999	1999,998	1998,06	0,940	K.AELIANSLATAGDGJLIER.K	P35232	PHB_HUMAN	Prohibitin	PHB			
			1999,99	0,994	R.GGFFAAFEPELLAQDIR.K	P07099	HYEP_HUMAN	Epoxide hydrolase 1 (EC 3.3.2.9) (Epoxide hydratase) (Microsomal epoxide hydrolase) (mEH)	EPHX1			
			1999,99	0,010	R.GGFFAAFEPELLAQDIR.K	P07099	HYEP_HUMAN	Epoxide hydrolase 1 (EC 3.3.2.9) (Epoxide hydratase) (Microsomal epoxide hydrolase) (mEH)	EPHX1			
			2001,01	2000,005	2002,006	2002,02	2001,014	2003,016	2003,97	0,948	R.DGFIKEDLHDM.LASLGK.N	P24844
2003,02	2002,018	2004,021										
			2003,97	0,948	R.DGFIKEDLHDM.LASLGK.N	O14950	ML12B_HUMAN	Myosin regulatory light chain 12B (MLC-2A) (MLC-2) (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2) (SHUJUN-1)	MYL12B			
			2003,98	2002,977	2004,981	2003,97	0,012	R.DGFIKEDLHDM.LASLGK.N	P24844	MYL9_HUMAN	Myosin regulatory light polypeptide 9 (20 kDa myosin light chain) (LC20) (MLC-2C) (Myosin RLC) (Myosin regulatory light chain 2, smooth muscle isoform) (Myosin regulatory light chain 9) (Myosin regulatory light chain MRLC1)	MYL9
			2003,97	0,012	R.DGFIKEDLHDM.LASLGK.N	O14950	ML12B_HUMAN	Myosin regulatory light chain 12B (MLC-2A) (MLC-2) (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2) (SHUJUN-1)	MYL12B			
			2004,98	2003,973	2005,978	2005,00	0,026	R.VVAQGVGIPEDSIFTMADR.G	P02760	AMBP_HUMAN	Protein AMBP [Cleared into: Alpha-1-microglobulin (Protein HC) (Alpha-1 microglycoprotein) (Complex-forming glycoprotein heterogeneous in charge); Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (EDC1) (HI-30) (Uronic-acid-rich protein); Trypstatin]	AMBP
						2005,92	0,940	R.DRGPMYDDPTLPEGWTR.K	P51608	MECP2_HUMAN	Methyl-CpG-binding protein 2 (MeCp-2 protein) (MeCp2)	MECP2
2005,93	0,957	K.EFQDAGEQVSSPADVAEK.A				P31937	3HIDH_HUMAN	3-hydroxyisobutyrate dehydrogenase, mitochondrial (HIBADH) (EC 1.1.1.31)	HIBADH			
2005,98	2004,977	2006,983				2005,93	0,048	K.EFQDAGEQVSSPADVAEK.A	P31937	3HIDH_HUMAN	3-hydroxyisobutyrate dehydrogenase, mitochondrial (HIBADH) (EC 1.1.1.31)	HIBADH
			2005,92	0,065	R.DRGPMYDDPTLPEGWTR.K	P51608	MECP2_HUMAN	Methyl-CpG-binding protein 2 (MeCp-2 protein) (MeCp2)	MECP2			
			2006,93	0,952	R.LAENFCVCHLATGDM.LR.A	P54819	KAD2_HUMAN	Adenylate kinase 2, mitochondrial (AK 2) (EC 2.7.4.3) (ATP-AMP transphosphorylase 2) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) [Cleared into: Adenylate kinase 2, mitochondrial, N-terminally processed]	AK2			
			2005,00	0,979	R.VVAQGVGIPEDSIFTMADR.G	P02760	AMBP_HUMAN	Protein AMBP [Cleared into: Alpha-1-microglobulin (Protein HC) (Alpha-1 microglycoprotein) (Complex-forming glycoprotein heterogeneous in charge); Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (EDC1) (HI-30) (Uronic-acid-rich protein); Trypstatin]	AMBP			
			2006,99	2005,988	2007,995	2006,93	0,059	R.LAENFCVCHLATGDM.LR.A	P54819	KAD2_HUMAN	Adenylate kinase 2, mitochondrial (AK 2) (EC 2.7.4.3) (ATP-AMP transphosphorylase 2) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) [Cleared into: Adenylate kinase 2, mitochondrial, N-terminally processed]	AK2
			2007,89	0,902	K.MAGNEVYGFSNATFQSER.E	O94925	GLSK_HUMAN	Glutaminase kidney isoform, mitochondrial (GLS) (EC 3.5.1.2) (K-glutaminase) (L-glutamine amidohydrolase) [Cleared into: Glutaminase kidney isoform, mitochondrial 68 kDa chain; Glutaminase kidney isoform, mitochondrial 65 kDa chain]	GLS			
			2007,91	0,916	K.TIGGGDDSFNTFFSETGAGK.H	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleared into: Detyrosinated tubulin alpha-1A chain]	TUBA1A			
			2007,91	0,916	K.TIGGGDDSFNTFFSETGAGK.H	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleared into: Detyrosinated tubulin alpha-1B chain]	TUBA1B			
			2007,44	2006,437	2008,445	2007,89	0,453	K.MAGNEVYGFSNATFQSER.E	O94925	GLSK_HUMAN	Glutaminase kidney isoform, mitochondrial (GLS) (EC 3.5.1.2) (K-glutaminase) (L-glutamine amidohydrolase) [Cleared into: Glutaminase kidney isoform, mitochondrial 68 kDa chain; Glutaminase kidney isoform, mitochondrial 65 kDa chain]	GLS
			2007,91	0,467	K.TIGGGDDSFNTFFSETGAGK.H	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleared into: Detyrosinated tubulin alpha-1A chain]	TUBA1A			
			2007,91	0,467	K.TIGGGDDSFNTFFSETGAGK.H	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleared into: Detyrosinated tubulin alpha-1B chain]	TUBA1B			
2006,93	0,509	R.LAENFCVCHLATGDM.LR.A	P54819	KAD2_HUMAN	Adenylate kinase 2, mitochondrial (AK 2) (EC 2.7.4.3) (ATP-AMP phosphotransferase) (Adenylate monophosphate kinase) [Cleared into: Adenylate kinase 2, mitochondrial, N-terminally processed]	AK2						

2007,61	2006,607	2008,614	2007,89	0,283	K.MAGNEYVGFSNATFQSER.E	O94925	GLSK_HUMAN	Glutaminase kidney isoform, mitochondrial (GLS) (EC 3.5.1.2) (K-glutaminase) (L-glutamine amidohydrolase) [Cleaved into: Glutaminase kidney isoform, mitochondrial 68 kDa chain; Glutaminase kidney isoform, mitochondrial 65 kDa chain]	GLS
			2007,91	0,298	K.TIGGGDDSFNTFFSETGAGK.H	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			2007,91	0,298	K.TIGGGDDSFNTFFSETGAGK.H	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2006,93	0,678	R.LAENFCVCHLATGDMRL.A	P54819	KAD2_HUMAN	Adenylate kinase 2, mitochondrial (AK 2) (EC 2.7.4.3) (ATP-AMP transphosphorylase 2) (ATP-AMP phosphotransferase) (Adenylate monophosphate kinase) [Cleaved into: Adenylate kinase 2, mitochondrial, N-terminally processed]	AK2
2007,99	2006,985	2008,993	2007,91	0,081	K.TIGGGDDSFNTFFSETGAGK.H	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			2007,91	0,081	K.TIGGGDDSFNTFFSETGAGK.H	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2007,89	0,096	K.MAGNEYVGFSNATFQSER.E	O94925	GLSK_HUMAN	Glutaminase kidney isoform, mitochondrial (GLS) (EC 3.5.1.2) (K-glutaminase) (L-glutamine amidohydrolase) [Cleaved into: Glutaminase kidney isoform, mitochondrial 68 kDa chain; Glutaminase kidney isoform, mitochondrial 65 kDa chain]	GLS
			2008,99	1,001	K.LGDVGMALCPGLHPSSR.L	P13489	RINI_HUMAN	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor) (Ribonuclease/angiogenin inhibitor 1) (RAI)	RNH1
2008,54	2007,532	2009,540	2008,99	0,454	K.LGDVGMALCPGLHPSSR.L	P13489	RINI_HUMAN	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor) (Ribonuclease/angiogenin inhibitor 1) (RAI)	RNH1
			2009,02	0,484	K.LTQAQIFDYGEIPNFR.S	P00491	PNPH_HUMAN	Purine nucleoside phosphorylase (PNP) (EC 2.4.2.1) (Inosine phosphorylase) (Inosine-guanosine phosphorylase)	PNP
			2007,91	0,628	K.TIGGGDDSFNTFFSETGAGK.H	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			2007,91	0,628	K.TIGGGDDSFNTFFSETGAGK.H	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2007,89	0,642	K.MAGNEYVGFSNATFQSER.E	O94925	GLSK_HUMAN	Glutaminase kidney isoform, mitochondrial (GLS) (EC 3.5.1.2) (K-glutaminase) (L-glutamine amidohydrolase) [Cleaved into: Glutaminase kidney isoform, mitochondrial 68 kDa chain; Glutaminase kidney isoform, mitochondrial 65 kDa chain]	GLS
2009,00	2007,994	2010,003	2008,99	0,008	K.LGDVGMALCPGLHPSSR.L	P13489	RINI_HUMAN	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor) (Ribonuclease/angiogenin inhibitor 1) (RAI)	RNH1
			2009,02	0,022	K.LTQAQIFDYGEIPNFR.S	P00491	PNPH_HUMAN	Purine nucleoside phosphorylase (PNP) (EC 2.4.2.1) (Inosine phosphorylase) (Inosine-guanosine phosphorylase)	PNP
			2010,00	1,002	R.FLGTEPEPDAVGLDSGHIR.G	Q16762	THTR_HUMAN	Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese)	TST
2009,99	2008,982	2010,992	2010,00	0,014	R.FLGTEPEPDAVGLDSGHIR.G	Q16762	THTR_HUMAN	Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese)	TST
			2009,02	0,967	K.LTQAQIFDYGEIPNFR.S	P00491	PNPH_HUMAN	Purine nucleoside phosphorylase (PNP) (EC 2.4.2.1) (Inosine phosphorylase) (Inosine-guanosine phosphorylase)	PNP
			2008,99	0,997	K.LGDVGMALCPGLHPSSR.L	P13489	RINI_HUMAN	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor) (Ribonuclease/angiogenin inhibitor 1) (RAI)	RNH1
2011,00	2009,999	2012,010	2010,00	1,003	R.FLGTEPEPDAVGLDSGHIR.G	Q16762	THTR_HUMAN	Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese)	TST
2012,01	2011,004	2013,016							
2013,01	2012,003	2014,016	2013,80	0,793	K.TNDDQTMCLDINECEC.D	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			2013,85	0,843	R.DENQSIHQMAQEDAQR.L	P20073	ANXA7_HUMAN	Annexin A7 (Annexin VII) (Annexin-7) (Synexin)	ANXA7
2014,00	2012,997	2015,011	2013,85	0,151	R.DENQSIHQMAQEDAQR.L	P20073	ANXA7_HUMAN	Annexin A7 (Annexin VII) (Annexin-7) (Synexin)	ANXA7
			2013,80	0,201	K.TNDDQTMCLDINECEC.D	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
2015,00	2013,991	2016,006	2015,04	0,046	K.VILHLKEDQTEYLEER.R	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			2015,04	0,046	K.VILHLKEDQTEYLEER.R	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP 2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
2015,99	2014,985	2017,001	2015,04	0,949	K.VILHLKEDQTEYLEER.R	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			2015,04	0,949	K.VILHLKEDQTEYLEER.R	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP 2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
			2016,98	0,984	R.HFDVAHVSTAATSNSFAVR.D	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2017,00	2015,994	2018,011	2016,98	0,025	R.HFDVAHVSTAATSNSFAVR.D	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2017,99	2016,980	2018,998							
2019,00	2017,987	2020,006							
2020,02	2019,012	2021,032	2020,07	0,048	K.ILATPPQEDAPSVDIANIR.M	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
2021,03	2020,015	2022,036	2021,95	0,925	R.EGMAALQSDPWQQELYR.N	P49748	ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial (VLCAD) (EC 1.3.8.9)	ACADVL
			2020,07	0,955	K.ILATPPQEDAPSVDIANIR.M	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
2021,49	2020,483	2022,505	2021,95	0,456	R.EGMAALQSDPWQQELYR.N	P49748	ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial (VLCAD) (EC 1.3.8.9)	ACADVL
2022,02	2021,009	2023,031	2021,95	0,070	R.EGMAALQSDPWQQELYR.N	P49748	ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial (VLCAD) (EC 1.3.8.9)	ACADVL
			2023,02	1,004	R.FLSQPFQVAEFTGHMGK.L	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
2022,45	2021,436	2023,458	2021,95	0,497	R.EGMAALQSDPWQQELYR.N	P49748	ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial (VLCAD) (EC 1.3.8.9)	ACADVL
			2023,02	0,578	R.FLSQPFQVAEFTGHMGK.L	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B

			2023,04	0,592	K.ITLPVDFVTADKF DENAK.T	P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1
2023,03	2022,015	2024,039	2023,02	0,002	R.FLSQPFQVAEVFTGHMGK.L	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP ATP5F1B synthase F1 subunit beta)	
			2023,04	0,012	K.ITLPVDFVTADKF DENAK.T	P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1
2024,02	2023,004	2025,028	2024,99	0,971	K.LGDVGMAELCPGLLHPSSR.L	P13489	RINI_HUMAN	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor) (Ribonuclease/angiogenin inhibitor 1) (RAI)	RNH1
			2023,04	0,977	K.ITLPVDFVTADKF DENAK.T	P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1
			2023,02	0,991	R.FLSQPFQVAEVFTGHMGK.L	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP ATP5F1B synthase F1 subunit beta)	
			2025,01	0,995	R.DEVQEVFVPAGTHTPGSR.L	Q96FV2	SCRN2_HUMAN	Secernin-2	SCRN2
2025,03	2024,015	2026,040	2025,01	0,016	R.DEVQEVFVPAGTHTPGSR.L	Q96FV2	SCRN2_HUMAN	Secernin-2	SCRN2
			2024,99	0,041	K.LGDVGMAELCPGLLHPSSR.L	P13489	RINI_HUMAN	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor) (Ribonuclease/angiogenin inhibitor 1) (RAI)	RNH1
			2026,02	0,991	R.GAQAAIVVYDITNTDTFAR.A	P51148	RAB5C_HUMAN	Ras-related protein Rab-5C (L1880) (RAB5L)	RAB5C
2026,04	2025,023	2027,049	2026,02	0,017	R.GAQAAIVVYDITNTDTFAR.A	P51148	RAB5C_HUMAN	Ras-related protein Rab-5C (L1880) (RAB5L)	RAB5C
2027,07	2026,057	2028,084	2027,07	0,003	K.NHLVEIPPNLPSLVELR.I	P21810	PGS1_HUMAN	Biglycan (Bone/cartilage proteoglycan I) (PG-S1)	BGN
2028,11	2027,091	2029,119	2028,94	0,833	R.ATENDIYNFFSLNPMR.V	P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 (hnRNP H2) (FTP-3) (Heterogeneous nuclear ribonucleoprotein H') (hnRNP H') [Cleaved into: Heterogeneous nuclear ribonucleoprotein H2, N-terminally processed]	HNRNPH2
			2029,00	0,896	K.IQVHYEDGNVQLVSHK.D	P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (CapZ alpha-1)	CAPZ1
			2029,00	0,896	K.IQVHYEDGNVQLVSHK.D	P47755	CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 (CapZ alpha-2)	CAPZ2
2029,09	2028,075	2030,104	2029,00	0,089	K.IQVHYEDGNVQLVSHK.D	P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (CapZ alpha-1)	CAPZ1
			2029,00	0,089	K.IQVHYEDGNVQLVSHK.D	P47755	CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 (CapZ alpha-2)	CAPZ2
			2028,94	0,151	R.ATENDIYNFFSLNPMR.V	P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 (hnRNP H2) (FTP-3) (Heterogeneous nuclear ribonucleoprotein H') (hnRNP H') [Cleaved into: Heterogeneous nuclear ribonucleoprotein H2, N-terminally processed]	HNRNPH2
			2029,85	0,756	R.DENQINHQMAQEDAQR.L	P20073	ANXA7_HUMAN	Annexin A7 (Annexin VII) (Annexin-7) (Synexin)	ANXA7
2030,02	2029,000	2031,030	2029,85	0,169	R.DENQINHQMAQEDAQR.L	P20073	ANXA7_HUMAN	Annexin A7 (Annexin VII) (Annexin-7) (Synexin)	ANXA7
			2030,99	0,976	R.NLHQSGFSLSGTQVDEGVR.S	Q14195	DPYL3_HUMAN	Dihydropyrimidine-related protein 3 (DRP-3) [Collapsin response mediator protein 4] (CRMP-4) (Unc-33-like phosphoprotein 1) (ULIP-1)	DPYSL3
			2031,01	0,994	K.LDFKQGAAGIPYFTAYR.A	Q08257	QOR_HUMAN	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-crystallin)	CRYZ
			2029,00	1,014	K.IQVHYEDGNVQLVSHK.D	P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (CapZ alpha-1)	CAPZ1
			2029,00	1,014	K.IQVHYEDGNVQLVSHK.D	P47755	CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 (CapZ alpha-2)	CAPZ2
2031,01	2029,999	2032,030	2031,01	0,006	K.LDFKQGAAGIPYFTAYR.A	Q08257	QOR_HUMAN	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-crystallin)	CRYZ
			2030,99	0,023	R.NLHQSGFSLSGTQVDEGVR.S	Q14195	DPYL3_HUMAN	Dihydropyrimidine-related protein 3 (DRP-3) [Collapsin response mediator protein 4] (CRMP-4) (Unc-33-like phosphoprotein 1) (ULIP-1)	DPYSL3
2032,01	2030,992	2033,024	2032,90	0,891	R.EYSELNAPSQESDSHPR.K	P49756	RBM25_HUMAN	RNA-binding protein 25 (Arg/Glu/Asp-rich protein of 120 kDa) (RED120) (Protein S164) (RNA-binding motif protein 25) (RNA-binding region-containing protein 7)	RBM25
			2031,01	0,999	K.LDFKQGAAGIPYFTAYR.A	Q08257	QOR_HUMAN	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-crystallin)	CRYZ
2033,01	2031,995	2034,028	2032,90	0,112	R.EYSELNAPSQESDSHPR.K	P49756	RBM25_HUMAN	RNA-binding protein 25 (Arg/Glu/Asp-rich protein of 120 kDa) (RED120) (Protein S164) (RNA-binding motif protein 25) (RNA-binding region-containing protein 7)	RBM25
2034,01	2032,995	2035,029	2034,94	0,928	K.AFTHTAQYDEAISDYFR.K	P31939	PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH [Cleaved into: Bifunctional purine biosynthesis protein PURH, N-terminally processed] [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (ATIC) (IMP synthase) (Inosinase)]	ATIC
			2034,96	0,946	K.QQLSAELDAQLDAYNAR.M	Q86V81	THOC4_HUMAN	THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Aly/REF export factor) (Transcriptional coactivator Aly/REF) (bZIP-enhancing factor BEF)	ALYREF
2035,00	2033,979	2036,014	2034,96	0,038	K.QQLSAELDAQLDAYNAR.M	Q86V81	THOC4_HUMAN	THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Aly/REF export factor) (Transcriptional coactivator Aly/REF) (bZIP-enhancing factor BEF)	ALYREF
			2034,94	0,056	K.AFTHTAQYDEAISDYFR.K	P31939	PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH [Cleaved into: Bifunctional purine biosynthesis protein PURH, N-terminally processed] [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (ATIC) (IMP synthase) (Inosinase)]	ATIC
			2035,86	0,867	R.GDQPAASGSDSDDDEPPLPR.L	O00264	PGR1_HUMAN	Membrane-associated progesterone receptor component 1 (mPR) (Dap1) (IZA)	PGRMC1
2035,99	2034,976	2037,012	2035,86	0,131	R.GDQPAASGSDSDDDEPPLPR.L	O00264	PGR1_HUMAN	Membrane-associated progesterone receptor component 1 (mPR) (Dap1) (IZA)	PGRMC1
2037,00	2035,978	2038,015	2037,06	0,060	R.VIHLNLPHSGYSDSAULK.L	P43243	MATR3_HUMAN	Matrin-3	MATR3
			2037,98	0,979	R.ATTPADGEEPAPAEALAAAR.E	Q96544	PRPK_HUMAN	EKC/KEOPS complex subunit TP53RK (EC 3.6.-.-) (Atypical serine/threonine protein kinase TP53RK) (Nori-2) (TP53-regulating kinase) (EC 2.7.11.1) (p53-related protein kinase)	TP53RK
2038,02	2037,005	2039,043	2038,06	0,034	K.VVIEDEQLVLGASQEPVGR.W	Q61850	TWF2_HUMAN	Twinfilin-2 (A6-related protein) (hA6RP) (Protein tyrosine kinase 9-like) (Twinfilin-1-like protein)	TWF2
			2037,98	0,048	R.ATTPADGEEPAPAEALAAAR.E	Q96544	PRPK_HUMAN	EKC/KEOPS complex subunit TP53RK (EC 3.6.-.-) (Atypical serine/threonine protein kinase TP53RK) (Nori-2) (TP53-regulating kinase) (EC 2.7.11.1) (p53-related protein kinase)	TP53RK
			2037,06	0,967	R.VIHLNLPHSGYSDSAULK.L	P43243	MATR3_HUMAN	Matrin-3	MATR3
			2039,00	0,973	R.FLSQPFQVAEVFTGHMGK.L	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP ATP5F1B synthase F1 subunit beta)	

2039,01	2037,992	2040,031	2039,00	0,015	R.FLSQPFQVAEFTGHMGK.L	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP ATP5F1B synthase F1 subunit beta)	
			2039,92	0,906	K.GESDPAYQQYQDAANNLR.E	P13667	PDIA4_HUMAN	Protein disulfide-isomerase A4 (EC 5.3.4.1) (Endoplasmic reticulum resident protein 70) (ER protein 70) (ERp70) (Endoplasmic reticulum resident protein 72) (ER protein 72) (ERp-72) (ERp72)	PDIA4
			2038,06	0,954	K.VVIEDEQLVLGASQEPVGR.W	Q6I8S0	TWF2_HUMAN	Twinfilin-2 (A6-related protein) (hA6RP) (Protein tyrosine kinase 9-like) (Twinfilin-1-like protein)	TWF2
2039,01	2037,992	2040,031	2039,00	0,015	R.FLSQPFQVAEFTGHMGK.L	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP ATP5F1B synthase F1 subunit beta)	
			2039,92	0,906	K.GESDPAYQQYQDAANNLR.E	P13667	PDIA4_HUMAN	Protein disulfide-isomerase A4 (EC 5.3.4.1) (Endoplasmic reticulum resident protein 70) (ER protein 70) (ERp70) (Endoplasmic reticulum resident protein 72) (ER protein 72) (ERp-72) (ERp72)	PDIA4
			2038,06	0,954	K.VVIEDEQLVLGASQEPVGR.W	Q6I8S0	TWF2_HUMAN	Twinfilin-2 (A6-related protein) (hA6RP) (Protein tyrosine kinase 9-like) (Twinfilin-1-like protein)	TWF2
2040,00	2038,981	2041,021	2039,92	0,083	K.GESDPAYQQYQDAANNLR.E	P13667	PDIA4_HUMAN	Protein disulfide-isomerase A4 (EC 5.3.4.1) (Endoplasmic reticulum resident protein 70) (ER protein 70) (ERp70) (Endoplasmic reticulum resident protein 72) (ER protein 72) (ERp-72) (ERp72)	PDIA4
			2040,95	0,948	K.GIVDQSQQAYQEAFEISK.K	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
			2039,00	1,004	R.FLSQPFQVAEFTGHMGK.L	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP ATP5F1B synthase F1 subunit beta)	
2040,00	2038,981	2041,021	2039,92	0,083	K.GESDPAYQQYQDAANNLR.E	P13667	PDIA4_HUMAN	Protein disulfide-isomerase A4 (EC 5.3.4.1) (Endoplasmic reticulum resident protein 70) (ER protein 70) (ERp70) (Endoplasmic reticulum resident protein 72) (ER protein 72) (ERp-72) (ERp72)	PDIA4
			2040,95	0,948	K.GIVDQSQQAYQEAFEISK.K	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
			2039,00	1,004	R.FLSQPFQVAEFTGHMGK.L	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP ATP5F1B synthase F1 subunit beta)	
2041,00	2039,981	2042,022	2040,95	0,053	K.GIVDQSQQAYQEAFEISK.K	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
			2040,95	0,752	K.GIVDQSQQAYQEAFEISK.K	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
2041,70	2040,679	2042,721	2040,95	0,752	K.GIVDQSQQAYQEAFEISK.K	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
			2042,02	0,927	K.TAFYQALQNSLGGEDSDAR.V	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2042,02	2040,994	2043,036	2043,01	0,992	K.AAWGKVGGAHAGEYGAEALER.M	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			2042,58	0,359	K.TAFYQALQNSLGGEDSDAR.V	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2042,58	2041,563	2043,605	2043,01	0,424	K.AAWGKVGGAHAGEYGAEALER.M	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			2042,62	0,321	K.TAFYQALQNSLGGEDSDAR.V	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2042,62	2041,600	2043,643	2043,01	0,386	K.AAWGKVGGAHAGEYGAEALER.M	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			2043,00	0,008	K.AAWGKVGGAHAGEYGAEALER.M	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
2043,00	2041,978	2044,021	2042,94	0,056	K.TAFYQALQNSLGGEDSDAR.V	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2044,02	1,018	K.KGFIGPGIDVPAPDMSTGER.E	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			2043,72	0,293	K.KGFIGPGIDVPAPDMSTGER.E	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
2043,72	2042,702	2044,745	2044,02	0,323	R.LPFTALGSGQDAALAVLEDR.F	P40306	PSB10_HUMAN	Proteasome subunit beta type-10 (EC 3.4.25.1) (Low molecular mass protein 10) (Macropain subunit MECl-1) (Multicatalytic endopeptidase complex subunit MECl-1) (Proteasome MECl-1) (Proteasome subunit beta-2i)	PSMB10
			2044,05	0,323	R.LPFTALGSGQDAALAVLEDR.F	P40306	PSB10_HUMAN	Proteasome subunit beta type-10 (EC 3.4.25.1) (Low molecular mass protein 10) (Macropain subunit MECl-1) (Multicatalytic endopeptidase complex subunit MECl-1) (Proteasome MECl-1) (Proteasome subunit beta-2i)	PSMB10
			2043,01	0,716	K.AAWGKVGGAHAGEYGAEALER.M	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
2044,56	2043,540	2045,585	2042,94	0,781	K.TAFYQALQNSLGGEDSDAR.V	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2044,94	0,382	R.NQEQMKPLEEKQEER.S	P62191	PRS4_HUMAN	26S proteasome regulatory subunit 4 (P26s4) (26S proteasome AAA-ATPase subunit RPT2) (Proteasome 26S subunit ATPase 1)	PSMC1
			2044,95	0,390	R.FFESFGDLSPPDAVMGNPK.V	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
2044,56	2043,540	2045,585	2045,05	0,490	R.ELFSPHLALNFGIGGDTTR.H	P68402	PA1B2_HUMAN	Platelet-activating factor acetylhydrolase IB subunit beta (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH subunit beta) (PAFAH subunit beta)	PAFAH1B2
			2044,05	0,516	R.LPFTALGSGQDAALAVLEDR.F	P40306	PSB10_HUMAN	Proteasome subunit beta type-10 (EC 3.4.25.1) (Low molecular mass protein 10) (Macropain subunit MECl-1) (Multicatalytic endopeptidase complex subunit MECl-1) (Proteasome MECl-1) (Proteasome subunit beta-2i)	PSMB10
			2045,09	0,531	K.VFDEFKPLVEEPQNLIK.Q	P02768	ALBU_HUMAN	Serum albumin	ALB
2044,56	2043,540	2045,585	2044,02	0,545	K.KGFIGPGIDVPAPDMSTGER.E	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			2045,00	0,048	R.ELFSPHLALNFGIGGDTTR.H	P68402	PA1B2_HUMAN	Platelet-activating factor acetylhydrolase IB subunit beta (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH subunit beta) (PAFAH subunit beta)	PAFAH1B2
			2044,95	0,052	R.FFESFGDLSPPDAVMGNPK.V	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
2044,56	2043,540	2045,585	2044,94	0,060	R.NQEQMKPLEEKQEER.S	P62191	PRS4_HUMAN	26S proteasome regulatory subunit 4 (P26s4) (26S proteasome AAA-ATPase subunit RPT2) (Proteasome 26S subunit ATPase 1)	PSMC1
			2045,09	0,090	K.VFDEFKPLVEEPQNLIK.Q	P02768	ALBU_HUMAN	Serum albumin	ALB
			2044,05	0,957	R.LPFTALGSGQDAALAVLEDR.F	P40306	PSB10_HUMAN	Proteasome subunit beta type-10 (EC 3.4.25.1) (Low molecular mass protein 10) (Macropain subunit MECl-1) (Multicatalytic endopeptidase complex subunit MECl-1) (Proteasome MECl-1) (Proteasome subunit beta-2i)	PSMB10
2044,56	2043,540	2045,585	2044,02	0,987	K.KGFIGPGIDVPAPDMSTGER.E	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			2045,51	0,414	K.VFDEFKPLVEEPQNLIK.Q	P02768	ALBU_HUMAN	Serum albumin	ALB
			2045,05	0,456	R.ELFSPHLALNFGIGGDTTR.H	P68402	PA1B2_HUMAN	Platelet-activating factor acetylhydrolase IB subunit beta (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH subunit beta) (PAFAH subunit beta)	PAFAH1B2

			2044,95	0,556	R.FFESFGDLSPPDAVMGNPK.V	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
			2044,94	0,563	R.NQEQMKPLEEKQEER.S	P62191	PR54_HUMAN	26S proteasome regulatory subunit 4 (P26s4) (26S proteasome AAA-ATPase subunit RPT2) (Proteasome 26S subunit ATPase 1)	PSMC1
2046,00	2044,980	2047,026	2045,09	0,909	K.VFDEFKPLVEEPQNLK.Q	P02768	ALBU_HUMAN	Serum albumin	ALB
			2045,05	0,951	R.ELFSPHALNFGIGGDTTR.H	P68402	PA1B2_HUMAN	Platelet-activating factor acetylhydrolase IB subunit beta (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH subunit beta) (PAFAH subunit beta)	PAFAH1B2
2047,00	2045,979	2048,026	2047,08	0,074	K.VIRPLDQPS5FDATPYIK.D	Q86VP6	CAND1_HUMAN	Cullin-associated NEDD8-dissociated protein 1 (Cullin-associated and neddylation-dissociated protein 1) (TBP-interacting protein of 120 kDa A) (TBP-interacting protein 120A) (p120 CAND1)	CAND1
			2047,82	0,822	R.GFNCEKPEAETCFDK.Y	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anstellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
2048,03	2047,009	2049,057	2047,82	0,209	R.GFNCEKPEAETCFDK.Y	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anstellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			2047,08	0,957	K.VIRPLDQPS5FDATPYIK.D	Q86VP6	CAND1_HUMAN	Cullin-associated NEDD8-dissociated protein 1 (Cullin-associated and neddylation-dissociated protein 1) (TBP-interacting protein of 120 kDa A) (TBP-interacting protein 120A) (p120 CAND1)	CAND1
2049,09	2048,065	2050,114	2049,06	0,027	R.VILQDFTGVPVVDFAAMR.D	P21399	ACOC_HUMAN	Cytoplasmic aconitase hydratase (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase) (Ferritin repressor protein) (Iron regulatory protein 1) (IRP1) (Iron-responsive element-binding protein 1) (IRE-BP 1)	ACO1
			2049,75	0,664	R.GGHMDDGYSMNFMN5SSR.G	Q96E39	RMXL1_HUMAN	RNA binding motif protein, X-linked-like-1 (Heterogeneous nuclear ribonucleoprotein G-like 1)	RBML1
			2050,01	0,925	R.YTCHVQHEGLPEPLTLR.W	P30508	1C12_HUMAN	HLA class I histocompatibility antigen, Cw-12 alpha chain (MHC class I antigen Cw*12)	HLA-C
			2050,02	0,933	K.TTQVPQFILDFFIQNDR.A	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A (EC 3.6.4.13) (DEAH box protein 9) (DEXH-box helicase 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II) (RNA helicase A)	DHX9
2050,02	2048,994	2051,044	2050,02	0,004	K.TTQVPQFILDFFIQNDR.A	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A (EC 3.6.4.13) (DEAH box protein 9) (DEXH-box helicase 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II) (RNA helicase A)	DHX9
			2050,01	0,005	R.YTCHVQHEGLPEPLTLR.W	P30508	1C12_HUMAN	HLA class I histocompatibility antigen, Cw-12 alpha chain (MHC class I antigen Cw*12)	HLA-C
			2049,75	0,266	R.GGHMDDGYSMNFMN5SSR.G	Q96E39	RMXL1_HUMAN	RNA binding motif protein, X-linked-like-1 (Heterogeneous nuclear ribonucleoprotein G-like 1)	RBML1
			2049,06	0,956	R.VILQDFTGVPVVDFAAMR.D	P21399	ACOC_HUMAN	Cytoplasmic aconitase hydratase (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase) (Ferritin repressor protein) (Iron regulatory protein 1) (IRP1) (Iron-responsive element-binding protein 1) (IRE-BP 1)	ACO1
2050,97	2049,943	2051,994	2050,02	0,946	K.TTQVPQFILDFFIQNDR.A	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A (EC 3.6.4.13) (DEAH box protein 9) (DEXH-box helicase 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II) (RNA helicase A)	DHX9
			2050,01	0,954	R.YTCHVQHEGLPEPLTLR.W	P30508	1C12_HUMAN	HLA class I histocompatibility antigen, Cw-12 alpha chain (MHC class I antigen Cw*12)	HLA-C
2051,10	2050,071	2052,122	2052,01	0,916	R.LSNTQGVVSFAFSTMMSVHR.G	P48047	ATPO_HUMAN	ATP synthase subunit O, mitochondrial (ATP synthase peripheral stalk subunit OSCP) (Oligomycin sensitivity conferral protein) (OSCP)	ATP5PO
			2052,01	0,008	R.LSNTQGVVSFAFSTMMSVHR.G	P48047	ATPO_HUMAN	ATP synthase subunit O, mitochondrial (ATP synthase peripheral stalk subunit OSCP) (Oligomycin sensitivity conferral protein) (OSCP)	ATP5PO
	2050,978	2053,030	2052,93	0,924	K.TYGADLASVDFQHASEDAR.K	P30740	ILEU_HUMAN	Leukocyte elastase inhibitor (LEI) (Monocyte/neutrophil elastase inhibitor) (EI) (M/NEI) (Peptidase inhibitor 2) (Pi-2) (Serpine B1)	SERPINB1
			2053,03	0,008	R.WVTYFNKPDIDAWELR.K	P20674	COX5A_HUMAN	Cytochrome c oxidase subunit 5A, mitochondrial (Cytochrome c oxidase polypeptide Va)	COX5A
	2051,998	2054,051	2052,93	0,096	K.TYGADLASVDFQHASEDAR.K	P30740	ILEU_HUMAN	Leukocyte elastase inhibitor (LEI) (Monocyte/neutrophil elastase inhibitor) (EI) (M/NEI) (Peptidase inhibitor 2) (Pi-2) (Serpine B1)	SERPINB1
			2053,97	0,949	R.NALVSHLDGTPVCEDIGR.S	P31930	QCR1_HUMAN	Cytochrome b-c1 complex subunit 1, mitochondrial (Complex III subunit 1) (Core protein I) (Ubiquinol-cytochrome-c reductase complex core protein 1)	UQCRC1
			2052,01	1,012	R.LSNTQGVVSFAFSTMMSVHR.G	P48047	ATPO_HUMAN	ATP synthase subunit O, mitochondrial (ATP synthase peripheral stalk subunit OSCP) (Oligomycin sensitivity conferral protein) (OSCP)	ATP5PO
2054,03	2053,005	2055,059	2053,97	0,059	R.NALVSHLDGTPVCEDIGR.S	P31930	QCR1_HUMAN	Cytochrome b-c1 complex subunit 1, mitochondrial (Complex III subunit 1) (Core protein I) (Ubiquinol-cytochrome-c reductase complex core protein 1)	UQCRC1
			2053,03	1,000	R.WVTYFNKPDIDAWELR.K	P20674	COX5A_HUMAN	Cytochrome c oxidase subunit 5A, mitochondrial (Cytochrome c oxidase polypeptide Va)	COX5A
2054,98	2053,953	2056,008	2055,09	0,111	K.LEGVLAQVAHYQDTLIR.A	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
			2053,97	1,007	R.NALVSHLDGTPVCEDIGR.S	P31930	QCR1_HUMAN	Cytochrome b-c1 complex subunit 1, mitochondrial (Complex III subunit 1) (Core protein I) (Ubiquinol-cytochrome-c reductase complex core protein 1)	UQCRC1
2055,03	2054,003	2056,058	2055,09	0,062	K.LEGVLAQVAHYQDTLIR.A	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
2056,08	2055,056	2057,112	2055,09	0,992	K.LEGVLAQVAHYQDTLIR.A	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
2056,68	2055,649	2057,705							
2057,00	2055,969	2058,026							
2057,43	2056,399	2058,457							
2057,63	2056,604	2058,662							
2057,98	2056,952	2059,010	2058,95	0,972	R.FFESFGDLSPPDAVMGNPK.V	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2058,97	2057,945	2060,004	2058,95	0,022	R.FFESFGDLSPPDAVMGNPK.V	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2060,02	2058,989	2061,049	2060,96	0,940	K.VLAVNQENEHLMEDYK.L	Q43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
			2060,99	0,971	R.EGNDLYHEMIESGVNLK.D	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B

2060,99	2059,955	2062,016	2060,99	0,005	R.EGNDLYHEMIESGVINLK.D	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP ATP5F1B synthase F1 subunit beta)	
			2060,96	0,027	K.VLAVNQENEHLMEDYEK.L	O43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
2061,97	2060,944	2063,006	2060,99	0,984	R.EGNDLYHEMIESGVINLK.D	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP ATP5F1B synthase F1 subunit beta)	
			2060,96	1,016	K.VLAVNQENEHLMEDYEK.L	O43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
2063,00	2061,972	2064,035	2063,04	0,037	K.ETDLLDDSLVSIFGNRR.L	P30044	PRDX5_HUMAN	Peroxisiredoxin-5, mitochondrial (EC 1.11.1.15) (Alu corepressor 1) (Antioxidant enzyme B166) (AOEB166) (Liver tissue 2D-page spot 718) (PLP) (Peroxisiredoxin V) (Prx-V) (Peroxisomal antioxidant enzyme) (TPx type VI) (Thioredoxin peroxidase PMP20)	PRDX5
2063,62	2062,587	2064,651	2063,04	0,579	K.ETDLLDDSLVSIFGNRR.L	P30044	PRDX5_HUMAN	Peroxisiredoxin-5, mitochondrial (EC 1.11.1.15) (Alu corepressor 1) (Antioxidant enzyme B166) (AOEB166) (Liver tissue 2D-page spot 718) (PLP) (Peroxisiredoxin V) (Prx-V) (Peroxisomal antioxidant enzyme) (TPx type VI) (Thioredoxin peroxidase PMP20)	PRDX5
2064,59	2063,562	2065,627	2064,99	0,393	R.RAEDGSVIDYELIDQDAR.D	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			2065,07	0,471	K.MIPCDFLIPVQTQHPIR.K	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
2065,65	2064,614	2066,680	2065,07	0,581	K.MIPCDFLIPVQTQHPIR.K	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
			2064,99	0,660	R.RAEDGSVIDYELIDQDAR.D	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
2065,97	2064,938	2067,004	2065,07	0,906	K.MIPCDFLIPVQTQHPIR.K	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
			2066,93	0,962	K.SEEWADNHLPLTDAELAR.I	O60664	PLIN3_HUMAN	Perilipin-3 (47 kDa mannose 6-phosphate receptor-binding protein) (47 kDa MPR-binding protein) (Cargo selection protein TIP47) (Mannose-6-phosphate receptor-binding protein 1) (Placental protein 17) (PP17)	PLIN3
			2064,99	0,984	R.RAEDGSVIDYELIDQDAR.D	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
2066,55	2065,515	2067,582	2066,93	0,385	K.SEEWADNHLPLTDAELAR.I	O60664	PLIN3_HUMAN	Perilipin-3 (47 kDa mannose 6-phosphate receptor-binding protein) (47 kDa MPR-binding protein) (Cargo selection protein TIP47) (Mannose-6-phosphate receptor-binding protein 1) (Placental protein 17) (PP17)	PLIN3
			2067,01	0,457	K.SLPADILYEDQQCLVFR.D	Q9BX68	HINT2_HUMAN	Histidine triad nucleotide-binding protein 2, mitochondrial (HINT-2) (EC 3.---) (HINT-3) (HIT-17kDa) (PKCI-1-related HIT protein)	HINT2
			2067,05	0,506	R.YTIKVLFSQEIAPSPFR.V	O75369	FLNB_HUMAN	Filamin-B (FLN-B) (ABP-278) (ABP-280 homolog) (Actin-binding-like protein) (Beta-filamin) (Filamin homolog 1) (Fh1) (Filamin-3) (Thyroid autoantigen) (Truncated actin-binding protein) (Truncated ABP)	FLNB
2067,02	2065,986	2068,053	2067,01	0,014	K.SLPADILYEDQQCLVFR.D	Q9BX68	HINT2_HUMAN	Histidine triad nucleotide-binding protein 2, mitochondrial (HINT-2) (EC 3.---) (HINT-3) (HIT-17kDa) (PKCI-1-related HIT protein)	HINT2
			2067,05	0,035	R.YTIKVLFSQEIAPSPFR.V	O75369	FLNB_HUMAN	Filamin-B (FLN-B) (ABP-278) (ABP-280 homolog) (Actin-binding-like protein) (Beta-filamin) (Filamin homolog 1) (Fh1) (Filamin-3) (Thyroid autoantigen) (Truncated actin-binding protein) (Truncated ABP)	FLNB
			2066,93	0,086	K.SEEWADNHLPLTDAELAR.I	O60664	PLIN3_HUMAN	Perilipin-3 (47 kDa mannose 6-phosphate receptor-binding protein) (47 kDa MPR-binding protein) (Cargo selection protein TIP47) (Mannose-6-phosphate receptor-binding protein 1) (Placental protein 17) (PP17)	PLIN3
			2067,86	0,845	K.GDRSEDFGVNEDLADSDAR.A	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
2068,04	2067,005	2069,073	2067,86	0,175	K.GDRSEDFGVNEDLADSDAR.A	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
			2069,01	0,974	R.LGQSDPAPLQHQMIDIYQK.R	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
			2067,05	0,984	R.YTIKVLFSQEIAPSPFR.V	O75369	FLNB_HUMAN	Filamin-B (FLN-B) (ABP-278) (ABP-280 homolog) (Actin-binding-like protein) (Beta-filamin) (Filamin homolog 1) (Fh1) (Filamin-3) (Thyroid autoantigen) (Truncated actin-binding protein) (Truncated ABP)	FLNB
			2067,01	1,033	K.SLPADILYEDQQCLVFR.D	Q9BX68	HINT2_HUMAN	Histidine triad nucleotide-binding protein 2, mitochondrial (HINT-2) (EC 3.---) (HINT-3) (HIT-17kDa) (PKCI-1-related HIT protein)	HINT2
2068,91	2067,876	2069,945	2069,01	0,102	R.LGQSDPAPLQHQMIDIYQK.R	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
			2069,92	1,008	R.APVAGTCYQAEWDDYVPK.L	P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPPp) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleared into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1
			2069,92	1,010	K.AYSDPSTGEPATYGELQQR.C	Q15149	PLEC_HUMAN	Plectin (PCN) (PLTN) (Hemidesmosomal protein 1) (HD1) (Plectin-1)	PLEC
2069,05	2068,020	2070,089	2069,01	0,042	R.LGQSDPAPLQHQMIDIYQK.R	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
			2069,92	0,864	R.APVAGTCYQAEWDDYVPK.L	P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPPp) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleared into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1
			2069,92	0,866	K.AYSDPSTGEPATYGELQQR.C	Q15149	PLEC_HUMAN	Plectin (PCN) (PLTN) (Hemidesmosomal protein 1) (HD1) (Plectin-1)	PLEC
			2070,02	0,969	K.FGKHGGTIPVPTAEFQDR.I	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1

2069,97	2068,935	2071,005	2069,92	0,050	K.AYSDPSTGEPATYGELQQR.C	Q15149	PLEC_HUMAN	Plectin (PCN) (PLTN) (Hemidesmosomal protein 1) (HD1)	PLEC
			2069,92	0,051	R.APVAGTCYQAEWDDYVPK.L	P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPPp) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1
			2070,02	0,053	K.FGKHGGTIPVPTAEFQDR.I	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			2069,01 2070,95	0,957 0,985	R.LGQSDPAPLQHQMDIYQK.R K.IHVSQDELQSANASVDDSR.L	P29401 P22314	TKT_HUMAN UBA1_HUMAN	Transketolase (TK) (EC 2.2.1.1) Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	TKT UBA1
2070,06	2069,029	2071,099	2070,02	0,040	K.FGKHGGTIPVPTAEFQDR.I	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			2069,92	0,143	K.AYSDPSTGEPATYGELQQR.C	Q15149	PLEC_HUMAN	Plectin (PCN) (PLTN) (Hemidesmosomal protein 1) (HD1)	PLEC
			2069,92	0,145	R.APVAGTCYQAEWDDYVPK.L	P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPPp) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1
			2070,95	0,891	K.IHVSQDELQSANASVDDSR.L	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
2070,99	2069,954	2072,025	2070,95	0,035	K.IHVSQDELQSANASVDDSR.L	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
			2070,02	0,966	K.FGKHGGTIPVPTAEFQDR.I	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			2071,97	0,978	K.ICHQIEYYFGDFNLPR.D	P05455	LA_HUMAN	Lupus La protein (La autoantigen) (La ribonucleoprotein) (Sjogren syndrome type B antigen) (SS-B)	SSB
2072,08	2071,046	2073,118	2071,97	0,115	K.ICHQIEYYFGDFNLPR.D	P05455	LA_HUMAN	Lupus La protein (La autoantigen) (La ribonucleoprotein) (Sjogren syndrome type B antigen) (SS-B)	SSB
			2073,02	0,937	R.VENQENVSNLVIEDTELK.Q	Q01518	CAP1_HUMAN	Adenylyl cyclase-associated protein 1 (CAP 1)	CAP1
2073,08	2072,043	2074,117	2073,02	0,061	R.VENQENVSNLVIEDTELK.Q	Q01518	CAP1_HUMAN	Adenylyl cyclase-associated protein 1 (CAP 1)	CAP1
2074,07	2073,035	2075,109	2074,95	0,880	R.FFESFGDLSTPDAVMGNPK.V	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2075,04	2074,004	2076,079	2074,95	0,090	R.FFESFGDLSTPDAVMGNPK.V	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2075,94	2074,903	2076,979	2074,95	0,989	R.FFESFGDLSTPDAVMGNPK.V	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2076,07 2077,05 2078,05 2079,04 2079,69 2080,01	2075,030 2076,013 2077,013 2077,996 2078,648 2078,971	2077,106 2078,090 2079,091 2080,075 2080,727 2081,051	2080,94	0,933	R.QTSGGPVDASSEYQQLER.E	P18859	ATP5J_HUMAN	ATP synthase-coupling factor 6, mitochondrial (ATPase subunit F6) (ATP synthase peripheral stalk subunit F6)	ATP5PF
2080,66	2079,617	2081,697	2080,94	0,287	R.QTSGGPVDASSEYQQLER.E	P18859	ATP5J_HUMAN	ATP synthase-coupling factor 6, mitochondrial (ATPase subunit F6) (ATP synthase peripheral stalk subunit F6)	ATP5PF
			2081,06	0,400	K.MIPCDFLIPVQTQHPIR.K	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
2081,01	2079,973	2082,054	2081,06	0,043	K.MIPCDFLIPVQTQHPIR.K	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
			2080,94	0,070	R.QTSGGPVDASSEYQQLER.E	P18859	ATP5J_HUMAN	ATP synthase-coupling factor 6, mitochondrial (ATPase subunit F6) (ATP synthase peripheral stalk subunit F6)	ATP5PF
			2081,98	0,971	K.NVMLLPVGSADDAHAHSQNEK.L	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
			2082,00	0,983	K.FYPEDVSEELIQDITQR.L	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
2082,02	2080,982	2083,064	2082,00	0,027	K.FYPEDVSEELIQDITQR.L	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			2081,98	0,039	K.NVMLLPVGSADDAHAHSQNEK.L	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
			2081,06	0,966	K.MIPCDFLIPVQTQHPIR.K	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
			2082,00	1,030	K.FYPEDVSEELIQDITQR.L	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
2084,01 2084,99	2082,971 2083,950	2085,055 2086,035	2085,17	0,177	R.VMTIAPGLFGTPLLTLSPK.V	Q99714	HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2 (EC 1.1.1.35) (17- HSD17B10 beta-hydroxysteroid dehydrogenase 10) (17-beta-HSD 10) (EC 1.1.1.51) (2-methyl-3-hydroxybutyryl-CoA dehydrogenase) (MHBd) (3-hydroxy-2-methylbutyryl-CoA dehydrogenase) (EC 1.1.1.178) (3-hydroxyacyl-CoA dehydrogenase type II) (Endoplasmic reticulum-associated amyloid beta-peptide-binding protein) (Mitochondrial ribonuclease P protein 2) (Mitochondrial RNase P protein 2) (Short chain dehydrogenase/reductase family 5C member 1) (Short-chain type dehydrogenase/reductase XH98G2) (Type II HADH)	
2086,00	2084,958	2087,044	2086,83	0,829	K.VHTECHGDLLECADDR.A	P02768	ALBU_HUMAN	Serum albumin	ALB

			2085,17	0,832	R.VMTIAPGLGFLPTLLTSLPEK.V	Q99714	HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2 (EC 1.1.1.35) (17-HSD17B10 beta-hydroxysteroid dehydrogenase 10) (17-beta-HSD 10) (EC 1.1.1.51) (2-methyl-3-hydroxybutyryl-CoA dehydrogenase) (MHB0) (3-hydroxy-2-methylbutyryl-CoA dehydrogenase) (EC 1.1.1.178) (3-hydroxyacyl-CoA dehydrogenase type II) (Endoplasmic reticulum-associated amyloid beta-peptide-binding protein) (Mitochondrial ribonuclease P protein 2) (Mitochondrial RNase P protein 2) (Short chain dehydrogenase/reductase family 5C member 1) (Short-chain type dehydrogenase/reductase XH98G2) (Type II HADH)	
2086,63	2085,586	2087,673	2086,83	0,200	K.VHTECCHGDLLECADDR.A	P02768	ALBU_HUMAN	Serum albumin	ALB
2086,94	2085,900	2087,987	2086,83	0,114	K.VHTECCHGDLLECADDR.A	P02768	ALBU_HUMAN	Serum albumin	ALB
2087,10	2086,055	2088,142	2086,83	0,269	K.VHTECCHGDLLECADDR.A	P02768	ALBU_HUMAN	Serum albumin	ALB
			2088,07	0,970	K.RLLFSFGNSQGGATPAAIEK.A	P12109	CO6A1_HUMAN	Collagen alpha-1(VI) chain	COL6A1
			2088,08	0,987	R.EAEAIIYHLQFEEELRR.L	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
			2088,09	0,989	R.VNPCIGGVILFHETLYQK.A	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
2088,05	2087,002	2089,090	2088,07	0,023	K.RLLFSFGNSQGGATPAAIEK.A	P12109	CO6A1_HUMAN	Collagen alpha-1(VI) chain	COL6A1
			2088,08	0,039	R.EAEAIIYHLQFEEELRR.L	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
			2088,09	0,042	R.VNPCIGGVILFHETLYQK.A	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
			2089,02	0,973	K.FITHAPPGEFNEFVNDVR.L	P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (CapZ alpha-1)	CAPZA1
2088,39	2087,344	2089,432	2088,09	0,301	R.VNPCIGGVILFHETLYQK.A	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
			2088,08	0,303	R.EAEAIIYHLQFEEELRR.L	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
			2088,07	0,320	K.RLLFSFGNSQGGATPAAIEK.A	P12109	CO6A1_HUMAN	Collagen alpha-1(VI) chain	COL6A1
			2089,02	0,630	K.FITHAPPGEFNEFVNDVR.L	P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (CapZ alpha-1)	CAPZA1
2089,05	2088,008	2090,097	2089,02	0,033	K.FITHAPPGEFNEFVNDVR.L	P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (CapZ alpha-1)	CAPZA1
			2089,97	0,922	R.ESGAQVQVAGDMLPNSTER.A	Q15365	PCBP1_HUMAN	Poly(rC)-binding protein 1 (Alpha-CP1) (Heterogeneous nuclear ribonucleoprotein E1) (hnRNP E1) (Nucleic acid-binding protein SUB2.3)	PCBP1
			2089,97	0,922	R.ESGAQVQVAGDMLPNSTER.A	Q15366	PCBP2_HUMAN	Poly(rC)-binding protein 2 (Alpha-CP2) (Heterogeneous nuclear ribonucleoprotein E2) (hnRNP E2)	PCBP2
			2088,09	0,964	R.VNPCIGGVILFHETLYQK.A	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
			2088,08	0,967	R.EAEAIIYHLQFEEELRR.L	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
			2088,07	0,984	K.RLLFSFGNSQGGATPAAIEK.A	P12109	CO6A1_HUMAN	Collagen alpha-1(VI) chain	COL6A1
2090,03	2088,985	2091,075	2089,97	0,056	R.ESGAQVQVAGDMLPNSTER.A	Q15365	PCBP1_HUMAN	Poly(rC)-binding protein 1 (Alpha-CP1) (Heterogeneous nuclear ribonucleoprotein E1) (hnRNP E1) (Nucleic acid-binding protein SUB2.3)	PCBP1
			2089,97	0,056	R.ESGAQVQVAGDMLPNSTER.A	Q15366	PCBP2_HUMAN	Poly(rC)-binding protein 2 (Alpha-CP2) (Heterogeneous nuclear ribonucleoprotein E2) (hnRNP E2)	PCBP2
			2090,96	0,928	R.GWGPHEICPFQGTVAFK.K	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			2090,99	0,955	R.ATSNVFMFMDQSQIQEFK.E	O14950	ML12B_HUMAN	Myosin regulatory light chain 12B (MLC-2A) (MLC-2) (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2) (SHUJUN-1)	MYL12B
			2090,99	0,955	R.ATSNVFMFMDQSQIQEFK.E	P24844	MYL9_HUMAN	Myosin regulatory light polypeptide 9 (20 kDa myosin light chain) (LC20) (MLC-2C) (Myosin RLC) (Myosin regulatory light chain 2, smooth muscle isoform) (Myosin regulatory light chain 9) (Myosin regulatory light chain MRLC1)	MYL9
			2089,02	1,011	K.FITHAPPGEFNEFVNDVR.L	P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (CapZ alpha-1)	CAPZA1
2091,00	2089,957	2092,048	2090,99	0,017	R.ATSNVFMFMDQSQIQEFK.E	O14950	ML12B_HUMAN	Myosin regulatory light chain 12B (MLC-2A) (MLC-2) (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2) (SHUJUN-1)	MYL12B
			2090,99	0,017	R.ATSNVFMFMDQSQIQEFK.E	P24844	MYL9_HUMAN	Myosin regulatory light polypeptide 9 (20 kDa myosin light chain) (LC20) (MLC-2C) (Myosin RLC) (Myosin regulatory light chain 2, smooth muscle isoform) (Myosin regulatory light chain 9) (Myosin regulatory light chain MRLC1)	MYL9
			2090,96	0,045	R.GWGPHEICPFQGTVAFK.K	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			2091,88	0,879	R.DTYHPMSEYTYHTHGR.Y	P15941	MUC1_HUMAN	Mucin-1 (MUC-1) (Breast carcinoma-associated antigen DF3) (Cancer antigen 15-3) (CA 15-3) (Carcinoma-associated mucin) (Episialin) (H23AG) (Krebs von den Lungen-6) (KL-6) (PEMT) (Peanut-reactive urinary mucin) (PUM) (Polymorphic epithelial mucin) (PEM) (Tumor-associated epithelial membrane antigen) (EMA) (Tumor-associated mucin) (CD antigen CD227) [Cleaved into: Mucin-1 subunit alpha (MUC1-NT) (MUC1-alpha); Mucin-1 subunit beta (MUC1-beta) (MUC1-CT)]	MUC1
			2091,96	0,959	R.QVQCNGPPEQVFELYQR.W	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2089,97	1,029	R.ESGAQVQVAGDMLPNSTER.A	Q15365	PCBP1_HUMAN	Poly(rC)-binding protein 1 (Alpha-CP1) (Heterogeneous nuclear ribonucleoprotein E1) (hnRNP E1) (Nucleic acid-binding protein SUB2.3)	PCBP1
			2089,97	1,029	R.ESGAQVQVAGDMLPNSTER.A	Q15366	PCBP2_HUMAN	Poly(rC)-binding protein 2 (Alpha-CP2) (Heterogeneous nuclear ribonucleoprotein E2) (hnRNP E2)	PCBP2
			2092,04	1,039	K.LDKDNLSYIEHIFEISR.R	Q15121	PEA15_HUMAN	Astrocytic phosphoprotein PEA-15 (15 kDa phosphoprotein enriched in astrocytes) (Phosphoprotein enriched in diabetes) (PED)	PEA15

2091,01	2089,962	2092,053	2090,99	0,022	R.ATSNVFMFQDSQIQEFK.E	O14950	ML12B_HUMAN	Myosin regulatory light chain 12B (MLC-2A) (MLC-2) (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2) (SHUJUN-1)	MYL12B
			2090,99	0,022	R.ATSNVFMFQDSQIQEFK.E	P24844	MYL9_HUMAN	Myosin regulatory light polypeptide 9 (20 kDa myosin light chain) (LC20) (MLC-2C) (Myosin RLC) (Myosin regulatory light chain 2, smooth muscle isoform) (Myosin regulatory light chain 9) (Myosin regulatory light chain MRLC1)	MYL9
			2090,96	0,050	R.GWGPHEICPFQGTVAFAK.K	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			2091,88	0,875	R.DTYHPMSEPTYHTHGR.Y	P15941	MUC1_HUMAN	Mucin-1 (MUC-1) (Breast carcinoma-associated antigen DF3) (Cancer antigen 15-3) (CA 15-3) (Carcinoma-associated mucin) (Episialin) (H23AG) (Krebs von den Lungen-6) (KL-6) (PEMT) (Peanut-reactive urinary mucin) (PUM) (Polymorphic epithelial mucin) (PEM) (Tumor-associated epithelial membrane antigen) (EMA) (Tumor-associated mucin) (CD antigen CD227) [Cleaved into: Mucin-1 subunit alpha (MUC1-NT) (MUC1-alpha); Mucin-1 subunit beta (MUC1-beta) (MUC1-CT)]	MUC1
			2091,96	0,954	R.QVQCNGPPEQVFELYQR.W	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2089,97	1,033	R.ESSTAQVQVAGDMLPNSTER.A	Q15365	PCBP1_HUMAN	Poly(rC)-binding protein 1 (Alpha-CP1) (Heterogeneous nuclear ribonucleoprotein E1) (hnRNP E1) (Nucleic acid-binding protein SUB2.3)	PCBP1
			2089,97	1,033	R.ESSTAQVQVAGDMLPNSTER.A	Q15366	PCBP2_HUMAN	Poly(rC)-binding protein 2 (Alpha-CP2) (Heterogeneous nuclear ribonucleoprotein E2) (hnRNP E2)	PCBP2
			2092,04	1,035	K.LDKDNLSYIEHIFEISR.R	Q15121	PEA15_HUMAN	Astrocytic phosphoprotein PEA-15 (15 kDa phosphoprotein enriched in astrocytes) (Phosphoprotein enriched in diabetes) (PED)	PEA15
2092,00	2090,953	2093,045	2091,96	0,038	R.QVQCNGPPEQVFELYQR.W	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2092,04	0,042	K.LDKDNLSYIEHIFEISR.R	Q15121	PEA15_HUMAN	Astrocytic phosphoprotein PEA-15 (15 kDa phosphoprotein enriched in astrocytes) (Phosphoprotein enriched in diabetes) (PED)	PEA15
			2091,88	0,117	R.DTYHPMSEPTYHTHGR.Y	P15941	MUC1_HUMAN	Mucin-1 (MUC-1) (Breast carcinoma-associated antigen DF3) (Cancer antigen 15-3) (CA 15-3) (Carcinoma-associated mucin) (Episialin) (H23AG) (Krebs von den Lungen-6) (KL-6) (PEMT) (Peanut-reactive urinary mucin) (PUM) (Polymorphic epithelial mucin) (PEM) (Tumor-associated epithelial membrane antigen) (EMA) (Tumor-associated mucin) (CD antigen CD227) [Cleaved into: Mucin-1 subunit alpha (MUC1-NT) (MUC1-alpha); Mucin-1 subunit beta (MUC1-beta) (MUC1-CT)]	MUC1
			2092,91	0,908	R.SQEATEAAPSCVGMADTPR.D	Q9UHD8	SEPT9_HUMAN	Septin-9 (MLL septin-like fusion protein MSF-A) (MLL septin-like fusion protein) (Ovarian/Breast septin) (Ov/Br septin) (Septin D1)	SEPT9
			2090,99	1,014	R.ATSNVFMFQDSQIQEFK.E	O14950	ML12B_HUMAN	Myosin regulatory light chain 12B (MLC-2A) (MLC-2) (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2) (SHUJUN-1)	MYL12B
			2090,99	1,014	R.ATSNVFMFQDSQIQEFK.E	P24844	MYL9_HUMAN	Myosin regulatory light polypeptide 9 (20 kDa myosin light chain) (LC20) (MLC-2C) (Myosin RLC) (Myosin regulatory light chain 2, smooth muscle isoform) (Myosin regulatory light chain 9) (Myosin regulatory light chain MRLC1)	MYL9
			2090,96	1,042	R.GWGPHEICPFQGTVAFAK.K	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
2092,99	2091,946	2094,039	2092,91	0,085	R.SQEATEAAPSCVGMADTPR.D	Q9UHD8	SEPT9_HUMAN	Septin-9 (MLL septin-like fusion protein MSF-A) (MLL septin-like fusion protein) (Ovarian/Breast septin) (Ov/Br septin) (Septin D1)	SEPT9
			2092,04	0,950	K.LDKDNLSYIEHIFEISR.R	Q15121	PEA15_HUMAN	Astrocytic phosphoprotein PEA-15 (15 kDa phosphoprotein enriched in astrocytes) (Phosphoprotein enriched in diabetes) (PED)	PEA15
			2091,96	1,031	R.QVQCNGPPEQVFELYQR.W	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2094,02	2092,975	2095,070	2094,87	0,849	K.NCMDIDECQRDPLLCR.G	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
2095,03	2093,983	2096,078	2094,87	0,158	K.NCMDIDECQRDPLLCR.G	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			2095,95	0,924	K.AAGIDEQENWHEGKENIR.A	P28838	AMPL_HUMAN	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase 3) (LAP-3) (Leucyl aminopeptidase) (Peptidase S) (Proline aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase)	LAP3
2096,02	2094,969	2097,065	2095,95	0,063	K.AAGIDEQENWHEGKENIR.A	P28838	AMPL_HUMAN	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase 3) (LAP-3) (Leucyl aminopeptidase) (Peptidase S) (Proline aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase)	LAP3
2096,91	2095,861	2097,957	2095,95	0,955	K.AAGIDEQENWHEGKENIR.A	P28838	AMPL_HUMAN	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase 3) (LAP-3) (Leucyl aminopeptidase) (Peptidase S) (Proline aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase)	LAP3
			2097,93	1,019	K.TTTTNTQVEGDDEAAFLER.L	Q05682	CALD1_HUMAN	Caldesmon (CDM)	CALD1
2097,07	2096,018	2098,115	2097,93	0,862	K.TTTTNTQVEGDDEAAFLER.L	Q05682	CALD1_HUMAN	Caldesmon (CDM)	CALD1
2098,02	2096,971	2099,069	2097,93	0,091	K.TTTTNTQVEGDDEAAFLER.L	Q05682	CALD1_HUMAN	Caldesmon (CDM)	CALD1
2098,93	2097,880	2099,979	2099,08	0,153	K.ASPSEVFLDDIGANLKPAR.D	P34913	HYES_HUMAN	Bifunctional epoxide hydrolase 2 [Includes: Cytosolic epoxide hydrolase 2 (CEH) (EC 3.3.2.10) (Epoxide hydratase) (Soluble epoxide hydrolase) (SEH); Lipid-phosphate phosphatase (EC 3.1.3.76)]	EPHX2
			2097,93	1,001	K.TTTTNTQVEGDDEAAFLER.L	Q05682	CALD1_HUMAN	Caldesmon (CDM)	CALD1
2099,08	2098,035	2100,134	2099,08	0,001	K.ASPSEVFLDDIGANLKPAR.D	P34913	HYES_HUMAN	Bifunctional epoxide hydrolase 2 [Includes: Cytosolic epoxide hydrolase 2 (CEH) (EC 3.3.2.10) (Epoxide hydratase) (Soluble epoxide hydrolase) (SEH); Lipid-phosphate phosphatase (EC 3.1.3.76)]	EPHX2
2099,92	2098,868	2100,968	2100,14	0,217	R.AAVFDLDGVLALPAVGVGLGR.T	P34913	HYES_HUMAN	Bifunctional epoxide hydrolase 2 [Includes: Cytosolic epoxide hydrolase 2 (CEH) (EC 3.3.2.10) (Epoxide hydratase) (Soluble epoxide hydrolase) (SEH); Lipid-phosphate phosphatase (EC 3.1.3.76)]	EPHX2
			2099,08	0,835	K.ASPSEVFLDDIGANLKPAR.D	P34913	HYES_HUMAN	Bifunctional epoxide hydrolase 2 [Includes: Cytosolic epoxide hydrolase 2 (CEH) (EC 3.3.2.10) (Epoxide hydratase) (Soluble epoxide hydrolase) (SEH); Lipid-phosphate phosphatase (EC 3.1.3.76)]	EPHX2

2100,07	2099,016	2101,116	2100,14	0,069	R.AAVFDLDGVLALPAVFGVLGR.T	P34913	HYE5_HUMAN	Bifunctional epoxide hydrolase 2 [Includes: Cytosolic epoxide hydrolase 2 (CEH) (EC 3.3.2.10) (Epoxide hydratase) (Soluble epoxide hydrolase) (SEH); Lipid-phosphate phosphatase (EC 3.1.3.76)]	EPHX2
			2101,04	0,974	K.FIIHAPPGEFNEVFNDVR.L	P47755	CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 (CapZ alpha-2)	CAPZA2
			2099,08	0,983	K.ASPSEVFLDDIGANLKPAR.D	P34913	HYE5_HUMAN	Bifunctional epoxide hydrolase 2 [Includes: Cytosolic epoxide hydrolase 2 (CEH) (EC 3.3.2.10) (Epoxide hydratase) (Soluble epoxide hydrolase) (SEH); Lipid-phosphate phosphatase (EC 3.1.3.76)]	EPHX2
2100,98	2099,925	2102,026	2101,04	0,065	K.FIIHAPPGEFNEVFNDVR.L	P47755	CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 (CapZ alpha-2)	CAPZA2
			2101,14	0,168	R.VMTIAPGLFGTPLLTLSPK.V	Q99714	HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2 (EC 1.1.1.35) (17-beta-HSD10) (EC 1.1.1.51) (2-methyl-3-hydroxybutyryl-CoA dehydrogenase) (MHBd) (3-hydroxy-2-methylbutyryl-CoA dehydrogenase) (EC 1.1.1.178) (3-hydroxyacyl-CoA dehydrogenase type II) (Endoplasmic reticulum-associated amyloid beta-peptide-binding protein) (Mitochondrial ribonuclease P protein 2) (Mitochondrial RNase P protein 2) (Short chain dehydrogenase/reductase family 5C member 1) (Short-chain type dehydrogenase/reductase XH98G2) (Type II HADH)	HSD17B10
			2100,14	0,841	R.AAVFDLDGVLALPAVFGVLGR.T	P34913	HYE5_HUMAN	Bifunctional epoxide hydrolase 2 [Includes: Cytosolic epoxide hydrolase 2 (CEH) (EC 3.3.2.10) (Epoxide hydratase) (Soluble epoxide hydrolase) (SEH); Lipid-phosphate phosphatase (EC 3.1.3.76)]	EPHX2
2101,98	2100,925	2103,027	2102,04	0,068	K.TANKDHLVTAYNHLFETK.R	Q00688	FKBP3_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP3 (PPIase FKBP3) (EC 5.2.1.8) (25 kDa FK506-binding protein) (25 kDa FKBP) (FKBP-25) (FK506-binding protein 3) (FKBP-3) (Immunophilin FKBP25) (Rapamycin-selective 25 kDa immunophilin) (Rotamase)	FKBP3
			2101,14	0,833	R.VMTIAPGLFGTPLLTLSPK.V	Q99714	HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2 (EC 1.1.1.35) (17-beta-HSD10) (EC 1.1.1.51) (2-methyl-3-hydroxybutyryl-CoA dehydrogenase) (MHBd) (3-hydroxy-2-methylbutyryl-CoA dehydrogenase) (EC 1.1.1.178) (3-hydroxyacyl-CoA dehydrogenase type II) (Endoplasmic reticulum-associated amyloid beta-peptide-binding protein) (Mitochondrial ribonuclease P protein 2) (Mitochondrial RNase P protein 2) (Short chain dehydrogenase/reductase family 5C member 1) (Short-chain type dehydrogenase/reductase XH98G2) (Type II HADH)	HSD17B10
			2101,04	0,936	K.FIIHAPPGEFNEVFNDVR.L	P47755	CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 (CapZ alpha-2)	CAPZA2
2102,97	2101,915	2104,018	2102,04	0,922	K.TANKDHLVTAYNHLFETK.R	Q00688	FKBP3_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP3 (PPIase FKBP3) (EC 5.2.1.8) (25 kDa FK506-binding protein) (25 kDa FKBP) (FKBP-25) (FK506-binding protein 3) (FKBP-3) (Immunophilin FKBP25) (Rapamycin-selective 25 kDa immunophilin) (Rotamase)	FKBP3
2104,07	2103,013	2105,118	2105,09	1,026	K.VFLENVIRDAVITYTEHAK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
2105,04	2103,989	2106,094	2105,09	0,051	K.VFLENVIRDAVITYTEHAK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
2106,01	2104,953	2107,059	2105,09	0,914	K.VFLENVIRDAVITYTEHAK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
2106,04	2104,982	2107,088	2105,09	0,943	K.VFLENVIRDAVITYTEHAK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4

2106,98	2105,925	2108,032	2107,10	0,116	K.IGEHTPSALAIMENANVLAR.Y	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
2107,02	2105,964	2108,071	2107,10	0,077	K.IGEHTPSALAIMENANVLAR.Y	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
2108,01	2106,959	2109,067	2107,10	0,918	K.IGEHTPSALAIMENANVLAR.Y	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
			2109,01	0,993	R.ELQSQSDTSVLSMDNSR.S	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
			2109,04	1,028	R.GADTAPTLAPEALPSQGEVER.E	Q81ZL8	PELP1_HUMAN	Proline-, glutamic acid- and leucine-rich protein 1 (Modulator of non-genomic activity of estrogen receptor) (Transcription factor HMX3)	PELP1
2109,06	2108,004	2110,113	2109,04	0,018	R.GADTAPTLAPEALPSQGEVER.E	Q81ZL8	PELP1_HUMAN	Proline-, glutamic acid- and leucine-rich protein 1 (Modulator of non-genomic activity of estrogen receptor) (Transcription factor HMX3)	PELP1
			2109,01	0,053	R.ELQSQSDTSVLSMDNSR.S	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
			2109,95	0,888	K.LGEMWNNTAADDKQPYEK.K	P09429	HMGB1_HUMAN	High mobility group protein B1 (High mobility group protein 1) (HMG-1)	HMGB1
2110,03	2108,979	2111,089	2109,95	0,087	K.LGEMWNNTAADDKQPYEK.K	P09429	HMGB1_HUMAN	High mobility group protein B1 (High mobility group protein 1) (HMG-1)	HMGB1
			2110,99	0,955	K.VNPDTGYINYDQLEENAR.L	P34896	GLYC_HUMAN	Serine hydroxymethyltransferase, cytosolic (SHMT) (EC 2.1.2.1) (Glycine hydroxymethyltransferase) (Serine methylase)	SHMT1
			2109,04	0,993	R.GADTAPTLAPEALPSQGEVER.E	Q81ZL8	PELP1_HUMAN	Proline-, glutamic acid- and leucine-rich protein 1 (Modulator of non-genomic activity of estrogen receptor) (Transcription factor HMX3)	PELP1
2111,05	2109,992	2112,103	2110,99	0,059	K.VNPDTGYINYDQLEENAR.L	P34896	GLYC_HUMAN	Serine hydroxymethyltransferase, cytosolic (SHMT) (EC 2.1.2.1) (Glycine hydroxymethyltransferase) (Serine methylase)	SHMT1
			2111,91	0,866	K.SKSEEAHAEDSVMDDHFR.K	Q8NC51	PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein (PAI1 RNA-binding protein 1) (PAI-RBP1) (SERPINE1 mRNA-binding protein 1)	SERBP1
			2111,94	0,897	R.APEAWDYGQGFVNEEMIR.D	P00387	NBSR3_HUMAN	NADH-cytochrome b5 reductase 3 (B5R) (Cytochrome b5 reductase) (EC 1.6.2.2) (Diaphorase-1) [Cleaved into: NADH-cytochrome b5 reductase 3 membrane-bound form; NADH-cytochrome b5 reductase 3 soluble form]	CYB5R3
2112,03	2110,972	2113,084	2111,94	0,083	R.APEAWDYGQGFVNEEMIR.D	P00387	NBSR3_HUMAN	NADH-cytochrome b5 reductase 3 (B5R) (Cytochrome b5 reductase) (EC 1.6.2.2) (Diaphorase-1) [Cleaved into: NADH-cytochrome b5 reductase 3 membrane-bound form; NADH-cytochrome b5 reductase 3 soluble form]	CYB5R3
			2111,91	0,114	K.SKSEEAHAEDSVMDDHFR.K	Q8NC51	PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein (PAI1 RNA-binding protein 1) (PAI-RBP1) (SERPINE1 mRNA-binding protein 1)	SERBP1
			2113,07	1,039	R.TPMGIVDALEQQEEGINR.L	075915	PRAF3_HUMAN	PRA1 family protein 3 (ADP-ribosylation factor-like protein 6-interacting protein 5) (ARL-6-interacting protein 5) (Aip-5) (Cytoskeleton-related vitamin A-responsive protein) (Dermal papilla-derived protein 11) (GTRAP3-18) (Glutamate transporter EAAC1-interacting protein) (JMS) (Prenylated Rab acceptor protein 2) (Protein JWa) (Putative MAPK-activating protein PM27)	ARL6IP5
2113,03	2111,972	2114,085	2110,99	1,039	K.VNPDTGYINYDQLEENAR.L	P34896	GLYC_HUMAN	Serine hydroxymethyltransferase, cytosolic (SHMT) (EC 2.1.2.1) (Glycine hydroxymethyltransferase) (Serine methylase)	SHMT1
			2113,07	0,039	R.TPMGIVDALEQQEEGINR.L	075915	PRAF3_HUMAN	PRA1 family protein 3 (ADP-ribosylation factor-like protein 6-interacting protein 5) (ARL-6-interacting protein 5) (Aip-5) (Cytoskeleton-related vitamin A-responsive protein) (Dermal papilla-derived protein 11) (GTRAP3-18) (Glutamate transporter EAAC1-interacting protein) (JMS) (Prenylated Rab acceptor protein 2) (Protein JWa) (Putative MAPK-activating protein PM27)	ARL6IP5
			2113,97	0,942	R.QLEVYTGSGDPESVAGEYGR.H	Q9Y262	EIF3L_HUMAN	Eukaryotic translation initiation factor 3 subunit L (eIF3L) (Eukaryotic translation initiation factor 3 subunit 6-interacting protein) (Eukaryotic translation initiation factor 3 subunit E-interacting protein)	EIF3L
2114,03	2112,973	2115,087	2113,97	0,059	R.QLEVYTGSGDPESVAGEYGR.H	Q9Y262	EIF3L_HUMAN	Eukaryotic translation initiation factor 3 subunit L (eIF3L) (Eukaryotic translation initiation factor 3 subunit 6-interacting protein) (Eukaryotic translation initiation factor 3 subunit E-interacting protein)	EIF3L
			2113,07	0,963	R.TPMGIVDALEQQEEGINR.L	075915	PRAF3_HUMAN	PRA1 family protein 3 (ADP-ribosylation factor-like protein 6-interacting protein 5) (ARL-6-interacting protein 5) (Aip-5) (Cytoskeleton-related vitamin A-responsive protein) (Dermal papilla-derived protein 11) (GTRAP3-18) (Glutamate transporter EAAC1-interacting protein) (JMS) (Prenylated Rab acceptor protein 2) (Protein JWa) (Putative MAPK-activating protein PM27)	ARL6IP5
			2115,03	1,000	R.GLVVLGFPCNQFGHQENAK.N	P07203	GPX1_HUMAN	Glutathione peroxidase 1 (GPx-1) (GSHPx-1) (EC 1.11.1.9) (Cellular glutathione peroxidase)	GPX1
2115,10	2114,043	2116,158	2115,12	0,019	K.NLKPDKPMQFLGDEETVR.K	P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG- dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	PGAM1
			2115,03	0,071	R.GLVVLGFPCNQFGHQENAK.N	P07203	GPX1_HUMAN	Glutathione peroxidase 1 (GPx-1) (GSHPx-1) (EC 1.11.1.9) (Cellular glutathione peroxidase)	GPX1
			2115,97	0,872	K.TTHFVEGGDAGNREDQINR.L	P18124	RL7_HUMAN	60S ribosomal protein L7 (Large ribosomal subunit protein uL30)	RPL7
2116,10	2115,044	2117,160	2115,97	0,129	K.TTHFVEGGDAGNREDQINR.L	P18124	RL7_HUMAN	60S ribosomal protein L7 (Large ribosomal subunit protein uL30)	RPL7
			2117,06	0,961	R.VISSGSVASVVTSPQGFQFR.R	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
			2115,12	0,982	K.NLKPDKPMQFLGDEETVR.K	P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG- dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	PGAM1
2117,10	2116,043	2118,160	2117,10	0,993	K.ESVPISDTIIPAVPPTDLR.F	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			2117,10	0,006	K.ESVPISDTIIPAVPPTDLR.F	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1

2118,09	2117,029	2119,147	2117,06	0,039	R.VISSGSVASVYVTSPPQGFQFR.R	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2			
			2117,90	0,794	K.LSEGSQPAEEEEEDQETPSR.N	Q9UKV3	ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus (Acinus)	ACIN1			
			2117,90	0,192	K.LSEGSQPAEEEEEDQETPSR.N	Q9UKV3	ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus (Acinus)	ACIN1			
			2117,10	0,993	K.ESVPISDTIPAVPPPTDLR.F	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1			
2118,09	2117,029	2119,147	2117,06	1,025	R.VISSGSVASVYVTSPPQGFQFR.R	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2			
			2117,90	0,192	K.LSEGSQPAEEEEEDQETPSR.N	Q9UKV3	ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus (Acinus)	ACIN1			
			2117,10	0,993	K.ESVPISDTIPAVPPPTDLR.F	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1			
			2117,06	1,025	R.VISSGSVASVYVTSPPQGFQFR.R	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2			
2119,08	2118,025	2120,144	2123,09	0,105	K.IGEHTPSALAIMENANVLAR.Y	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA			
2120,07	2119,011	2121,131										
2121,01	2119,946	2122,067										
2121,99	2120,925	2123,047										
2122,98	2121,919	2124,042	2123,98	2122,920	2125,044	2123,09	0,896	K.IGEHTPSALAIMENANVLAR.Y	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
2125,02	2123,962	2126,087				2124,94	0,956	R.KVEEGESPGDPPDHEASTQGR.T	Q9NZT2	OGFR_HUMAN	Opioid growth factor receptor (OGFr) (Protein 7-60) (Zeta-type opioid receptor)	OGFR
						2124,98	0,998	R.EGAHAFAQYNMDQFTPVK.I	P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (Cap2 alpha-1)	CAP2A1
						2124,98	0,045	R.EGAHAFAQYNMDQFTPVK.I	P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (Cap2 alpha-1)	CAP2A1
2126,05	2124,984	2127,110	2124,94	0,086	R.KVEEGESPGDPPDHEASTQGR.T	Q9NZT2	OGFR_HUMAN	Opioid growth factor receptor (OGFr) (Protein 7-60) (Zeta-type opioid receptor)	OGFR			
			2125,12	0,100	K.AQFAQPEILIGTIPGAGGTQR.L	P30084	ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial (EC 4.2.1.17) (Enoyl-CoA hydratase 1) (Short-chain enoyl-CoA hydratase) (SCEH)	ECHS1			
			2125,12	0,923	K.AQFAQPEILIGTIPGAGGTQR.L	P30084	ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial (EC 4.2.1.17) (Enoyl-CoA hydratase 1) (Short-chain enoyl-CoA hydratase) (SCEH)	ECHS1			
			2127,08	1,035	K.HQLYIDETVNSNIPTNLR.V	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB			
2127,06	2125,993	2128,120	2128,05	2126,987	2129,115	2127,08	0,025	K.HQLYIDETVNSNIPTNLR.V	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
2130,05	2128,984	2131,114				2126,15	0,902	K.ALPGQLKPFETLLSQNQGKG.T	P09211	GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1)	GSTP1
						2128,86	0,806	R.EGYAWAEDKEHCEEYGR.M	Q9Y310	RTCB_HUMAN	tRNA-splicing ligase RtcB homolog (EC 6.5.1.3)	RTCB
						2127,08	0,969	K.HQLYIDETVNSNIPTNLR.V	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
2129,02	2127,959	2130,088	2130,05	2128,984	2131,114	2129,17	0,148	R.DLEKPFLLPVEAVVSPGR.G	P49411	EFTU_HUMAN	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	TUFM
2128,86	0,166	R.EGYAWAEDKEHCEEYGR.M				Q9Y310	RTCB_HUMAN	tRNA-splicing ligase RtcB homolog (EC 6.5.1.3)	RTCB			
2129,17	0,878	R.DLEKPFLLPVEAVVSPGR.G				P49411	EFTU_HUMAN	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	TUFM			
2130,22	0,176	R.QIIQQNPSSLIPALLQIQJGR.E				P54727	RD23B_HUMAN	UV excision repair protein RAD23 homolog B (HR23B) (hHR23B) (XP-C repair-complementing complex 58 kDa protein) (p58)	RAD23B			
2131,06	2129,995	2132,126	2132,07	2131,007	2133,139	2129,17	0,878	R.DLEKPFLLPVEAVVSPGR.G	P49411	EFTU_HUMAN	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	TUFM
2133,07	2132,004	2134,137				2130,22	0,836	R.QIIQQNPSSLIPALLQIQJGR.E	P54727	RD23B_HUMAN	UV excision repair protein RAD23 homolog B (HR23B) (hHR23B) (XP-C repair-complementing complex 58 kDa protein) (p58)	RAD23B
2134,05	2132,987	2135,121				2134,03	0,965	K.QYYIGDIHPSDLKPESGSK.D	O43169	CYB5B_HUMAN	Cytochrome b5 type B (Cytochrome b5 outer mitochondrial membrane isoform)	CYB5B
						2134,11	1,036	R.LEGSDVQLLEYEASAAGLR.S	Q9NY33	DPP3_HUMAN	Dipeptidyl peptidase 3 (EC 3.4.14.4) (Dipeptidyl aminopeptidase III) (Dipeptidyl arylamidase III) (Dipeptidyl peptidase III) (DPP III) (Enkephalinase B)	DPP3
			2134,03	0,019	K.QYYIGDIHPSDLKPESGSK.D	O43169	CYB5B_HUMAN	Cytochrome b5 type B (Cytochrome b5 outer mitochondrial membrane isoform)	CYB5B			
2134,05	2132,987	2135,121	2134,11	0,052	R.LEGSDVQLLEYEASAAGLR.S	Q9NY33	DPP3_HUMAN	Dipeptidyl peptidase 3 (EC 3.4.14.4) (Dipeptidyl aminopeptidase III) (Dipeptidyl arylamidase III) (Dipeptidyl peptidase III) (DPP III) (Enkephalinase B)	DPP3			
			2135,11	1,051	R.ETIELVHTEPTDVAQLPSR.V	Q6I8S0	TWF2_HUMAN	Twinfilin-2 (A6-related protein) (hA6RP) (Protein tyrosine kinase 9-like) (Twinfilin-1-like protein)	TWF2			
			2135,11	0,063	R.ETIELVHTEPTDVAQLPSR.V	Q6I8S0	TWF2_HUMAN	Twinfilin-2 (A6-related protein) (hA6RP) (Protein tyrosine kinase 9-like) (Twinfilin-1-like protein)	TWF2			
			2134,11	0,936	R.LEGSDVQLLEYEASAAGLR.S	Q9NY33	DPP3_HUMAN	Dipeptidyl peptidase 3 (EC 3.4.14.4) (Dipeptidyl aminopeptidase III) (Dipeptidyl arylamidase III) (Dipeptidyl peptidase III) (DPP III) (Enkephalinase B)	DPP3			
2135,04	2133,974	2136,109	2137,08	2136,013	2138,150	2135,98	0,941	K.VDNALQSGNSQESVTEQDSK.D	P01834	IGKC_HUMAN	Immunoglobulin kappa constant (Ig kappa chain C region) (Ig kappa chain C region AG) (Ig kappa chain C region CUM) (Ig kappa chain C region EU) (Ig kappa chain C region OU) (Ig kappa chain C region ROY) (Ig kappa chain C region TI)	IGKC
2135,99	0,945	R.FSGWYDADLSAPGHEEAKR.G				P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG- dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	PGAM1			
2134,03	1,007	K.QYYIGDIHPSDLKPESGSK.D				O43169	CYB5B_HUMAN	Cytochrome b5 type B (Cytochrome b5 outer mitochondrial membrane isoform)	CYB5B			
2136,81	0,267	R.ECYCPDPFSPALYCDSR.N				P51888	PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	PRELP			
2137,08	2136,013	2138,150	2138,01	0,925	K.SEIIPMFNSLASDEQDSVR.L	P30153	ZAAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform (Medium tumor antigen-associated 61 kDa protein) (PP2A subunit A isoform PR65-alpha) (PP2A subunit A isoform R1-alpha)	PPP2R1A			

2138,08	2137,015	2139,153	2138,01	0,077	K.SEIIPMFSNLASDEQDSVR.L	P30153	ZAAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform (Medium tumor antigen-associated 61 kDa protein) (PP2A subunit A isoform PR65-alpha) (PP2A subunit A isoform R1-alpha)	PPP2R1A
			2139,02	0,941	R.TPEVTCVVVDVSHEDPEVK.F	P01857	IGHG1_HUMAN	Immunoglobulin heavy constant gamma 1 (Ig gamma-1 chain C region) (Ig gamma-1 chain C region EU) (Ig gamma-1 chain C region KOL) (Ig gamma-1 chain C region NIE)	IGHG1
2139,07	2137,999	2140,138	2139,02	0,044	R.TPEVTCVVVDVSHEDPEVK.F	P01857	IGHG1_HUMAN	Immunoglobulin heavy constant gamma 1 (Ig gamma-1 chain C region) (Ig gamma-1 chain C region EU) (Ig gamma-1 chain C region KOL) (Ig gamma-1 chain C region NIE)	IGHG1
			2139,95	0,877	R.TTISAGAFSQTHCVTDQQR.N	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2138,01	1,062	K.SEIIPMFSNLASDEQDSVR.L	P30153	ZAAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform (Medium tumor antigen-associated 61 kDa protein) (PP2A subunit A isoform PR65-alpha) (PP2A subunit A isoform R1-alpha)	PPP2R1A
2140,07	2138,997	2141,138	2139,95	0,121	R.TTISAGAFSQTHCVTDQQR.N	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2141,01	0,938	K.QAWFIENEQEYVQTVK.S	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
			2141,10	1,031	K.SPLYLYGLGELPQGFR.L	P50395	GDI8_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
			2141,10	1,031	K.SPLYLYGLGELPQGFR.L	P31150	GDI8_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			2139,02	1,043	R.TPEVTCVVVDVSHEDPEVK.F	P01857	IGHG1_HUMAN	Immunoglobulin heavy constant gamma 1 (Ig gamma-1 chain C region) (Ig gamma-1 chain C region EU) (Ig gamma-1 chain C region KOL) (Ig gamma-1 chain C region NIE)	IGHG1
2141,06	2139,994	2142,135	2141,10	0,034	K.SPLYLYGLGELPQGFR.L	P50395	GDI8_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
			2141,10	0,034	K.SPLYLYGLGELPQGFR.L	P31150	GDI8_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			2141,01	0,059	K.QAWFIENEQEYVQTVK.S	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
2142,05	2140,983	2143,125	2141,10	0,956	K.SPLYLYGLGELPQGFR.L	P50395	GDI8_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
			2141,10	0,956	K.SPLYLYGLGELPQGFR.L	P31150	GDI8_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			2143,07	1,013	K.ARPPDGLAEDIDKGEVSAR.Q	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
			2141,01	1,049	K.QAWFIENEQEYVQTVK.S	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
2143,02	2141,950	2144,093	2143,07	0,045	K.ARPPDGLAEDIDKGEVSAR.Q	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
			2143,97	0,948	R.VADPDHDTGFLTEYVATR.W	P28482	MK01_HUMAN	Mitogen-activated protein kinase 1 (MAP kinase 1) (MAPK 1) (EC 2.7.11.24) (ERT1) (Extracellular signal-regulated kinase 2) (ERK-2) (MAP kinase isoform p42) (p42-MAPK) (Mitogen-activated protein kinase 2) (MAP kinase 2) (MAPK 2)	MAPK1
2144,03	2142,958	2145,102	2143,97	0,060	R.VADPDHDTGFLTEYVATR.W	P28482	MK01_HUMAN	Mitogen-activated protein kinase 1 (MAP kinase 1) (MAPK 1) (EC 2.7.11.24) (ERT1) (Extracellular signal-regulated kinase 2) (ERK-2) (MAP kinase isoform p42) (p42-MAPK) (Mitogen-activated protein kinase 2) (MAP kinase 2) (MAPK 2)	MAPK1
			2143,07	0,963	K.ARPPDGLAEDIDKGEVSAR.Q	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
			2145,06	1,029	R.YVQLPADEVDTQLLQDAAR.K	Q9Y333	LSM2_HUMAN	U6 snRNA-associated 5m-like protein Lsm2 (Protein G7b) (Small nuclear ribonuclear protein D homolog) (snRNP core 5m-like protein Sm-x5)	LSM2
2145,03	2143,960	2146,105	2145,06	0,027	R.YVQLPADEVDTQLLQDAAR.K	Q9Y333	LSM2_HUMAN	U6 snRNA-associated 5m-like protein Lsm2 (Protein G7b) (Small nuclear ribonuclear protein D homolog) (snRNP core 5m-like protein Sm-x5)	LSM2
			2143,97	1,062	R.VADPDHDTGFLTEYVATR.W	P28482	MK01_HUMAN	Mitogen-activated protein kinase 1 (MAP kinase 1) (MAPK 1) (EC 2.7.11.24) (ERT1) (Extracellular signal-regulated kinase 2) (ERK-2) (MAP kinase isoform p42) (p42-MAPK) (Mitogen-activated protein kinase 2) (MAP kinase 2) (MAPK 2)	MAPK1
2146,05	2144,975	2147,121	2145,06	0,989	R.YVQLPADEVDTQLLQDAAR.K	Q9Y333	LSM2_HUMAN	U6 snRNA-associated 5m-like protein Lsm2 (Protein G7b) (Small nuclear ribonuclear protein D homolog) (snRNP core 5m-like protein Sm-x5)	LSM2
2147,05	2145,980	2148,128	2147,98	0,928	K.SDESLEQYFYFVAMCR.N	Q8TD26	CHD6_HUMAN	Chromodomain-helicase-DNA-binding protein 6 (CHD-6) (EC 3.6.4.12) (ATP-dependent helicase CHD6) (Radiation-induced gene B protein)	CHD6
2148,05	2146,980	2149,128	2147,98	0,072	K.SDESLEQYFYFVAMCR.N	Q8TD26	CHD6_HUMAN	Chromodomain-helicase-DNA-binding protein 6 (CHD-6) (EC 3.6.4.12) (ATP-dependent helicase CHD6) (Radiation-induced gene B protein)	CHD6
2149,05	2147,975	2150,124	2150,07	1,019	K.QATVGDINTERPGMLDFTGK.A	P07108	ACBP_HUMAN	Acyl-CoA-binding protein (ACBP) (Diazepam-binding inhibitor) (DBI) (Endozepine) (EP)	DBI
			2147,98	1,067	K.SDESLEQYFYFVAMCR.N	Q8TD26	CHD6_HUMAN	Chromodomain-helicase-DNA-binding protein 6 (CHD-6) (EC 3.6.4.12) (ATP-dependent helicase CHD6) (Radiation-induced gene B protein)	CHD6
2150,04	2148,967	2151,117	2150,07	0,026	K.QATVGDINTERPGMLDFTGK.A	P07108	ACBP_HUMAN	Acyl-CoA-binding protein (ACBP) (Diazepam-binding inhibitor) (DBI) (Endozepine) (EP)	DBI
2151,04	2149,969	2152,120	2150,07	0,976	K.QATVGDINTERPGMLDFTGK.A	P07108	ACBP_HUMAN	Acyl-CoA-binding protein (ACBP) (Diazepam-binding inhibitor) (DBI) (Endozepine) (EP)	DBI
2152,05	2150,971	2153,123							
2153,06	2151,986	2154,139							
2154,06	2152,985	2155,139	2154,98	0,914	R.VSQGSKDPAEGDGAQPEETPR.D	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			2155,08	1,015	K.YISLIYTNFYAGKDDYVK.A	P09211	GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1)	GSTP1

2155,06	2153,986	2156,141	2155,08	0,013	K.YISLIYTNYEAGKDDYVK.A	P09211	GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1)	GSTP1
			2154,98	0,088	R.VSQGSKDPAEGDGAQPEETPR.D	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			2155,99	0,927	R.QTNPSAMEVEEDDPVPEIR.R	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
2156,01	2154,934	2157,090	2155,99	0,021	R.QTNPSAMEVEEDDPVPEIR.R	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			2156,94	0,931	R.VYCDMNTENGWTVIQNR.Q	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
			2155,08	0,935	K.YISLIYTNYEAGKDDYVK.A	P09211	GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1)	GSTP1
			2154,98	1,036	R.VSQGSKDPAEGDGAQPEETPR.D	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			2157,09	1,075	R.ILLQGTTPVAQMTEDAVDAER.L	P01024	CO3_HUMAN	Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
2157,02	2155,937	2158,094	2157,09	0,072	R.ILLQGTTPVAQMTEDAVDAER.L	P01024	CO3_HUMAN	Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
			2156,94	0,072	R.VYCDMNTENGWTVIQNR.Q	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
			2155,99	1,024	R.QTNPSAMEVEEDDPVPEIR.R	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
2158,05	2156,968	2159,126	2158,98	0,930	K.FHYLPFLPSTEDVYDCR.V	P01903	DRA_HUMAN	HLA class II histocompatibility antigen, DR alpha chain (MHC class II antigen DRA)	HLA-DRA
			2157,09	0,960	R.ILLQGTTPVAQMTEDAVDAER.L	P01024	CO3_HUMAN	Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
			2159,03	0,983	K.QTTVSNSQQAYQEAFAISK.K	P31946	1433B_HUMAN	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHAH
2159,05	2157,973	2160,132	2159,03	0,022	K.QTTVSNSQQAYQEAFAISK.K	P31946	1433B_HUMAN	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHAH
			2158,98	0,075	K.FHYLPFLPSTEDVYDCR.V	P01903	DRA_HUMAN	HLA class II histocompatibility antigen, DR alpha chain (MHC class II antigen DRA)	HLA-DRA
			2159,99	0,934	R.EHINLGCDMDFDIAGPSIR.G	P21796	VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal porin) (Porin 31HL) (Porin 31HM)	VDAC1
2160,06	2158,978	2161,138	2159,99	0,072	R.EHINLGCDMDFDIAGPSIR.G	P21796	VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal porin) (Porin 31HL) (Porin 31HM)	VDAC1
			2160,92	0,858	K.AQPAQPADEPAEKADPEMEH.-	P25786	PSA1_HUMAN	Proteasome subunit alpha type-1 (EC 3.4.25.1) (30 kDa prosomal protein) (PROS-30) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome component C2) (Proteasome nu chain)	PSMA1
			2161,01	0,948	K.KYEDICPSTHNMDEVPIK.R	P63241	IF5A1_HUMAN	Eukaryotic translation initiation factor 5A-1 (eIF-5A-1) (eIF-5A1) (Eukaryotic initiation factor 5A isoform 1) (eIF-5A) (Rev-binding factor) (eIF-4D)	EIF5A
			2161,03	0,976	K.LIGEVSSGSGETFSYPDFLR.M	P55008	AIF1_HUMAN	Allograft inflammatory factor 1 (AIF-1) (Ionized calcium-binding adapter molecule 1) (Protein G1)	AIF1
			2159,03	1,028	K.QTTVSNSQQAYQEAFAISK.K	P31946	1433B_HUMAN	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHAH
2161,06	2159,981	2162,142	2161,03	0,027	K.LIGEVSSGSGETFSYPDFLR.M	P55008	AIF1_HUMAN	Allograft inflammatory factor 1 (AIF-1) (Ionized calcium-binding adapter molecule 1) (Protein G1)	AIF1
			2161,01	0,055	K.KYEDICPSTHNMDEVPIK.R	P63241	IF5A1_HUMAN	Eukaryotic translation initiation factor 5A-1 (eIF-5A-1) (eIF-5A1) (Eukaryotic initiation factor 5A isoform 1) (eIF-5A) (Rev-binding factor) (eIF-4D)	EIF5A
			2160,92	0,146	K.AQPAQPADEPAEKADPEMEH.-	P25786	PSA1_HUMAN	Proteasome subunit alpha type-1 (EC 3.4.25.1) (30 kDa prosomal protein) (PROS-30) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome component C2) (Proteasome nu chain)	PSMA1
			2161,94	0,876	K.FIQQTPSGSGEEQACYCR.A	Q8WUM4	PDC6I_HUMAN	Programmed cell death 6-interacting protein (PDCD6-interacting protein) (ALG-2-interacting protein 1) (ALG-2-interacting protein X) (Hp95)	PDCD6IP
			2162,09	1,027	R.TNLVNYLPQNMTQDEL.R.S	Q15717	ELAV1_HUMAN	ELAV-like protein 1 (Hu-antigen R) (HuR)	ELAVL1
2162,06	2160,982	2163,144	2159,99	1,076	R.EHINLGCDMDFDIAGPSIR.G	P21796	VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal porin) (Porin 31HL) (Porin 31HM)	VDAC1
			2162,09	0,026	R.TNLVNYLPQNMTQDEL.R.S	Q15717	ELAV1_HUMAN	ELAV-like protein 1 (Hu-antigen R) (HuR)	ELAVL1
			2161,94	0,125	K.FIQQTPSGSGEEQACYCR.A	Q8WUM4	PDC6I_HUMAN	Programmed cell death 6-interacting protein (PDCD6-interacting protein) (ALG-2-interacting protein 1) (ALG-2-interacting protein X) (Hp95)	PDCD6IP
2162,06	2160,982	2163,144	2162,94	0,882	K.AENNSEVGASGYGPGPTWDR.G	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A (EC 3.6.4.13) (DEAH box protein 9) (DEXH-box helicase 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II) (RNA helicase A)	DHX9

2163,99	2162,907	2165,071	2162,95	0,883	K.GPQLFHMDSGTFVQCDA.R.A	P28066	PSA5_HUMAN	Proteasome subunit alpha type-5 (EC 3.4.25.1) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta chain) (Proteasome zeta chain)	PSMA5
			2163,07	1,007	R.FGQAATMEGIGAIGGTPPAFNR.A	Q15233	NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrbb)) (p54nrbb)	NONO
			2161,03	1,029	K.LIGEVSSSGSETFSYPDFLR.M	P55008	AIF1_HUMAN	Allograft inflammatory factor 1 (AIF-1) (Ionized calcium-binding adapter molecule 1) (Protein G1)	AIF1
			2161,01	1,057	K.KYEDICPSTHNDVDPNIK.R	P63241	IF5A1_HUMAN	Eukaryotic translation initiation factor 5A-1 (eIF-5A-1) (eIF-5A1) (Eukaryotic initiation factor 5A isoform 1) (eIF-5A) (Rev-binding factor) (eIF-4D)	EIF5A
			2163,89	0,103	R.IQEQESSGEEDSDLSPEER.E	P41236	IPP2_HUMAN	Protein phosphatase inhibitor 2 (IPP-2)	PPP1R2
			2163,07	0,919	R.FGQAATMEGIGAIGGTPPAFNR.A	Q15233	NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrbb)) (p54nrbb)	NONO
			2165,01	1,022	K.QLSSSVTGLTNEIEENCQR.Y	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
			2162,95	1,043	K.GPQLFHMDSGTFVQCDA.R.A	P28066	PSA5_HUMAN	Proteasome subunit alpha type-5 (EC 3.4.25.1) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta chain) (Proteasome zeta chain)	PSMA5
			2162,94	1,044	K.AENNSEVGSAGYGVPGPTWDR.G	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A (EC 3.6.4.13) (DEAH box protein 9) (DEXH-box helicase 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II) (RNA helicase A)	DHX9
			2165,01	0,031	K.QLSSSVTGLTNEIEENCQR.Y	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
			2165,94	0,964	R.GPGASGEQPEPGEAAGGAAEEAR.R	Q9H3P7	GCP60_HUMAN	Golgi resident protein GCP60 (Acyl-CoA-binding domain-containing protein 3) (Golgi complex-associated protein 1) (GOCAP1) (Golgi phosphoprotein 1) (GOLPH1) (PBR- and PKA-associated protein 7) (Peripheral benzodiazepine receptor-associated protein PAP7) [Cleaved into: Golgi resident protein GCP60, N-terminally processed]	ACBD3
			2166,04	1,062	K.QATVGDINTERPGMLDFTGK.A	P07108	ACBP_HUMAN	Acyl-CoA-binding protein (ACBP) (Diazepam-binding inhibitor) (DBI) (Endozepine) (EP)	DBI
2166,00	2164,913	2167,079	2166,04	0,046	K.QATVGDINTERPGMLDFTGK.A	P07108	ACBP_HUMAN	Acyl-CoA-binding protein (ACBP) (Diazepam-binding inhibitor) (DBI) (Endozepine) (EP)	DBI
			2165,94	0,052	R.GPGASGEQPEPGEAAGGAAEEAR.R	Q9H3P7	GCP60_HUMAN	Golgi resident protein GCP60 (Acyl-CoA-binding domain-containing protein 3) (Golgi complex-associated protein 1) (GOCAP1) (Golgi phosphoprotein 1) (GOLPH1) (PBR- and PKA-associated protein 7) (Peripheral benzodiazepine receptor-associated protein PAP7) [Cleaved into: Golgi resident protein GCP60, N-terminally processed]	ACBD3
			2166,08	0,086	K.EILVGDVGQTVDDPYATFVK.M	P23528	COF1_HUMAN	Cofilin-1 (18 kDa phosphoprotein) (p18) (Cofilin, non-muscle isoform)	CFL1
			2166,90	0,900	K.KGDVEGSQSQDEGSGESER.G	Q9UQE7	SMC3_HUMAN	Structural maintenance of chromosomes protein 3 (SMC protein 3) (SMC-3) (Basement membrane-associated chondroitin proteoglycan) (Bamacan) (Chondroitin sulfate proteoglycan 6) (Chromosome-associated polypeptide) (hCAP)	SMC3
			2165,01	0,985	K.QLSSSVTGLTNEIEENCQR.Y	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
			2167,05	1,058	K.SGVSDHWALDDHHAHLTR.K	Q9HCC0	MCCB_HUMAN	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial (MCCase subunit beta) (EC 6.4.1.4) (3-methylcrotonyl-CoA carboxylase 2) (3-methylcrotonyl-CoA carboxylase non-biotin-containing subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase subunit beta)	MCCC2
			2167,05	0,036	K.SGVSDHWALDDHHAHLTR.K	Q9HCC0	MCCB_HUMAN	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial (MCCase subunit beta) (EC 6.4.1.4) (3-methylcrotonyl-CoA carboxylase 2) (3-methylcrotonyl-CoA carboxylase non-biotin-containing subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase subunit beta)	MCCC2
			2166,90	0,122	K.KGDVEGSQSQDEGSGESER.G	Q9UQE7	SMC3_HUMAN	Structural maintenance of chromosomes protein 3 (SMC protein 3) (SMC-3) (Basement membrane-associated chondroitin proteoglycan) (Bamacan) (Chondroitin sulfate proteoglycan 6) (Chromosome-associated polypeptide) (hCAP)	SMC3
			2166,08	0,936	K.EILVGDVGQTVDDPYATFVK.M	P23528	COF1_HUMAN	Cofilin-1 (18 kDa phosphoprotein) (p18) (Cofilin, non-muscle isoform)	CFL1
			2166,04	0,976	K.QATVGDINTERPGMLDFTGK.A	P07108	ACBP_HUMAN	Acyl-CoA-binding protein (ACBP) (Diazepam-binding inhibitor) (DBI) (Endozepine) (EP)	DBI
			2168,05	1,035	R.ITYGETGGNSPVQEFTVPGSK.S	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			2165,94	1,074	R.GPGASGEQPEPGEAAGGAAEEAR.R	Q9H3P7	GCP60_HUMAN	Golgi resident protein GCP60 (Acyl-CoA-binding domain-containing protein 3) (Golgi complex-associated protein 1) (GOCAP1) (Golgi phosphoprotein 1) (GOLPH1) (PBR- and PKA-associated protein 7) (Peripheral benzodiazepine receptor-associated protein PAP7) [Cleaved into: Golgi resident protein GCP60, N-terminally processed]	ACBD3
2167,99	2166,908	2169,076	2168,05	0,061	R.ITYGETGGNSPVQEFTVPGSK.S	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			2167,05	0,939	K.SGVSDHWALDDHHAHLTR.K	Q9HCC0	MCCB_HUMAN	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial (MCCase subunit beta) (EC 6.4.1.4) (3-methylcrotonyl-CoA carboxylase 2) (3-methylcrotonyl-CoA carboxylase non-biotin-containing subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase subunit beta)	MCCC2
2168,98	2167,892	2170,061	2168,05	0,924	R.ITYGETGGNSPVQEFTVPGSK.S	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
2169,99	2168,910	2171,080	2171,09	0,071	R.SAGWNIPIGLLYCDLPEPR.K	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
2171,02	2169,932	2172,103	2171,88	0,863	R.ECP5DECGAGVFMASHFDR.H	P62979	RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a (Ubiquitin carboxyl extension protein 80) [Cleaved into: Ubiquitin; 40S ribosomal protein S27a (Small ribosomal subunit protein eS31)]	RPS27A
2172,02	2170,932	2173,104	2171,88	0,137	R.ECP5DECGAGVFMASHFDR.H	P62979	RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a (Ubiquitin carboxyl extension protein 80) [Cleaved into: Ubiquitin; 40S ribosomal protein S27a (Small ribosomal subunit protein eS31)]	RPS27A

			2172,90	0,886	R.DQSGSCGSCWAFGAVEAISDR.I	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
			2171,09	0,929	R.SAGWNIPIGLLYCDLPEPR.K	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			2173,08	1,062	R.ILLQGTVPVQMTEDAVDAER.L	P01024	CO3_HUMAN	Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
2173,01	2171,925	2174,098	2173,08	0,068	R.ILLQGTVPVQMTEDAVDAER.L	P01024	CO3_HUMAN	Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
			2172,90	0,108	R.DQSGSCGSCWAFGAVEAISDR.I	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
			2174,02	1,011	K.HESENLISIACDKPQQVR.N	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
2173,98	2172,891	2175,065	2174,09	1,074	R.QGSWSVFPPGPLICSLESGR.W	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2174,02	0,045	K.HESENLISIACDKPQQVR.N	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
			2174,09	0,108	R.QGSWSVFPPGPLICSLESGR.W	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2173,08	0,898	R.ILLQGTVPVQMTEDAVDAER.L	P01024	CO3_HUMAN	Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
			2172,90	1,074	R.DQSGSCGSCWAFGAVEAISDR.I	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
2175,03	2173,946	2176,121	2175,16	0,128	K.SRLEDIPVASLPDLHDIER.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2175,96	0,924	K.MHEGDEGPGHHHKPLGEGTP.-	P06702	S10A9_HUMAN	Protein S100-A9 (Calgranulin-B) (Calprotectin L1H subunit) (Leukocyte L1 complex heavy chain) (Migration inhibitory factor-related protein 14) (MRP-14) (p14) (S100 calcium-binding protein A9)	S100A9
			2174,09	0,947	R.QGSWSVFPPGPLICSLESGR.W	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2176,04	1,007	K.WNTDNTLGTETVEDQLAR.G	P21796	VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal porin) (Porin 31HL) (Porin 31HM)	VDAC1
			2174,02	1,010	K.HESENLISIACDKPQQVR.N	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
			2176,04	0,004	K.WNTDNTLGTETVEDQLAR.G	P21796	VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal porin) (Porin 31HL) (Porin 31HM)	VDAC1
			2175,96	0,086	K.MHEGDEGPGHHHKPLGEGTP.-	P06702	S10A9_HUMAN	Protein S100-A9 (Calgranulin-B) (Calprotectin L1H subunit) (Leukocyte L1 complex heavy chain) (Migration inhibitory factor-related protein 14) (MRP-14) (p14) (S100 calcium-binding protein A9)	S100A9
			2175,16	0,883	K.SRLEDIPVASLPDLHDIER.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2176,96	0,911	R.YHTSQSGDEMTSLSEVVS.R.M	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
2177,06	2175,971	2178,148	2176,96	0,104	R.YHTSQSGDEMTSLSEVVS.R.M	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			2178,01	0,952	R.ATGEADVEFVTHEDAVAAMSK.D	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNPH3
			2178,06	1,004	K.GIGMGNIGPAGMGMEGIGFGINK.M	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			2176,04	1,020	K.WNTDNTLGTETVEDQLAR.G	P21796	VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal porin) (Porin 31HL) (Porin 31HM)	VDAC1
			2178,06	0,002	K.GIGMGNIGPAGMGMEGIGFGINK.M	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			2178,01	0,050	R.ATGEADVEFVTHEDAVAAMSK.D	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNPH3
2179,07	2177,976	2180,155	2178,06	1,002	K.GIGMGNIGPAGMGMEGIGFGINK.M	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			2180,12	1,052	R.SVLLLAYKPMEGNFEEIAR.D	Q16531	DDB1_HUMAN	DNA damage-binding protein 1 (DDB p127 subunit) (DNA damage-binding protein a) (DDBa) (Damage-specific DNA-binding protein 1) (HBV X-associated protein 1) (XAP-1) (UV-damaged DNA-binding factor) (UV-damaged DNA-binding protein 1) (UV-DDB 1) (XPE-binding factor) (XPE-BF) (Xeroderma pigmentosum group E-complementing protein) (XPCe)	DDB1
			2178,01	1,054	R.ATGEADVEFVTHEDAVAAMSK.D	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNPH3
2180,04	2178,948	2181,128	2180,12	0,080	R.SVLLLAYKPMEGNFEEIAR.D	Q16531	DDB1_HUMAN	DNA damage-binding protein 1 (DDB p127 subunit) (DNA damage-binding protein a) (DDBa) (Damage-specific DNA-binding protein 1) (HBV X-associated protein 1) (XAP-1) (UV-damaged DNA-binding factor) (UV-damaged DNA-binding protein 1) (UV-DDB 1) (XPE-binding factor) (XPE-BF) (Xeroderma pigmentosum group E-complementing protein) (XPCe)	DDB1

2181,03	2179,941	2182,122	2180,12	0,914	R.SVLLLAYKPMEGNFEEIAR.D	Q16531	DDB1_HUMAN	DNA damage-binding protein 1 (DDB p127 subunit) (DNA damage-binding protein a) (DDBa) (Damage-specific DNA-binding protein 1) (HBV X-associated protein 1) (XAP-1) (UV-damaged DNA-binding factor) (UV-damaged DNA-binding protein 1) (UV-DDB 1) (XPE-binding factor) (XPE-BF) (Xeroderma pigmentosum group E-complementing protein) (XPCe)	DDB1
2182,04 2183,05	2180,948 2181,962	2183,130 2184,145	2184,07	1,019	R.QLGLGPPDPDHAAYHPFR.R	Q14624	ITIH4_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H4 (ITI heavy chain H4) (ITI-HC4) (Inter-alpha-inhibitor heavy chain 4) (Inter-alpha-trypsin inhibitor family heavy chain-related protein) (IHRP) (Plasma kallikrein sensitive glycoprotein 120) (Gp120) (PK-120) [Cleaved into: 70 kDa inter-alpha-trypsin inhibitor heavy chain H4; 35 kDa inter-alpha-trypsin inhibitor heavy chain H4]	ITIH4
2184,03	2182,934	2185,118	2184,07	0,047	R.QLGLGPPDPDHAAYHPFR.R	Q14624	ITIH4_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H4 (ITI heavy chain H4) (ITI-HC4) (Inter-alpha-inhibitor heavy chain 4) (Inter-alpha-trypsin inhibitor family heavy chain-related protein) (IHRP) (Plasma kallikrein sensitive glycoprotein 120) (Gp120) (PK-120) [Cleaved into: 70 kDa inter-alpha-trypsin inhibitor heavy chain H4; 35 kDa inter-alpha-trypsin inhibitor heavy chain H4]	ITIH4
			2184,16	0,133	K.VFHLPTTTFIGGQESALPLR.E	Q02218	ODO1_HUMAN	2-oxoglutarate dehydrogenase, mitochondrial (EC 1.2.4.2) (2-oxoglutarate dehydrogenase complex component E1) (OGDC-E1) (Alpha-ketoglutarate dehydrogenase)	OGDH
2185,04	2183,944	2186,129	2184,16	0,878	K.VFHLPTTTFIGGQESALPLR.E	Q02218	ODO1_HUMAN	2-oxoglutarate dehydrogenase, mitochondrial (EC 1.2.4.2) (2-oxoglutarate dehydrogenase complex component E1) (OGDC-E1) (Alpha-ketoglutarate dehydrogenase)	OGDH
			2184,07	0,964	R.QLGLGPPDPDHAAYHPFR.R	Q14624	ITIH4_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H4 (ITI heavy chain H4) (ITI-HC4) (Inter-alpha-inhibitor heavy chain 4) (Inter-alpha-trypsin inhibitor family heavy chain-related protein) (IHRP) (Plasma kallikrein sensitive glycoprotein 120) (Gp120) (PK-120) [Cleaved into: 70 kDa inter-alpha-trypsin inhibitor heavy chain H4; 35 kDa inter-alpha-trypsin inhibitor heavy chain H4]	ITIH4
			2186,04	1,008	K.LYHSEAFTVNFGDTEAAKK.Q	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiprotease) (Serpine A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
2186,01	2184,914	2187,100	2186,04	0,038	K.LYHSEAFTVNFGDTEAAKK.Q	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiprotease) (Serpine A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
			2186,95	0,944	R.EMENFAVEAANYQDTIGR.L	P08670	VIME_HUMAN	Vimentin	VIM
2186,98	2185,886	2188,073	2186,95	0,029	R.EMENFAVEAANYQDTIGR.L	P08670	VIME_HUMAN	Vimentin	VIM
			2186,04	0,935	K.LYHSEAFTVNFGDTEAAKK.Q	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiprotease) (Serpine A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
2187,97	2186,878	2189,066	2186,95	1,022	R.EMENFAVEAANYQDTIGR.L	P08670	VIME_HUMAN	Vimentin	VIM
2188,99	2187,895	2190,084	2189,07	0,078	R.GPLLVDVVFTDEMAHFDR.E	P04040	CATA_HUMAN	Catalase (EC 1.11.1.6)	CAT
			2189,91	0,920	R.NMGGPYGGNYGPGSGSGGYGGR.S	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			2190,03	1,043	R.NEHVDYVDVGGAYVGTQNR.I	P21397	AOFA_HUMAN	Amine oxidase [flavin-containing] A (EC 1.4.3.4) (Monoamine oxidase type A) (MAO-A)	MAOA
2189,97	2188,874	2191,064	2189,91	0,059	R.NMGGPYGGNYGPGSGSGGYGGR.S	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			2190,03	0,064	R.NEHVDYVDVGGAYVGTQNR.I	P21397	AOFA_HUMAN	Amine oxidase [flavin-containing] A (EC 1.4.3.4) (Monoamine oxidase type A) (MAO-A)	MAOA
			2189,07	0,901	R.GPLLVDVVFTDEMAHFDR.E	P04040	CATA_HUMAN	Catalase (EC 1.11.1.6)	CAT
2191,00	2189,902	2192,093	2191,94	0,941	K.MHEGDEGPGHHHKPLGEGTP.-	P06702	S10A9_HUMAN	Protein S100-A9 (Calgranulin-B) (Calprotectin L1H subunit) (Leukocyte L1 complex heavy chain) (Migration inhibitory factor-related protein 14) (MRP-14) (p14) (S100 calcium-binding protein A9)	S100A9
			2190,03	0,965	R.NEHVDYVDVGGAYVGTQNR.I	P21397	AOFA_HUMAN	Amine oxidase [flavin-containing] A (EC 1.4.3.4) (Monoamine oxidase type A) (MAO-A)	MAOA
			2192,07	1,070	K.VPADTEVVCAPPTAYIDFAR.Q	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP11
			2189,91	1,087	R.NMGGPYGGNYGPGSGSGGYGGR.S	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
2191,99	2190,893	2193,085	2191,94	0,051	K.MHEGDEGPGHHHKPLGEGTP.-	P06702	S10A9_HUMAN	Protein S100-A9 (Calgranulin-B) (Calprotectin L1H subunit) (Leukocyte L1 complex heavy chain) (Migration inhibitory factor-related protein 14) (MRP-14) (p14) (S100 calcium-binding protein A9)	S100A9
			2192,07	0,078	K.VPADTEVVCAPPTAYIDFAR.Q	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP11
2192,99	2191,889	2194,082	2193,14	0,156	K.ALAPTWEQLALGLEHSETVK.I	Q8NB59	TXND5_HUMAN	Thioredoxin domain-containing protein 5 (Endoplasmic reticulum resident protein 46) (ER protein 46) (Erp46) (Thioredoxin-like protein p46)	TXNDC5
			2192,07	0,918	K.VPADTEVVCAPPTAYIDFAR.Q	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP11
			2191,94	1,047	K.MHEGDEGPGHHHKPLGEGTP.-	P06702	S10A9_HUMAN	Protein S100-A9 (Calgranulin-B) (Calprotectin L1H subunit) (Leukocyte L1 complex heavy chain) (Migration inhibitory factor-related protein 14) (MRP-14) (p14) (S100 calcium-binding protein A9)	S100A9
			2194,04	1,057	R.YGGLHFSDDQVEVSPGSDR.A	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
2193,98	2192,879	2195,073	2194,04	0,066	R.YGGLHFSDDQVEVSPGSDR.A	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
			2193,14	0,835	K.ALAPTWEQLALGLEHSETVK.I	Q8NB59	TXND5_HUMAN	Thioredoxin domain-containing protein 5 (Endoplasmic reticulum resident protein 46) (ER protein 46) (Erp46) (Thioredoxin-like protein p46)	TXNDC5
			2195,03	1,057	K.EQQAIEHIDEVQNEIDR.L	Q01105	SET_HUMAN	Protein SET (HLA-DR-associated protein II) (Inhibitor of granzyme A-activated DNase) (IGAAD) (PHAPII) (Phosphatase 2A inhibitor I2PP2A) (I-2PP2A) (Template-activating factor I) (TAF-I)	SET
2194,99	2193,893	2196,088	2195,03	0,043	K.EQQAIEHIDEVQNEIDR.L	Q01105	SET_HUMAN	Protein SET (HLA-DR-associated protein II) (Inhibitor of granzyme A-activated DNase) (IGAAD) (PHAPII) (Phosphatase 2A inhibitor I2PP2A) (I-2PP2A) (Template-activating factor I) (TAF-I)	SET

2196,01	2194,910	2197,106	2195,10	0,111	K.VGEQAQVVIDMNDPSNPIR.R	Q00610	CLH1_HUMAN	Clathrin heavy chain 1 (Clathrin heavy chain on chromosome 17) (CLH-17)	CLTC
			2194,04	0,949	R.YGGLHFDQVEVSPGSDR.A	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
			2195,10	0,906	K.VGEQAQVVIDMNDPSNPIR.R	Q00610	CLH1_HUMAN	Clathrin heavy chain 1 (Clathrin heavy chain on chromosome 17) (CLH-17)	CLTC
			2196,93	0,921	R.QDGHLCWSTTSNYEQDQK.Y	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
2197,08	2195,980	2198,177	2195,03	0,974	K.EQQAIEHIDEVQNEIDR.L	Q01105	SET_HUMAN	Protein SET (HLA-DR-associated protein II) (Inhibitor of granzyme A-activated DNase) (IGAAD) (PHAP II) (Phosphatase 2A inhibitor I2PP2A) (I-2PP2A) (Template-activating factor I) (TAF-I)	SET
			2197,10	1,093	R.TVQPKPDYGAAVAFFETAR.Q	Q03154	ACY1_HUMAN	Aminoacylase-1 (ACY-1) (EC 3.5.1.14) (N-acyl-L-amino-acid amidohydrolase)	ACY1
			2197,10	0,022	R.TVQPKPDYGAAVAFFETAR.Q	Q03154	ACY1_HUMAN	Aminoacylase-1 (ACY-1) (EC 3.5.1.14) (N-acyl-L-amino-acid amidohydrolase)	ACY1
			2196,93	0,149	R.QDGHLCWSTTSNYEQDQK.Y	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
2198,08	2196,982	2199,180	2197,10	0,981	R.TVQPKPDYGAAVAFFETAR.Q	Q03154	ACY1_HUMAN	Aminoacylase-1 (ACY-1) (EC 3.5.1.14) (N-acyl-L-amino-acid amidohydrolase)	ACY1
2198,97	2197,873	2200,071	2200,00	1,032	K.GDVEEDETIPDSEQDIRPR.F	Q92973	TNPO1_HUMAN	Transportin-1 (Importin beta-2) (Karyopherin beta-2) (M9 region interaction protein) (MIP)	TNPO1
2199,96	2198,859	2201,059	2200,04	1,068	K.GLSEDTTEETLKESFDGSVR.A	P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL
			2200,00	0,045	K.GDVEEDETIPDSEQDIRPR.F	Q92973	TNPO1_HUMAN	Transportin-1 (Importin beta-2) (Karyopherin beta-2) (M9 region interaction protein) (MIP)	TNPO1
			2200,04	0,081	K.GLSEDTTEETLKESFDGSVR.A	P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL
			2201,02	1,060	K.DLYANTVLSGGSTMYPGIADR.M	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
2200,92	2199,821	2202,022	2201,02	0,098	K.DLYANTVLSGGSTMYPGIADR.M	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			2201,15	0,226	R.YNEDELEDAIHTAILTK.E	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
			2200,04	0,882	K.GLSEDTTEETLKESFDGSVR.A	P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL
			2200,00	0,918	K.GDVEEDETIPDSEQDIRPR.F	Q92973	TNPO1_HUMAN	Transportin-1 (Importin beta-2) (Karyopherin beta-2) (M9 region interaction protein) (MIP)	TNPO1
2200,98	2199,876	2202,077	2201,02	0,043	K.DLYANTVLSGGSTMYPGIADR.M	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			2201,15	0,171	R.YNEDELEDAIHTAILTK.E	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
			2200,04	0,937	K.GLSEDTTEETLKESFDGSVR.A	P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL
			2200,00	0,972	K.GDVEEDETIPDSEQDIRPR.F	Q92973	TNPO1_HUMAN	Transportin-1 (Importin beta-2) (Karyopherin beta-2) (M9 region interaction protein) (MIP)	TNPO1
2201,96	2200,863	2203,065	2201,15	0,816	R.YNEDELEDAIHTAILTK.E	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
			2201,02	0,945	K.DLYANTVLSGGSTMYPGIADR.M	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			2202,95	0,983	R.EMENFAVEAANYQDTIGR.L	P08670	VIME_HUMAN	Vimentin	VIM
			2203,02	1,052	R.ASFNFHDKDHGGALGPEEFK.A	Q43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
2203,03	2201,926	2204,129	2203,02	0,011	R.ASFNFHDKDHGGALGPEEFK.A	Q43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
			2203,10	0,077	R.IGQPTLLLYVDAGPETMTQR.L	P00568	KAD1_HUMAN	Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP-AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	AK1
			2202,95	0,080	R.EMENFAVEAANYQDTIGR.L	P08670	VIME_HUMAN	Vimentin	VIM
			2204,15	0,185	R.GNIIIPGINEAUAATEEHK.L	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
2203,97	2202,866	2205,070	2203,10	0,864	R.IGQPTLLLYVDAGPETMTQR.L	P00568	KAD1_HUMAN	Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP-AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	AK1
			2203,02	0,953	R.ASFNFHDKDHGGALGPEEFK.A	Q43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
			2202,95	1,021	R.EMENFAVEAANYQDTIGR.L	P08670	VIME_HUMAN	Vimentin	VIM
			2204,15	0,862	R.GNIIIPGINEAUAATEEHK.L	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
2206,99	2205,890	2208,097	2205,92	0,907	R.EAQGGDATENFEDVGHSTDAE	P00167	CYB5_HUMAN	Cytochrome b5 (Microsomal cytochrome b5 type A) (MCB5)	CYB5A
			2205,98	0,961	K.SDAEEDGGTVSQEEDRKPK.A	P27824	CALX_HUMAN	Calnexin (IP90) (Major histocompatibility complex class I antigen-binding protein p88) (p90)	CANX
			2207,04	0,045	K.EFGFHLSPGTTFEVLGNEK.I	P02679	FIBG_HUMAN	Fibrinogen gamma chain	FGG
			2205,98	1,018	K.SDAEEDGGTVSQEEDRKPK.A	P27824	CALX_HUMAN	Calnexin (IP90) (Major histocompatibility complex class I antigen-binding protein p88) (p90)	CANX
2207,99	2206,882	2209,090	2205,92	1,071	R.EAQGGDATENFEDVGHSTDAE	P00167	CYB5_HUMAN	Cytochrome b5 (Microsomal cytochrome b5 type A) (MCB5)	CYB5A
			2207,04	0,948	K.EFGFHLSPGTTFEVLGNEK.I	P02679	FIBG_HUMAN	Fibrinogen gamma chain	FGG
			2209,03	1,044	K.GDTFSCMVHGHEALPLAFTQK.T	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
			2209,06	1,073	K.ISSEAWPPVGTTPSSESEPV.R	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
2209,00	2207,893	2210,102	2209,03	0,032	K.GDTFSCMVHGHEALPLAFTQK.T	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
			2209,06	0,062	K.ISSEAWPPVGTTPSSESEPV.R	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
			2209,06	0,934	K.ISSEAWPPVGTTPSSESEPV.R	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
			2209,03	0,964	K.GDTFSCMVHGHEALPLAFTQK.T	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
2215,04	2213,929	2216,144	2215,07	0,036	K.DLYANTVLSGGTTPMYPGIADR.M	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB

2216,04	2214,930	2217,146	2215,07	0,966	K.DLYANTVLSGGTTMYPGIADR.M	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			2217,13	1,095	K.ASAFALQEQPVVNAVIDDTTK.E	P36957	ODO2_HUMAN	Dihydrolipoylysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex) (E2K)	DLST
2217,03	2215,918	2218,135	2217,13	0,108	K.ASAFALQEQPVVNAVIDDTTK.E	P36957	ODO2_HUMAN	Dihydrolipoylysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex) (E2K)	DLST
			2218,03	1,008	R.SPWSNKYDPPLEDGAMPARS.L	P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta (CapZ beta)	CAPZB
2218,03	2216,920	2219,138	2218,03	0,006	R.SPWSNKYDPPLEDGAMPARS.L	P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta (CapZ beta)	CAPZB
			2218,14	0,109	K.TLYVEEVVPNVIEPSFGLGR.I	P41250	GARS_HUMAN		GARS
			2217,13	0,895	K.ASAFALQEQPVVNAVIDDTTK.E	P36957	ODO2_HUMAN	Dihydrolipoylysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex) (E2K)	DLST
2219,02	2217,915	2220,134	2218,14	0,887	K.TLYVEEVVPNVIEPSFGLGR.I	P41250	GARS_HUMAN		GARS
			2218,03	0,990	R.SPWSNKYDPPLEDGAMPARS.L	P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta (CapZ beta)	CAPZB
			2220,08	1,051	R.GSTDDKGPVAGWINALEAYQK.T	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
2220,01	2218,899	2221,119	2220,08	0,066	R.GSTDDKGPVAGWINALEAYQK.T	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
2221,02	2219,907	2222,128	2220,08	0,942	R.GSTDDKGPVAGWINALEAYQK.T	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
2222,02	2220,909	2223,131	2222,93	0,906	R.MREDYDVEQDGEPEGPQR.S	Q9Y5S9	RBM8A_HUMAN	RNA-binding protein 8A (Binder of OVCA1-1) (BOV-1) (RNA-binding motif protein 8A) (RNA-binding protein Y14) (Ribonucleoprotein RBM8A)	
2223,02	2221,908	2224,131	2222,93	0,094	R.MREDYDVEQDGEPEGPQR.S	Q9Y5S9	RBM8A_HUMAN	RNA-binding protein 8A (Binder of OVCA1-1) (BOV-1) (RNA-binding motif protein 8A) (RNA-binding protein Y14) (Ribonucleoprotein RBM8A)	
2224,05	2222,939	2225,163							
2225,05	2223,941	2226,166	2226,20	0,146	K.LLYPADTPVGNDQLLELNK.L	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
			2227,10	1,052	R.DVVFLLDGSQSAGPEFQVVR.T	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
2226,05	2224,939	2227,165							
2227,09	2225,976	2228,203	2227,10	0,015	R.DVVFLLDGSQSAGPEFQVVR.T	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			2226,20	0,891	K.LLYPADTPVGNDQLLELNK.L	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
			2228,06	0,971	K.YTPSGQAGAAASESLFVSNHAY.-	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
			2228,07	0,982	K.DLYANNVLSGGTTMYPGIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2228,07	0,982	K.DLYANNVLSGGTTMYPGIADR.M	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2228,16	1,067	K.SAVTALWGKVVNDEVGGEALGR.L	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2228,06	2226,946	2229,175	2228,06	0,000	K.YTPSGQAGAAASESLFVSNHAY.-	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
			2228,07	0,011	K.DLYANNVLSGGTTMYPGIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2228,07	0,011	K.DLYANNVLSGGTTMYPGIADR.M	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2228,16	0,096	K.SAVTALWGKVVNDEVGGEALGR.L	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			2228,97	0,907	K.KEDGTFYFEGEDIPEAPER.L	O43776	SYNC_HUMAN	Asparagine--tRNA ligase, cytoplasmic (EC 6.1.1.22) (Asparaginyl-tRNA synthetase) (AsnRS)	NARS
			2227,10	0,956	R.DVVFLLDGSQSAGPEFQVVR.T	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			2229,04	0,978	K.EVFGDTLINESRDPDRPPER.Y	Q96CX2	KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 (Pftin) (Predominantly fetal expressed T1 domain)	KCTD12
2229,06	2227,942	2230,171	2229,04	0,018	K.EVFGDTLINESRDPDRPPER.Y	Q96CX2	KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 (Pftin) (Predominantly fetal expressed T1 domain)	KCTD12
			2228,97	0,089	K.KEDGTFYFEGEDIPEAPER.L	O43776	SYNC_HUMAN	Asparagine--tRNA ligase, cytoplasmic (EC 6.1.1.22) (Asparaginyl-tRNA synthetase) (AsnRS)	NARS
			2228,16	0,900	K.SAVTALWGKVVNDEVGGEALGR.L	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			2228,07	0,985	K.DLYANNVLSGGTTMYPGIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2228,07	0,985	K.DLYANNVLSGGTTMYPGIADR.M	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2228,06	0,996	K.YTPSGQAGAAASESLFVSNHAY.-	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
			2230,06	1,006	K.TTLSRFVAVWMNGLSVYQIK.V	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
2230,04	2228,928	2231,158	2230,06	0,020	K.TTLSRFVAVWMNGLSVYQIK.V	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
			2229,04	1,004	K.EVFGDTLINESRDPDRPPER.Y	Q96CX2	KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 (Pftin) (Predominantly fetal expressed T1 domain)	KCTD12
			2231,06	1,014	K.DLYANTVLSGGTTMYPGIADR.M	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			2228,97	1,075	K.KEDGTFYFEGEDIPEAPER.L	O43776	SYNC_HUMAN	Asparagine--tRNA ligase, cytoplasmic (EC 6.1.1.22) (Asparaginyl-tRNA synthetase) (AsnRS)	NARS

2231,08	2229,965	2232,196	2231,06	0,024	K.DLYANTVLSGGTTMYPGIADR.M	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			2232,00	0,915	R.DGEDQQTQDELTVETRPAGDR.T	P30493	1B55_HUMAN	HLA class I histocompatibility antigen, B-55 alpha chain (Bw-55) (HLA class I histocompatibility antigen, B-12 alpha chain) (MHC class I antigen B*55)	HLA-B
			2230,06	1,018	K.TTSLRFVAVWMNGLSVYQIK.V	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
2232,05	2230,935	2233,167	2232,00	0,056	R.DGEDQQTQDELTVETRPAGDR.T	P30493	1B55_HUMAN	HLA class I histocompatibility antigen, B-55 alpha chain (Bw-55) (HLA class I histocompatibility antigen, B-12 alpha chain) (MHC class I antigen B*55)	HLA-B
			2231,06	0,995	K.DLYANTVLSGGTTMYPGIADR.M	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
2233,06	2231,948	2234,181	2232,00	1,070	R.DGEDQQTQDELTVETRPAGDR.T	P30493	1B55_HUMAN	HLA class I histocompatibility antigen, B-55 alpha chain (Bw-55) (HLA class I histocompatibility antigen, B-12 alpha chain) (MHC class I antigen B*55)	HLA-B
2234,07	2232,949	2235,183	2234,19	0,125	R.ISQAEEDQQLGLHLLLVAK.Q	Q9BX68	HINT2_HUMAN	Histidine triad nucleotide-binding protein 2, mitochondrial (HINT-2) (EC 3.-.-.-) (HINT-3) (HIT-17kDa) (PKC1-related HIT protein)	HINT2
2235,01	2233,892	2236,127	2234,19	0,819	R.ISQAEEDQQLGLHLLLVAK.Q	Q9BX68	HINT2_HUMAN	Histidine triad nucleotide-binding protein 2, mitochondrial (HINT-2) (EC 3.-.-.-) (HINT-3) (HIT-17kDa) (PKC1-related HIT protein)	HINT2
			2235,94	0,930	R.SHTEEDCTEELDFDLHAR.D	P07919	QCR6_HUMAN	Cytochrome b-c1 complex subunit 6, mitochondrial (Complex III subunit 6) (Complex III subunit VIII) (Cytochrome c1 non-heme 11 kDa protein) (Mitochondrial hinge protein) (Ubiquinol-cytochrome c reductase complex 11 kDa protein)	UQCRH
2236,04	2234,926	2237,163	2235,94	0,105	R.SHTEEDCTEELDFDLHAR.D	P07919	QCR6_HUMAN	Cytochrome b-c1 complex subunit 6, mitochondrial (Complex III subunit 6) (Complex III subunit VIII) (Cytochrome c1 non-heme 11 kDa protein) (Mitochondrial hinge protein) (Ubiquinol-cytochrome c reductase complex 11 kDa protein)	UQCRH
2237,06	2235,943	2238,180	2243,13	1,065	K.NNQFQALLQYADPVSAQHAK.L	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
2238,06	2236,937	2239,175							
2239,06	2237,940	2240,179							
2240,09	2238,973	2241,213							
2241,05	2239,925	2242,166							
2242,06	2240,944	2243,186							
2242,18	2241,057	2243,299	2243,13	0,952	K.NNQFQALLQYADPVSAQHAK.L	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
2242,99	2241,869	2244,112	2243,13	0,139	K.NNQFQALLQYADPVSAQHAK.L	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
			2244,07	1,079	K.DLYANNVLSGGTTMYPGIADR.M	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2244,07	1,079	K.DLYANNVLSGGTTMYPGIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2244,09	1,096	R.SVMTEEEKVPDGMVGFIIGR.G	Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1) (DNA helicase V) (hDH V)	FUBP1
2243,17	2242,053	2244,296	2243,13	0,045	K.NNQFQALLQYADPVSAQHAK.L	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
			2244,07	0,895	K.DLYANNVLSGGTTMYPGIADR.M	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2244,07	0,895	K.DLYANNVLSGGTTMYPGIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2244,09	0,912	R.SVMTEEEKVPDGMVGFIIGR.G	Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1) (DNA helicase V) (hDH V)	FUBP1
			2244,12	2242,996	2245,240	2244,09	0,031	R.SVMTEEEKVPDGMVGFIIGR.G	Q96AE4
2244,12	2242,996	2245,240	2244,07	0,048	K.DLYANNVLSGGTTMYPGIADR.M	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2244,07	0,048	K.DLYANNVLSGGTTMYPGIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2245,08	0,961	K.IEGYEDQVLITEHGDLGNSR.F	P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (CapZ alpha-1)	CAPZA1
			2243,13	0,988	K.NNQFQALLQYADPVSAQHAK.L	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
			2245,01	2243,889	2246,134	2245,08	0,067	K.IEGYEDQVLITEHGDLGNSR.F	P52907
2245,01	2243,889	2246,134	2244,09	0,925	R.SVMTEEEKVPDGMVGFIIGR.G	Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1) (DNA helicase V) (hDH V)	FUBP1
			2244,07	0,942	K.DLYANNVLSGGTTMYPGIADR.M	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2244,07	0,942	K.DLYANNVLSGGTTMYPGIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2246,01	0,997	K.DLYANNVLSGGTTMYPGIADR.M	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			2245,17	2244,048	2246,293	2245,08	0,091	K.IEGYEDQVLITEHGDLGNSR.F	P52907
2245,17	2244,048	2246,293	2246,01	0,838	K.DLYANNVLSGGTTMYPGIADR.M	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			2244,09	1,083	R.SVMTEEEKVPDGMVGFIIGR.G	Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1) (DNA helicase V) (hDH V)	FUBP1
			2244,07	1,100	K.DLYANNVLSGGTTMYPGIADR.M	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2244,07	1,100	K.DLYANNVLSGGTTMYPGIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2246,12	2244,994	2247,240	2246,01	0,109	K.DLYANNVLSGGTTMYPGIADR.M	P68133
2246,12	2244,994	2247,240	2245,08	1,038	K.IEGYEDQVLITEHGDLGNSR.F	P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (CapZ alpha-1)	CAPZA1

2247,12	2245,999	2248,246	2246,01	1,114	K.DLYANNVMGGTMYPGIADR.M	P68133	ACT5_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
2248,13	2247,004	2249,252							
2249,11	2247,988	2250,237							
2250,11	2248,981	2251,231							
2251,09	2249,967	2252,218							
2252,09	2250,967	2253,220	2253,04	0,950	K.AMEVDERPTEQYSDIGGLDK.Q	P17980	PR56A_HUMAN	26S proteasome regulatory subunit 6A (26S proteasome AAA-ATPase subunit RPT5) (Proteasome 26S subunit ATPase 3) (Proteasome subunit P50) (Tat-binding protein 1) (TBP-1)	PSMC3
2253,10	2251,975	2254,228	2253,04	0,058	K.AMEVDERPTEQYSDIGGLDK.Q	P17980	PR56A_HUMAN	26S proteasome regulatory subunit 6A (26S proteasome AAA-ATPase subunit RPT5) (Proteasome 26S subunit ATPase 3) (Proteasome subunit P50) (Tat-binding protein 1) (TBP-1)	PSMC3
			2254,16	1,059	R.VAEEHAPSIVFIDEIDAIGTK.R	P62191	PR54_HUMAN	26S proteasome regulatory subunit 4 (P26s4) (26S proteasome AAA-ATPase subunit RPT2) (Proteasome 26S subunit ATPase 1)	PSMC1
2254,06	2252,936	2255,190	2254,16	0,097	R.VAEEHAPSIVFIDEIDAIGTK.R	P62191	PR54_HUMAN	26S proteasome regulatory subunit 4 (P26s4) (26S proteasome AAA-ATPase subunit RPT2) (Proteasome 26S subunit ATPase 1)	PSMC1
			2253,04	1,020	K.AMEVDERPTEQYSDIGGLDK.Q	P17980	PR56A_HUMAN	26S proteasome regulatory subunit 6A (26S proteasome AAA-ATPase subunit RPT5) (Proteasome 26S subunit ATPase 3) (Proteasome subunit P50) (Tat-binding protein 1) (TBP-1)	PSMC3
2255,06	2253,935	2256,190	2254,16	0,903	R.VAEEHAPSIVFIDEIDAIGTK.R	P62191	PR54_HUMAN	26S proteasome regulatory subunit 4 (P26s4) (26S proteasome AAA-ATPase subunit RPT2) (Proteasome 26S subunit ATPase 1)	PSMC1
			2255,99	0,925	K.HNDDEQYAWESSAGGSFTVR.A	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			2255,99	0,925	K.HNDDEQYAWESSAGGSFTVR.T	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP 2) (LP5-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
			2256,02	0,953	K.EIINVGHSHFVNFDNDNR.S	P00915	CAH1_HUMAN	Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase I) (Carbonic anhydrase B) (CAB) (Carbonic anhydrase I) (CA-I)	CA1
2256,08	2254,952	2257,208	2256,02	0,064	K.EIINVGHSHFVNFDNDNR.S	P00915	CAH1_HUMAN	Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase I) (Carbonic anhydrase B) (CAB) (Carbonic anhydrase I) (CA-I)	CA1
			2255,99	0,092	K.HNDDEQYAWESSAGGSFTVR.A	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			2255,99	0,092	K.HNDDEQYAWESSAGGSFTVR.T	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP 2) (LP5-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
			2257,06	0,981	K.GGETSEMYLIQPDSSVKPYR.V	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
			2257,18	1,099	-MDPQEMVVKNPYAHISIPR.A	A8MQ03	CRTP1_HUMAN	Cysteine-rich tail protein 1	CYSRT1
2257,11	2255,977	2258,234	2257,06	0,044	K.GGETSEMYLIQPDSSVKPYR.V	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
			2257,18	0,074	-MDPQEMVVKNPYAHISIPR.A	A8MQ03	CRTP1_HUMAN	Cysteine-rich tail protein 1	CYSRT1
			2256,02	1,090	K.EIINVGHSHFVNFDNDNR.S	P00915	CAH1_HUMAN	Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase I) (Carbonic anhydrase B) (CAB) (Carbonic anhydrase I) (CA-I)	CA1
			2258,20	1,094	K.VSLDSWQSLALSSVVDPISIR.H	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2258,99	1,117	K.HNDDEQYAWESSAGGSFTVR.A	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			2255,99	1,117	K.HNDDEQYAWESSAGGSFTVR.T	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP 2) (LP5-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
2258,13	2257,002	2259,260	2258,20	0,068	K.VSLDSWQSLALSSVVDPISIR.H	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2257,18	0,952	-MDPQEMVVKNPYAHISIPR.A	A8MQ03	CRTP1_HUMAN	Cysteine-rich tail protein 1	CYSRT1
			2259,15	1,022	K.GTEAAGAMFLEAIPMSIPEVK.F	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiprotease) (Serp1 A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
			2257,06	1,070	K.GGETSEMYLIQPDSSVKPYR.V	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
2259,15	2258,020	2260,279	2259,15	0,003	K.GTEAAGAMFLEAIPMSIPEVK.F	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiprotease) (Serp1 A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
			2260,02	0,871	K.EFNAETFTFHADICTLSEK.E	P02768	ALBU_HUMAN	Serum albumin	ALB
			2260,07	0,923	R.FQSSHPTDITSLDQYVER.M	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			2258,20	0,950	K.VSLDSWQSLALSSVVDPISIR.H	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2260,14	0,988	K.VAVPSTIHCDHLEAQVGGEK.D	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
			2260,14	0,992	K.SINPDEAVAYGAQAALSGDK.S	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LP5-associated protein 1)	HSPA8
2260,09	2258,961	2261,221	2260,07	0,018	R.FQSSHPTDITSLDQYVER.M	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			2260,14	0,047	K.VAVPSTIHCDHLEAQVGGEK.D	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
			2260,14	0,051	K.SINPDEAVAYGAQAALSGDK.S	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LP5-associated protein 1)	HSPA8
			2260,02	0,071	K.EFNAETFTFHADICTLSEK.E	P02768	ALBU_HUMAN	Serum albumin	ALB
			2259,15	0,938	K.GTEAAGAMFLEAIPMSIPEVK.F	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiprotease) (Serp1 A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
			2261,10	1,007	R.GGMGSGGLATGIAGGLAGMGGIQNEK.E	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
2261,10	2259,971	2262,232	2261,10	0,003	R.GGMGSGGLATGIAGGLAGMGGIQNEK.E	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
			2261,98	0,875	K.DLYANNVMGGTMYPGIADR.M	P68133	ACT5_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			2262,00	0,902	K.DLYANNVMGGTMYPGIADR.M	P68133	ACT5_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1

2262,12	2260,987	2263,249	2260,14	0,959	K.SINPDEAVAYGAAVQAAILSGDK.S	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LP5-associated protein 1)	HSPA8
			2260,14	0,964	K.VAVPSTIHCDHUIEAQVGGEK.D	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
			2260,07	1,028	R.FQSSHPTDITSLDQIVER.M	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			2260,02	1,081	K.FNAETFTFHADICTSEK.E	P02768	ALBU_HUMAN	Serum albumin	ALB
			2262,00	0,114	K.DLYANNVMSGGTTMYPGIADR.M	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
2263,12	2261,993	2264,256	2261,98	0,142	K.DLYANNVMSGGTTMYPGIADR.M	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			2261,10	1,019	R.GGMGSGGLATGIAGGLAGMGGIQNEK.E	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
			2262,00	1,121	K.DLYANNVMSGGTTMYPGIADR.M	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			2265,04	0,902	K.ADRDESSPYAAMLAQDVAQR.C	P62263	RS14_HUMAN	40S ribosomal protein S14 (Small ribosomal subunit protein uS11)	RPS14
			2265,06	0,917	K.TFPGFFSPMLGEFVSETESR.G	P02671	FIBA_HUMAN	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	FGA
2265,15	2264,022	2266,287	2265,06	0,096	K.TFPGFFSPMLGEFVSETESR.G	P02671	FIBA_HUMAN	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	FGA
			2265,04	0,111	K.ADRDESSPYAAMLAQDVAQR.C	P62263	RS14_HUMAN	40S ribosomal protein S14 (Small ribosomal subunit protein uS11)	RPS14
			2266,09	0,937	R.IPSAVGYQPTLATDMGTMQER.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			2266,09	0,007	R.IPSAVGYQPTLATDMGTMQER.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			2265,06	1,040	K.TFPGFFSPMLGEFVSETESR.G	P02671	FIBA_HUMAN	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	FGA
2266,10	2264,966	2267,232	2265,04	1,056	K.ADRDESSPYAAMLAQDVAQR.C	P62263	RS14_HUMAN	40S ribosomal protein S14 (Small ribosomal subunit protein uS11)	RPS14
			2266,09	1,011	R.IPSAVGYQPTLATDMGTMQER.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			2267,00	0,900	R.VYQSLCPTSWVTDWDEQR.A	P14854	CX6B1_HUMAN	Cytochrome c oxidase subunit 6B1 (Cytochrome c oxidase subunit Vlb isoform 1) (COX Vlb-1)	COX6B1
			2267,08	0,976	R.NIELICQENEGENDPVLQR.I	Q15691	MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1) (End-binding protein 1) (EB1)	MAPRE1
			2270,13	1,024	K.GPAFVNPLIPESPEEEELFR.Q	Q9Y305	ACOT9_HUMAN	Acyl-coenzyme A thioesterase 9, mitochondrial (Acyl-CoA thioesterase 9) (EC 3.1.2.-) (Acyl-CoA thioester hydrolase 9)	ACOT9
2270,10	2268,963	2271,233	2270,08	0,021	R.NIELICQENEGENDPVLQR.I	Q15691	MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1) (End-binding protein 1) (EB1)	MAPRE1
			2270,13	0,028	K.GPAFVNPLIPESPEEEELFR.Q	Q9Y305	ACOT9_HUMAN	Acyl-coenzyme A thioesterase 9, mitochondrial (Acyl-CoA thioesterase 9) (EC 3.1.2.-) (Acyl-CoA thioester hydrolase 9)	ACOT9
			2270,00	0,097	R.VYQSLCPTSWVTDWDEQR.A	P14854	CX6B1_HUMAN	Cytochrome c oxidase subunit 6B1 (Cytochrome c oxidase subunit Vlb isoform 1) (COX Vlb-1)	COX6B1
			2270,08	0,021	R.NIELICQENEGENDPVLQR.I	Q15691	MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1) (End-binding protein 1) (EB1)	MAPRE1
			2270,13	0,028	K.GPAFVNPLIPESPEEEELFR.Q	Q9Y305	ACOT9_HUMAN	Acyl-coenzyme A thioesterase 9, mitochondrial (Acyl-CoA thioesterase 9) (EC 3.1.2.-) (Acyl-CoA thioester hydrolase 9)	ACOT9
2270,10	2268,963	2271,233	2270,00	0,097	R.VYQSLCPTSWVTDWDEQR.A	P14854	CX6B1_HUMAN	Cytochrome c oxidase subunit 6B1 (Cytochrome c oxidase subunit Vlb isoform 1) (COX Vlb-1)	COX6B1
			2270,13	0,970	K.GPAFVNPLIPESPEEEELFR.Q	Q9Y305	ACOT9_HUMAN	Acyl-coenzyme A thioesterase 9, mitochondrial (Acyl-CoA thioesterase 9) (EC 3.1.2.-) (Acyl-CoA thioester hydrolase 9)	ACOT9
			2272,09	0,996	K.NIDGTSRDPYSHALVAGIDR.Y	P61353	RL27_HUMAN	60S ribosomal protein L27 (Large ribosomal subunit protein eL27)	RPL27
			2272,11	1,016	R.AQPQVQVAEGSEPDGFWEALGGK.A	P06396	GELS_HUMAN	Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF) (Brevin)	GSN
			2270,08	1,019	R.NIELICQENEGENDPVLQR.I	Q15691	MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1) (End-binding protein 1) (EB1)	MAPRE1
2271,10	2269,960	2272,231	2272,13	1,036	K.GVVPLAGTNGETTQGLDGLSER.C	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
			2272,18	1,083	R.TQTSDPAMPLPTMIGLAEAGVR.L	O43175	SERA_HUMAN	D-3-phosphoglycerate dehydrogenase (3-PGDH) (EC 1.1.1.95) (2-oxoglutarate reductase) (EC 1.1.1.399) (Malate dehydrogenase) (EC 1.1.1.37)	PHGDH
			2270,00	1,094	R.VYQSLCPTSWVTDWDEQR.A	P14854	CX6B1_HUMAN	Cytochrome c oxidase subunit 6B1 (Cytochrome c oxidase subunit Vlb isoform 1) (COX Vlb-1)	COX6B1
			2272,11	0,001	R.AQPQVQVAEGSEPDGFWEALGGK.A	P06396	GELS_HUMAN	Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF) (Brevin)	GSN
			2272,09	0,019	K.NIDGTSRDPYSHALVAGIDR.Y	P61353	RL27_HUMAN	60S ribosomal protein L27 (Large ribosomal subunit protein eL27)	RPL27
2272,11	2270,974	2273,246	2272,13	0,021	K.GVVPLAGTNGETTQGLDGLSER.C	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
			2272,18	0,068	R.TQTSDPAMPLPTMIGLAEAGVR.L	O43175	SERA_HUMAN	D-3-phosphoglycerate dehydrogenase (3-PGDH) (EC 1.1.1.95) (2-oxoglutarate reductase) (EC 1.1.1.399) (Malate dehydrogenase) (EC 1.1.1.37)	PHGDH
			2273,10	0,992	R.NPYYGESASITPLEDLKYR.F	P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GD12
			2273,12	1,014	K.GVVPLAGTDGETTQGLDGLSER.C	P09972	ALDOC_HUMAN	Fructose-bisphosphate aldolase C (EC 4.1.2.13) (Brain-type aldolase)	ALDOC
			2273,12	0,004	K.GVVPLAGTDGETTQGLDGLSER.C	P09972	ALDOC_HUMAN	Fructose-bisphosphate aldolase C (EC 4.1.2.13) (Brain-type aldolase)	ALDOC
2273,13	2271,991	2274,265	2273,10	0,026	R.NPYYGESASITPLEDLKYR.F	P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GD12
			2272,18	0,949	R.TQTSDPAMPLPTMIGLAEAGVR.L	O43175	SERA_HUMAN	D-3-phosphoglycerate dehydrogenase (3-PGDH) (EC 1.1.1.95) (2-oxoglutarate reductase) (EC 1.1.1.399) (Malate dehydrogenase) (EC 1.1.1.37)	PHGDH
			2272,13	0,996	K.GVVPLAGTNGETTQGLDGLSER.C	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA

			2272,11	1,017	R.AQPVQVAEGSEPDGFWEALGGK.A	P06396	GELS_HUMAN	Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF (Brevin))	GSN
			2272,09	1,037	K.NIDDGTSRPPYSHALVAGIDR.Y	P61353	RL27_HUMAN	60S ribosomal protein L27 (Large ribosomal subunit protein eL27)	RPL27
2274,15	2273,010	2275,284	2273,12	1,022	K.GVVPLAGTGETTQTGLDGLSER.C	P09972	ALDOC_HUMAN	Fructose-bisphosphate aldolase C (EC 4.1.2.13) (Brain-type aldolase)	ALDOC
			2273,10	1,044	R.NPYYGGEASITPLEDLYKR.F	P50395	GDI8_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
			2275,28	1,135	R.IAIPGLAGAGNSVLLVSNLNPER.V	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
			2275,28	0,126	R.IAIPGLAGAGNSVLLVSNLNPER.V	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
2276,15	2275,016	2277,292	2275,28	0,873	R.IAIPGLAGAGNSVLLVSNLNPER.V	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
			2277,04	0,887	K.WGDAGAEEVVESTGVFTTMEK.A	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
			2277,04	0,025	K.WGDAGAEEVVESTGVFTTMEK.A	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
			2278,16	1,096	K.SILENRGVHNASLALSASIGR.V	O15230	LAMA5_HUMAN	Laminin subunit alpha-5 (Laminin-10 subunit alpha) (Laminin-11 subunit alpha) (Laminin-15 subunit alpha)	LAMA5
			2278,16	0,065	K.SILENRGVHNASLALSASIGR.V	O15230	LAMA5_HUMAN	Laminin subunit alpha-5 (Laminin-10 subunit alpha) (Laminin-11 subunit alpha) (Laminin-15 subunit alpha)	LAMA5
2278,10	2276,958	2279,236	2277,04	1,056	K.WGDAGAEEVVESTGVFTTMEK.A	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
			2278,16	0,954	K.SILENRGVHNASLALSASIGR.V	O15230	LAMA5_HUMAN	Laminin subunit alpha-5 (Laminin-10 subunit alpha) (Laminin-11 subunit alpha) (Laminin-15 subunit alpha)	LAMA5
2280,12	2278,982	2281,262	2282,09	0,971	R.IPSAVGYQPTLATDMGTMQER.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			2282,21	1,092	K.VVPLADIITPNQFEALLSGR.K	O00764	PDXK_HUMAN	Pyridoxal kinase (EC 2.7.1.35) (Pyridoxine kinase)	PDXK
2282,12	2280,983	2283,266	2282,09	0,034	R.IPSAVGYQPTLATDMGTMQER.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			2282,21	0,087	K.VVPLADIITPNQFEALLSGR.K	O00764	PDXK_HUMAN	Pyridoxal kinase (EC 2.7.1.35) (Pyridoxine kinase)	PDXK
2283,10	2281,960	2284,244	2282,21	0,890	K.VVPLADIITPNQFEALLSGR.K	O00764	PDXK_HUMAN	Pyridoxal kinase (EC 2.7.1.35) (Pyridoxine kinase)	PDXK
			2282,09	1,012	R.IPSAVGYQPTLATDMGTMQER.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
2284,11	2282,967	2285,251	2286,12	1,025	R.FFESFGDLSTPDVAMGNPKVK.A	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			2286,12	0,031	R.FFESFGDLSTPDVAMGNPKVK.A	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2286,09	2284,945	2287,231	2286,14	1,047	K.EISPDTTLLDLQNNDISLR.K	P21810	PGS1_HUMAN	Biglycan (Bone/cartilage proteoglycan I) (PG-S1)	BGN
			2287,05	0,959	R.QMEKDETVSDCSPIANIGR.L	P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta (CapZ beta)	CAPZB
2286,09	2284,945	2287,231	2286,12	0,031	R.FFESFGDLSTPDVAMGNPKVK.A	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			2286,14	0,053	K.EISPDTTLLDLQNNDISLR.K	P21810	PGS1_HUMAN	Biglycan (Bone/cartilage proteoglycan I) (PG-S1)	BGN
			2287,05	0,959	R.QMEKDETVSDCSPIANIGR.L	P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta (CapZ beta)	CAPZB
2287,15	2286,005	2288,292	2286,14	1,007	K.EISPDTTLLDLQNNDISLR.K	P21810	PGS1_HUMAN	Biglycan (Bone/cartilage proteoglycan I) (PG-S1)	BGN
			2286,12	1,029	R.FFESFGDLSTPDVAMGNPKVK.A	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2288,15	2287,010	2289,299	2287,05	1,108	R.QMEKDETVSDCSPIANIGR.L	P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta (CapZ beta)	CAPZB
			2291,18	1,067	R.CLAFHDISPQAPTHFLVIPK.K	P49773	HINT1_HUMAN	Histidine triad nucleotide-binding protein 1 (EC 3.-.-.-) (Adenosine 5'-monophosphoramidase) (Protein kinase C inhibitor 1) (Protein kinase C-interacting protein 1) (PKCI-1)	HINT1
			2291,19	1,077	K.VAGHPNIVINNAAGNFISPTER.L	Q16698	DECR_HUMAN	2,4-dienoyl-CoA reductase, mitochondrial (EC 1.3.1.34) (2,4-dienoyl-CoA reductase [NADPH]) (4-enoyl-CoA reductase [NADPH]) (Short chain dehydrogenase/reductase family 18C member 1)	DECR1
			2291,18	0,076	R.CLAFHDISPQAPTHFLVIPK.K	P49773	HINT1_HUMAN	Histidine triad nucleotide-binding protein 1 (EC 3.-.-.-) (Adenosine 5'-monophosphoramidase) (Protein kinase C inhibitor 1) (Protein kinase C-interacting protein 1) (PKCI-1)	HINT1
			2291,19	0,086	K.VAGHPNIVINNAAGNFISPTER.L	Q16698	DECR_HUMAN	2,4-dienoyl-CoA reductase, mitochondrial (EC 1.3.1.34) (2,4-dienoyl-CoA reductase [NADPH]) (4-enoyl-CoA reductase [NADPH]) (Short chain dehydrogenase/reductase family 18C member 1)	DECR1
			2292,07	0,965	R.SAYQTIDSAEAPDPFAVPEGR.S	Q6RW13	ATRAP_HUMAN	Type-1 angiotensin II receptor-associated protein (AT1 receptor-associated protein)	AGTRAP
2292,11	2290,964	2293,256	2292,07	0,039	R.SAYQTIDSAEAPDPFAVPEGR.S	Q6RW13	ATRAP_HUMAN	Type-1 angiotensin II receptor-associated protein (AT1 receptor-associated protein)	AGTRAP
			2291,19	0,918	K.VAGHPNIVINNAAGNFISPTER.L	Q16698	DECR_HUMAN	2,4-dienoyl-CoA reductase, mitochondrial (EC 1.3.1.34) (2,4-dienoyl-CoA reductase [NADPH]) (4-enoyl-CoA reductase [NADPH]) (Short chain dehydrogenase/reductase family 18C member 1)	DECR1
			2291,18	0,928	R.CLAFHDISPQAPTHFLVIPK.K	P49773	HINT1_HUMAN	Histidine triad nucleotide-binding protein 1 (EC 3.-.-.-) (Adenosine 5'-monophosphoramidase) (Protein kinase C inhibitor 1) (Protein kinase C-interacting protein 1) (PKCI-1)	HINT1
			2292,07	1,027	R.SAYQTIDSAEAPDPFAVPEGR.S	Q6RW13	ATRAP_HUMAN	Type-1 angiotensin II receptor-associated protein (AT1 receptor-associated protein)	AGTRAP

2294,09	2292,942	2295,237	2295,14	1,050	K.TSPVADAAGWVDVDKETLQHR.R	Q9Y6N5	SQOR_HUMAN	Sulfide:quinone oxidoreductase, mitochondrial, SQOR, EC 1.8.5.- (Sulfide dehydrogenase-like) (Sulfide quinone oxidoreductase)	SQOR
2295,10	2293,957	2296,252	2295,14	0,035	K.TSPVADAAGWVDVDKETLQHR.R	Q9Y6N5	SQOR_HUMAN	Sulfide:quinone oxidoreductase, mitochondrial, SQOR, EC 1.8.5.- (Sulfide dehydrogenase-like) (Sulfide quinone oxidoreductase)	SQOR
			2295,25	0,150	R.VAPEEHVLLTEAPLNPKANR.E	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			2295,96	0,858	K.EGEEPTVYSDEEEKPKDESAR.K	O00264	PGR1_HUMAN	Membrane-associated progesterone receptor component 1 (mPR) (Dap1) (IZA)	PGRMC1
2296,08	2294,933	2297,229	2295,96	0,118	K.EGEEPTVYSDEEEKPKDESAR.K	O00264	PGR1_HUMAN	Membrane-associated progesterone receptor component 1 (mPR) (Dap1) (IZA)	PGRMC1
			2295,25	0,827	R.VAPEEHVLLTEAPLNPKANR.E	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			2296,93	0,852	K.EDAGEYECHASNQQQASASAK.I	Q16270	IBP7_HUMAN	Insulin-like growth factor-binding protein 7 (IBP-7) (IGF-binding protein 7) (IGFBP-7) (IGFBP-rP1) (MAC25 protein) (PGI2-stimulating factor) (Prostacyclin-stimulating factor) (Tumor-derived adhesion factor) (TAF)	IGFBP7
			2295,14	0,941	K.TSPVADAAGWVDVDKETLQHR.R	Q9Y6N5	SQOR_HUMAN	Sulfide:quinone oxidoreductase, mitochondrial, SQOR, EC 1.8.5.- (Sulfide dehydrogenase-like) (Sulfide quinone oxidoreductase)	SQOR
2297,08	2295,928	2298,225	2296,93	0,144	K.EDAGEYECHASNQQQASASAK.I	Q16270	IBP7_HUMAN	Insulin-like growth factor-binding protein 7 (IBP-7) (IGF-binding protein 7) (IGFBP-7) (IGFBP-rP1) (MAC25 protein) (PGI2-stimulating factor) (Prostacyclin-stimulating factor) (Tumor-derived adhesion factor) (TAF)	IGFBP7
			2295,96	1,114	K.EGEEPTVYSDEEEKPKDESAR.K	O00264	PGR1_HUMAN	Membrane-associated progesterone receptor component 1 (mPR) (Dap1) (IZA)	PGRMC1
2298,10	2296,947	2299,245							
2299,09	2297,944	2300,243	2300,06	0,964	R.VNIAFNYDMPEDSDTYLHR.V	Q13838	DX39B_HUMAN	Spliceosome RNA helicase DDX39B (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	DX39B
2300,09	2298,939	2301,239	2300,06	0,032	R.VNIAFNYDMPEDSDTYLHR.V	Q13838	DX39B_HUMAN	Spliceosome RNA helicase DDX39B (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	DX39B
2301,10	2299,947	2302,248	2300,06	1,040	R.VNIAFNYDMPEDSDTYLHR.V	Q13838	DX39B_HUMAN	Spliceosome RNA helicase DDX39B (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	DX39B
2302,08	2300,925	2303,227							
2303,13	2301,975	2304,278	2304,14	1,018	K.SINPDEAVAYGAAVQAAILMGDK.S	P0DMV8	HS71A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
2304,12	2302,971	2305,276	2304,14	0,021	K.SINPDEAVAYGAAVQAAILMGDK.S	P0DMV8	HS71A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
2305,11	2303,955	2306,260	2304,14	0,964	K.SINPDEAVAYGAAVQAAILMGDK.S	P0DMV8	HS71A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
			2306,14	1,037	R.NLPLGLVQEGEPFSEATLFTK.E	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
2306,11	2304,960	2307,266	2306,14	0,032	R.NLPLGLVQEGEPFSEATLFTK.E	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
			2307,17	1,060	R.IQYQLVDISQDNALRDEM.R	Q9H299	SH3L3_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 3 (SH3 domain-binding protein 1) (SH3BP-1)	SH3BGL3
2307,13	2305,975	2308,282	2307,17	0,044	R.IQYQLVDISQDNALRDEM.R	Q9H299	SH3L3_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 3 (SH3 domain-binding protein 1) (SH3BP-1)	SH3BGL3
			2306,14	0,984	R.NLPLGLVQEGEPFSEATLFTK.E	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
			2308,13	0,998	K.SGYHQSAEHLVVIADPDSR.G	P10768	ESTD_HUMAN	S-formylglutathione hydrolase (FGH) (EC 3.1.2.12) (Esterase D) (Methylumbelliferyl-acetate deacetylase) (EC 3.1.1.56)	ESD
2308,14	2306,982	2309,290	2308,13	0,009	K.SGYHQSAEHLVVIADPDSR.G	P10768	ESTD_HUMAN	S-formylglutathione hydrolase (FGH) (EC 3.1.2.12) (Esterase D) (Methylumbelliferyl-acetate deacetylase) (EC 3.1.1.56)	ESD
			2307,17	0,963	R.IQYQLVDISQDNALRDEM.R	Q9H299	SH3L3_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 3 (SH3 domain-binding protein 1) (SH3BP-1)	SH3BGL3
			2309,17	1,032	K.QGQYSPMAIEEQVAVIYAGVR.G	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
2309,11	2307,960	2310,269	2309,17	0,053	K.QGQYSPMAIEEQVAVIYAGVR.G	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
			2310,07	0,959	R.LYFGTSGYFSQHDLFSSPEK.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2308,13	0,988	K.SGYHQSAEHLVVIADPDSR.G	P10768	ESTD_HUMAN	S-formylglutathione hydrolase (FGH) (EC 3.1.2.12) (Esterase D) (Methylumbelliferyl-acetate deacetylase) (EC 3.1.1.56)	ESD
2310,13	2308,973	2311,283	2310,07	0,054	R.LYFGTSGYFSQHDLFSSPEK.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2309,17	0,960	K.QGQYSPMAIEEQVAVIYAGVR.G	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
			2311,22	1,094	R.VPATLQVLQTLPENYQVLR.F	Q07960	RHG01_HUMAN	Rho GTPase-activating protein 1 (CDC42 GTPase-activating protein) (GTPase-activating protein rhoGAP) (Rho-related small GTPase protein activator) (Rho-type GTPase-activating protein 1) (p50-RhoGAP)	ARHGAP1
2311,20	2310,044	2312,355	2311,22	0,023	R.VPATLQVLQTLPENYQVLR.F	Q07960	RHG01_HUMAN	Rho GTPase-activating protein 1 (CDC42 GTPase-activating protein) (GTPase-activating protein rhoGAP) (Rho-related small GTPase protein activator) (Rho-type GTPase-activating protein 1) (p50-RhoGAP)	ARHGAP1
			2312,03	0,831	R.NDYATMLPDSTEIDQDTINR.I	P12110	COL6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
			2312,13	0,928	K.DGYAVTYVPLTAGMYTLTKM.Y	O75369	FLNB_HUMAN	Filamin-B (FLN-B) (ABP-278) (ABP-280 homolog) (Actin-binding-like protein) (Beta-filamin) (Filamin homolog 1) (Fh1) (Filamin-3) (Thyroid autoantigen) (Truncated actin-binding protein) (Truncated ABP)	FLNB
			2310,07	1,125	R.LYFGTSGYFSQHDLFSSPEK.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG

2312,19	2311,031	2313,344	2312,13	0,061	K.DGTAYVTYVPLTAGMYLTMK.Y	075369	FLNB_HUMAN	Filamin-B (FLN-B) (ABP-278) (ABP-280 homolog) (Actin-binding-like protein) (Beta-filamin) (Filamin homolog 1) (Fh1) (Filamin-3) (Thyroid autoantigen) (Truncated actin-binding protein) (Truncated ABP)	FLNB
			2312,03	0,158	R.NDYATMLPDSIEDQDTINR.I	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
			2313,11	0,921	R.SAGQGEVLVYVEDPAGHQEEAK.V	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			2313,15	0,960	R.GSTGFGQDSILSLPGNVGHQDVK.D	P13798	ACPH_HUMAN	Acylamino-acid-releasing enzyme (AARE) (EC 3.4.19.1) (Acyl-peptide hydrolase) (APH) (Acyllaminoacyl-peptidase) (Oxidized protein hydrolase) (OPH)	APEH
			2311,22	0,966	R.VPATQLVLQTLPEENYQVLR.F	Q07960	RHG01_HUMAN	Rho GTPase-activating protein 1 (CDC42 GTPase-activating protein) (GTPase-activating protein rhoGAP) (Rho-related small GTPase protein activator) (Rho-type GTPase-activating protein 1) (p50-RhoGAP)	ARHGAP1
2313,12	2311,959	2314,272	2313,11	0,008	R.SAGQGEVLVYVEDPAGHQEEAK.V	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			2313,15	0,032	R.GSTGFGQDSILSLPGNVGHQDVK.D	P13798	ACPH_HUMAN	Acylamino-acid-releasing enzyme (AARE) (EC 3.4.19.1) (Acyl-peptide hydrolase) (APH) (Acyllaminoacyl-peptidase) (Oxidized protein hydrolase) (OPH)	APEH
			2312,13	0,989	K.DGTAYVTYVPLTAGMYLTMK.Y	075369	FLNB_HUMAN	Filamin-B (FLN-B) (ABP-278) (ABP-280 homolog) (Actin-binding-like protein) (Beta-filamin) (Filamin homolog 1) (Fh1) (Filamin-3) (Thyroid autoantigen) (Truncated actin-binding protein) (Truncated ABP)	FLNB
			2314,12	1,008	R.LVAFEPATGGLTSWQFYSVK.L	Q9NZM6	PK2L2_HUMAN	Polycystic kidney disease 2-like 2 protein (Polycystin-2L2) (Polycystin-L2)	PKD2L2
			2312,03	1,086	R.NDYATMLPDSIEDQDTINR.I	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
2314,12	2312,962	2315,276	2314,12	0,005	R.LVAFEPATGGLTSWQFYSVK.L	Q9NZM6	PK2L2_HUMAN	Polycystic kidney disease 2-like 2 protein (Polycystin-2L2) (Polycystin-L2)	PKD2L2
			2313,15	0,971	R.GSTGFGQDSILSLPGNVGHQDVK.D	P13798	ACPH_HUMAN	Acylamino-acid-releasing enzyme (AARE) (EC 3.4.19.1) (Acyl-peptide hydrolase) (APH) (Acyllaminoacyl-peptidase) (Oxidized protein hydrolase) (OPH)	APEH
			2313,11	1,010	R.SAGQGEVLVYVEDPAGHQEEAK.V	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
2315,14	2313,983	2316,298	2314,12	1,017	R.LVAFEPATGGLTSWQFYSVK.L	Q9NZM6	PK2L2_HUMAN	Polycystic kidney disease 2-like 2 protein (Polycystin-2L2) (Polycystin-L2)	PKD2L2
2316,12 2317,12	2314,965 2315,957	2317,281 2318,274	2318,14	1,023	R.GEVPCVTTSASPLEEATLSELK.T	P48047	ATPO_HUMAN	ATP synthase subunit O, mitochondrial (ATP synthase peripheral stalk subunit OSCP) (Oligomycin sensitivity conferral protein) (OSCP)	ATP5PO
2317,12	2315,957	2318,274	2318,14	1,023	R.GEVPCVTTSASPLEEATLSELK.T	P48047	ATPO_HUMAN	ATP synthase subunit O, mitochondrial (ATP synthase peripheral stalk subunit OSCP) (Oligomycin sensitivity conferral protein) (OSCP)	ATP5PO
2318,10	2316,937	2319,255	2318,14	0,042	R.GEVPCVTTSASPLEEATLSELK.T	P48047	ATPO_HUMAN	ATP synthase subunit O, mitochondrial (ATP synthase peripheral stalk subunit OSCP) (Oligomycin sensitivity conferral protein) (OSCP)	ATP5PO
2319,13	2317,967	2320,286	2320,09	0,965	R.NPPGFAFVEFEDPRDAADAVR.E	P84103	SRSF3_HUMAN	Serine/arginine-rich splicing factor 3 (Pre-mRNA-splicing factor SRP20) (Splicing factor, arginine/serine-rich 3)	SRSF3
			2318,14	0,988	R.GEVPCVTTSASPLEEATLSELK.T	P48047	ATPO_HUMAN	ATP synthase subunit O, mitochondrial (ATP synthase peripheral stalk subunit OSCP) (Oligomycin sensitivity conferral protein) (OSCP)	ATP5PO
2320,14	2318,983	2321,304	2320,09	0,052	R.NPPGFAFVEFEDPRDAADAVR.E	P84103	SRSF3_HUMAN	Serine/arginine-rich splicing factor 3 (Pre-mRNA-splicing factor SRP20) (Splicing factor, arginine/serine-rich 3)	SRSF3
2321,13	2319,971	2322,292	2321,94	0,806	K.GEGWGDPCLECPTEPDEAFR.Q	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			2320,09	1,040	R.NPPGFAFVEFEDPRDAADAVR.E	P84103	SRSF3_HUMAN	Serine/arginine-rich splicing factor 3 (Pre-mRNA-splicing factor SRP20) (Splicing factor, arginine/serine-rich 3)	SRSF3
2322,12	2320,956	2323,278	2321,94	0,179	K.GEGWGDPCLECPTEPDEAFR.Q	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
2323,13 2324,09	2321,968 2322,930	2324,291 2325,255	2325,14	1,046	R.IIDSEITKEDDALWPPPPDR.V	P61326	MGN_HUMAN	Protein mago nashi homolog	MAGOH
			2325,21	1,121	K.ISFPAIQAAFSNSFPQIFR.D	P23381	SYWC_HUMAN	Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleaved into: T1-TrpRS; T2-TrpRS]	WARS
2325,10	2323,939	2326,265	2325,14	0,037	R.IIDSEITKEDDALWPPPPDR.V	P61326	MGN_HUMAN	Protein mago nashi homolog	MAGOH
			2325,21	0,112	K.ISFPAIQAAFSNSFPQIFR.D	P23381	SYWC_HUMAN	Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleaved into: T1-TrpRS; T2-TrpRS]	WARS
2326,11	2324,951	2327,277	2325,21	0,900	K.ISFPAIQAAFSNSFPQIFR.D	P23381	SYWC_HUMAN	Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleaved into: T1-TrpRS; T2-TrpRS]	WARS
			2325,14	0,975	R.IIDSEITKEDDALWPPPPDR.V	P61326	MGN_HUMAN	Protein mago nashi homolog	MAGOH
2327,11	2325,949	2328,276	2328,18	1,068	R.VVHCSDLGLTSVPTNIPFDTR.M	Q98XN1	ASPN_HUMAN	Asporin (Periodontal ligament-associated protein 1) (PLAP- ASPN 1)	ASPN 1
2328,11	2326,943	2329,271	2328,18	0,073	R.VVHCSDLGLTSVPTNIPFDTR.M	Q98XN1	ASPN_HUMAN	Asporin (Periodontal ligament-associated protein 1) (PLAP- ASPN 1)	ASPN 1
2329,12	2327,957	2330,286	2330,02	0,903	R.AFVHWYVGEGMEEGFSEAR.E	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			2330,02	0,903	R.AFVHWYVGEGMEEGFSEAR.E	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
			2330,02	0,903	R.AFVHWYVGEGMEEGFSEAR.E	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2328,18	0,942	R.VVHCSDLGLTSVPTNIPFDTR.M	Q98XN1	ASPN_HUMAN	Asporin (Periodontal ligament-associated protein 1) (PLAP- ASPN 1)	ASPN 1
			2330,16	1,035	R.IPIHNEDITYDELVLMMQR.V	Q92734	TFG_HUMAN	Protein TFG (TRK-fused gene protein)	TFG
2330,13	2328,965	2331,295	2330,16	0,026	R.IPIHNEDITYDELVLMMQR.V	Q92734	TFG_HUMAN	Protein TFG (TRK-fused gene protein)	TFG

2331,14	2329,970	2332,301	2330,02	0,105	R.AFVHWYVVGEGMEEGFSEAR.E	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			2330,02	0,105	R.AFVHWYVVGEGMEEGFSEAR.E	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
			2330,02	0,105	R.AFVHWYVVGEGMEEGFSEAR.E	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2332,09	0,959	R.QPYAVSELAGHQTSAESWGTR.G	P36578	RL4_HUMAN	60S ribosomal protein L4 (60S ribosomal protein L1) (Large ribosomal subunit protein uL4)	RPL4
			2330,16	0,979	R.IPIHNEDITYDELVLMMQR.V	Q92734	TFG_HUMAN	Protein TFG (TRK-fused gene protein)	TFG
			2330,02	1,111	R.AFVHWYVVGEGMEEGFSEAR.E	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			2330,02	1,111	R.AFVHWYVVGEGMEEGFSEAR.E	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
			2330,02	1,111	R.AFVHWYVVGEGMEEGFSEAR.E	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2332,09	0,025	R.QPYAVSELAGHQTSAESWGTR.G	P36578	RL4_HUMAN	60S ribosomal protein L4 (60S ribosomal protein L1) (Large ribosomal subunit protein uL4)	RPL4
			2333,00	0,880	K.MFSFGSDFTNQHTVQTENR.F	Q9UB53	DNJB9_HUMAN	DnaJ homolog subfamily B member 9 (Endoplasmic reticulum DNA J domain-containing protein 4) (ER-resident protein ERdj4) (ERdj4) (Microvascular endothelial differentiation gene 1 protein) (Mdg-1)	DNAJB9
2333,11	2331,945	2334,278	2333,00	0,112	K.MFSFGSDFTNQHTVQTENR.F	Q9UB53	DNJB9_HUMAN	DnaJ homolog subfamily B member 9 (Endoplasmic reticulum DNA J domain-containing protein 4) (ER-resident protein ERdj4) (ERdj4) (Microvascular endothelial differentiation gene 1 protein) (Mdg-1)	DNAJB9
			2334,09	0,980	K.MYGISLCQAILDETKGDYEK.I	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
			2332,09	1,017	R.QPYAVSELAGHQTSAESWGTR.G	P36578	RL4_HUMAN	60S ribosomal protein L4 (60S ribosomal protein L1) (Large ribosomal subunit protein uL4)	RPL4
2334,11	2332,944	2335,278	2334,09	0,020	K.MYGISLCQAILDETKGDYEK.I	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
			2335,06	0,951	R.QVQFSEEHVWHESGRPVQR.A	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
			2333,00	1,112	K.MFSFGSDFTNQHTVQTENR.F	Q9UB53	DNJB9_HUMAN	DnaJ homolog subfamily B member 9 (Endoplasmic reticulum DNA J domain-containing protein 4) (ER-resident protein ERdj4) (ERdj4) (Microvascular endothelial differentiation gene 1 protein) (Mdg-1)	DNAJB9
2335,11	2333,946	2336,281	2335,06	0,051	R.QVQFSEEHVWHESGRPVQR.A	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
			2334,09	1,022	K.MYGISLCQAILDETKGDYEK.I	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
2336,11	2334,945	2337,281	2337,14	1,032	K.KGDTFSCMVGEALPLAFTQK.T	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
			2335,06	1,050	R.QVQFSEEHVWHESGRPVQR.A	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
2337,13	2335,960	2338,297	2337,14	0,016	K.KGDTFSCMVGEALPLAFTQK.T	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
			2338,16	1,035	R.EVAFAAQFGSDLDAAATQQLLSR.G	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
2338,09	2336,923	2339,262	2338,16	0,071	R.EVAFAAQFGSDLDAAATQQLLSR.G	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
			2337,14	0,948	K.KGDTFSCMVGEALPLAFTQK.T	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
2339,03	2337,864	2340,203	2338,16	0,870	R.EVAFAAQFGSDLDAAATQQLLSR.G	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
2340,05	2338,875	2341,215	2343,05	0,952	K.EAEVVLGGTSMQAPYCVR.N	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2
2341,07	2339,903	2342,244			R.KDLYANTVLSGGTMYPGIADR.M	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
2342,10	2340,926	2343,268	2343,16	1,064	R.KDLYANTVLSGGTMYPGIADR.M	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
2343,14	2341,968	2344,311	2343,16	0,021	R.KDLYANTVLSGGTMYPGIADR.M	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			2343,05	0,091	K.EAEVVLGGTSMQAPYCVR.N	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2
			2345,06	0,913	R.TDPHLCDFLETHFLDEEVK.L	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
2344,15	2342,979	2345,323	2343,16	0,990	R.KDLYANTVLSGGTMYPGIADR.M	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			2343,05	1,101	K.EAEVVLGGTSMQAPYCVR.N	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2
2345,16	2343,983	2346,328	2345,06	0,092	R.TDPHLCDFLETHFLDEEVK.L	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
2346,16	2344,987	2347,333	2347,17	1,013	R.MLPITIADNAGYDSADLVAQLR.A	P78371	TCPB_HUMAN	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	CCT2
			2345,06	1,097	R.TDPHLCDFLETHFLDEEVK.L	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
2347,16	2345,983	2348,330	2347,17	0,017	R.MLPITIADNAGYDSADLVAQLR.A	P78371	TCPB_HUMAN	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	CCT2
2348,15	2346,974	2349,322	2347,17	0,975	R.MLPITIADNAGYDSADLVAQLR.A	P78371	TCPB_HUMAN	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	CCT2

2349,13	2347,960	2350,309	2350,03	0,895	R.NAFACFDEEATGTIQEDYLR.E	O14950	ML12B_HUMAN	Myosin regulatory light chain 12B (MLC-2A) (MLC-2) (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2) (SHUJUN-1)	MYL12B
			2350,07	0,932	R.VAGEAAETDSEPEPEPTAAPR.D	Q6QNY0	BL1S3_HUMAN	Biogenesis of lysosome-related organelles complex 1 subunit 3 (BLOC-1 subunit 3)	BLOC1S3
			2350,08	0,941	R.LLEGEDAHLSSQQASQSGSYSSR.E	P08779	K1C16_HUMAN	Keratin, type I cytoskeletal 16 (Cytokeratin-16) (CK-16) (Keratin-16) (K16)	KRT16
			2350,18	1,050	K.AVAFQNPQTHVIEHLHAAAYR.N	P22695	QCR2_HUMAN	Cytochrome b-c1 complex subunit 2, mitochondrial (Complex III subunit 2) (Core protein II) (Ubiquinol-cytochrome-c reductase complex core protein 2)	UQCRC2
2350,16	2348,983	2351,334	2350,18	0,026	K.AVAFQNPQTHVIEHLHAAAYR.N	P22695	QCR2_HUMAN	Cytochrome b-c1 complex subunit 2, mitochondrial (Complex III subunit 2) (Core protein II) (Ubiquinol-cytochrome-c reductase complex core protein 2)	UQCRC2
			2350,08	0,083	R.LLEGEDAHLSSQQASQSGSYSSR.E	P08779	K1C16_HUMAN	Keratin, type I cytoskeletal 16 (Cytokeratin-16) (CK-16) (Keratin-16) (K16)	KRT16
			2350,07	0,092	R.VAGEAAETDSEPEPEPTAAPR.D	Q6QNY0	BL1S3_HUMAN	Biogenesis of lysosome-related organelles complex 1 subunit 3 (BLOC-1 subunit 3)	BLOC1S3
			2350,03	0,129	R.NAFACFDEEATGTIQEDYLR.E	O14950	ML12B_HUMAN	Myosin regulatory light chain 12B (MLC-2A) (MLC-2) (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2) (SHUJUN-1)	MYL12B
			2351,05	0,893	R.HQGVMMVGMGQKDSYVGDEAQS.K	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			2351,05	0,893	R.HQGVMMVGMGQKDSYVGDEAQS.K	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2351,05	0,893	R.HQGVMMVGMGQKDSYVGDEAQS.K	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			2351,05	0,893	R.HQGVMMVGMGQKDSYVGDEAQS.K	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
2351,19	2350,010	2352,361	2351,05	0,134	R.HQGVMMVGMGQKDSYVGDEAQS.K	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			2351,05	0,134	R.HQGVMMVGMGQKDSYVGDEAQS.K	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2351,05	0,134	R.HQGVMMVGMGQKDSYVGDEAQS.K	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			2351,05	0,134	R.HQGVMMVGMGQKDSYVGDEAQS.K	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2350,18	1,001	K.AVAFQNPQTHVIEHLHAAAYR.N	P22695	QCR2_HUMAN	Cytochrome b-c1 complex subunit 2, mitochondrial (Complex III subunit 2) (Core protein II) (Ubiquinol-cytochrome-c reductase complex core protein 2)	UQCRC2
			2350,08	1,110	R.LLEGEDAHLSSQQASQSGSYSSR.E	P08779	K1C16_HUMAN	Keratin, type I cytoskeletal 16 (Cytokeratin-16) (CK-16) (Keratin-16) (K16)	KRT16
			2350,07	1,119	R.VAGEAAETDSEPEPEPTAAPR.D	Q6QNY0	BL1S3_HUMAN	Biogenesis of lysosome-related organelles complex 1 subunit 3 (BLOC-1 subunit 3)	BLOC1S3
			2350,03	1,156	R.NAFACFDEEATGTIQEDYLR.E	O14950	ML12B_HUMAN	Myosin regulatory light chain 12B (MLC-2A) (MLC-2) (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2) (SHUJUN-1)	MYL12B
2352,17	2350,996	2353,348	2353,14	0,966	K.KGDTFSCMVGHEALPLAFTQK.T	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
			2351,05	1,120	R.HQGVMMVGMGQKDSYVGDEAQS.K	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			2351,05	1,120	R.HQGVMMVGMGQKDSYVGDEAQS.K	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2351,05	1,120	R.HQGVMMVGMGQKDSYVGDEAQS.K	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			2351,05	1,120	R.HQGVMMVGMGQKDSYVGDEAQS.K	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
2353,15	2351,978	2354,331	2353,14	0,016	K.KGDTFSCMVGHEALPLAFTQK.T	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
2354,15	2352,970	2355,324	2355,13	0,984	K.VLQHYQESDKGEELGPGNVQK.E	Q9Y6C9	MTCH2_HUMAN	Mitochondrial carrier homolog 2 (Met-induced mitochondrial protein)	MTCH2
			2353,14	1,008	K.KGDTFSCMVGHEALPLAFTQK.T	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
2355,13	2353,955	2356,310	2355,13	0,001	K.VLQHYQESDKGEELGPGNVQK.E	Q9Y6C9	MTCH2_HUMAN	Mitochondrial carrier homolog 2 (Met-induced mitochondrial protein)	MTCH2
			2356,10	0,965	R.LTESPCALVASQYGSWSGNMER.I	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			2356,16	1,024	R.KDLYANNVLSGGTTPYPGIADR.M	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2356,16	1,024	R.KDLYANNVLSGGTTPYPGIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2356,17	1,038	K.GGPGSAVSPYPTFNPSSDVAAHLK.A	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
2356,10	2354,919	2357,275	2356,10	0,001	R.LTESPCALVASQYGSWSGNMER.I	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			2356,16	0,060	R.KDLYANNVLSGGTTPYPGIADR.M	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2356,16	0,060	R.KDLYANNVLSGGTTPYPGIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2356,17	0,074	K.GGPGSAVSPYPTFNPSSDVAAHLK.A	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
			2355,13	0,966	K.VLQHYQESDKGEELGPGNVQK.E	Q9Y6C9	MTCH2_HUMAN	Mitochondrial carrier homolog 2 (Met-induced mitochondrial protein)	MTCH2

2357,15	2355,970	2358,327	2356,17	0,978	K.GGPGSAVSPYPTFNPSSDVAALHK.A	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	
			2356,16	0,992	R.KDLYANNVLSGGTTPYPIADR.M	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2356,16	0,992	R.KDLYANNVLSGGTTPYPIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2356,10	1,050	R.LTESPCALVASQYWGSGNMER.I	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
2358,18	2356,999	2359,357	2359,14	0,963	R.KDLYANTVLSGGTTPYPIADR.M	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
2359,16	2357,975	2360,335	2359,14	0,014	R.KDLYANTVLSGGTTPYPIADR.M	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
2360,12	2358,941	2361,301	2359,14	0,980	R.KDLYANTVLSGGTTPYPIADR.M	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
2361,13 2362,14 2363,19	2359,950 2360,959 2362,005	2362,311 2363,321 2364,368	2364,17	0,982	K.LLQDEFFGIPSPDLAAVECHR.G	P02790	HEMO_HUMAN	Hemopexin (Beta-1B-glycoprotein)	HPX
2364,20	2363,022	2365,386	2364,17	0,035	K.LLQDEFFGIPSPDLAAVECHR.G	P02790	HEMO_HUMAN	Hemopexin (Beta-1B-glycoprotein)	HPX
			2365,04	0,837	R.NAFACFDEEASGFIHEDHLR.E	P24844	MYL9_HUMAN	Myosin regulatory light polypeptide 9 (20 kDa myosin light chain) (LC20) (MLC-2C) (Myosin RLC) (Myosin regulatory light chain 2, smooth muscle isoform) (Myosin regulatory light chain 9) (Myosin regulatory light chain MRLC1)	MYL9
2365,20	2364,022	2366,387	2365,23	1,023	R.LTYDIAHTPGVAADLSHIETK.A	P40926	MDHM_HUMAN	Malate dehydrogenase, mitochondrial (EC 1.1.1.37)	MDH2
			2365,23	0,022	R.LTYDIAHTPGVAADLSHIETK.A	P40926	MDHM_HUMAN	Malate dehydrogenase, mitochondrial (EC 1.1.1.37)	MDH2
			2365,04	0,164	R.NAFACFDEEASGFIHEDHLR.E	P24844	MYL9_HUMAN	Myosin regulatory light polypeptide 9 (20 kDa myosin light chain) (LC20) (MLC-2C) (Myosin RLC) (Myosin regulatory light chain 2, smooth muscle isoform) (Myosin regulatory light chain 9) (Myosin regulatory light chain MRLC1)	MYL9
			2365,99	0,787	R.KVVDYSQFQESDDADEDYGR.D	Q9H1E3	NUCKS_HUMAN	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 (P1)	NUCKS1
2366,19	2365,008	2367,374	2364,17	1,036	K.LLQDEFFGIPSPDLAAVECHR.G	P02790	HEMO_HUMAN	Hemopexin (Beta-1B-glycoprotein)	HPX
			2365,99	0,199	R.KVVDYSQFQESDDADEDYGR.D	Q9H1E3	NUCKS_HUMAN	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 (P1)	NUCKS1
			2365,23	0,964	R.LTYDIAHTPGVAADLSHIETK.A	P40926	MDHM_HUMAN	Malate dehydrogenase, mitochondrial (EC 1.1.1.37)	MDH2
			2367,27	1,077	K.FENAFLSHVVSQHQALLGTIR.A	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
2366,19	2365,008	2367,374	2365,04	1,150	R.NAFACFDEEASGFIHEDHLR.E	P24844	MYL9_HUMAN	Myosin regulatory light polypeptide 9 (20 kDa myosin light chain) (LC20) (MLC-2C) (Myosin RLC) (Myosin regulatory light chain 2, smooth muscle isoform) (Myosin regulatory light chain 9) (Myosin regulatory light chain MRLC1)	MYL9
2367,20	2366,017	2368,384	2367,27	0,068	K.FENAFLSHVVSQHQALLGTIR.A	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
2368,21	2367,021	2369,389	2367,27	0,937	K.FENAFLSHVVSQHQALLGTIR.A	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
2369,20	2368,020	2370,389	2370,12	0,917	R.ASPAPGSGHPEGPGAHLDMNSLDR.A	O94826	TOM70_HUMAN	Mitochondrial import receptor subunit TOM70 (Mitochondrial precursor proteins import receptor) (Translocase of outer membrane 70 kDa subunit) (Translocase of outer mitochondrial membrane protein 70)	TOMM70
2370,19	2369,004	2371,374	2370,12	0,068	R.ASPAPGSGHPEGPGAHLDMNSLDR.A	O94826	TOM70_HUMAN	Mitochondrial import receptor subunit TOM70 (Mitochondrial precursor proteins import receptor) (Translocase of outer membrane 70 kDa subunit) (Translocase of outer mitochondrial membrane protein 70)	TOMM70
2371,18	2369,999	2372,370	2372,18	0,997	R.KDLYANNVLSGGTTPYPIADR.M	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2372,18	0,997	R.KDLYANNVLSGGTTPYPIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2370,12	1,063	R.ASPAPGSGHPEGPGAHLDMNSLDR.A	O94826	TOM70_HUMAN	Mitochondrial import receptor subunit TOM70 (Mitochondrial precursor proteins import receptor) (Translocase of outer membrane 70 kDa subunit) (Translocase of outer mitochondrial membrane protein 70)	TOMM70
2372,19	2371,003	2373,375	2372,18	0,008	R.KDLYANNVLSGGTTPYPIADR.M	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2372,18	0,008	R.KDLYANNVLSGGTTPYPIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2373,17	0,984	K.YEVLALLYHEPPDDKASQR.Q	P31415	CASQ1_HUMAN	Calsequestrin-1 (Calmitine) (Calsequestrin, skeletal muscle isoform)	CASQ1
2373,19	2372,006	2374,379	2373,17	0,020	K.YEVLALLYHEPPDDKASQR.Q	P31415	CASQ1_HUMAN	Calsequestrin-1 (Calmitine) (Calsequestrin, skeletal muscle isoform)	CASQ1
			2374,14	0,945	R.KDLYANNVMSGGTTMYPPIADR.M	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			2372,18	1,011	R.KDLYANNVLSGGTTPYPIADR.M	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2372,18	1,011	R.KDLYANNVLSGGTTPYPIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
2374,20	2373,012	2375,386	2374,14	0,062	R.KDLYANNVMSGGTTMYPPIADR.M	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			2373,17	1,026	K.YEVLALLYHEPPDDKASQR.Q	P31415	CASQ1_HUMAN	Calsequestrin-1 (Calmitine) (Calsequestrin, skeletal muscle isoform)	CASQ1
2375,20	2374,016	2376,391	2374,14	1,067	R.KDLYANNVMSGGTTMYPPIADR.M	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
2376,19	2375,001	2377,378	2377,17	0,976	R.QVQSLTCEVDALKGTNESLER.Q	P08670	VIME_HUMAN	Vimentin	VIM

2377,19	2376,001	2378,378	2377,17	0,023	R.QVQSLTCEVDALKGTNESLER.Q	P08670	VIME_HUMAN	Vimentin	VIM	
2378,17	2376,981	2379,359	2377,17	1,004	R.QVQSLTCEVDALKGTNESLER.Q	P08670	VIME_HUMAN	Vimentin	VIM	
2379,17	2377,985	2380,364	2381,21 2381,27	1,028	K.LLAVAATAPPDAPNREEVFDER.A	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL	
2380,19	2378,997	2381,377		1,085	K.LLAVSGPFHYWGPVIDGHFLR.E	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG	
2381,21	2380,021	2382,402	2381,21 2381,27	0,003	K.LLAVAATAPPDAPNREEVFDER.A	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL	
				0,061	K.LLAVSGPFHYWGPVIDGHFLR.E	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG	
2382,22	2381,026	2383,408	2381,27 2383,19	0,945	K.LLAVSGPFHYWGPVIDGHFLR.E	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG	
				0,972	K.TFYEPGEITYSCKPGYVSR.G	P02749	APOH_HUMAN	Beta-2-glycoprotein 1 (APC inhibitor) (Activated protein C-binding protein) (Anticardiolipin cofactor) (Apolipoprotein H) (Apo-H) (Beta-2-glycoprotein I) (B2GPI) (Beta(2)GPI)	APOH	
			2381,21	1,002	K.LLAVAATAPPDAPNREEVFDER.A	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL	
2383,21	2382,018	2384,401	2383,19	0,020	K.TFYEPGEITYSCKPGYVSR.G	P02749	APOH_HUMAN	Beta-2-glycoprotein 1 (APC inhibitor) (Activated protein C-binding protein) (Anticardiolipin cofactor) (Apolipoprotein H) (Apo-H) (Beta-2-glycoprotein I) (B2GPI) (Beta(2)GPI)	APOH	
					0,724	R.GGGGGGYSGGSSYSGGGSYSGGGGGGGF	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
2384,21	2383,017	2385,401	2383,93	0,275	R.GGGGGGYSGGSSYSGGGSYSGGGGGGGF	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1	
					0,971	R.KGGETSEMYLIQPDSSVKPYR.V	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
					1,020	K.TFYEPGEITYSCKPGYVSR.G	P02749	APOH_HUMAN	Beta-2-glycoprotein 1 (APC inhibitor) (Activated protein C-binding protein) (Anticardiolipin cofactor) (Apolipoprotein H) (Apo-H) (Beta-2-glycoprotein I) (B2GPI) (Beta(2)GPI)	APOH
2385,20	2384,003	2386,388	2385,18	0,015	R.KGGETSEMYLIQPDSSVKPYR.V	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB	
2386,19	2384,994	2387,380	2387,14	0,953	R.DPDQDTGLGLSYLSSHIANVER.V	P06396	GELS_HUMAN	Gelsolin (AGE1) (Actin-depolymerizing factor) (ADF) (Brevin)	GSN	
				1,007	R.KGGETSEMYLIQPDSSVKPYR.V	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB	
2387,16	2385,967	2388,354	2387,14	0,021	R.DPDQDTGLGLSYLSSHIANVER.V	P06396	GELS_HUMAN	Gelsolin (AGE1) (Actin-depolymerizing factor) (ADF) (Brevin)	GSN	
2388,16	2386,964	2389,352	2387,14	1,018	R.DPDQDTGLGLSYLSSHIANVER.V	P06396	GELS_HUMAN	Gelsolin (AGE1) (Actin-depolymerizing factor) (ADF) (Brevin)	GSN	
				1,051	R.FLHNPDAAQGFVGCALSSTIQR.F	Q13228	SBP1_HUMAN	Methanethiol oxidase (MTO) (EC 1.8.3.4) (56 kDa selenium-binding protein) (SBP56) (SP56) (Selenium-binding protein 1)	SELENBP1	
2389,18	2387,985	2390,374	2389,21	0,029	R.FLHNPDAAQGFVGCALSSTIQR.F	Q13228	SBP1_HUMAN	Methanethiol oxidase (MTO) (EC 1.8.3.4) (56 kDa selenium-binding protein) (SBP56) (SP56) (Selenium-binding protein 1)	SELENBP1	
					0,961	R.KDLYANNVMSGGTTMYPGIADR.M	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
2390,20	2389,008	2391,398	2390,14	0,063	R.KDLYANNVMSGGTTMYPGIADR.M	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1	
					0,994	R.FLHNPDAAQGFVGCALSSTIQR.F	Q13228	SBP1_HUMAN	Methanethiol oxidase (MTO) (EC 1.8.3.4) (56 kDa selenium-binding protein) (SBP56) (SP56) (Selenium-binding protein 1)	SELENBP1
2391,21	2390,015	2392,406	2392,11	0,900	K.MQENMKPQEQLTLEPYER.D	P22087	FBRL_HUMAN	rRNA 2'-O-methyltransferase fibrillar (EC 2.1.1.-) (34 kDa nucleolar scleroderma antigen) (Histone-glutamine methyltransferase)	FBL	
					1,070	R.KDLYANNVMSGGTTMYPGIADR.M	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
2392,20	2391,004	2393,396	2392,11	0,090	K.MQENMKPQEQLTLEPYER.D	P22087	FBRL_HUMAN	rRNA 2'-O-methyltransferase fibrillar (EC 2.1.1.-) (34 kDa nucleolar scleroderma antigen) (Histone-glutamine methyltransferase)	FBL	
					0,842	R.EGYCFTEVLQNMCGSSNR.N	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
2393,19	2391,996	2394,389	2393,04 2392,11	0,151	R.EGYCFTEVLQNMCGSSNR.N	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1	
				1,083	K.MQENMKPQEQLTLEPYER.D	P22087	FBRL_HUMAN	rRNA 2'-O-methyltransferase fibrillar (EC 2.1.1.-) (34 kDa nucleolar scleroderma antigen) (Histone-glutamine methyltransferase)	FBL	
2394,18	2392,985	2395,380	2395,08 2395,32 2393,04	0,901	R.DLGDVMTETVLSQCEQTPER.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG	
				1,138	R.KPGISLLSYEASVSPISTHGR.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG	
				1,141	R.EGYCFTEVLQNMCGSSNR.N	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1	
2395,32	2394,123	2396,518	2395,32 2395,08 2396,10	0,000	R.KPGISLLSYEASVSPISTHGR.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG	
				0,237	R.DLGDVMTETVLSQCEQTPER.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG	
				0,778	R.RPGGEPSEPTGTGQSYNQYSQR.Y	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1	
2396,34	2395,138	2397,534	2396,10	0,238	R.RPGGEPSEPTGTGQSYNQYSQR.Y	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1	
					1,016	R.KPGISLLSYEASVSPISTHGR.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2397,25	2396,055	2398,452	2396,10	1,156	R.RPGGEPSEPTGTGQSYNQYSQR.Y	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1	
2398,23 2399,19	2397,028 2397,990	2399,426 2400,390	2400,26	1,066	R.DFVAEMPGEKPVGSLAGIEVLGK.K	O75531	BAF_HUMAN	Barrier-to-autointegration factor (Breakpoint cluster region protein 1) [Cleaved into: Barrier-to-autointegration factor, N-terminally processed]	BANF1	
2400,19	2398,995	2401,395			0,061	R.DFVAEMPGEKPVGSLAGIEVLGK.K	O75531	BAF_HUMAN	Barrier-to-autointegration factor (Breakpoint cluster region protein 1) [Cleaved into: Barrier-to-autointegration factor, N-terminally processed]	BANF1
2401,17	2399,971	2402,372	2400,26	0,916	R.DFVAEMPGEKPVGSLAGIEVLGK.K	O75531	BAF_HUMAN	Barrier-to-autointegration factor (Breakpoint cluster region protein 1) [Cleaved into: Barrier-to-autointegration factor, N-terminally processed]	BANF1	
2402,18 2403,18 2404,17	2400,982 2401,979 2402,969	2403,384 2404,382 2405,373								

2405,17 2406,17 2407,19 2408,20	2403,971 2404,968 2405,985 2406,998	2406,376 2407,374 2408,392 2409,406	2409,20	0,994	R.FDGALNVDLTFEQTNLVPPYR.I	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
	R.FDGALNVDLTFEQTNLVPPYR.I	Q71U36			TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A		
	R.FDGALNVDLTFEQTNLVPPYR.I	P68366			TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A		
2409,17	2407,968 2410,377	2411,376	2409,20	0,024	R.FDGALNVDLTFEQTNLVPPYR.I	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2409,20	0,024	R.FDGALNVDLTFEQTNLVPPYR.I	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			2409,20	0,024	R.FDGALNVDLTFEQTNLVPPYR.I	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
2410,17	2408,965 2411,376	2411,376	2411,08	0,910	R.DLGDVMTVLSSQTCQTPER.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2409,20	0,974	R.FDGALNVDLTFEQTNLVPPYR.I	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2409,20	0,974	R.FDGALNVDLTFEQTNLVPPYR.I	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
2411,17	2409,968 2410,976 2411,980	2412,379 2413,388 2414,393	2409,20	0,974	R.FDGALNVDLTFEQTNLVPPYR.I	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
			2411,08	0,093	R.DLGDVMTVLSSQTCQTPER.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2412,18	1,101	R.DLGDVMTVLSSQTCQTPER.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2413,19	2411,980	2414,393	2414,14	0,956	K.VLHEAEGHIVTCETNTGEVYR.G	P62318	SMD3_HUMAN	Small nuclear ribonucleoprotein Sm D3 (Sm-D3) (snRNP core protein D3)	SNRPD3
2414,20	2412,990 2415,404	2415,404	2414,14	0,055	K.VLHEAEGHIVTCETNTGEVYR.G	P62318	SMD3_HUMAN	Small nuclear ribonucleoprotein Sm D3 (Sm-D3) (snRNP core protein D3)	SNRPD3
			2415,16	0,961	R.QGPVNLLSDPEQGEVVTGQYER.E	Q14624	ITIH4_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H4 (ITI heavy chain H4) (ITI-HC4) (Inter-alpha-inhibitor heavy chain 4) (Inter-alpha-trypsin inhibitor family heavy chain-related protein) (IHRP) (Plasma kallikrein sensitive glycoprotein 120) (Gp120) (PK-120) [Cleaved into: 70 kDa inter-alpha-trypsin inhibitor heavy chain H4; 35 kDa inter-alpha-trypsin inhibitor heavy chain H4]	ITIH4
			2415,20	0,998	R.QLFHPEQLTGKEDAANNYAR.G	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
2415,19	2413,984 2416,399	2416,399	2415,20	0,998	R.QLFHPEQLTGKEDAANNYAR.G	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2415,20	0,998	R.QLFHPEQLTGKEDAANNYAR.G	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			2415,20	0,004	R.QLFHPEQLTGKEDAANNYAR.G	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
2415,19	2413,984 2416,399	2416,399	2415,20	0,004	R.QLFHPEQLTGKEDAANNYAR.G	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2415,20	0,004	R.QLFHPEQLTGKEDAANNYAR.G	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			2415,16	0,033	R.QGPVNLLSDPEQGEVVTGQYER.E	Q14624	ITIH4_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H4 (ITI heavy chain H4) (ITI-HC4) (Inter-alpha-inhibitor heavy chain 4) (Inter-alpha-trypsin inhibitor family heavy chain-related protein) (IHRP) (Plasma kallikrein sensitive glycoprotein 120) (Gp120) (PK-120) [Cleaved into: 70 kDa inter-alpha-trypsin inhibitor heavy chain H4; 35 kDa inter-alpha-trypsin inhibitor heavy chain H4]	ITIH4
2414,20	2412,990 2415,404	2415,404	2414,14	1,049	K.VLHEAEGHIVTCETNTGEVYR.G	P62318	SMD3_HUMAN	Small nuclear ribonucleoprotein Sm D3 (Sm-D3) (snRNP core protein D3)	SNRPD3
			2416,25	1,055	R.DFVAEPMGEKPVGSLAGIEVLGK.K	O75531	BAF_HUMAN	Barrier-to-autointegration factor (Breakpoint cluster region protein 1) [Cleaved into: Barrier-to-autointegration factor, N-terminally processed]	BANF1
			2416,20	0,044	R.DFVAEPMGEKPVGSLAGIEVLGK.K	O75531	BAF_HUMAN	Barrier-to-autointegration factor (Breakpoint cluster region protein 1) [Cleaved into: Barrier-to-autointegration factor, N-terminally processed]	BANF1
2416,20	2414,994 2417,410	2417,410	2416,25	0,044	R.DFVAEPMGEKPVGSLAGIEVLGK.K	O75531	BAF_HUMAN	Barrier-to-autointegration factor (Breakpoint cluster region protein 1) [Cleaved into: Barrier-to-autointegration factor, N-terminally processed]	BANF1
			2417,08	0,878	R.FGSYCPTTCGIADFLSTYQTK.V	P02679	FIBG_HUMAN	Fibrinogen gamma chain	FGG
			2417,13	0,925	R.SYDVPPPPMEPDHPFYSNISK.D	P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	PGAM1
2416,20	2414,994 2417,410	2417,410	2415,20	1,007	R.QLFHPEQLTGKEDAANNYAR.G	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
			2415,20	1,007	R.QLFHPEQLTGKEDAANNYAR.G	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2415,20	1,007	R.QLFHPEQLTGKEDAANNYAR.G	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
2416,20	2414,994 2417,410	2417,410	2415,16	1,044	R.QGPVNLLSDPEQGEVVTGQYER.E	Q14624	ITIH4_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H4 (ITI heavy chain H4) (ITI-HC4) (Inter-alpha-inhibitor heavy chain 4) (Inter-alpha-trypsin inhibitor family heavy chain-related protein) (IHRP) (Plasma kallikrein sensitive glycoprotein 120) (Gp120) (PK-120) [Cleaved into: 70 kDa inter-alpha-trypsin inhibitor heavy chain H4; 35 kDa inter-alpha-trypsin inhibitor heavy chain H4]	ITIH4
			2417,22	0,090	R.SYDVPPPPMEPDHPFYSNISK.D	P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	PGAM1
			2417,08	0,137	R.FGSYCPTTCGIADFLSTYQTK.V	P02679	FIBG_HUMAN	Fibrinogen gamma chain	FGG
2417,22	2416,009 2418,426	2418,426	2416,25	0,971	R.DFVAEPMGEKPVGSLAGIEVLGK.K	O75531	BAF_HUMAN	Barrier-to-autointegration factor (Breakpoint cluster region protein 1) [Cleaved into: Barrier-to-autointegration factor, N-terminally processed]	BANF1

			2418,24	1,028	R.NIDNPALADIYTEHAHQVVVAK.Y	O75083	WDR1_HUMAN	WD repeat-containing protein 1 (Actin-interacting protein 1) (AIP1) (NORI-1)	WDR1
2418,21	2417,000	2419,418	2418,24	0,036	R.NIDNPALADIYTEHAHQVVVAK.Y	O75083	WDR1_HUMAN	WD repeat-containing protein 1 (Actin-interacting protein 1) (AIP1) (NORI-1)	WDR1
			2417,13	1,082	R.SYDVPPPPMEPDHPFYSNISK.D	P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG-dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	PGAM1
			2417,08	1,129	R.FGSYCPTTCGIADFLSTYQTK.V	P02679	FIBG_HUMAN	Fibrinogen gamma chain	FGG
2419,20	2417,989	2420,408	2418,24	0,954	R.NIDNPALADIYTEHAHQVVVAK.Y	O75083	WDR1_HUMAN	WD repeat-containing protein 1 (Actin-interacting protein 1) (AIP1) (NORI-1)	WDR1
2420,19	2418,976	2421,396							
2421,19	2419,976	2422,397							
2422,19	2420,982	2423,405	2423,11	0,919	K.TVETRDGQVINETSQHDDLE.-	P08670	VIME_HUMAN	Vimentin	VIM
2423,18	2421,968	2424,391	2423,11	0,067	K.TVETRDGQVINETSQHDDLE.-	P08670	VIME_HUMAN	Vimentin	VIM
2424,18	2422,965	2425,389	2425,17	0,989	R.YADLTEDQLPSCESLKDTIAR.A	P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG-dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	PGAM1
			2425,19	1,008	R.VLLNDGGYYDPETGVFTAPLAGR.Y	Q9Y6C2	EMIL1_HUMAN	EMILIN-1 (Elastin microfibril interface-located protein 1) (Elastin microfibril interfacar 1)	EMILIN1
			2423,11	1,065	K.TVETRDGQVINETSQHDDLE.-	P08670	VIME_HUMAN	Vimentin	VIM
2425,18	2423,966	2426,391	2425,19	0,007	R.VLLNDGGYYDPETGVFTAPLAGR.Y	Q9Y6C2	EMIL1_HUMAN	EMILIN-1 (Elastin microfibril interface-located protein 1) (Elastin microfibril interfacar 1)	EMILIN1
			2425,17	0,012	R.YADLTEDQLPSCESLKDTIAR.A	P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG-dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	PGAM1
2426,19	2424,973	2427,400	2425,19	1,001	R.VLLNDGGYYDPETGVFTAPLAGR.Y	Q9Y6C2	EMIL1_HUMAN	EMILIN-1 (Elastin microfibril interface-located protein 1) (Elastin microfibril interfacar 1)	EMILIN1
			2425,17	1,021	R.YADLTEDQLPSCESLKDTIAR.A	P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG-dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	PGAM1
2427,17	2425,958	2428,385	2428,14	0,971	K.DKLESEMEDAYHEHQANLLR.Q	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMp100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
2428,17	2426,957	2429,386	2428,14	0,029	K.DKLESEMEDAYHEHQANLLR.Q	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMp100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
2429,18	2427,961	2430,390	2428,14	1,033	K.DKLESEMEDAYHEHQANLLR.Q	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMp100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
2430,19	2428,977	2431,408							
2431,20	2429,983	2432,414	2432,12	0,918	R.LVSSPCCVITYSTYGWTANMER.I	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HS90AB1
2432,20	2430,987	2433,420	2432,12	0,087	R.LVSSPCCVITYSTYGWTANMER.I	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HS90AB1
			2433,06	0,860	R.NAGDLAPAGGAASASTDEAADAESGTR.N	Q9NXV6	CARF_HUMAN	CDKN2A-interacting protein (Collaborator of ARF)	CDKN2AIP
2433,20	2431,983	2434,416	2433,06	0,136	R.NAGDLAPAGGAASASTDEAADAESGTR.N	Q9NXV6	CARF_HUMAN	CDKN2A-interacting protein (Collaborator of ARF)	CDKN2AIP
			2432,12	1,082	R.LVSSPCCVITYSTYGWTANMER.I	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HS90AB1
2434,20	2432,986	2435,420	2433,06	1,139	R.NAGDLAPAGGAASASTDEAADAESGTR.N	Q9NXV6	CARF_HUMAN	CDKN2A-interacting protein (Collaborator of ARF)	CDKN2AIP
2435,19	2433,975	2436,410							
2436,18	2434,966	2437,402							
2437,18	2435,963	2438,400							
2438,20	2436,976	2439,415							
2439,20	2437,977	2440,417							
2440,25	2439,026	2441,466							
2441,25	2440,034	2442,476	2442,22	0,969	K.ITDLANLSAANHDAIIFPGGFGAAK.N	P0DPI2	GAL3A_HUMAN	Glutamine amidotransferase-like class 1 domain-containing protein 3A, mitochondrial	GATD3A
2442,20	2440,977	2443,419	2442,22	0,025	K.ITDLANLSAANHDAIIFPGGFGAAK.N	P0DPI2	GAL3A_HUMAN	Glutamine amidotransferase-like class 1 domain-containing protein 3A, mitochondrial	GATD3A
			2443,07	0,875	R.TREEECHFYAGGQVYPGEASR.V	Q13162	PRDX4_HUMAN	Peroxioredoxin-4 (EC 1.11.1.15) (Antioxidant enzyme AOE372) (AOE37-2) (Peroxioredoxin IV) (Prx-IV) (Thioredoxin peroxidase A0372) (Thioredoxin-dependent peroxide reductase A0372)	PRDX4
2443,20	2441,975	2444,418	2443,07	0,123	R.TREEECHFYAGGQVYPGEASR.V	Q13162	PRDX4_HUMAN	Peroxioredoxin-4 (EC 1.11.1.15) (Antioxidant enzyme AOE372) (AOE37-2) (Peroxioredoxin IV) (Prx-IV) (Thioredoxin peroxidase A0372) (Thioredoxin-dependent peroxide reductase A0372)	PRDX4
			2442,22	0,973	K.ITDLANLSAANHDAIIFPGGFGAAK.N	P0DPI2	GAL3A_HUMAN	Glutamine amidotransferase-like class 1 domain-containing protein 3A, mitochondrial	GATD3A
			2444,19	0,997	K.GVDDLDFFIGDEAIEKPTYATK.W	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
2444,19	2442,968	2445,412	2444,19	0,003	K.GVDDLDFFIGDEAIEKPTYATK.W	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
			2443,07	1,117	R.TREEECHFYAGGQVYPGEASR.V	Q13162	PRDX4_HUMAN	Peroxioredoxin-4 (EC 1.11.1.15) (Antioxidant enzyme AOE372) (AOE37-2) (Peroxioredoxin IV) (Prx-IV) (Thioredoxin peroxidase A0372) (Thioredoxin-dependent peroxide reductase A0372)	PRDX4
2445,19	2443,968	2446,413	2444,19	0,997	K.GVDDLDFFIGDEAIEKPTYATK.W	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
2446,20	2444,980	2447,426	2447,19	0,984	K.TPALIVYGDQDPMGQTSFEHLK.Q	Q96IU4	ABHEB_HUMAN	Protein ABHD14B (EC 3.-.-.-) (Alpha/beta hydrolase domain-containing protein 14B) (Abhydrolase domain-containing protein 14B) (CCG1-interacting factor B)	ABHD14B
2447,20	2445,974	2448,421	2447,19	0,011	K.TPALIVYGDQDPMGQTSFEHLK.Q	Q96IU4	ABHEB_HUMAN	Protein ABHD14B (EC 3.-.-.-) (Alpha/beta hydrolase domain-containing protein 14B) (Abhydrolase domain-containing protein 14B) (CCG1-interacting factor B)	ABHD14B
			2448,14	0,944	R.GFEVVMTEPIDEYCVQQLK.E	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HS90AB1
2448,21	2446,982	2449,430	2448,14	0,064	R.GFEVVMTEPIDEYCVQQLK.E	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HS90AB1

			2447,19	1,019	K.TPALIVYGDQPMGQTQFEHLK.Q	Q96IU4	ABHEB_HUMAN	Protein ABHD14B (EC 3.---) (Alpha/beta hydrolase domain-containing protein 14B) (Abhydrolase domain-containing protein 14B) (CCG1-interacting factor B)	ABHD14B
2449,20	2447,976	2450,425	2448,14	1,058	R.GFEVVMTEPIDEYCVQQLK.E	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
2450,20 2451,20	2448,976 2449,979	2451,426 2452,430	2452,13	0,930	R.TVEGGSSSVFSMFDQTIQEFK.E	Q96A32	MLRS_HUMAN	Myosin regulatory light chain 2, skeletal muscle isoform (Fast skeletal myosin light chain 2) (MLC2B)	MYLPF
2452,22	2450,991	2453,443	2452,13	0,083	R.TVEGGSSSVFSMFDQTIQEFK.E	Q96A32	MLRS_HUMAN	Myosin regulatory light chain 2, skeletal muscle isoform (Fast skeletal myosin light chain 2) (MLC2B)	MYLPF
2453,21	2451,984	2454,437	2452,13	1,077	R.TVEGGSSSVFSMFDQTIQEFK.E	Q96A32	MLRS_HUMAN	Myosin regulatory light chain 2, skeletal muscle isoform (Fast skeletal myosin light chain 2) (MLC2B)	MYLPF
2454,24	2453,010	2455,464	2455,14	0,904	K.TSESGELHGLTTEEFVEGIYK.V	P02766	TTHY_HUMAN	Transthyretin (ATTR) (Prealbumin) (TBPA)	TTR
2455,24	2454,015	2456,470	2455,14	0,101	K.TSESGELHGLTTEEFVEGIYK.V	P02766	TTHY_HUMAN	Transthyretin (ATTR) (Prealbumin) (TBPA)	TTR
2456,28	2455,052	2457,508	2455,14	1,139	K.TSESGELHGLTTEEFVEGIYK.V	P02766	TTHY_HUMAN	Transthyretin (ATTR) (Prealbumin) (TBPA)	TTR
2457,23 2458,23	2455,998 2456,997	2458,456 2459,455	2459,14	0,912	K.THIQDNHDGTTYVAVVPDVTGR.Y	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
2459,21	2457,982	2460,441	2459,14	0,074	K.THIQDNHDGTTYVAVVPDVTGR.Y	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
2460,21	2458,983	2461,443	2461,15 2459,14	0,940 1,075	K.NVMSAFGLTDDQVSGPPSPAEDR.S K.THIQDNHDGTTYVAVVPDVTGR.Y	Q92734 P21333	TFG_HUMAN FLNA_HUMAN	Protein TFG (TRK-fused gene protein) Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	TFG FLNA
2460,21	2458,983	2461,443	2461,15 2459,14	0,940 1,075	K.NVMSAFGLTDDQVSGPPSPAEDR.S K.THIQDNHDGTTYVAVVPDVTGR.Y	Q92734 P21333	TFG_HUMAN FLNA_HUMAN	Protein TFG (TRK-fused gene protein) Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	TFG FLNA
2461,21	2459,984	2462,445	2461,15	0,062	K.NVMSAFGLTDDQVSGPPSPAEDR.S	Q92734	TFG_HUMAN	Protein TFG (TRK-fused gene protein)	TFG
2462,21	2460,983	2463,445	2461,15	1,061	K.NVMSAFGLTDDQVSGPPSPAEDR.S	Q92734	TFG_HUMAN	Protein TFG (TRK-fused gene protein)	TFG
2463,23	2461,996	2464,459	2464,01	0,780	R.CMFYADTQSCTHSLQGQNCRL.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2464,15	2462,923	2465,387	2464,01 2465,29	0,147 1,136	R.CMFYADTQSCTHSLQGQNCRL.L R.TATESFASDPILYRPVAVALDTK.G	P01266 P14618	THYG_HUMAN KPYM_HUMAN	Thyroglobulin (Tg) Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	TG PKM
2464,21	2462,979	2465,443	2464,01 2465,29	0,203 1,080	R.CMFYADTQSCTHSLQGQNCRL.L R.TATESFASDPILYRPVAVALDTK.G	P01266 P14618	THYG_HUMAN KPYM_HUMAN	Thyroglobulin (Tg) Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	TG PKM
2465,24	2464,008	2466,473	2465,29	0,050	R.TATESFASDPILYRPVAVALDTK.G	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
2466,24	2465,008	2467,475	2466,16 2465,29	0,922 0,079 0,951	R.LYFGTSGYFSQHDLFSSPEKR.W R.LYFGTSGYFSQHDLFSSPEKR.W R.TATESFASDPILYRPVAVALDTK.G	P01266 P01266 P14618	THYG_HUMAN THYG_HUMAN KPYM_HUMAN	Thyroglobulin (Tg) Thyroglobulin (Tg) Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	TG TG PKM
2467,27	2466,034	2468,501	2467,20	0,962	K.FNEEHIPDSPFVVPVPSGSDAR.R	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			2468,21	0,941	K.FVDGLMIHSGDPVNYVDTAVR.H	P23396	RS3_HUMAN	40S ribosomal protein S3 (EC 4.2.99.18) (Small ribosomal subunit protein uS3)	RPS3
			2466,16	1,104	R.LYFGTSGYFSQHDLFSSPEKR.W	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2468,28	2467,042	2469,511	2468,21	0,068	K.FVDGLMIHSGDPVNYVDTAVR.H	P23396	RS3_HUMAN	40S ribosomal protein S3 (EC 4.2.99.18) (Small ribosomal subunit protein uS3)	RPS3
			2467,20	1,073	K.FNEEHIPDSPFVVPVPSGSDAR.R	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
2469,24	2468,008	2470,477	2468,21	1,034	K.FVDGLMIHSGDPVNYVDTAVR.H	P23396	RS3_HUMAN	40S ribosomal protein S3 (EC 4.2.99.18) (Small ribosomal subunit protein uS3)	RPS3
2470,25 2471,24 2471,24 2472,24 2473,23 2474,23	2469,010 2470,009 2470,009 2471,004 2471,997 2472,992	2471,480 2472,481 2472,481 2473,476 2474,470 2475,467	2475,30 2475,31	1,068 1,080	R.AITPPHPASQANIIFDITEGNLR.D K.DDKESVPISDTIIPAVPPPTDLR.F	P23142 P02751	FBLN1_HUMAN FINC_HUMAN	Fibulin-1 (FIBL-1) Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FBLN1 FN1
2475,23	2473,996	2476,471	2475,30 2475,31	0,064 0,076	R.AITPPHPASQANIIFDITEGNLR.D K.DDKESVPISDTIIPAVPPPTDLR.F	P23142 P02751	FBLN1_HUMAN FINC_HUMAN	Fibulin-1 (FIBL-1) Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FBLN1 FN1
2476,25	2475,007	2477,484	2475,31	0,936	K.DDKESVPISDTIIPAVPPPTDLR.F	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			2475,30	0,948	R.AITPPHPASQANIIFDITEGNLR.D	P23142	FBLN1_HUMAN	Fibulin-1 (FIBL-1)	FBLN1
2477,22 2478,22	2475,986 2476,977	2478,463 2479,455							

2478,22 2479,21	2476,977 2477,974	2479,455 2480,453	2480,00 2480,06	0,785 0,845	R.CMFYADTQSCTHSLQGQNC.R.L R.QDHPSSMGVYGQESGFGSPGENR.S	P01266 Q01844	THYG_HUMAN EWS_HUMAN	Thyroglobulin (Tg) RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein)	TG EWSR1
2480,23	2478,987	2481,467	2480,06 2480,00	0,169 0,229	R.QDHPSSMGVYGQESGFGSPGENR.S R.CMFYADTQSCTHSLQGQNC.R.L	Q01844 P01266	EWS_HUMAN THYG_HUMAN	RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein) Thyroglobulin (Tg)	EWSR1 TG
2481,23	2479,986	2482,467	2482,19 2480,06 2480,00	0,966 1,168 1,228	R.AEPEDHYFLLTEPLNTPENR.E R.QDHPSSMGVYGQESGFGSPGENR.S R.CMFYADTQSCTHSLQGQNC.R.L	P61158 Q01844 P01266	ARP3_HUMAN EWS_HUMAN THYG_HUMAN	Actin-related protein 3 (Actin-like protein 3) RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein) Thyroglobulin (Tg)	ACTR3 EWSR1 TG
2482,23	2480,993	2483,475	2482,19 2483,28	0,041 1,043	R.AEPEDHYFLLTEPLNTPENR.E R.VTASDPLDTLGSEGALSPGGVASLLR.L	P61158 P0C0L5	ARP3_HUMAN CO4B_HUMAN	Actin-related protein 3 (Actin-like protein 3) Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-8; C4d-8; Complement C4 gamma chain]	ACTR3 C4B; C4B_2
2483,24	2481,999	2484,482	2483,28 2482,19	0,037 1,048	R.VTASDPLDTLGSEGALSPGGVASLLR.L R.AEPEDHYFLLTEPLNTPENR.E	P0C0L5 P61158	CO4B_HUMAN ARP3_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-8; C4d-8; Complement C4 gamma chain] Actin-related protein 3 (Actin-like protein 3)	C4B; C4B_2 ACTR3
2484,24	2483,001	2485,486	2483,28 2485,37	0,966 1,124	R.VTASDPLDTLGSEGALSPGGVASLLR.L R.IGYPKALLHSTFFPALQGAQTK.M	P0C0L5 P23381	CO4B_HUMAN SYWC_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-8; C4d-8; Complement C4 gamma chain] Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleaved into: T1-TrpRS; T2-TrpRS]	C4B; C4B_2 WARS
2485,26	2484,015	2486,500	2485,37 2486,02	0,110 0,762	R.IGYPKALLHSTFFPALQGAQTK.M K.GTMDDISQEEGSSQGEDSVSGSQR.I	P23381 Q14683	SYWC_HUMAN SMC1A_HUMAN	Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleaved into: T1-TrpRS; T2-TrpRS] Structural maintenance of chromosomes protein 1A (SMC protein 1A) (SMC-1-alpha) (SMC-1A) (Sb1.8)	WARS SMC1A
2486,26	2485,017	2487,504	2486,02 2485,37	0,242 0,893	K.GTMDDISQEEGSSQGEDSVSGSQR.I R.IGYPKALLHSTFFPALQGAQTK.M	Q14683 P23381	SMC1A_HUMAN SYWC_HUMAN	Structural maintenance of chromosomes protein 1A (SMC protein 1A) (SMC-1-alpha) (SMC-1A) (Sb1.8) Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleaved into: T1-TrpRS; T2-TrpRS]	SMC1A WARS
2487,26	2486,012	2488,499	2486,02	1,237	K.GTMDDISQEEGSSQGEDSVSGSQR.I	Q14683	SMC1A_HUMAN	Structural maintenance of chromosomes protein 1A (SMC protein 1A) (SMC-1-alpha) (SMC-1A) (Sb1.8)	SMC1A
2488,26	2487,015	2489,503	2489,32	1,063	R.AWRDPDEPVLLEPVLVLALEA.Y	P14550	AK1A1_HUMAN	Aldo-keto reductase family 1 member A1 (EC 1.1.1.2) (EC 1.1.1.372) (EC 1.1.1.54) (Alcohol dehydrogenase [NADP(+)] (Aldehyde reductase) (Glucuronate reductase) (EC 1.1.1.19) (Glucuronolactone reductase) (EC 1.1.1.20)	AKR1A1
2489,25	2488,005	2490,494	2489,32	0,072	R.AWRDPDEPVLLEPVLVLALEA.Y	P14550	AK1A1_HUMAN	Aldo-keto reductase family 1 member A1 (EC 1.1.1.2) (EC 1.1.1.372) (EC 1.1.1.54) (Alcohol dehydrogenase [NADP(+)] (Aldehyde reductase) (Glucuronate reductase) (EC 1.1.1.19) (Glucuronolactone reductase) (EC 1.1.1.20)	AKR1A1
2490,25	2489,002	2491,492	2489,32	0,925	R.AWRDPDEPVLLEPVLVLALEA.Y	P14550	AK1A1_HUMAN	Aldo-keto reductase family 1 member A1 (EC 1.1.1.2) (EC 1.1.1.372) (EC 1.1.1.54) (Alcohol dehydrogenase [NADP(+)] (Aldehyde reductase) (Glucuronate reductase) (EC 1.1.1.19) (Glucuronolactone reductase) (EC 1.1.1.20)	AKR1A1
2491,24	2489,999	2492,490	2492,13 2492,25	0,890 1,007	R.LPWWETEAPLEDSQCLMMQK.F R.FPNGVQLSPAEDFVLVAETTMAR.I	P01266 Q9HDC9	THYG_HUMAN APMAP_HUMAN	Thyroglobulin (Tg) Adipocyte plasma membrane-associated protein (Protein BSCv)	TG APMAP
2492,25	2491,004	2493,496	2492,25 2492,13	0,001 0,115	R.FPNGVQLSPAEDFVLVAETTMAR.I R.LPWWETEAPLEDSQCLMMQK.F	Q9HDC9 P01266	APMAP_HUMAN THYG_HUMAN	Adipocyte plasma membrane-associated protein (Protein BSCv) Thyroglobulin (Tg)	APMAP TG
2493,23	2491,988	2494,481	2494,14 2492,25 2492,13	0,905 0,984 1,100	R.AEGSDVANAVLDGADCIMLSGETAK.G R.FPNGVQLSPAEDFVLVAETTMAR.I R.LPWWETEAPLEDSQCLMMQK.F	P14618 Q9HDC9 P01266	KPYM_HUMAN APMAP_HUMAN THYG_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58) Adipocyte plasma membrane-associated protein (Protein BSCv) Thyroglobulin (Tg)	PKM APMAP TG
2494,23	2492,987	2495,481	2494,14	0,095	R.AEGSDVANAVLDGADCIMLSGETAK.G	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
2495,23	2493,981	2496,476	2496,05 2494,14	0,818 1,089	R.QDHPSSMGVYGQESGFGSPGENR.S R.AEGSDVANAVLDGADCIMLSGETAK.G	Q01844 P14618	EWS_HUMAN KPYM_HUMAN	RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein) Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	EWSR1 PKM
2496,25	2495,004	2497,500	2496,05 2497,17 2497,21	0,205 0,913 0,957	R.QDHPSSMGVYGQESGFGSPGENR.S K.LASGETVAAFLTEPSSGSDAASIR.T R.VVTNNYSAHQDNLLIYEYF.N	Q01844 P49748 P21980	EWS_HUMAN ACADV_HUMAN TGM2_HUMAN	RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein) Very long-chain specific acyl-CoA dehydrogenase, mitochondrial (VLCAD) (EC 1.3.8.9) Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (Transglutaminase C) (TG(C)) (TGC) (TGase C) (Transglutaminase H) (TGase H) (Transglutaminase-2) (TGase-2)	EWSR1 ACADV.L TGM2

2497,24	2495,989	2498,486	2497,21	0,029	R.VVTNYSNHAHDQNSNLLIEYF.R.N	P21980	TGM2_HUMAN	Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (Transglutaminase C) (TG(C)) (TGC) (TGase C) (Transglutaminase H) (TGase H) (Transglutaminase-2) (TGase-2)	TGM2
			2497,17	0,073	K.LASGETVAACFLETPSSGSDAASIR.T	P49748	ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial (VLCAD) (EC 1.3.8.9)	ACADVL
			2498,24	1,002	K.EVGTPHGIILSDVDAAFICPGSSR.L	P02790	HEMO_HUMAN	Hemopexin (Beta-1B-glycoprotein)	HPX
			2498,25	1,017	R.ETVVEVPQVTWEDIGGLEDVKR.E	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			2496,05	1,191	R.QDHPSMVGVGQESGGFSGPGENR.S	Q01844	EWS_HUMAN	RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein)	EWSR1
2498,24	2496,986	2499,485	2498,24	0,005	K.EVGTPHGIILSDVDAAFICPGSSR.L	P02790	HEMO_HUMAN	Hemopexin (Beta-1B-glycoprotein)	HPX
			2498,25	0,019	R.ETVVEVPQVTWEDIGGLEDVKR.E	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			2498,98	0,746	R.GFSLDQTGSSCEDVDECEGNHR.C	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			2497,21	1,027	R.VVTNYSNHAHDQNSNLLIEYF.R.N	P21980	TGM2_HUMAN	Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (Transglutaminase C) (TG(C)) (TGC) (TGase C) (Transglutaminase H) (TGase H) (Transglutaminase-2) (TGase-2)	TGM2
			2497,17	1,070	K.LASGETVAACFLETPSSGSDAASIR.T	P49748	ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial (VLCAD) (EC 1.3.8.9)	ACADVL
2499,25	2497,998	2500,497	2498,98	0,266	R.GFSLDQTGSSCEDVDECEGNHR.C	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			2498,25	0,992	R.ETVVEVPQVTWEDIGGLEDVKR.E	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			2498,24	1,007	K.EVGTPHGIILSDVDAAFICPGSSR.L	P02790	HEMO_HUMAN	Hemopexin (Beta-1B-glycoprotein)	HPX
2500,24	2498,994	2501,494							
2501,24	2499,990	2502,491							
2504,25	2502,995	2505,499	2503,29	0,957	R.YHVPVVVPEGSADTHEQAILR.L	P04844	RPN2_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 (Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit) (RIBIIR) (Ribophorin II) (RPN-II) (Ribophorin-2)	RPN2
2505,24	2503,984	2506,489							
2506,24	2504,989	2507,495	2507,23	0,983	K.AVTLHDQGTAAQWADLSSQFYLR.E	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
2507,24	2505,984	2508,492	2507,23	0,013	K.AVTLHDQGTAAQWADLSSQFYLR.E	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
			2508,22	0,982	R.TSRPENAIYNNNEDFQVGOAK.V	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
2508,23	2506,979	2509,488	2508,22	0,014	R.TSRPENAIYNNNEDFQVGOAK.V	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
			2509,13	0,895	R.LQEVPHGPMCDLLWSDPDDR.G	P62714	PP2AB_HUMAN	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform (PP2A-beta) (EC 3.1.3.16)	PPP2CB
			2507,23	1,008	K.AVTLHDQGTAAQWADLSSQFYLR.E	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
			2509,33	1,100	K.EFTPPVQAAYQKVAVGANALAHK.Y	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2509,22	2507,967	2510,476	2509,13	0,093	R.LQEVPHGPMCDLLWSDPDDR.G	P62714	PP2AB_HUMAN	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform (PP2A-beta) (EC 3.1.3.16)	PPP2CB
			2509,33	0,112	K.EFTPPVQAAYQKVAVGANALAHK.Y	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			2510,17	0,951	K.EIETYHNLLEGGQEDFESSGAGK.I	P35527	K1C9_HUMAN	Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9) (Keratin-9) (K9)	KRT9
			2508,22	1,002	R.TSRPENAIYNNNEDFQVGOAK.V	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
2510,22	2508,966	2511,476	2510,17	0,049	K.EIETYHNLLEGGQEDFESSGAGK.I	P35527	K1C9_HUMAN	Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9) (Keratin-9) (K9)	KRT9
			2509,33	0,887	K.EFTPPVQAAYQKVAVGANALAHK.Y	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			2509,13	1,093	R.LQEVPHGPMCDLLWSDPDDR.G	P62714	PP2AB_HUMAN	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform (PP2A-beta) (EC 3.1.3.16)	PPP2CB
2511,24	2509,983	2512,494	2510,17	1,066	K.EIETYHNLLEGGQEDFESSGAGK.I	P35527	K1C9_HUMAN	Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9) (Keratin-9) (K9)	KRT9
2512,24	2510,986	2513,498							
2513,23	2511,977	2514,491							
2514,23	2512,977	2515,491							
2515,25	2513,990	2516,506							
2516,26	2514,998	2517,514	2517,34	1,089	R.LPPLPVTGMEGAGVVIAGGEGVSDR.K	Q99536	VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog (EC 1.-.-. VAT1 -.)	VAT1
2517,26	2516,005	2518,522	2517,34	0,081	R.LPPLPVTGMEGAGVVIAGGEGVSDR.K	Q99536	VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog (EC 1.-.-. VAT1 -.)	VAT1
			2518,23	0,969	R.MPCAEDYLSVLNLQCLVHEK.T	P02768	ALBU_HUMAN	Serum albumin	ALB
2519,25	2517,988	2520,508	2518,23	1,016	R.MPCAEDYLSVLNLQCLVHEK.T	P02768	ALBU_HUMAN	Serum albumin	ALB
2520,25	2518,987	2521,507	2521,36	1,113	K.LAQQYVLVYQEPIPTAQLVQR.V	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
2521,24	2519,978	2522,499	2521,36	0,122	K.LAQQYVLVYQEPIPTAQLVQR.V	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
2522,23	2520,973	2523,495	2521,36	0,874	K.LAQQYVLVYQEPIPTAQLVQR.V	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
2523,25	2521,984	2524,507							
2524,26	2522,994	2525,519							
2525,26	2523,997	2526,522							
2526,28	2525,012	2527,538							
2527,26	2525,994	2528,521							
2528,25	2526,986	2529,515							
2529,25	2527,989	2530,518							
2530,28	2529,012	2531,542							
2531,25	2529,985	2532,517	2532,20	0,950	K.QAFTDVATGSLGQGLGAACGMAYTGK.Y	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT

2532,25	2530,988	2533,520	2532,20	0,052	K.QAFTDVATGSLGQGLGAACGMAYTGK.Y	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
2533,25	2531,986	2534,520	2532,20	1,052	K.QAFTDVATGSLGQGLGAACGMAYTGK.Y	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
2534,26 2535,25	2532,991 2533,987	2535,525 2536,522	2536,05	0,795	R.SDGSGESAQPPEDSSPPASSESSSTR.D	Q72627	HUWE1_HUMAN	E3 ubiquitin-protein ligase HUWE1 (EC 2.3.2.26) (ARF-binding protein 1) (ARF-BP1) (HECT, UBA and WWE domain-containing protein 1) (HECT-type E3 ubiquitin transferase HUWE1) (Homologous to E6AP carboxyl terminus homologous protein 9) (HectH9) (Large structure of UREB1) (LASU1) (Mcl-1 ubiquitin ligase E3) (Mule) (Upstream regulatory element-binding protein 1) (URE-B1) (URE-binding protein 1)	HUWE1
			2536,17	0,914	K.LCVVALDFENEMATAASSSSLEK.S	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2536,17	0,914	K.LCVVALDFENEMATAASSSSLEK.S	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			2536,17	0,914	K.LCVVALDFENEMATAASSSSLEK.S	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2536,28	1,025	K.NIPTVNENLENYLEVNQLEK.F	P51884	LUM_HUMAN	Lumican (Keratan sulfate proteoglycan lumican) (KSPG lumican)	LUM
2536,26	2534,990	2537,526	2536,28	0,022	K.NIPTVNENLENYLEVNQLEK.F	P51884	LUM_HUMAN	Lumican (Keratan sulfate proteoglycan lumican) (KSPG lumican)	LUM
			2536,17	0,090	K.LCVVALDFENEMATAASSSSLEK.S	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2536,17	0,090	K.LCVVALDFENEMATAASSSSLEK.S	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			2536,17	0,090	K.LCVVALDFENEMATAASSSSLEK.S	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2536,05	0,208	R.SDGSGESAQPPEDSSPPASSESSSTR.D	Q72627	HUWE1_HUMAN	E3 ubiquitin-protein ligase HUWE1 (EC 2.3.2.26) (ARF-binding protein 1) (ARF-BP1) (HECT, UBA and WWE domain-containing protein 1) (HECT-type E3 ubiquitin transferase HUWE1) (Homologous to E6AP carboxyl terminus homologous protein 9) (HectH9) (Large structure of UREB1) (LASU1) (Mcl-1 ubiquitin ligase E3) (Mule) (Upstream regulatory element-binding protein 1) (URE-B1) (URE-binding protein 1)	HUWE1
2537,27	2536,004	2538,542	2536,28	0,994	K.NIPTVNENLENYLEVNQLEK.F	P51884	LUM_HUMAN	Lumican (Keratan sulfate proteoglycan lumican) (KSPG lumican)	LUM
			2536,17	1,105	K.LCVVALDFENEMATAASSSSLEK.S	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2536,17	1,105	K.LCVVALDFENEMATAASSSSLEK.S	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1
			2536,17	1,105	K.LCVVALDFENEMATAASSSSLEK.S	P62736	ACTA_HUMAN	Actin, aortic smooth muscle (Alpha-actin-2) (Cell growth-inhibiting gene 46 protein) [Cleaved into: Actin, aortic smooth muscle, intermediate form]	ACTA2
			2536,05	1,223	R.SDGSGESAQPPEDSSPPASSESSSTR.D	Q72627	HUWE1_HUMAN	E3 ubiquitin-protein ligase HUWE1 (EC 2.3.2.26) (ARF-binding protein 1) (ARF-BP1) (HECT, UBA and WWE domain-containing protein 1) (HECT-type E3 ubiquitin transferase HUWE1) (Homologous to E6AP carboxyl terminus homologous protein 9) (HectH9) (Large structure of UREB1) (LASU1) (Mcl-1 ubiquitin ligase E3) (Mule) (Upstream regulatory element-binding protein 1) (URE-B1) (URE-binding protein 1)	HUWE1
2538,30	2537,035	2539,573	2539,21	0,909	R.YPALHKPENQDIDWGALEGETR.E	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
2539,22	2537,947	2540,486	2539,21	0,003	R.YPALHKPENQDIDWGALEGETR.E	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
2540,20	2538,932	2541,472	2539,21	0,989	R.YPALHKPENQDIDWGALEGETR.E	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
2541,21 2542,25	2539,940 2540,976	2542,481 2543,519	2543,10	0,849	R.GMGHGYGGAGDASSFGHGPHVHMR.G	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNPH3
2543,26	2541,989	2544,532	2543,10	0,164	R.GMGHGYGGAGDASSFGHGPHVHMR.G	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNPH3
			2544,26	1,003	K.GLVEPVDVVDNADGTQTVNVYPSR.E	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
2544,27	2542,993	2545,538	2544,26	0,002	K.GLVEPVDVVDNADGTQTVNVYPSR.E	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			2543,10	1,169	R.GMGHGYGGAGDASSFGHGPHVHMR.G	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNPH3
2545,26	2543,990	2546,536	2544,26	0,999	K.GLVEPVDVVDNADGTQTVNVYPSR.E	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
2546,27 2547,27 2548,26 2549,26	2544,998 2545,996 2546,991 2547,989	2547,545 2548,544 2549,539 2550,538	2550,19	0,925	K.LCVVALDFEQEMATAASSSSLEK.S	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			2550,19	0,925	K.LCVVALDFEQEMATAASSSSLEK.S	Q658J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
2550,25	2548,974	2551,524	2550,19	0,061	K.LCVVALDFEQEMATAASSSSLEK.S	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			2550,19	0,061	K.LCVVALDFEQEMATAASSSSLEK.S	Q658J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			2551,24	0,990	R.VFTSSTISGGYAEYALAADHTVYK.L	Q08257	QOR_HUMAN	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-crystallin)	CRYZ
2551,24	2549,965	2552,516	2551,24	0,001	R.VFTSSTISGGYAEYALAADHTVYK.L	Q08257	QOR_HUMAN	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-crystallin)	CRYZ

			2550,19	1,052	K.LCYVALDFEQEMATAASSSSLEK.S	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			2550,19	1,052	K.LCYVALDFEQEMATAASSSSLEK.S	Q658J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
2552,24	2550,967	2553,519	2551,24	1,004	R.VFTSSTISGGYAEYALAADHTVYK.L	Q08257	QOR_HUMAN	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-crystallin)	CRYZ
2553,21 2554,19 2555,20 2556,22	2551,929 2552,914 2553,919 2554,939	2554,482 2555,468 2556,474 2557,495	2557,27	1,053	K.TEAASDPQHPPAASEGAAAAASPILLR.C	Q99536	VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog (EC 1.-. VAT1 -.)	
2557,23	2555,955	2558,512	2557,27	0,036	K.TEAASDPQHPPAASEGAAAAASPILLR.C	Q99536	VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog (EC 1.-. VAT1 -.)	
2558,25	2556,968	2559,526	2559,09	0,843	R.GMGGHGYGGAGDASSGFHGGHFVHMR.G	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNP3
			2557,27	0,977	K.TEAASDPQHPPAASEGAAAAASPILLR.C	Q99536	VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog (EC 1.-. VAT1 -.)	
2559,26	2557,982	2560,541	2559,09	0,172	R.GMGGHGYGGAGDASSGFHGGHFVHMR.G	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNP3
			2560,25	0,985	K.LVQDVANNTNEEAGDGTATTATVLAR.S	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
2560,24	2558,963	2561,524	2560,25	0,003	K.LVQDVANNTNEEAGDGTATTATVLAR.S	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
			2561,17	0,929	K.GSFTFYAPSN-EAWDNLSDIR.R.G	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
			2561,25	1,011	R.VANILHDDCAFLSAGDVSFKPER.Y	Q9B526	ERP44_HUMAN	Endoplasmic reticulum resident protein 44 (ER protein 44) (ERp44) (Thioredoxin domain-containing protein 4)	ERP44
			2559,09	1,154	R.GMGGHGYGGAGDASSGFHGGHFVHMR.G	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNP3
2561,26	2559,981	2562,542	2561,25	0,007	R.VANILHDDCAFLSAGDVSFKPER.Y	Q9B526	ERP44_HUMAN	Endoplasmic reticulum resident protein 44 (ER protein 44) (ERp44) (Thioredoxin domain-containing protein 4)	ERP44
			2561,17	0,089	K.GSFTFYAPSN-EAWDNLSDIR.R.G	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
			2560,25	1,015	K.LVQDVANNTNEEAGDGTATTATVLAR.S	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
2562,23	2560,949	2563,511	2561,25	0,976	R.VANILHDDCAFLSAGDVSFKPER.Y	Q9B526	ERP44_HUMAN	Endoplasmic reticulum resident protein 44 (ER protein 44) (ERp44) (Thioredoxin domain-containing protein 4)	ERP44
			2561,17	1,058	K.GSFTFYAPSN-EAWDNLSDIR.R.G	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
2563,26 2565,26	2561,974 2563,975	2564,537 2566,540	2566,20	0,939	K.LCYVALDFEQEMATAASSSSLEK.S	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			2566,20	0,939	K.LCYVALDFEQEMATAASSSSLEK.S	Q658J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
2566,25	2564,967	2567,534	2566,20	0,054	K.LCYVALDFEQEMATAASSSSLEK.S	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			2566,20	0,054	K.LCYVALDFEQEMATAASSSSLEK.S	Q658J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
2567,24	2565,960	2568,527	2566,20	1,047	K.LCYVALDFEQEMATAASSSSLEK.S	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB
			2566,20	1,047	K.LCYVALDFEQEMATAASSSSLEK.S	Q658J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			2568,31	1,063	R.SEPTQALELTEDDIKEDGIVPLR.Y	Q43396	TXNL1_HUMAN	Thioredoxin-like protein 1 (32 kDa thioredoxin-related protein)	TXNL1
2568,28	2567,000	2569,569	2568,31	0,022	R.SEPTQALELTEDDIKEDGIVPLR.Y	Q43396	TXNL1_HUMAN	Thioredoxin-like protein 1 (32 kDa thioredoxin-related protein)	TXNL1
2569,25	2567,967	2570,537	2568,31	0,945	R.SEPTQALELTEDDIKEDGIVPLR.Y	Q43396	TXNL1_HUMAN	Thioredoxin-like protein 1 (32 kDa thioredoxin-related protein)	TXNL1
2570,27 2571,27 2572,27 2573,23 2574,23	2568,986 2569,986 2570,987 2571,946 2572,945	2571,557 2572,557 2573,559 2574,519 2575,519	2575,33	1,095	K.TFSHELSDFGLESTAGEIPVVAIR.T	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	
2575,24	2573,955	2576,530	2575,33	0,085	K.TFSHELSDFGLESTAGEIPVVAIR.T	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	
2576,29	2575,001	2577,577	2575,33	0,962	K.TFSHELSDFGLESTAGEIPVVAIR.T	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	
2577,32	2576,027	2578,604							

[illegible]

2607,30	2605,998	2608,605	2608,24 2606,19	0,942 1,113	R.SQENPSPKDLFVPACLETGEYAR.L R.QQSHFAMMHGGTGFAGIDSSSEPVK.G	P01266 Q15365	THYG_HUMAN PCBP1_HUMAN	Thyroglobulin (Tg) Poly(rC)-binding protein 1 (Alpha-CP1) (Heterogeneous nuclear ribonucleoprotein E1) (hnRNP E1) (Nucleic acid-binding protein SUB2.3)	TG PCBP1
2608,30	2606,995	2609,603	2608,24	0,055	R.SQENPSPKDLFVPACLETGEYAR.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2609,29	2607,981	2610,591	2608,24	1,042	R.SQENPSPKDLFVPACLETGEYAR.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2610,28	2608,975	2611,586	2611,35	1,074	K.VIHDNFGIVEGLMTTVTHAITATQK.T	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine 5-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
2611,28	2609,977	2612,588	2611,35	0,072	K.VIHDNFGIVEGLMTTVTHAITATQK.T	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine 5-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
			2612,29	1,010	R.NQINALTsfVDASmVYGSEELAR.N	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
2612,28	2610,978	2613,590	2612,29	0,009	R.NQINALTsfVDASmVYGSEELAR.N	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
			2611,35	0,929	K.VIHDNFGIVEGLMTTVTHAITATQK.T	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine 5-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
2613,32	2612,010	2614,623	2612,29	1,024	R.NQINALTsfVDASmVYGSEELAR.N	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
2614,30	2612,998	2615,612							
2617,32	2616,012	2618,629	2616,28	1,041	K.SLTPLEGTDQDTFTNFQVYLWK.D	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2618,32	2617,009	2619,627							
2619,33	2618,022	2620,642	2620,12	0,786	K.FGFCPMAAHEEICTTNEGVMYR.I	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anstellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
2623,34	2622,025	2624,648	2622,34	0,997	R.LTGPGLSEGEPSISVMVTGGPWPTR.L	Q8WU39	MZB1_HUMAN	Marginal zone B- and B1-cell-specific protein (Mesenteric estrogen-dependent adipose 7) (MEDA-7) (Plasma cell-induced resident endoplasmic reticulum protein) (Plasma cell-induced resident ER protein) (pERp1) (Proapoptotic caspase adapter protein)	MZB1
2625,32	2624,011	2626,636	2626,16	0,834	R.EGGHIVYDQLPTPSSPDESENQAR.V	P78540	ARGI2_HUMAN	Arginase-2, mitochondrial (EC 3.5.3.1) (Arginase II) (Kidney- ARG2 type arginase) (Non-hepatic arginase) (Type II arginase)	
2626,32	2625,011	2627,638	2626,16	0,167	R.EGGHIVYDQLPTPSSPDESENQAR.V	P78540	ARGI2_HUMAN	Arginase-2, mitochondrial (EC 3.5.3.1) (Arginase II) (Kidney- ARG2 type arginase) (Non-hepatic arginase) (Type II arginase)	
2628,31	2626,996	2629,624	2628,11	0,205	R.EDGNEEDKENQGDETQGGQPPQR.R	P67809	YBOX1_HUMAN	Nuclease-sensitive element-binding protein 1 (CCAAT-binding transcription factor I subunit A) (CBF-A) (DNA-binding protein B) (DBPB) (Enhancer factor I subunit A) (EFI-A) (Y-box transcription factor) (Y-box-binding protein 1) (YB-1)	YBX1
2629,32	2628,005	2630,635	2628,11	1,215	R.EDGNEEDKENQGDETQGGQPPQR.R	P67809	YBOX1_HUMAN	Nuclease-sensitive element-binding protein 1 (CCAAT-binding transcription factor I subunit A) (CBF-A) (DNA-binding protein B) (DBPB) (Enhancer factor I subunit A) (EFI-A) (Y-box transcription factor) (Y-box-binding protein 1) (YB-1)	YBX1
2636,34	2635,018	2637,655	2636,21	0,128	K.AAEAAAAAESAAPAAGEEPSKEEGEPK.K	P80723	BASP1_HUMAN	Brain acid soluble protein 1 (22 kDa neuronal tissue-enriched acidic protein) (Neuronal axonal membrane protein NAP-22)	BASP1
			2637,20	0,865	R.DGEDQTQDTELVEPTRPAGDGTfQK.W	P16190	1A33_HUMAN	HLA class I histocompatibility antigen, A-33 alpha chain (Aw-19) (Aw-33) (MHC class I antigen A*33)	HLA-A
			2637,20	0,865	R.DGEDQTQDTELVEPTRPAGDGTfQK.W	P30508	1C12_HUMAN	HLA class I histocompatibility antigen, Cw-12 alpha chain (MHC class I antigen Cw*12)	HLA-C
2637,32	2635,998	2638,636	2637,20	0,116	R.DGEDQTQDTELVEPTRPAGDGTfQK.W	P16190	1A33_HUMAN	HLA class I histocompatibility antigen, A-33 alpha chain (Aw-19) (Aw-33) (MHC class I antigen A*33)	HLA-A
			2637,20	0,116	R.DGEDQTQDTELVEPTRPAGDGTfQK.W	P30508	1C12_HUMAN	HLA class I histocompatibility antigen, Cw-12 alpha chain (MHC class I antigen Cw*12)	HLA-C
			2636,21	1,109	K.AAEAAAAAESAAPAAGEEPSKEEGEPK.K	P80723	BASP1_HUMAN	Brain acid soluble protein 1 (22 kDa neuronal tissue-enriched acidic protein) (Neuronal axonal membrane protein NAP-22)	BASP1
2638,33	2637,014	2639,653	2637,20	1,132	R.DGEDQTQDTELVEPTRPAGDGTfQK.W	P16190	1A33_HUMAN	HLA class I histocompatibility antigen, A-33 alpha chain (Aw-19) (Aw-33) (MHC class I antigen A*33)	HLA-A
			2637,20	1,132	R.DGEDQTQDTELVEPTRPAGDGTfQK.W	P30508	1C12_HUMAN	HLA class I histocompatibility antigen, Cw-12 alpha chain (MHC class I antigen Cw*12)	HLA-C
2639,33	2638,006	2640,646							
2640,33	2639,006	2641,646							
2641,32	2639,997	2642,639							
2642,30	2640,983	2643,625							
2643,31	2641,986	2644,629	2644,34	1,035	R.TSQENISFETMYDLVSTKPVLNK.L	Q13510	ASAH1_HUMAN	Acid ceramidase (AC) (ACDase) (Acid CDase) (EC 3.5.1.23) (Acylsphingosine deacylase) (N-acylethanolamine hydrolase ASAH1) (EC 3.5.1.-) (N-acylsphingosine amidohydrolase) (Putative 32 kDa heart protein) (PHP32) [Cleaved into: Acid ceramidase subunit alpha; Acid ceramidase subunit beta]	ASAH1
2644,32	2642,996	2645,640	2644,34	0,025	R.TSQENISFETMYDLVSTKPVLNK.L	Q13510	ASAH1_HUMAN	Acid ceramidase (AC) (ACDase) (Acid CDase) (EC 3.5.1.23) (Acylsphingosine deacylase) (N-acylethanolamine hydrolase ASAH1) (EC 3.5.1.-) (N-acylsphingosine amidohydrolase) (Putative 32 kDa heart protein) (PHP32) [Cleaved into: Acid ceramidase subunit alpha; Acid ceramidase subunit beta]	ASAH1
2645,33	2644,012	2646,657	2644,34	0,992	R.TSQENISFETMYDLVSTKPVLNK.L	Q13510	ASAH1_HUMAN	Acid ceramidase (AC) (ACDase) (Acid CDase) (EC 3.5.1.23) (Acylsphingosine deacylase) (N-acylethanolamine hydrolase ASAH1) (EC 3.5.1.-) (N-acylsphingosine amidohydrolase) (Putative 32 kDa heart protein) (PHP32) [Cleaved into: Acid ceramidase subunit alpha; Acid ceramidase subunit beta]	ASAH1
2646,34	2645,015	2647,662							

2648,33	2647,007	2649,655							
2649,32	2647,998	2650,647							
2651,34	2650,016	2652,667	2651,20	0,138	R.TCLHYLGEFGEDQIYEAHQQR.G	Q8WU39	MZB1_HUMAN	Marginal zone B- and B1-cell-specific protein (Mesenteric estrogen-dependent adipose 7) (MEDA-7) (Plasma cell-induced resident endoplasmic reticulum protein) (Plasma cell-induced resident ER protein) (pERp1) (Proapoptotic caspase adapter protein)	MZB1
2655,31	2653,981	2656,636							
2656,31	2654,984	2657,641							
2658,30	2656,968	2659,627							
2659,29	2657,962	2660,621							
2660,30	2658,965	2661,626							
2660,39	2659,056	2661,717							
2661,44	2660,112	2662,773							
2662,68	2661,353	2664,015							
2664,30	2662,972	2665,636							
2665,29	2663,962	2666,627							
2666,30	2664,972	2667,638							
2667,33	2665,997	2668,664							
2668,36	2667,022	2669,690	2669,21	0,853	R.VEAAATWYYSLEHSTDDYASF.SR.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2670,31	2668,971	2671,641	2671,09	0,783	R.NGDYQAVQCQTEGPCWCVDAQGK.E	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2669,21	1,097	R.VEAAATWYYSLEHSTDDYASF.SR.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2671,32	2669,982	2672,653	2671,09	0,228	R.NGDYQAVQCQTEGPCWCVDAQGK.E	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2672,33	2670,990	2673,662	2671,09	1,237	R.NGDYQAVQCQTEGPCWCVDAQGK.E	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2673,31	2671,970	2674,643	2674,40	1,092	K.YILGNPLTPGVGTQGPQIDKEQYDK.I	P00352	AL1A1_HUMAN	Retinal dehydrogenase 1 (RALDH 1) (RalDH1) (EC 1.2.1.-) (EC 1.2.1.36) (ALDH-E1) (ALHDII) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic)	ALDH1A1
2674,29	2672,957	2675,631	2674,40	0,105	K.YILGNPLTPGVGTQGPQIDKEQYDK.I	P00352	AL1A1_HUMAN	Retinal dehydrogenase 1 (RALDH 1) (RalDH1) (EC 1.2.1.-) (EC 1.2.1.36) (ALDH-E1) (ALHDII) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic)	ALDH1A1
			2675,30	1,006	R.SGEVYTCQVEHPSLTSPLTVEWR.A	P13760	2B14_HUMAN	HLA class II histocompatibility antigen, DRB1-4 beta chain (MHC class II antigen DRB1*4) (DR-4) (DR4)	HLA-DRB1
2675,28	2673,946	2676,621	2675,30	0,017	R.SGEVYTCQVEHPSLTSPLTVEWR.A	P13760	2B14_HUMAN	HLA class II histocompatibility antigen, DRB1-4 beta chain (MHC class II antigen DRB1*4) (DR-4) (DR4)	HLA-DRB1
			2674,40	0,885	K.YILGNPLTPGVGTQGPQIDKEQYDK.I	P00352	AL1A1_HUMAN	Retinal dehydrogenase 1 (RALDH 1) (RalDH1) (EC 1.2.1.-) (EC 1.2.1.36) (ALDH-E1) (ALHDII) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic)	ALDH1A1
2675,71	2674,372	2677,047	2675,30	0,409	R.SGEVYTCQVEHPSLTSPLTVEWR.A	P13760	2B14_HUMAN	HLA class II histocompatibility antigen, DRB1-4 beta chain (MHC class II antigen DRB1*4) (DR-4) (DR4)	HLA-DRB1
			2674,40	1,311	K.YILGNPLTPGVGTQGPQIDKEQYDK.I	P00352	AL1A1_HUMAN	Retinal dehydrogenase 1 (RALDH 1) (RalDH1) (EC 1.2.1.-) (EC 1.2.1.36) (ALDH-E1) (ALHDII) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic)	ALDH1A1
2676,29	2674,951	2677,628	2675,30	0,989	R.SGEVYTCQVEHPSLTSPLTVEWR.A	P13760	2B14_HUMAN	HLA class II histocompatibility antigen, DRB1-4 beta chain (MHC class II antigen DRB1*4) (DR-4) (DR4)	HLA-DRB1
2676,43	2675,089	2677,765	2675,30	1,127	R.SGEVYTCQVEHPSLTSPLTVEWR.A	P13760	2B14_HUMAN	HLA class II histocompatibility antigen, DRB1-4 beta chain (MHC class II antigen DRB1*4) (DR-4) (DR4)	HLA-DRB1
2677,43	2676,092	2678,769							
2678,39	2677,048	2679,726							
2679,29	2677,953	2680,632	2680,30	1,005	R.YVSHFETEGPHVLLYFDSVPTS.R.E	POCOL5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
2679,78	2678,436	2681,116	2680,30	0,521	R.YVSHFETEGPHVLLYFDSVPTS.R.E	POCOL5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
2680,48	2679,144	2681,824	2680,30	0,187	R.YVSHFETEGPHVLLYFDSVPTS.R.E	POCOL5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
2681,29	2679,951	2682,633	2680,30	0,995	R.YVSHFETEGPHVLLYFDSVPTS.R.E	POCOL5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
2681,73	2680,393	2683,075							
2682,30	2680,957	2683,639	2683,34	1,039	K.IHVSQELQSANASVDDSRLEELK.A	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A1S9) (Ubiquitin-activating enzyme E1)	UBA1
2683,30	2681,957	2684,641	2683,34	0,038	K.IHVSQELQSANASVDDSRLEELK.A	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A1S9) (Ubiquitin-activating enzyme E1)	UBA1
2684,34	2682,994	2685,679	2683,34	1,000	K.IHVSQELQSANASVDDSRLEELK.A	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A1S9) (Ubiquitin-activating enzyme E1)	UBA1
2687,28	2685,940	2688,628	2686,39	0,889	R.LEQQVPVNVQVFGQDEMIDVIGVTK.G	P39023	RL3_HUMAN	60S ribosomal protein L3 (HIV-1 TAR RNA-binding protein B) (TARBP-B) (Large ribosomal subunit protein uL3)	RPL3
2688,28	2686,941	2689,629	2689,34	1,059	R.EIGNLHPSVPISNDEVDNKNVER.I	P49591	SYSC_HUMAN	Serine--tRNA ligase, cytoplasmic (EC 6.1.1.11) (Seryl-tRNA synthetase) (SerRS) (Seryl-tRNA(Ser/Sec) synthetase)	SARS
			2689,41	1,120	R.LPPGEYVVVPTSTFEPNKEGDFVLR.F	P07384	CAN1_HUMAN	Calpain-1 catalytic subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase 1) (CANP 1) (Calpain mu-type) (Calpain-1 large subunit) (Cell proliferation-inducing gene 30 protein) (Micromolar-calpain) (muCANP)	CAPN1

2689,29	2687,949	2690,638	2689,34	0,051	R.EIGNLLHPSVPISNDEDDVDNKVER.I	P49591	SYSC_HUMAN	Serine--tRNA ligase, cytoplasmic (EC 6.1.1.11) (Seryl-tRNA synthetase) (SerRS) (Seryl-tRNA(Ser/Sec) synthetase)	SARS
			2689,41	0,112	R.LPPGEYVVVPSTFEPNKEGDFVLR.F	P07384	CAN1_HUMAN	Calpain-1 catalytic subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase 1) (CANP 1) (Calpain mu-type) (Calpain-1 large subunit) (Cell proliferation-inducing gene 30 protein) (Micromolar-calpain) (muCANP)	CAPN1
2690,31	2688,964	2691,654	2689,41	0,904	R.LPPGEYVVVPSTFEPNKEGDFVLR.F	P07384	CAN1_HUMAN	Calpain-1 catalytic subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase 1) (CANP 1) (Calpain mu-type) (Calpain-1 large subunit) (Cell proliferation-inducing gene 30 protein) (Micromolar-calpain) (muCANP)	CAPN1
			2689,34	0,965	R.EIGNLLHPSVPISNDEDDVDNKVER.I	P49591	SYSC_HUMAN	Serine--tRNA ligase, cytoplasmic (EC 6.1.1.11) (Seryl-tRNA synthetase) (SerRS) (Seryl-tRNA(Ser/Sec) synthetase)	SARS
2691,31	2689,965	2692,656							
2691,88	2690,530	2693,221							
2692,37	2691,020	2693,712							
2693,36	2692,018	2694,711							
2694,45	2693,103	2695,798							
2695,32	2693,969	2696,664							
2696,29	2694,937	2697,634							
2697,28	2695,930	2698,628							
2697,28	2695,930	2698,628							
2697,73	2696,379	2699,077							
2698,68	2697,327	2700,026							
2700,31	2698,963	2701,663							
2701,32	2699,969	2702,671	2702,28	0,957	K.YIYDQCFAVAGYGPIEQLPDYNRI	P31930	QCR1_HUMAN	Cytochrome b-c1 complex subunit 1, mitochondrial (Complex III subunit 1) (Core protein I) (Ubiquinol-cytochrome-c reductase complex core protein 1)	UQCRC1
2703,30	2701,943	2704,647	2702,28	1,018	K.YIYDQCFAVAGYGPIEQLPDYNRI	P31930	QCR1_HUMAN	Cytochrome b-c1 complex subunit 1, mitochondrial (Complex III subunit 1) (Core protein I) (Ubiquinol-cytochrome-c reductase complex core protein 1)	UQCRC1
2704,29	2702,943	2705,647							
2705,30	2703,945	2706,650							
2706,28	2704,925	2707,632	2707,19	0,912	K.SSSSVTTSETQPCTPSSSDYDLQR.V	P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP)	VASP
2706,29	2704,938	2707,645	2707,19	0,899	K.SSSSVTTSETQPCTPSSSDYDLQR.V	P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP)	VASP
2707,28	2705,929	2708,636	2707,19	0,092	K.SSSSVTTSETQPCTPSSSDYDLQR.V	P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP)	VASP
2707,30	2705,944	2708,651	2707,19	0,107	K.SSSSVTTSETQPCTPSSSDYDLQR.V	P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP)	VASP
2708,29	2706,933	2709,641	2707,19	1,096	K.SSSSVTTSETQPCTPSSSDYDLQR.V	P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP)	VASP
2708,33	2706,977	2709,685	2707,19	1,140	K.SSSSVTTSETQPCTPSSSDYDLQR.V	P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP)	VASP
2709,37	2708,012	2710,721							
2710,29	2708,939	2711,649							
2711,29	2709,934	2712,646							
2711,89	2710,536	2713,248							
2712,28	2710,921	2713,634							
2712,80	2711,449	2714,161							
2713,91	2712,552	2715,266							
2715,29	2713,935	2716,651	2716,30	1,010	R.LVDEPGHCADFHPSGTVVAIGHSGR.W	Q9HC35	EMAL4_HUMAN	Echinoderm microtubule-associated protein-like 4 (EMAP-4) (Restrictedly overexpressed proliferation-associated protein) (Ropp 120)	EML4
2716,33	2714,971	2717,687	2716,30	0,026	R.LVDEPGHCADFHPSGTVVAIGHSGR.W	Q9HC35	EMAL4_HUMAN	Echinoderm microtubule-associated protein-like 4 (EMAP-4) (Restrictedly overexpressed proliferation-associated protein) (Ropp 120)	EML4
2717,34	2715,986	2718,703	2718,38	1,034	R.KPQVLPHSHVEEDTPNSVHSIPR.S	P98095	FBLN2_HUMAN	Fibulin-2 (FBL-2)	FBLN2
			2716,30	1,042	R.LVDEPGHCADFHPSGTVVAIGHSGR.W	Q9HC35	EMAL4_HUMAN	Echinoderm microtubule-associated protein-like 4 (EMAP-4) (Restrictedly overexpressed proliferation-associated protein) (Ropp 120)	EML4
2719,30	2717,944	2720,663	2719,33	0,024	R.LLDSLEPPGEPGPSTNIPENDTVDGR.E	Q92734	TFG_HUMAN	Protein TFG (TRK-fused gene protein)	TFG
			2718,38	0,926	R.KPQVLPHSHVEEDTPNSVHSIPR.S	P98095	FBLN2_HUMAN	Fibulin-2 (FBL-2)	FBLN2
2720,30	2718,943	2721,663	2719,33	0,975	R.LLDSLEPPGEPGPSTNIPENDTVDGR.E	Q92734	TFG_HUMAN	Protein TFG (TRK-fused gene protein)	TFG
2721,29	2719,932	2722,653							
2722,31	2720,950	2723,673							
2723,31	2721,953	2724,677	2724,37	1,058	K.EKPYFPIPEEYTHQNVPLEDR.V	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) [Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
2727,31	2725,944	2728,671							
2728,34	2726,972	2729,700							
2729,35	2727,982	2730,712							
2730,32	2728,950	2731,680							
2731,33	2729,967	2732,698							
2743,30	2741,933	2744,676							
2744,31	2742,934	2745,679							
2745,32	2743,944	2746,689							
2750,33	2748,957	2751,708	2750,31	0,021	K.AYHEQLSVAEITNACFEPANQMVK.C	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			2750,31	0,021	K.AYHEQLSVAEITNACFEPANQMVK.C	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A
			2750,31	0,021	K.AYHEQLSVAEITNACFEPANQMVK.C	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2751,34	1,012	K.VSPETVDSVIMGNVLQSSSDAIYLAR.H	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2
2751,34	2749,965	2752,717	2751,34	0,003	K.VSPETVDSVIMGNVLQSSSDAIYLAR.H	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2
			2750,31	1,029	K.AYHEQLSVAEITNACFEPANQMVK.C	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain) [Cleaved into: Detyrosinated tubulin alpha-1A chain]	TUBA1A
			2750,31	1,029	K.AYHEQLSVAEITNACFEPANQMVK.C	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	TUBA4A

			2750,31	1,029	K.AYHEQLSVAEITNACFEPANQMVK.C	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2752,46	1,119	K.AFLADPSAFVAAAPVAAATAAPAAAAAPAK.V	P05388	RLA0_HUMAN	60S acidic ribosomal protein P0 (60S ribosomal protein L10E) (Large ribosomal subunit protein uL10)	RPLP0
2762,41	2761,024	2763,787	2763,35	0,949	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
2763,41	2762,033	2764,796	2763,35	0,060	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
2764,41	2763,029	2765,794	2765,31	0,903	R.APLTATAPQLDDEEMYSAHMPAHLR.C	Q8WU39	MZB1_HUMAN	Marginal zone B- and B1-cell-specific protein (Mesenteric estrogen-dependent adipose 7) (MEDA-7) (Plasma cell-induced resident endoplasmic reticulum protein) (Plasma cell-induced resident ER protein) (pERp1) (Proapoptotic caspase adapter protein)	MZB1
			2763,35	1,057	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
2765,40	2764,016	2766,781	2765,31	0,084	R.APLTATAPQLDDEEMYSAHMPAHLR.C	Q8WU39	MZB1_HUMAN	Marginal zone B- and B1-cell-specific protein (Mesenteric estrogen-dependent adipose 7) (MEDA-7) (Plasma cell-induced resident endoplasmic reticulum protein) (Plasma cell-induced resident ER protein) (pERp1) (Proapoptotic caspase adapter protein)	MZB1
			2766,00	0,600	R.MDACCSCVGAAGWTECEECPEMR.N	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
2777,40	2776,011	2778,788	2778,32	0,925	R.STQDVTIALDALSAYWIASHTTEER.G	P0C0L5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and P2P-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
			2778,37	0,975	R.LVRPEVDVMCTAFHDNEETFLKK.Y	P02768	ALBU_HUMAN	Serum albumin	ALB
2778,41	2777,016	2779,795	2778,37	0,031	R.LVRPEVDVMCTAFHDNEETFLKK.Y	P02768	ALBU_HUMAN	Serum albumin	ALB
			2778,32	0,081	R.STQDVTIALDALSAYWIASHTTEER.G	P0C0L5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and P2P-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
2798,40	2796,999	2799,797	2798,33	0,068	R.SGPFQGI FRPDNFVFGQSGAGNNWAK.G	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			2798,33	0,068	R.SGPFQGI FRPDNFVFGQSGAGNNWAK.G	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			2799,50	1,105	K.GLKPGVVYEGQLSIQIQYGHQEVTR.F	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
2799,41	2798,008	2800,808	2799,50	0,095	K.GLKPGVVYEGQLSIQIQYGHQEVTR.F	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			2798,33	1,078	R.SGPFQGI FRPDNFVFGQSGAGNNWAK.G	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			2798,33	1,078	R.SGPFQGI FRPDNFVFGQSGAGNNWAK.G	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
2800,41	2799,009	2801,810	2801,26	0,854	R.WQQGNVFCSCVMHEALHNHYTQK.S	P01859	IGHG2_HUMAN	Immunoglobulin heavy constant gamma 2 (Ig gamma-2 chain C region) (Ig gamma-2 chain C region DOT) (Ig gamma-2 chain C region TIL) (Ig gamma-2 chain C region ZIE)	IGHG2
			2801,26	0,854	R.WQQGNVFCSCVMHEALHNHYTQK.S	P01857	IGHG1_HUMAN	Immunoglobulin heavy constant gamma 1 (Ig gamma-1 chain C region) (Ig gamma-1 chain C region EU) (Ig gamma-1 chain C region KOL) (Ig gamma-1 chain C region NIE)	IGHG1
			2799,50	0,907	K.GLKPGVVYEGQLSIQIQYGHQEVTR.F	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
2801,41	2800,013	2802,815	2801,26	0,151	R.WQQGNVFCSCVMHEALHNHYTQK.S	P01859	IGHG2_HUMAN	Immunoglobulin heavy constant gamma 2 (Ig gamma-2 chain C region) (Ig gamma-2 chain C region DOT) (Ig gamma-2 chain C region TIL) (Ig gamma-2 chain C region ZIE)	IGHG2
			2801,26	0,151	R.WQQGNVFCSCVMHEALHNHYTQK.S	P01857	IGHG1_HUMAN	Immunoglobulin heavy constant gamma 1 (Ig gamma-1 chain C region) (Ig gamma-1 chain C region EU) (Ig gamma-1 chain C region KOL) (Ig gamma-1 chain C region NIE)	IGHG1
2803,48	2802,075	2804,879							
2832,42	2831,006	2833,838							
2833,41	2831,995	2834,828							
2833,41	2831,995	2834,828							
2834,41	2832,997	2835,831							
2835,42	2833,999	2836,835							
2836,43	2835,009	2837,846							
2837,43	2836,009	2838,846							
2846,45	2845,030	2847,877	2846,33	0,128	R.EPTSSEQGGLSGSAAAGEGKPALEEER.Q	Q04323	UBXN1_HUMAN	UBX domain-containing protein 1 (SAPK substrate protein 1) (UBA/UBX 33.3 kDa protein)	UBXN1
2847,45	2846,030	2848,877	2848,32	0,865	K.SEPVKEESSELEQPFQAQDTSSVGPDR.K	Q15424	SAFB1_HUMAN	Scaffold attachment factor B1 (SAF-B) (SAF-B1) (HSP27 estrogen response element-TATA box-binding protein) (HSP27 ERE-TATA-binding protein)	SAFB
			2846,33	1,127	R.EPTSSEQGGLSGSAAAGEGKPALEEER.Q	Q04323	UBXN1_HUMAN	UBX domain-containing protein 1 (SAPK substrate protein 1) (UBA/UBX 33.3 kDa protein)	UBXN1
2848,47	2847,045	2849,893	2848,32	0,150	K.SEPVKEESSELEQPFQAQDTSSVGPDR.K	Q15424	SAFB1_HUMAN	Scaffold attachment factor B1 (SAF-B) (SAF-B1) (HSP27 estrogen response element-TATA box-binding protein) (HSP27 ERE-TATA-binding protein)	SAFB
2849,46	2848,036	2850,885	2848,32	1,142	K.SEPVKEESSELEQPFQAQDTSSVGPDR.K	Q15424	SAFB1_HUMAN	Scaffold attachment factor B1 (SAF-B) (SAF-B1) (HSP27 estrogen response element-TATA box-binding protein) (HSP27 ERE-TATA-binding protein)	SAFB
2850,61	2849,187	2852,037							
2851,60	2850,178	2853,030							
2852,61	2851,186	2854,039							
2853,46	2852,037	2854,891							
2854,45	2853,024	2855,878							
2855,44	2854,010	2856,865							
2856,44	2855,008	2857,864							
2857,43	2855,997	2858,854							
2858,45	2857,022	2859,880							
2865,49	2864,053	2866,919							
2866,49	2865,052	2867,918							
2867,49	2866,053	2868,920							
2868,49	2867,056	2869,925							

2869,50	2868,062	2870,931	2873,31	0,845	R.VPFDAATLHTSTAMAAQHGMDDDDGTGQK.Q P06396	GELS_HUMAN	Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF) (Brevin)	GSN
2870,48	2869,046	2871,916						
2871,50	2870,061	2872,933						
2872,47	2871,032	2873,905						
2873,47	2872,028	2874,902	2873,31	0,151	R.VPFDAATLHTSTAMAAQHGMDDDDGTGQK.Q P06396	GELS_HUMAN	Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF) (Brevin)	GSN
2874,46	2873,021	2875,896	2873,31	1,145	R.VPFDAATLHTSTAMAAQHGMDDDDGTGQK.Q P06396	GELS_HUMAN	Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF) (Brevin)	GSN
2875,45	2874,009	2876,884	2880,29	0,829	R.SPEGPREEEAAGGEEESPDSPPHGEASR.G Q96NY7	CLIC6_HUMAN	Chloride intracellular channel protein 6 (Parchorin)	CLIC6
2876,44	2874,999	2877,875						
2877,43	2875,996	2878,873						
2878,44	2877,002	2879,881						
2879,46	2878,025	2880,904	2880,29	0,182	R.SPEGPREEEAAGGEEESPDSPPHGEASR.G Q96NY7	CLIC6_HUMAN	Chloride intracellular channel protein 6 (Parchorin)	CLIC6
2880,48	2879,036	2881,916	2880,29	1,193	R.SPEGPREEEAAGGEEESPDSPPHGEASR.G Q96NY7	CLIC6_HUMAN	Chloride intracellular channel protein 6 (Parchorin)	CLIC6
2881,49	2880,046	2882,927	2880,29	0,813	K.NDQDTWDYTNPNLSGQGDGPGSNPNKR.Q P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
2882,48	2881,042	2883,925	2890,29	1,182	K.NDQDTWDYTNPNLSGQGDGPGSNPNKR.Q P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
2883,49	2882,047	2884,931						
2884,49	2883,050	2885,935						
2885,49	2884,047	2886,932						
2886,49	2885,047	2887,933	2908,35	0,118	K.MGQAVPAPTGAPPGGQPDYSAAWAEYYR.Q Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1) (DNA helicase V) (hDH V)	FUBP1
2887,49	2886,046	2888,934						
2888,49	2887,046	2889,934						
2889,48	2888,035	2890,924						
2891,47	2890,029	2892,920	2890,29	1,118	K.MGQAVPAPTGAPPGGQPDYSAAWAEYYR.Q Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1) (DNA helicase V) (hDH V)	FUBP1
2892,47	2891,027	2893,919	2915,52	0,066	K.VSDSISAQYPVVDHEFDVAVVGAGGAGLR.A P31040	SDHA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) (Flavoprotein subunit of complex II) (Fp)	SDHA
2893,48	2892,030	2894,924						
2894,51	2893,060	2895,954						
2895,49	2894,041	2896,937						
2896,47	2895,017	2897,914	2915,52	1,107	K.VSDSISAQYPVVDHEFDVAVVGAGGAGLR.A P31040	SDHA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) (Flavoprotein subunit of complex II) (Fp)	SDHA
2897,45	2896,004	2898,901						
2908,47	2907,018	2909,926						
2909,47	2908,017	2910,926						
2915,59	2914,130	2917,046	2915,52	0,066	K.VSDSISAQYPVVDHEFDVAVVGAGGAGLR.A P31040	SDHA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) (Flavoprotein subunit of complex II) (Fp)	SDHA
2916,63	2915,171	2918,087	2915,52	1,107	K.VSDSISAQYPVVDHEFDVAVVGAGGAGLR.A P31040	SDHA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) (Flavoprotein subunit of complex II) (Fp)	SDHA
2917,63	2916,169	2919,086	2974,38	0,828	K.SHCIAEVENDEMPADLPSLADFVESK.D P02768	ALBU_HUMAN	Serum albumin	ALB
2918,58	2917,122	2920,041						
2934,58	2933,110	2936,045						
2935,57	2934,102	2937,037						
2936,57	2935,104	2938,041	2981,24	0,649	K.TDNAGDQHGSGGGGGGAGAGGGGGG P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
2937,58	2936,111	2939,048						
2950,56	2949,080	2952,030						
2951,55	2950,075	2953,027						
2952,53	2951,059	2954,011	2981,24	0,274	K.TDNAGDQHGSGGGGGGAGAGGGGGG P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
2952,55	2951,078	2954,031						
2953,56	2952,088	2955,041						
2954,55	2953,077	2956,031						
2955,54	2954,059	2957,014	2981,24	1,296	K.TDNAGDQHGSGGGGGGAGAGGGGGG P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
2957,64	2956,160	2959,118						
2958,63	2957,148	2960,107						
2959,56	2958,079	2961,038						
2960,51	2959,029	2961,990	2992,41	0,188	K.VLDNYLTSPLPEEVDSETSADEGVSR.K O00299	CLIC1_HUMAN	Chloride intracellular channel protein 1 (Chloride channel ABP) (Nuclear chloride ion channel 27) (NCC27) (Regulatory nuclear chloride ion channel protein) (hRNCC)	CLIC1
2961,51	2960,031	2962,992						
2962,46	2960,982	2963,945						
2962,53	2961,053	2964,016						
2963,46	2961,983	2964,946	2991,50	1,098	R.MLLADQGQGSQKEEVVTWETWQESLK.A P09211	GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1)	GSTP1
2964,49	2963,012	2965,977						
2965,53	2964,044	2967,010						
2966,01	2964,526	2967,492						
2966,54	2965,060	2968,027	2996,47	1,077	R.ADHQPLTEASYVNLPTIALCNTDSPLR.Y P08865	RSSA_HUMAN	40S ribosomal protein SA (37 kDa laminin receptor precursor) (37LRP) (37/67 kDa laminin receptor) (LRP/LR) (67 kDa laminin receptor) (67LR) (Colon carcinoma laminin-binding protein) (Laminin receptor 1) (LamR) (Laminin-binding protein precursor p40) (LBP/p40) (Multidrug resistance-associated protein MGr1-Ag) (NEM/1CHD4) (Small ribosomal subunit protein uS2)	RPSA
2967,98	2966,497	2969,465						
2972,55	2971,068	2974,040						
2973,55	2972,063	2975,037						
2974,55	2973,058	2976,033	2974,38	0,168	K.SHCIAEVENDEMPADLPSLADFVESK.D P02768	ALBU_HUMAN	Serum albumin	ALB
2975,55	2974,067	2977,042	2974,38	1,177	K.SHCIAEVENDEMPADLPSLADFVESK.D P02768	ALBU_HUMAN	Serum albumin	ALB
2976,55	2975,058	2978,035	2981,24	0,649	K.TDNAGDQHGSGGGGGGAGAGGGGGG P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
2977,54	2976,053	2979,030						
2979,58	2978,091	2981,070						
2980,59	2979,097	2982,077						
2981,51	2980,019	2983,000	2981,24	0,274	K.TDNAGDQHGSGGGGGGAGAGGGGGG P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
2982,53	2981,041	2984,023	2981,24	1,296	K.TDNAGDQHGSGGGGGGAGAGGGGGG P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
2983,47	2981,974	2984,958	2992,41	0,188	K.VLDNYLTSPLPEEVDSETSADEGVSR.K O00299	CLIC1_HUMAN	Chloride intracellular channel protein 1 (Chloride channel ABP) (Nuclear chloride ion channel 27) (NCC27) (Regulatory nuclear chloride ion channel protein) (hRNCC)	CLIC1
2984,47	2982,982	2985,967						
2989,55	2988,054	2991,043						
2992,60	2991,104	2994,097						
2997,55	2996,047	2999,045	2996,47	1,077	R.ADHQPLTEASYVNLPTIALCNTDSPLR.Y P08865	RSSA_HUMAN	40S ribosomal protein SA (37 kDa laminin receptor precursor) (37LRP) (37/67 kDa laminin receptor) (LRP/LR) (67 kDa laminin receptor) (67LR) (Colon carcinoma laminin-binding protein) (Laminin receptor 1) (LamR) (Laminin-binding protein precursor p40) (LBP/p40) (Multidrug resistance-associated protein MGr1-Ag) (NEM/1CHD4) (Small ribosomal subunit protein uS2)	RPSA
			2996,45	1,095	K.VADALTNAAVHVDMPNALSALDHAHK.L P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2

[illegible]

Table S2.B. Hypothetical identity of molecular components detected by MSI; annotation with peptides identified in samples of cancer-containing lymph nodes; empty spaces in LC-MS/MS - related information denote no match found for a given MSI component.

MSI molecular component (m/z)	m/z tolerance - minimum	m/z tolerance - maximum	LC-MS/MS measured peptide m/z	Δ delta m/z	amino acid sequence	entry ID	entry name	protein name	primary gene name
699,45	699,102	699,802							
699,62	699,272	699,972							
699,87	699,518	700,218							
700,18	699,830	700,530							
700,38	700,028	700,728							
701,31	700,964	701,665							
701,40	701,052	701,753							
702,33	701,982	702,685							
702,40	702,052	702,754							
703,39	703,034	703,738							
704,39	704,042	704,747							
705,40	705,049	705,754							
706,39	706,035	706,741							
707,39	707,039	707,747							
708,33	707,974	708,683							
708,38	708,021	708,729							
709,34	708,983	709,693							
710,36	710,009	710,719							
711,42	711,069	711,781							
712,40	712,041	712,753							
713,42	713,065	713,779							
714,42	714,065	714,779							
715,42	715,063	715,778							
716,33	715,976	716,692							
716,44	716,079	716,795							
717,42	717,057	717,775							
718,38	718,017	718,735							
718,41	718,054	718,772							
719,41	719,046	719,765							
720,41	720,052	720,773							
721,42	721,062	721,784							
722,39	722,030	722,752							
723,37	723,010	723,733							
723,46	723,102	723,825							
724,36	724,001	724,725							
724,41	724,051	724,776							
725,42	725,061	725,786							
726,40	726,040	726,766							
727,42	727,061	727,788							
728,42	728,058	728,786							
729,43	729,065	729,795							
730,38	730,018	730,749							
731,40	731,030	731,761							
731,43	731,065	731,796							
731,72	731,356	732,088							
732,41	732,047	732,779							
733,18	732,815	733,549							
733,42	733,049	733,783							
733,42	733,055	733,788							
734,43	734,063	734,798							
735,31	734,942	735,677							
735,42	735,055	735,790							
735,60	735,235	735,971							
736,33	735,958	736,694							
736,42	736,048	736,784							
737,42	737,046	737,784							
737,79	737,418	738,156							
738,39	738,022	738,760							
739,38	739,009	739,748							
739,44	739,071	739,810							
740,40	740,033	740,773							
741,43	741,055	741,796							
742,38	742,012	742,754							
742,45	742,080	742,823							
743,46	743,088	743,832							
744,41	744,040	744,784							
745,44	745,071	745,816							
746,34	745,964	746,710							
746,42	746,051	746,797							
747,52	747,144	747,892							
748,42	748,048	748,797							
749,42	749,047	749,796							
750,42	750,042	750,792							
751,42	751,049	751,800							
752,40	752,020	752,772							
753,42	753,042	753,796							
754,42	754,048	754,802							
755,40	755,025	755,780							
755,53	755,155	755,910							
756,45	756,076	756,833							
757,43	757,054	757,812							
757,44	757,064	757,822							
758,41	758,034	758,792							
759,39	759,005	759,765							
759,45	759,069	759,829							
760,42	760,038	760,798							
761,41	761,032	761,793							
762,40	762,014	762,777							
763,51	763,130	763,894							
764,41	764,028	764,792							
764,45	764,070	764,835							
765,44	765,054	765,819							
766,42	766,039	766,805							
767,42	767,041	767,808							
768,35	767,965	768,734							
768,43	768,042	768,811							
769,31	768,925	769,694							
769,44	769,057	769,826							
770,42	770,036	770,806							
771,42	771,033	771,805							
772,43	772,045	772,817							
773,43	773,045	773,818							
774,42	774,030	774,805							
775,37	774,987	775,762							
775,49	775,104	775,879							

[illegible]

			807,404	0,024	R.LAADDFR.T	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
808,43	808,024	808,832							
808,71	808,310	809,119							
809,47	809,068	809,878							
810,46	810,050	810,860							
811,44	811,039	811,850	811,427	0,018	K.YAISMAR.K	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LCG4P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
			811,464	0,019	R.QALPQVR.L	Q99829	CPNE1_HUMAN	Copine-1 (Chromobindin 17) (Copine I)	CPNE1
			811,499	0,054	K.ALEIIPR.Q	Q99832	TCPH_HUMAN	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein) [Cleaved into: T-complex protein 1 subunit eta, N-terminally processed]	CCT7
812,46	812,053	812,865	812,477	0,017	R.LELQGPR.G	P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL
			812,419	0,041	K.YLPTYR.S	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
813,43	813,028	813,842							
813,46	813,052	813,865							
814,44	814,030	814,845							
814,45	814,045	814,859							
815,42	815,016	815,832	815,429	0,005	R.HFWGLR.V	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
			815,471	0,047	R.ELIGDR.Q	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
			815,509	0,085	R.ALLFVPR.R	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
816,44	816,035	816,851	816,459	0,016	R.EIQTAVR.L	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
			816,459	0,016	R.EIQTAVR.L	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
			816,459	0,016	R.ELKEAAR.Q	Q9BV73	CP250_HUMAN	Centrosome-associated protein CEP250 (250 kDa centrosomal protein) (Cep250) (Centrosomal Nek2-associated protein 1) (C-Nap1) (Centrosomal protein 2)	CEP250
			816,469	0,026	R.GFIPNIR.T	P35555	FBN1_HUMAN	Fibrillin-1 [Cleaved into: Asprosin]	FBN1
			816,496	0,053	K.QLMRLR.K	P40429	RL13A_HUMAN	60S ribosomal protein L13a (23 kDa highly basic protein) (Large ribosomal subunit protein uL13)	RPL13A
817,35	816,942	817,759							
817,44	817,035	817,852							
818,43	818,018	818,836	818,441	0,014	R.VDPVNF.K.L	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			818,454	0,027	K.SEALKDR.H	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
			818,468	0,041	K.LTVDKSR.W	P01860	IGHG3_HUMAN	Immunoglobulin heavy constant gamma 3 (HDC) (Heavy chain disease protein) (Ig gamma-3 chain C region)	IGHG3
819,43	819,021	819,840	819,481	0,050	K.FIEIAAR.K	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
820,42	820,014	820,834	820,438	0,013	R.VGFAEAAR.L	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
820,48	820,073	820,894	820,438	0,046	R.VGFAEAAR.L	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
821,22	820,809	821,631	821,439	0,219	R.TILMMGR.Y	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
			821,447	0,227	K.QLYLER.V	P61160	ARP2_HUMAN	Actin-related protein 2 (Actin-like protein 2)	ACTR2
			821,455	0,234	K.ALADYIR.Q	Q9BS26	ERP44_HUMAN	Endoplasmic reticulum resident protein 44 (ER protein 44) (ERp44) (Thioredoxin domain-containing protein 4)	ERP44
821,42	821,010	821,832	821,439	0,018	R.TILMMGR.Y	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
			821,447	0,026	K.QLYLER.V	P61160	ARP2_HUMAN	Actin-related protein 2 (Actin-like protein 2)	ACTR2
			821,455	0,033	K.ALADYIR.Q	Q9BS26	ERP44_HUMAN	Endoplasmic reticulum resident protein 44 (ER protein 44) (ERp44) (Thioredoxin domain-containing protein 4)	ERP44
821,83	821,423	822,245	821,455	0,380	K.ALADYIR.Q	Q9BS26	ERP44_HUMAN	Endoplasmic reticulum resident protein 44 (ER protein 44) (ERp44) (Thioredoxin domain-containing protein 4)	ERP44
			821,447	0,387	K.QLYLER.V	P61160	ARP2_HUMAN	Actin-related protein 2 (Actin-like protein 2)	ACTR2
			821,439	0,395	R.TILMMGR.Y	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
822,17	821,760	822,582							
822,42	822,004	822,826							
822,48	822,069	822,891							
823,11	822,695	823,518							
823,41	822,996	823,820							
823,44	823,028	823,852							
824,47	824,058	824,882	824,534	0,063	R.ILPKPTR.K	P62081	RS7_HUMAN	40S ribosomal protein S7 (Small ribosomal subunit protein eS7)	RPS7
824,70	824,289	825,114	824,534	0,168	R.ILPKPTR.K	P62081	RS7_HUMAN	40S ribosomal protein S7 (Small ribosomal subunit protein eS7)	RPS7
825,12	824,709	825,534							
825,37	824,955	825,780							
825,50	825,086	825,912							
826,45	826,033	826,859	826,536	0,090	K.VVLVLAGR.Y	P61353	RL27_HUMAN	60S ribosomal protein L27 (Large ribosomal subunit protein eL27)	RPL27
			826,544	0,097	R.IDKPIK.K.A	P62917	RL8_HUMAN	60S ribosomal protein L8 (Large ribosomal subunit protein uL2)	RPL8
826,47	826,059	826,886	826,536	0,063	K.VVLVLAGR.Y	P61353	RL27_HUMAN	60S ribosomal protein L27 (Large ribosomal subunit protein eL27)	RPL27

			826,544	0,071	R.IDKPILK.A	P62917	RL8_HUMAN	60S ribosomal protein L8 (Large ribosomal subunit protein uL2)	RPL8
827,39	826,974	827,801	827,538	0,151	R.LIVDVIR.F	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
			827,549	0,161	R.KVGLIAAR.R	P62917	RL8_HUMAN	60S ribosomal protein L8 (Large ribosomal subunit protein uL2)	RPL8
827,51	827,092	827,919	827,538	0,032	R.LIVDVIR.F	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
			827,549	0,043	R.KVGLIAAR.R	P62917	RL8_HUMAN	60S ribosomal protein L8 (Large ribosomal subunit protein uL2)	RPL8
828,40	827,981	828,810	828,460	0,064	K.DRSVPVR.L	P61009	SPCS3_HUMAN	Signal peptidase complex subunit 3 (EC 3.4.-.-) (Microsomal signal peptidase 22/23 kDa subunit) (SPC22/23) (SPase 22/23 kDa subunit)	SPCS3
828,48	828,068	828,897	828,460	0,023	K.DRSVPVR.L	P61009	SPCS3_HUMAN	Signal peptidase complex subunit 3 (EC 3.4.-.-) (Microsomal signal peptidase 22/23 kDa subunit) (SPC22/23) (SPase 22/23 kDa subunit)	SPCS3
829,46	829,049	829,879	829,478	0,013	R.LADLIER.D	P05091	ALDH2_HUMAN	Aldehyde dehydrogenase, mitochondrial (EC 1.2.1.3) (ALDH class 2) (ALDH-E2) (ALDH1)	ALDH2
			829,478	0,013	K.LADLIER.D	P00352	AL1A1_HUMAN	Retinal dehydrogenase 1 (RALDH 1) (RALDH1) (EC 1.2.1.-) (EC 1.2.1.36) (ALDH-E1) (ALHDI1) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic)	ALDH1A1
			829,432	0,032	R.HLQFER.F	Q9H8H3	MET7A_HUMAN	Methyltransferase-like protein 7A (EC 2.1.1.-)	METTL7A
			829,529	0,065	R.ALLFIPR.R	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
830,47	830,053	830,884	831,500	0,016	K.STELLIR.K	P84243	H33_HUMAN	Histone H3.3	H3F3A; H3F3B
831,48	831,068	831,899	831,503	0,020	R.VPFSLLR.G	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	HSPB1
			831,456	0,027	R.LTIAEER.D	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein eS4)	RP54X
832,38	831,966	832,798	833,386	0,316	R.FFSGYGR.L	Q13247	SRSF6_HUMAN	Serine/arginine-rich splicing factor 6 (Pre-mRNA-splicing factor SRP55) (Splicing factor, arginine/serine-rich 6)	SRSF6
832,49	832,071	832,904		0,407	R.VLFAPMR.M	Q14764	MVP_HUMAN	Major vault protein (MVP) (Lung resistance-related protein)	MVP
833,07	832,654	833,487		0,028	R.FFSGYGR.L	Q13247	SRSF6_HUMAN	Serine/arginine-rich splicing factor 6 (Pre-mRNA-splicing factor SRP55) (Splicing factor, arginine/serine-rich 6)	SRSF6
833,36	832,942	833,775	833,386	0,119	R.VLFAPMR.M	Q14764	MVP_HUMAN	Major vault protein (MVP) (Lung resistance-related protein)	MVP
833,48	833,060	833,894	833,478	0,000	R.VLFAPMR.M	Q14764	MVP_HUMAN	Major vault protein (MVP) (Lung resistance-related protein)	MVP
			833,386	0,091	R.FFSGYGR.L	Q13247	SRSF6_HUMAN	Serine/arginine-rich splicing factor 6 (Pre-mRNA-splicing factor SRP55) (Splicing factor, arginine/serine-rich 6)	SRSF6
834,41	833,993	834,827	835,431	0,016	K.DTLMISR.T	P01860	IGHG3_HUMAN	Immunoglobulin heavy constant gamma 3 (HDC) (Heavy chain disease protein) (Ig gamma-3 chain C region)	IGHG3
834,44	834,020	834,855		0,050	R.EAVTFLR.K	P36957	ODO2_HUMAN	Dihydropyridyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydropyridylsuccinyltransferase component of 2-oxoglutarate dehydrogenase complex) (E2K)	DLST
835,42	834,998	835,833		0,012	K.DTLMISR.T	P01860	IGHG3_HUMAN	Immunoglobulin heavy constant gamma 3 (HDC) (Heavy chain disease protein) (Ig gamma-3 chain C region)	IGHG3
			835,465	0,022	R.EAVTFLR.K	P36957	ODO2_HUMAN	Dihydropyridyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydropyridylsuccinyltransferase component of 2-oxoglutarate dehydrogenase complex) (E2K)	DLST
836,43	836,012	836,848	836,512	0,082	R.HLQLAVR.N	Q8IU66	H2A2B_HUMAN	Histone H2A type 2-B	HIST2H2AB
837,29	836,873	837,710	837,536	0,245	K.AIGVKPPR.G	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
837,43	837,015	837,852	837,536	0,103	K.AIGVKPPR.G	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
837,60	837,184	838,022	837,536	0,067	K.AIGVKPPR.G	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
838,44	838,023	838,861	838,503	0,061	K.ALPAPIEK.T	P01860	IGHG3_HUMAN	Immunoglobulin heavy constant gamma 3 (HDC) (Heavy chain disease protein) (Ig gamma-3 chain C region)	IGHG3
839,08	838,658	839,497							
839,21	838,789	839,628							

[illegible]

			850,532	0,025	R.HLQLAIR.N	Q93077	H2A1C_HUMAN	Histone H2A type 1-C (Histone H2A/I)	HIST1H2AC
			850,453	0,054	R.FGPGVAFR.A	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
850,80	850,378	851,229	850,532	0,271	R.HLQLAIR.G	Q71UI9	H2AV_HUMAN	Histone H2A.V (H2A.F/Z)	H2AFV
			850,532	0,271	R.HLQLAIR.N	Q6FI13	H2A2A_HUMAN	Histone H2A type 2-A (Histone H2A.2) (Histone H2A/o)	HIST2H2AA3; HIST2H2AA4
			850,532	0,271	R.HLQLAIR.N	P16104	H2AX_HUMAN	Histone H2AX (H2a/x) (Histone H2A.X)	H2AFX
			850,532	0,271	R.HLQLAIR.N	Q93077	H2A1C_HUMAN	Histone H2A type 1-C (Histone H2A/I)	HIST1H2AC
			850,485	0,319	K.RPDVAVHR.E	A4D2P6	GRD2I_HUMAN	Delphinin (Glutamate receptor, ionotropic, delta 2-interacting protein 1)	GRID2IP
			850,453	0,351	R.FGPGVAFR.A	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
851,44	851,015	851,866	851,439	0,002	K.DTLMISR.T	P01860	IGHG3_HUMAN	Immunoglobulin heavy constant gamma 3 (HDC) (Heavy chain disease protein) (Ig gamma-3 chain C region)	IGHG3
			851,431	0,010	K.KICMQR.F	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein e54)	RPS4X
			851,510	0,069	R.EHLLAR.Q	P49411	EFTU_HUMAN	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	TUFM
851,51	851,082	851,933	851,510	0,002	R.EHLLAR.Q	P49411	EFTU_HUMAN	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	TUFM
			851,439	0,069	K.DTLMISR.T	P01860	IGHG3_HUMAN	Immunoglobulin heavy constant gamma 3 (HDC) (Heavy chain disease protein) (Ig gamma-3 chain C region)	IGHG3
			851,431	0,077	K.KICMQR.F	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein e54)	RPS4X
852,42	851,992	852,844	852,568	0,150	R.GLVVPVIR.N	P36957	ODO2_HUMAN	Dihydropyridyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydropyridylamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex) (E2K)	DLST
852,42	851,997	852,849	852,568	0,145	R.GLVVPVIR.N	P36957	ODO2_HUMAN	Dihydropyridyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydropyridylamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex) (E2K)	DLST
852,69	852,262	853,114	852,568	0,120	R.GLVVPVIR.N	P36957	ODO2_HUMAN	Dihydropyridyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydropyridylamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex) (E2K)	DLST
853,43 854,43	853,003 854,007	853,856 854,862	854,511	0,076	R.DLAPIGIR.V	Q99714	HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2 (EC 1.1.1.35) (17-beta-hydroxysteroid dehydrogenase 10) (17-beta-HSD 10) (EC 1.1.1.51) (2-methyl-3-hydroxybutyryl-CoA dehydrogenase) (MHBd) (3-hydroxy-2-methylbutyryl-CoA dehydrogenase) (EC 1.1.1.178) (3-hydroxyacyl-CoA dehydrogenase type II) (Endoplasmic reticulum-associated amyloid beta-peptide-binding protein) (Mitochondrial ribonuclease P protein 2) (Mitochondrial RNase P protein 2) (Short chain dehydrogenase/reductase family 5C member 1) (Short-chain type dehydrogenase/reductase XH98G2) (Type II HADH)	HSD17B10
855,05 855,40	854,619 854,972	855,474 855,828	855,513	0,113	K.APNVVVTR.L	P52566	GDIR2_HUMAN	Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Ly-GDI) (Rho-GDI beta)	ARHGDI3
855,45	855,018	855,873	855,513	0,068	K.APNVVVTR.L	P52566	GDIR2_HUMAN	Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Ly-GDI) (Rho-GDI beta)	ARHGDI3
856,07	855,642	856,498	856,497	0,427	R.GNLANVIR.Y	P05141	ADT2_HUMAN	ADP/ATP translocase 2 (ADP,ATP carrier protein 2) (ADP,ATP carrier protein, fibroblast isoform) (Adenine nucleotide translocator 2) (ANT 2) (Solute carrier family 25 member 5) [Cleaved into: ADP/ATP translocase 2, N-terminally processed]	SLC25A5
856,34	855,916	856,772	856,497	0,153	R.GNLANVIR.Y	P05141	ADT2_HUMAN	ADP/ATP translocase 2 (ADP,ATP carrier protein 2) (ADP,ATP carrier protein, fibroblast isoform) (Adenine nucleotide translocator 2) (ANT 2) (Solute carrier family 25 member 5) [Cleaved into: ADP/ATP translocase 2, N-terminally processed]	SLC25A5
			856,499	0,155	K.TAVAPIER.V	P05141	ADT2_HUMAN	ADP/ATP translocase 2 (ADP,ATP carrier protein 2) (ADP,ATP carrier protein, fibroblast isoform) (Adenine nucleotide translocator 2) (ANT 2) (Solute carrier family 25 member 5) [Cleaved into: ADP/ATP translocase 2, N-terminally processed]	SLC25A5
			856,565	0,221	R.LLTVVRR.A	Q8IZQ1	WDFY3_HUMAN	WD repeat and FYVE domain-containing protein 3 (Autophagy-linked FYVE protein) (Alfy)	WDFY3
856,49	856,060	856,916	856,497	0,009	R.GNLANVIR.Y	P05141	ADT2_HUMAN	ADP/ATP translocase 2 (ADP,ATP carrier protein 2) (ADP,ATP carrier protein, fibroblast isoform) (Adenine nucleotide translocator 2) (ANT 2) (Solute carrier family 25 member 5) [Cleaved into: ADP/ATP translocase 2, N-terminally processed]	SLC25A5

856,57	856,141	856,998	856,499	0,011	K.TAVAPIER.V	P05141	ADT2_HUMAN	ADP/ATP translocase 2 (ADP,ATP carrier protein 2) (ADP,ATP carrier protein, fibroblast isoform) (Adenine nucleotide translocator 2) (ANT 2) (Solute carrier family 25 member 5) [Cleaved into: ADP/ATP translocase 2, N-terminally processed]	SLC25A5
			856,565	0,077	R.LLTVVRR.A	Q8IZQ1	WDFY3_HUMAN	WD repeat and FYVE domain-containing protein 3 (Autophagy-linked FYVE protein) (Alfy)	WDFY3
			856,565	0,004	R.LLTVVRR.A	Q8IZQ1	WDFY3_HUMAN	WD repeat and FYVE domain-containing protein 3 (Autophagy-linked FYVE protein) (Alfy)	WDFY3
			856,499	0,070	K.TAVAPIER.V	P05141	ADT2_HUMAN	ADP/ATP translocase 2 (ADP,ATP carrier protein 2) (ADP,ATP carrier protein, fibroblast isoform) (Adenine nucleotide translocator 2) (ANT 2) (Solute carrier family 25 member 5) [Cleaved into: ADP/ATP translocase 2, N-terminally processed]	SLC25A5
857,52	857,095	857,953	856,497	0,072	R.GNLANVIR.Y	P05141	ADT2_HUMAN	ADP/ATP translocase 2 (ADP,ATP carrier protein 2) (ADP,ATP carrier protein, fibroblast isoform) (Adenine nucleotide translocator 2) (ANT 2) (Solute carrier family 25 member 5) [Cleaved into: ADP/ATP translocase 2, N-terminally processed]	SLC25A5
			857,499	0,025	R.YAHVVLR.K	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
			857,499	0,038	R.YAHVVLR.K	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
			858,537	0,074	K.KIPVVFR.L	P10768	ESTD_HUMAN	S-formylglutathione hydrolase (FGH) (EC 3.1.2.12) (Esterase D) (Methylumbelliferyl-acetate deacetylase) (EC 3.1.1.56)	ESD
859,42	858,992	859,851	860,497	0,065	R.QMSLLR.R	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATPSF1A
859,49	859,057	859,916				P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATPSF1A
860,43	860,001	860,862							
860,49	860,059	860,919	860,497	0,008	R.QMSLLR.R				
861,13	860,699	861,560	862,474	0,340	R.IALDFQR.G	P17931	LEG3_HUMAN	Galectin-3 (Gal-3) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Galactose-specific lectin 3) (Galactoside-binding protein) (GALBP) (IgE-binding protein) (L-31) (Laminin-binding protein) (Lectin L-29) (Mac-2 antigen)	LGALS3
861,44	861,006	861,867							
862,13	861,703	862,565							
862,45	862,014	862,877	862,474	0,028	R.IALDFQR.G	P17931	LEG3_HUMAN	Galectin-3 (Gal-3) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Galactose-specific lectin 3) (Galactoside-binding protein) (GALBP) (IgE-binding protein) (L-31) (Laminin-binding protein) (Lectin L-29) (Mac-2 antigen)	LGALS3
862,51	862,084	862,946	862,474	0,041	R.IALDFQR.G	P17931	LEG3_HUMAN	Galectin-3 (Gal-3) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Galactose-specific lectin 3) (Galactoside-binding protein) (GALBP) (IgE-binding protein) (L-31) (Laminin-binding protein) (Lectin L-29) (Mac-2 antigen)	LGALS3
863,06	862,631	863,494	864,456	0,007	R.SSPVYVGR.V	P21980	TGM2_HUMAN	Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (Transglutaminase C) (TG(C)) (TGC) (TGase C) (Transglutaminase H) (TGase H) (Transglutaminase-2) (TGase-2)	TGM2
863,13	862,701	863,564				Q9UKM9	RALY_HUMAN	RNA-binding protein Raly (Autoantigen p542) (Heterogeneous nuclear ribonucleoprotein C-like 2) (hnRNP core protein C-like 2) (hnRNP associated with lethal yellow protein homolog)	RALY
863,49	863,054	863,918				Q9UKM9	RALY_HUMAN	RNA-binding protein Raly (Autoantigen p542) (Heterogeneous nuclear ribonucleoprotein C-like 2) (hnRNP core protein C-like 2) (hnRNP associated with lethal yellow protein homolog)	RALY
864,46	864,031	864,896	864,522	0,058	R.LSPVPVPR.A	P21980	TGM2_HUMAN	Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (Transglutaminase C) (TG(C)) (TGC) (TGase C) (Transglutaminase H) (TGase H) (Transglutaminase-2) (TGase-2)	TGM2
864,56	864,128	864,993	864,522	0,039	R.LSPVPVPR.A				
			864,456	0,104	R.SSPVYVGR.V				
865,41	864,981	865,847	868,488	0,038	R.MQHLIAR.E	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
865,53	865,094	865,959				P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
866,49	866,053	866,920				P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (CapZ alpha-1)	CAPZA1
867,45	867,015	867,882				P47755	CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 (CapZ alpha-2)	CAPZA2
868,45	868,015	868,884							
869,34	868,904	869,774	869,505	0,165	K.VIPELNGK.L	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
			869,530	0,191	R.RQLPVTR.T				
			869,530	0,191	R.RQLPVTR.T				
869,46	869,021	869,891	869,505	0,048	K.VIPELNGK.L				

			869,530	0,074	R.RQLPVTR.T	P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (CapZ alpha-1)	CAPZA1
			869,530	0,074	R.RQLPVTR.T	P47755	CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 (CapZ alpha-2)	CAPZA2
870,48	870,050	870,920	870,436	0,049	R.ISSSSFSR.V	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
870,55	870,110	870,980	870,436	0,109	R.ISSSSFSR.V	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
871,51	871,075	871,946	871,513	0,002	K.DIQLARR.I	P84243	H33_HUMAN	Histone H3.3	H3F3A; H3F3B
			871,535	0,024	R.GQVVSLIR.M	P07384	CAN1_HUMAN	Calpain-1 catalytic subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase 1) (CANP 1) (Calpain mu-type) (Calpain-1 large subunit) (Cell proliferation-inducing gene 30 protein) (Micromolar-calpain) (muCANP)	CAPN1
872,41	871,976	872,848	872,527	0,115	R.KNAALVTR.M	Q96AY2	EME1_HUMAN	Crossover junction endonuclease EME1 (EC 3.1.22.-) (MMS4 homolog) (hMMS4)	EME1
872,49	872,053	872,925	872,527	0,038	R.KNAALVTR.M	Q96AY2	EME1_HUMAN	Crossover junction endonuclease EME1 (EC 3.1.22.-) (MMS4 homolog) (hMMS4)	EME1
873,46	873,024	873,898	873,507	0,046	R.RGPPPPPR.S	P38159	RBMX_HUMAN	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX
874,42 875,43	873,982 874,990	874,857 875,866	875,515	0,086	R.LSQRFPK.A	P02768	ALBU_HUMAN	Serum albumin	ALB
876,46	876,021	876,898	876,461	0,001	K.TFEINPR.H	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			876,456	0,004	K.LPASFDAR.E	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
			876,488	0,028	R.TSVETALR.A	P47755	CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 (CapZ alpha-2)	CAPZA2
877,07	876,630	877,508	877,459	0,389	R.NYLSQPR.L	P21281	VATB2_HUMAN	V-type proton ATPase subunit B, brain isoform (V-ATPase subunit B 2) (Endomembrane proton pump 58 kDa subunit) (HO57) (Vacuolar proton pump subunit B 2)	ATP6V1B2
877,46	877,023	877,901	877,459	0,004	R.NYLSQPR.L	P21281	VATB2_HUMAN	V-type proton ATPase subunit B, brain isoform (V-ATPase subunit B 2) (Endomembrane proton pump 58 kDa subunit) (HO57) (Vacuolar proton pump subunit B 2)	ATP6V1B2
878,07 878,43	877,629 877,992	878,507 878,870	878,570	0,139	R.AVLHVALR.N	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
878,53	878,089	878,967	878,570	0,042	R.AVLHVALR.N	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
879,05 879,42 879,51 880,39	878,606 878,982 879,069 879,952	879,485 879,861 879,949 880,833	880,443 880,483	0,051 0,090	K.AEFAEVSK.L R.MAPHLRR.D	P02768 Q86WV1	ALBU_HUMAN SKAP1_HUMAN	Serum albumin Src kinase-associated phosphoprotein 1 (Src family-associated phosphoprotein 1) (Src kinase-associated phosphoprotein of 55 kDa) (SKAP-55) (pp55)	ALB SKAP1
880,50	880,063	880,943	880,483	0,020	R.MAPHLRR.D	Q86WV1	SKAP1_HUMAN	Src kinase-associated phosphoprotein 1 (Src family-associated phosphoprotein 1) (Src kinase-associated phosphoprotein of 55 kDa) (SKAP-55) (pp55)	SKAP1
			880,443	0,060	K.AEFAEVSK.L	P02768	ALBU_HUMAN	Serum albumin	ALB
881,40	880,956	881,837	881,518	0,122	K.SLQPLAPR.N	Q14764	MVP_HUMAN	Major vault protein (MVP) (Lung resistance-related protein)	MVP
881,48	881,040	881,922	881,518	0,037	K.SLQPLAPR.N	Q14764	MVP_HUMAN	Major vault protein (MVP) (Lung resistance-related protein)	MVP
882,44 882,50 883,41	881,997 882,057 882,972	882,879 882,939 883,856	883,432	0,018	R.AFFAGSQR.F	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			883,507	0,093	R.VGQDPVLR.Q	Q04837	SSBP_HUMAN	Single-stranded DNA-binding protein, mitochondrial (Mt-SSB) (MtSSB) (PWP1-interacting protein 17)	SSBP1
883,49	883,050	883,934	883,507	0,015	R.VGQDPVLR.Q	Q04837	SSBP_HUMAN	Single-stranded DNA-binding protein, mitochondrial (Mt-SSB) (MtSSB) (PWP1-interacting protein 17)	SSBP1
			883,432	0,059	R.AFFAGSQR.F	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
884,46	884,016	884,900	884,523	0,065	R.TLLVADPR.R	P62249	RS16_HUMAN	40S ribosomal protein S16 (Small ribosomal subunit protein uS9)	RPS16
884,48	884,037	884,922	884,523	0,043	R.TLLVADPR.R	P62249	RS16_HUMAN	40S ribosomal protein S16 (Small ribosomal subunit protein uS9)	RPS16

885,47	885,030	885,916	885,502	0,030	K.IVVSNTPR.T	Q92616	GCN1_HUMAN	elf-2-alpha kinase activator GCN1 (GCN1 eIF-2-alpha kinase activator homolog) (GCN1-like protein 1) (General control of amino-acid synthesis 1-like protein 1) (Translational activator GCN1) (HsGCN1)	GCN1
886,43	885,989	886,876	886,483	0,050	R.ILSHGGR.K	Q12905	ILF2_HUMAN	Interleukin enhancer-binding factor 2 (Nuclear factor of activated T-cells 45 kDa)	ILF2
887,44	886,997	887,884	887,420	0,020	R.MYSYPAR.V	P07910	HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1/C2)	HNRNPC
			887,471	0,030	K.HIDFSLR.S	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RP59
888,46	888,011	888,900							
889,45	889,002	889,892							
890,43	889,981	890,871	890,510	0,084	K.FSVSPVVR.V	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
891,43	890,989	891,880	891,424	0,011	K.LMSDNGVR.V	Q96I99	SUCB2_HUMAN	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial (EC 6.2.2.14) (GTP-specific succinyl-CoA synthetase subunit beta) (G-SCS) (GTPSCS) (Succinyl-CoA synthetase beta-G chain) (SCS-betaG)	SUCLG2
			891,424	0,011	R.LMEDLDR.N	P06703	S10A6_HUMAN	Protein S100-A6 (Calcylin) (Growth factor-inducible protein 2A9) (MLN 4) (Prolactin receptor-associated protein) (PRA) (S100 calcium-binding protein A6)	S100A6
			891,504	0,069	R.AYLQQLR.Q	O15145	ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3 (Arp2/3 complex 21 kDa subunit) (p21-ARC)	ARPC3
			891,506	0,071	R.IGASFLQR.F	P00505	AATM_HUMAN	Aspartate aminotransferase, mitochondrial (mAspAT) (EC 2.6.1.1) (EC 2.6.1.7) (Fatty acid-binding protein) (FABP-1) (Glutamate oxaloacetate transaminase 2) (Kynurenine aminotransferase 4) (Kynurenine aminotransferase IV) (Kynurenine--oxoglutarate transaminase 4) (Kynurenine--oxoglutarate transaminase IV) (Plasma membrane-associated fatty acid-binding protein) (FABPpm) (Transaminase A)	GOT2
892,39	891,943	892,836	892,490	0,101	K.LELAQYR.E	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
892,50	892,051	892,944	892,490	0,007	K.LELAQYR.E	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
893,01	892,563	893,456							
893,40	892,957	893,850	893,464	0,060	K.LQQWYR.E	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
			893,481	0,077	K.LHPHFSR.I	P19367	HXK1_HUMAN	Hexokinase-1 (EC 2.7.1.1) (Brain form hexokinase) (Hexokinase type I) (HK I)	HK1
			893,503	0,099	R.SILEYLR.V	Q8N1G4	LRC47_HUMAN	Leucine-rich repeat-containing protein 47	LRRC47
893,50	893,054	893,948	893,503	0,002	R.SILEYLR.V	Q8N1G4	LRC47_HUMAN	Leucine-rich repeat-containing protein 47	LRRC47
			893,481	0,020	K.LHPHFSR.I	P19367	HXK1_HUMAN	Hexokinase-1 (EC 2.7.1.1) (Brain form hexokinase) (Hexokinase type I) (HK I)	HK1
			893,464	0,037	K.LQQWYR.E	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
894,39	893,941	894,835	894,442	0,053	K.RYEPSDK.D	Q86VM9	ZCH18_HUMAN	Zinc finger CCCH domain-containing protein 18 (Nuclear protein NHN1)	ZC3H18
			894,442	0,053	R.FAVRDMR.Q	P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1
			894,497	0,108	K.ILTTGFSR.M	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
894,49	894,045	894,940	894,497	0,004	K.ILTTGFSR.M	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
			894,442	0,051	K.RYEPSDK.D	Q86VM9	ZCH18_HUMAN	Zinc finger CCCH domain-containing protein 18 (Nuclear protein NHN1)	ZC3H18
			894,442	0,051	R.FAVRDMR.Q	P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1
895,45	895,003	895,898	895,457	0,007	K.SILYDER.S	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
895,46	895,014	895,910	895,457	0,005	K.SILYDER.S	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
896,43	895,985	896,882	896,466	0,032	K.YLTWASR.Q	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
			896,534	0,100	K.LVAVGGQPR.M	Q6XQN6	PNCB_HUMAN	Nicotinate phosphoribosyltransferase (NAPRTase) (EC 6.3.4.21) (FHA-HIT-interacting protein) (Nicotinate phosphoribosyltransferase domain-containing protein 1)	NAPRT
897,44	896,992	897,889	897,546	0,105	R.SPAQILLR.W	P14550	AK1A1_HUMAN	Aldo-keto reductase family 1 member A1 (EC 1.1.1.2) (EC 1.1.1.372) (EC 1.1.1.54) (Alcohol dehydrogenase [NADP(+)]) (Aldehyde reductase) (Glucuronate reductase) (EC 1.1.1.19) (Glucuronolactone reductase) (EC 1.1.1.20)	AKR1A1

897,47	897,024	897,921	897,546	0,073	R.SPAQILLR.W	P14550	AK1A1_HUMAN	Aldo-keto reductase family 1 member A1 (EC 1.1.1.2) (EC 1.1.1.372) (EC 1.1.1.54) (Alcohol dehydrogenase [NADP(+)]) (Aldehyde reductase) (Glucuronate reductase) (EC 1.1.1.19) (Glucuronolactone reductase) (EC 1.1.1.20)	AKR1A1
898,50	898,049	898,948	898,483	0,015	K.QGYVIYR.I	P61313	RL15_HUMAN	60S ribosomal protein L15 (Large ribosomal subunit protein eL15)	RPL15
899,50	899,054	899,953	899,502	0,001	R.GTIEINPR.D	Q08257	QOR_HUMAN	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-crystallin)	CRYZ
900,39	899,935	900,836	901,504 901,504 901,504	0,002	R.LAHYNKR.S	Q6DRA6	H2B2D_HUMAN	Putative histone H2B type 2-D	HIST2H2BD
900,51	900,059	900,959		0,002	R.LAHYNKR.S	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
900,98	900,533	901,434		0,002	R.LAHYNKR.S	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
901,51	901,056	901,957	904,499	0,016	K.LFMPRPK.V	Q96T75	DSCR8_HUMAN	Down syndrome critical region protein 8 (Cancer/testis antigen 25) (CT25) (DCR1-24.0) (Malignant melanoma-associated protein 1) (MMA-1) (Protein MTAG2)	DSCR8
902,49	902,035	902,937		0,138	K.AYADFYR.N	P09669	COX6C_HUMAN	Cytochrome c oxidase subunit 6C (Cytochrome c oxidase polypeptide VIc)	COX6C
903,47	903,018	903,922		0,319	R.KVPVIPPR.I	P51888	PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	PRELP
904,48	904,032	904,936		0,067	K.AYADFYR.N	P09669	COX6C_HUMAN	Cytochrome c oxidase subunit 6C (Cytochrome c oxidase polypeptide VIc)	COX6C
905,28	904,825	905,731	905,597	0,114	R.KVPVIPPR.I	P51888	PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	PRELP
905,48	905,029	905,935	905,416	0,029	R.DVQEIFR.M	Q13838	DX39B_HUMAN	Spliceosome RNA helicase DDX39B (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	DDX39B
906,23	905,779	906,686	906,462	0,229	R.ARDELMR.K	Q9BV73	CP250_HUMAN	Centrosome-associated protein CEP250 (250 kDa centrosomal protein) (Cep250) (Centrosomal Nek2-associated protein 1) (C-Nap1) (Centrosomal protein 2)	CEP250
			906,474	0,241	R.NFDEILR.V	P30041	PRDX6_HUMAN	Peroxiredoxin-6 (EC 1.11.1.15) (1-Cys peroxiredoxin) (1-Cys PRX) (24 kDa protein) (Acidic calcium-independent phospholipase A2) (aiPLA2) (EC 3.1.1.4) (Antioxidant protein 2) (Liver 2D page spot 40) (Non-selenium glutathione peroxidase) (NSGPx) (Red blood cells page spot 12)	PRDX6
906,46	906,007	906,914	906,462	0,001	R.DVQEIFR.M	Q13838	DX39B_HUMAN	Spliceosome RNA helicase DDX39B (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	DDX39B
			906,462	0,001	R.ARDELMR.K	Q9BV73	CP250_HUMAN	Centrosome-associated protein CEP250 (250 kDa centrosomal protein) (Cep250) (Centrosomal Nek2-associated protein 1) (C-Nap1) (Centrosomal protein 2)	CEP250
			906,474	0,013	R.NFDEILR.V	P30041	PRDX6_HUMAN	Peroxiredoxin-6 (EC 1.11.1.15) (1-Cys peroxiredoxin) (1-Cys PRX) (24 kDa protein) (Acidic calcium-independent phospholipase A2) (aiPLA2) (EC 3.1.1.4) (Antioxidant protein 2) (Liver 2D page spot 40) (Non-selenium glutathione peroxidase) (NSGPx) (Red blood cells page spot 12)	PRDX6
907,46	907,003	907,910	907,462	0,005	R.MGPPVGGHR.R	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
			907,506	0,049	K.FLPLFDR.V	P61604	CH10_HUMAN	10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperonin) (Chaperonin 10) (CPN10) (Early-pregnancy factor) (EPF)	HSPE1
			907,525	0,069	R.NLLSVAYK.N	P31946	1433B_HUMAN	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHAH
			907,525	0,069	R.NLLSVAYK.N	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
908,48	908,022	908,930	908,463 908,495	0,013 0,019	R.SLQYLER.Y K.VFNLYPR.K	Q9ULE6 Q16555	PALD_HUMAN DPYL2_HUMAN	Paladin Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) (Unc-33-like phosphoprotein 2) (ULIP-2)	PALD1 DPYSL2
			908,452	0,025	R.ALYEAGER.R	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
909,40	908,950	909,859	909,418	0,013	R.DGFFGNPR.K	P01871	IGHM_HUMAN	Immunoglobulin heavy constant mu (Ig mu chain C region) (Ig mu chain C region BOT) (Ig mu chain C region GAL) (Ig mu chain C region OU)	IGHM
			909,428	0,023	K.MFDVGGQR.S	P04899	GNAI2_HUMAN	Guanine nucleotide-binding protein Gi(i) subunit alpha-2 (Adenylate cyclase-inhibiting G alpha protein)	GNAI2
			909,521	0,116	R.VAIEPGAPR.E	Q00796	DHSO_HUMAN	Sorbitol dehydrogenase (SDH) (EC 1.1.1.-) ((R,R)-butanediol dehydrogenase) (EC 1.1.1.4) (L-iditol 2-dehydrogenase) (EC 1.1.1.14) (Polyol dehydrogenase) (Ribitol dehydrogenase) (RDH) (EC 1.1.1.56) (Xylitol dehydrogenase) (XDH) (EC 1.1.1.9)	SORD

909,50	909,044	909,953	909,521	0,022	R.VAIEPGAPR.E	Q00796	DHSO_HUMAN	Sorbitol dehydrogenase (SDH) (EC 1.1.1.-) ((R,R)-butanediol dehydrogenase) (EC 1.1.1.4) (L-iditol 2-dehydrogenase) (EC 1.1.1.14) (Polyol dehydrogenase) (Ribitol dehydrogenase) (RDH) (EC 1.1.1.56) (Xylitol dehydrogenase) (XDH) (EC 1.1.1.9)	SORD
			909,428	0,071	K.MFDVGGQR.S	P04899	GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2 (Adenylate cyclase-inhibiting G alpha protein)	GNAI2
			909,418	0,081	R.DGFFGNPR.K	P01871	IGHM_HUMAN	Immunoglobulin heavy constant mu (Ig mu chain C region) (Ig mu chain C region BOT) (Ig mu chain C region GAL) (Ig mu chain C region OUI)	IGHM
910,49	910,036	910,946							
911,49	911,038	911,949	911,480	0,013	R.SSSMKSLR.I	Q99759	M3K3_HUMAN	Mitogen-activated protein kinase kinase kinase 3 (EC 2.7.11.25) (MAPK/ERK kinase kinase 3) (MEK kinase 3) (MEKK 3)	MAP3K3
912,49	912,031	912,944	912,526	0,038	R.LAYIAHPK.L	P47914	RL29_HUMAN	60S ribosomal protein L29 (Cell surface heparin-binding protein HIP) (Large ribosomal subunit protein eL29)	RPL29
913,10	912,648	913,561	913,428	0,324	R.QGYGEGFR.W	Q9NR31	SAR1A_HUMAN	GTP-binding protein SAR1a (COPII-associated small GTPase)	SAR1A
			913,529	0,425	M.AAVALAGGLVGK.G	Q8IZD4	DCP1B_HUMAN	mRNA-decapping enzyme 18 (EC 3.-.-.-)	DCP1B
913,43	912,969	913,882	913,428	0,003	R.QGYGEGFR.W	Q9NR31	SAR1A_HUMAN	GTP-binding protein SAR1a (COPII-associated small GTPase)	SAR1A
			913,529	0,103	M.AAVALAGGLVGK.G	Q8IZD4	DCP1B_HUMAN	mRNA-decapping enzyme 18 (EC 3.-.-.-)	DCP1B
			913,588	0,162	K.LVITAGAR.Q	P00338	LDHA_HUMAN	L-lactate dehydrogenase A chain (LDH-A) (EC 1.1.1.27) (Cell proliferation-inducing gene 19 protein) (LDH muscle subunit) (LDH-M) (Renal carcinoma antigen NY-REN-59)	LDHA
913,54	913,085	913,999	913,529	0,013	M.AAVALAGGLVGK.G	Q8IZD4	DCP1B_HUMAN	mRNA-decapping enzyme 18 (EC 3.-.-.-)	DCP1B
			913,588	0,045	K.LVITAGAR.Q	P00338	LDHA_HUMAN	L-lactate dehydrogenase A chain (LDH-A) (EC 1.1.1.27) (Cell proliferation-inducing gene 19 protein) (LDH muscle subunit) (LDH-M) (Renal carcinoma antigen NY-REN-59)	LDHA
			913,428	0,114	R.QGYGEGFR.W	Q9NR31	SAR1A_HUMAN	GTP-binding protein SAR1a (COPII-associated small GTPase)	SAR1A
914,49	914,034	914,948	914,490	0,001	R.FVHGEGLR.W	P30536	TSPO_HUMAN	Translocator protein (Mitochondrial benzodiazepine receptor) (PKBS) (Peripheral-type benzodiazepine receptor) (PBR)	TSPO
			914,461	0,030	R.SYVTSTR.T	P08670	VIME_HUMAN	Vimentin	VIM
			914,525	0,034	K.IALLEEAR.R	P15311	EZR_HUMAN	Ezrin (Cytovillin) (Villin-2) (p81)	EZR
			914,536	0,045	R.ARTGLSGPR.S	Q2TAZ0	ATG2A_HUMAN	Autophagy-related protein 2 homolog A	ATG2A
			914,555	0,064	R.QTVAVGVKA	P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1
915,51	915,048	915,964	915,494	0,012	K.LQDAEIAL.L	P06703	S10A6_HUMAN	Protein S100-A6 (Calcylin) (Growth factor-inducible protein 2A9) (MLN 4) (Prolactin receptor-associated protein) (PRA) (S100 calcium-binding protein A6)	S100A6
			915,543	0,037	R.AGVIFPVGR.L	Q9P0M6	H2AW_HUMAN	Core histone macro-H2A.2 (Histone macroH2A2) (mH2A2)	H2AFY2
			915,548	0,042	R.KLILDSAR.A	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
916,58	916,126	917,042							
917,53	917,068	917,985							
918,44	917,984	918,902	918,509	0,066	R.VGDVYIPR.D	Q01130	SRSF2_HUMAN	Serine/arginine-rich splicing factor 2 (Protein PR264) (Splicing component, 35 kDa) (Splicing factor SC35) (SC-35) (Splicing factor, arginine/serine-rich 2)	SRSF2
918,48	918,020	918,938	918,509	0,030	R.VGDVYIPR.D	Q01130	SRSF2_HUMAN	Serine/arginine-rich splicing factor 2 (Protein PR264) (Splicing component, 35 kDa) (Splicing factor SC35) (SC-35) (Splicing factor, arginine/serine-rich 2)	SRSF2
919,50	919,036	919,955	919,488	0,008	K.APAMFNIR.N	P61247	RS3A_HUMAN	40S ribosomal protein S3a (Small ribosomal subunit protein eS1) (v-fos transformation effector protein) (Fte-1)	RPS3A
			919,516	0,021	R.SYPQLRR.V	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
920,49	920,030	920,951	920,516	0,025	K.LIGEYGLR.N	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RPS9
921,50	921,043	921,965	921,485	0,018	K.AAYRTSPR.L	P06396	GELS_HUMAN	Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF) (Brevin)	GSN
922,51	922,051	922,973	922,512	0,000	K.IFNLYPR.K	Q14195	DPYL3_HUMAN	Dihydropyrimidinase-related protein 3 (DRP-3) (Collapsin response mediator protein 4) (CRMP-4) (Unc-33-like phosphoprotein 1) (ULIP-1)	DPYSL3
923,52	923,056	923,980	923,544	0,026	R.ILGGLHDAK.G	P00738	HPT_HUMAN	Haptoglobin (Zonulin) [Cleaved into: Haptoglobin alpha chain; Haptoglobin beta chain]	HP
			923,573	0,055	K.IIAPPERK.Y	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			923,573	0,055	K.IIAPPERK.Y	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			923,573	0,055	K.IIAPPERK.Y	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
924,38	923,914	924,838	924,443	0,067	K.TDEGIAYR.G	P32119	PRDX2_HUMAN	Peroxioredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2

924,50	924,038	924,962	924,443	0,057	K.TDEGIAYR.G	P32119	PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
925,48	925,016	925,942	925,500	0,021	K.GSSITFSVK.V	Q5V5T9	OBSCN_HUMAN	Obscurin (EC 2.7.11.1) (Obscurin-RhoGEF) (Obscurin-myosin light chain kinase) (Obscurin-MLCK)	OBSCN
			925,532	0,053	K.AIFAGYKR.G	P18077	RL35A_HUMAN	60S ribosomal protein L35a (Cell growth-inhibiting gene 33 protein) (Large ribosomal subunit protein eL33)	RPL35A
926,49	926,030	926,957	926,413	0,081	R.FCPFAER.T	P78417	GSTO1_HUMAN	Glutathione S-transferase omega-1 (GSTO-1) (EC 2.5.1.18) (Glutathione S-transferase omega 1-1) (GSTO 1-1) (Glutathione-dependent dehydroascorbate reductase) (EC 1.8.5.1) (Monomethylarsonic acid reductase) (MMA(V) reductase) (EC 1.20.4.2) (S-(Phenacyl)glutathione reductase) (SPG-R)	GSTO1
927,51	927,050	927,978	927,494	0,020	K.YLVEIAR.R	P02768	ALBU_HUMAN	Serum albumin	ALB
			927,491	0,023	R.LEPRGEAR.S	Q8WZ42	TITIN_HUMAN	Titin (EC 2.7.11.1) (Connectin) (Rhabdomyosarcoma antigen MU-RMS-40.14)	TTN
928,43	927,967	928,895							
928,50	928,041	928,969							
929,40	928,934	929,863	929,497	0,099	K.GVAPLWMR.Q	Q00325	MPCP_HUMAN	Phosphate carrier protein, mitochondrial (Phosphate transport protein) (PTP) (Solute carrier family 25 member 3)	SLC25A3
929,51	929,046	929,976	929,497	0,014	K.GVAPLWMR.Q	Q00325	MPCP_HUMAN	Phosphate carrier protein, mitochondrial (Phosphate transport protein) (PTP) (Solute carrier family 25 member 3)	SLC25A3
930,48	930,020	930,950							
931,48	931,019	931,951	931,541	0,056	K.LAPEFAKR.N	P30041	PRDX6_HUMAN	Peroxiredoxin-6 (EC 1.11.1.15) (1-Cys peroxiredoxin) (1-Cys PRX) (24 kDa protein) (Acidic calcium-independent phospholipase A2) (aiPLA2) (EC 3.1.1.4) (Antioxidant protein 2) (Liver 2D page spot 40) (Non-selenium glutathione peroxidase) (NSGPx) (Red blood cells page spot 12)	PRDX6
932,51	932,045	932,978	932,518	0,007	K.SAVTALWVK.V	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			932,518	0,007	K.QVMAIKSR.V	Q92616	GCN1_HUMAN	elf-2-alpha kinase activator GCN1 (GCN1 elf-2-alpha kinase activator homolog) (GCN1-like protein 1) (General control of amino-acid synthesis 1-like protein 1) (Translational activator GCN1) (HsGCN1)	GCN1
933,47	933,007	933,940	933,455	0,019	R.FDGVQDPR.I	O00264	PGRC1_HUMAN	Membrane-associated progesterone receptor component 1 (mPR) (Dap1) (IZA)	PGRMC1
934,48	934,010	934,945	934,490	0,013	K.FMRDPIR.I	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-I (eIF-4A-I) (eIF4A-I) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
			934,490	0,013	K.FMRDPIR.I	Q14240	IF4A2_HUMAN	Eukaryotic initiation factor 4A-II (eIF-4A-II) (eIF4A-II) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-2)	EIF4A2
			934,497	0,019	K.TFPAETIR.F	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
934,51	934,040	934,974	934,497	0,010	K.TFPAETIR.F	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			934,490	0,016	K.FMRDPIR.I	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-I (eIF-4A-I) (eIF4A-I) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
			934,490	0,016	K.FMRDPIR.I	Q14240	IF4A2_HUMAN	Eukaryotic initiation factor 4A-II (eIF-4A-II) (eIF4A-II) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-2)	EIF4A2
935,54	935,074	936,009	935,543	0,002	R.VPSHAVVAR.S	P02788	TRFL_HUMAN	Lactotransferrin (Lactoferrin) (EC 3.4.21.-) (Growth-inhibiting protein 12) (Tala lactoferrin) [Cleaved into: Lactoferricin-H (Lfcin-H); Kaliocin-1; Lactoferronin-A; Lactoferronin-B; Lactoferronin-C]	LTF
			935,437	0,104	R.YRDYYR.Q	Q1KMD3	HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 2 (Scaffold-attachment factor A2) (SAF-A2)	HNRNPUL2
936,52	936,049	936,986	936,490	0,028	R.ATNSQLFR.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
937,53	937,065	938,002							
938,52	938,049	938,987							
939,49	939,020	939,959							
940,50	940,031	940,971	940,498	0,003	K.ELSDIAHR.I	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
			940,470	0,031	R.NNFAVGYR.T	P45880	VDAC2_HUMAN	Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2) (Outer mitochondrial membrane protein porin 2)	VDAC2
			940,451	0,050	K.DDNPNLPR.L	P02768	ALBU_HUMAN	Serum albumin	ALB
941,50	941,029	941,970	941,554	0,055	R.AVVGVVAGGGR.I	P62917	RL8_HUMAN	60S ribosomal protein L8 (Large ribosomal subunit protein uL2)	RPL8
			941,580	0,080	K.VTEKIPVR.H	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPUL2
942,46	941,989	942,932	942,531	0,071	R.NIVEAAAVR.D	P62854	RS26_HUMAN	40S ribosomal protein S26 (Small ribosomal subunit protein eS26)	RPS26
942,52	942,048	942,990	942,531	0,012	R.NIVEAAAVR.D	P62854	RS26_HUMAN	40S ribosomal protein S26 (Small ribosomal subunit protein eS26)	RPS26
943,54	943,067	944,011	943,567	0,027	R.VPPPPPIAR.A	P07910	HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1/C2)	HNRNPC
			943,570	0,030	R.MPIIPFLL.-	Q9NZ01	TECR_HUMAN	Very-long-chain enoyl-CoA reductase (EC 1.3.1.93) (Synaptic glycoprotein SC2) (Trans-2,3-enoyl-CoA reductase) (TER)	TECR

			943,453	0,086	K.LTFDEYR.N	P12429	ANXA3_HUMAN	Annexin A3 (35-alpha calcimedin) (Annexin III) (Annexin-3) (Inositol 1,2-cyclic phosphate 2-phosphohydrolase) (Lipocortin III) (Placental anticoagulant protein III) (PAP-III)	ANXA3
944,52	944,044	944,989	944,529	0,013	R.AGLQFPVGR.V	Q6F113	H2A2A_HUMAN	Histone H2A type 2-A (Histone H2A.2) (Histone H2A/o)	HIST2H2AA3; HIST2H2AA4
			944,529	0,013	R.AGLQFPVGR.V	Q93077	H2A1C_HUMAN	Histone H2A type 1-C (Histone H2A/i)	HIST1H2AC
			944,529	0,013	R.AGLQFPVGR.V	P16104	H2AX_HUMAN	Histone H2AX (H2a/x) (Histone H2A.X)	H2AFX
			944,529	0,013	R.AGLQFPVGR.I	Q71U09	H2AV_HUMAN	Histone H2A.V (H2A.F/Z)	H2AFV
			944,529	0,013	R.AGLQFPVGR.V	Q8IU66	H2A2B_HUMAN	Histone H2A type 2-B	HIST2H2AB
944,74	944,266	945,211	944,529	0,209	R.AGLQFPVGR.V	Q6F113	H2A2A_HUMAN	Histone H2A type 2-A (Histone H2A.2) (Histone H2A/o)	HIST2H2AA3; HIST2H2AA4
			944,529	0,209	R.AGLQFPVGR.V	Q93077	H2A1C_HUMAN	Histone H2A type 1-C (Histone H2A/i)	HIST1H2AC
			944,529	0,209	R.AGLQFPVGR.V	P16104	H2AX_HUMAN	Histone H2AX (H2a/x) (Histone H2A.X)	H2AFX
			944,529	0,209	R.AGLQFPVGR.I	Q71U09	H2AV_HUMAN	Histone H2A.V (H2A.F/Z)	H2AFV
			944,529	0,209	R.AGLQFPVGR.V	Q8IU66	H2A2B_HUMAN	Histone H2A type 2-B	HIST2H2AB
945,52	945,047	945,992							
946,51	946,041	946,987							
946,52	946,044	946,991							
947,49	947,018	947,965	947,499	0,007	K.KEAEDSLR.R	O43776	SYNC_HUMAN	Asparagine--tRNA ligase, cytoplasmic (EC 6.1.1.22) (Asparaginyl-tRNA synthetase) (AsnRS)	NARS
			947,483	0,008	K.LSEELSGGR.L	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
			947,501	0,009	R.ISQLEMAR.Q	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
947,52	947,043	947,990	947,501	0,016	R.ISQLEMAR.Q	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			947,499	0,018	K.KEAEDSLR.R	O43776	SYNC_HUMAN	Asparagine--tRNA ligase, cytoplasmic (EC 6.1.1.22) (Asparaginyl-tRNA synthetase) (AsnRS)	NARS
			947,483	0,033	K.LSEELSGGR.L	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
948,50	948,022	948,971	948,515	0,019	R.LAVYQAGAR.E	P02649	APOE_HUMAN	Apolipoprotein E (Apo-E)	APOE
			948,476	0,020	R.DFTPAELR.R	O00264	PGRC1_HUMAN	Membrane-associated progesterone receptor component 1 (mPR) (Dap1) (iZA)	PGRMC1
			948,446	0,050	K.FYEQFSK.N	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
949,48	949,004	949,954	949,482	0,003	R.AAATLMSE.R	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
			949,500	0,021	R.LGDQEFIK.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
950,47	949,999	950,949	950,493	0,019	R.GFSLEELR.V	P26373	RL13_HUMAN	60S ribosomal protein L13 (Breast basic conserved protein 1) (Large ribosomal subunit protein eL13)	RPL13
			950,493	0,019	K.TVFDEAIR.A	P15153	RAC2_HUMAN	Ras-related C3 botulinum toxin substrate 2 (GX) (Small G protein) (p21-Rac2)	RAC2
			950,527	0,053	R.QPFFQKR.S	Q01105	SET_HUMAN	Protein SET (HLA-DR-associated protein II) (Inhibitor of granzyme A-activated DNase) (IGAAD) (PHAPII) (Phosphatase 2A inhibitor I2PP2A) (I-2PP2A) (Template-activating factor I) (TAF-I)	SET
951,51	951,031	951,983							
952,37	951,891	952,843							
952,51	952,034	952,986							
953,44	952,959	953,912	953,601	0,166	R.LLLPGELAK.H	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
			953,601	0,166	R.LLLPGELAK.H	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
953,46	952,986	953,940	953,601	0,138	R.LLLPGELAK.H	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
			953,601	0,138	R.LLLPGELAK.H	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
953,61	953,133	954,087	953,601	0,009	R.LLLPGELAK.H	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
			953,601	0,009	R.LLLPGELAK.H	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
954,50	954,021	954,976	954,478	0,020	K.FFVGGNWK.M	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP11
			954,470	0,028	R.IFGSYDPR.R	P08311	CATG_HUMAN	Cathepsin G (CG) (EC 3.4.21.20)	CTSG
			954,414	0,085	K.EDMEMKR.Q	P46939	UTRO_HUMAN	Utrophin (Dystrophin-related protein 1) (DRP-1)	UTRN
955,53	955,049	956,004							
956,41	955,933	956,890	956,412	0,000	R.FGSGMNMGR.I	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			956,515	0,103	R.LTFKYER.D	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
956,54	956,066	957,023	956,515	0,030	R.LTFKYER.D	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			956,412	0,133	R.FGSGMNMGR.I	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
957,43	956,949	957,906	957,494	0,066	R.YLSNAYAR.E	O00299	CLIC1_HUMAN	Chloride intracellular channel protein 1 (Chloride channel ABP) (Nuclear chloride ion channel 27) (NCC27) (Regulatory nuclear chloride ion channel protein) (hRNCC)	CLIC1
			957,539	0,111	R.TIGISVDPR.R	P26373	RL13_HUMAN	60S ribosomal protein L13 (Breast basic conserved protein 1) (Large ribosomal subunit protein eL13)	RPL13
			957,544	0,117	R.QINLSNIR.A	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
957,55	957,073	958,030	957,544	0,007	R.QINLSNIR.A	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1

			957,539	0,013	R.TIGISVDPR.R	P26373	RL13_HUMAN	60S ribosomal protein L13 (Breast basic conserved protein 1) (Large ribosomal subunit protein eL13)	RPL13
			957,494	0,058	R.YLSNAYAR.E	O00299	CLIC1_HUMAN	Chloride intracellular channel protein 1 (Chloride channel ABP) (Nuclear chloride ion channel 27) (NCC27) (Regulatory nuclear chloride ion channel protein) (hRNCC)	CLIC1
958,42	957,944	958,903	959,539	0,094	R.NFRNPLAK.-	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
958,56	958,077	959,035				P84243	H33_HUMAN	Histone H3.3	H3F3A; H3F3B
959,44	958,965	959,924							
			959,592	0,147	K.STELLIRK.L	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			959,539	0,025	R.NFRNPLAK.-	P84243	H33_HUMAN	Histone H3.3	H3F3A; H3F3B
			959,592	0,028	K.STELLIRK.L	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			959,539	0,025	R.NFRNPLAK.-	P84243	H33_HUMAN	Histone H3.3	H3F3A; H3F3B
960,45	959,965	960,926	960,547	0,101	K.FLSLPEVR.Q	Q9H3G5	CPVL_HUMAN	Probable serine carboxypeptidase CPVL (EC 3.4.16.-) (Carboxypeptidase, vitellogenic-like) (Vitellogenic carboxypeptidase-like protein) (VCP-like protein) (hVLP)	CPVL
			960,559	0,114	K.FQNALLVR.Y	P02768	ALBU_HUMAN	Serum albumin	ALB
			960,559	0,000	K.FQNALLVR.Y	P02768	ALBU_HUMAN	Serum albumin	ALB
			960,547	0,012	K.FLSLPEVR.Q	Q9H3G5	CPVL_HUMAN	Probable serine carboxypeptidase CPVL (EC 3.4.16.-) (Carboxypeptidase, vitellogenic-like) (Vitellogenic carboxypeptidase-like protein) (VCP-like protein) (hVLP)	CPVL
961,50	961,024	961,985	961,559	0,054	R.QEFLRR.F	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			962,44	0,007	R.RPDEPPPR.R	A4D2P6	GRD2I_HUMAN	Delphiin (Glutamate receptor, ionotropic, delta 2-interacting protein 1)	GRID2IP
			962,53			P26640	SYVC_HUMAN	Valine--tRNA ligase (EC 6.1.1.9) (Protein G7a) (Valyl-tRNA synthetase) (ValRS)	VARS
			963,51						
			963,498	0,032	R.ILPEAHQR.T	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
			963,537	0,156	K.HTLVALRR.V	O00408	PDE2A_HUMAN	cGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic GMP-stimulated phosphodiesterase) (CGS-PDE) (cGSPDE)	PDE2A
964,42	963,938	964,903	965,477	0,030	R.AQYDELAR.K	Q15102	PA1B3_HUMAN	Platelet-activating factor acetylhydrolase IB subunit gamma (EC 3.1.1.47) (PAF acetylhydrolase 29 kDa subunit) (PAF-AH 29 kDa subunit) (PAF-AH subunit gamma) (PAFAH subunit gamma)	PAFAH1B3
964,53	964,049	965,014				O00408	PDE2A_HUMAN	cGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic GMP-stimulated phosphodiesterase) (CGS-PDE) (cGSPDE)	PDE2A
965,45	964,965	965,930				P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
			965,603	0,156	K.HTLVALRR.V	Q15102	PA1B3_HUMAN	Platelet-activating factor acetylhydrolase IB subunit gamma (EC 3.1.1.47) (PAF acetylhydrolase 29 kDa subunit) (PAF-AH 29 kDa subunit) (PAF-AH subunit gamma) (PAFAH subunit gamma)	PAFAH1B3
			965,653	0,205	R.VVVLGLPR.G				
			965,603	0,051	K.HTLVALRR.V	P62906	RL10A_HUMAN	60S ribosomal protein L10a (CSA-19) (Large ribosomal subunit protein uL1) (Neural precursor cell expressed developmentally down-regulated protein 6) (NEDD-6)	RPL10A
			965,477	0,074	R.AQYDELAR.K	Q13535	ATR_HUMAN	Serine/threonine-protein kinase ATR (EC 2.7.11.1) (Ataxia telangiectasia and Rad3-related protein) (FRAP-related protein 1)	ATR
			965,653	0,101	R.VVVLGLPR.G	Q13535	ATR_HUMAN	Serine/threonine-protein kinase ATR (EC 2.7.11.1) (Ataxia telangiectasia and Rad3-related protein) (FRAP-related protein 1)	ATR
			966,489	0,008	R.DTLYEAVR.E	P02649	APOE_HUMAN	Apolipoprotein E (Apo-E)	APOE
						Q13535	ATR_HUMAN	Serine/threonine-protein kinase ATR (EC 2.7.11.1) (Ataxia telangiectasia and Rad3-related protein) (FRAP-related protein 1)	ATR
967,51	967,026	967,993	967,616	0,107	K.EPILALRR.A	P02649	APOE_HUMAN	Apolipoprotein E (Apo-E)	APOE
967,95	967,469	968,437	967,616	0,337	K.EPILALRR.A				
			968,564	0,467	R.LGPLVEQGR.V	P62081	RS7_HUMAN	40S ribosomal protein S7 (Small ribosomal subunit protein eS7)	RPS7
			967,616	0,481	K.EPILALRR.A	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
968,10	967,613	968,581	968,564	0,047	R.LGPLVEQGR.V	Q01433	AMPD2_HUMAN	AMP deaminase 2 (EC 3.5.4.6) (AMP deaminase isoform L)	AMPD2
			969,001	0,045	K.HVVFIAQR.R	P08670	VIME_HUMAN	Vimentin	VIM
			969,544			P00915	CAH1_HUMAN	Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase I) (Carbonic anhydrase B) (CAB) (Carbonic anhydrase I) (CA-I)	CA1
			969,031						
969,06	968,575	969,544	969,561	0,046	R.GGGQIIPTAR.R	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
969,52	969,031	970,000	969,562	0,046	R.RTNVPDIR.V				
			970,567	0,046	R.LRSSVPGVR.L				
			970,585	0,063	K.VLDALQAIK.T				
			970,597	0,076					
970,52	970,036	971,007	970,641	0,120	R.VLLPILFR.N				

971,54	971,056	972,028	971,528	0,014	K.DLLPSRDR.Q	P02671	FIBA_HUMAN	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	FGA
			971,478	0,064	K.QPHVGDYR.Q	Q06323	PSME1_HUMAN	Proteasome activator complex subunit 1 (11S regulator complex subunit alpha) (REG-alpha) (Activator of multicatalytic protease subunit 1) (Interferon gamma up-regulated I-5111 protein) (IGUP I-5111) (Proteasome activator 28 subunit alpha) (PA28a) (PA28alpha)	PSME1
972,45	971,967	972,940	972,481	0,027	K.ESAYLYAR.F	P20774	MIME_HUMAN	Mimecan (Osteoglycin) (Osteoinductive factor) (OIF)	OGN
			972,543	0,090	R.IGKPAPDFK.A	P32119	PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
972,55	972,068	973,040	972,543	0,011	R.IGKPAPDFK.A	P32119	PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
			972,481	0,074	K.ESAYLYAR.F	P20774	MIME_HUMAN	Mimecan (Osteoglycin) (Osteoinductive factor) (OIF)	OGN
973,53	973,041	974,014	973,578	0,051	K.LVPVGYGIR.K	P29692	EF1D_HUMAN	Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO-4)	EEF1D
			973,594	0,066	R.SGVSLAALKK.A	P16403	H12_HUMAN	Histone H1.2 (Histone H1c) (Histone H1d) (Histone H1s-1)	HIST1H1C
			973,621	0,093	R.SKILFPR.K	P26373	RL13_HUMAN	60S ribosomal protein L13 (Breast basic conserved protein 1) (Large ribosomal subunit protein eL13)	RPL13
974,49	974,007	974,982	974,508	0,013	R.GQVFDVGPR.Y	P28482	MK01_HUMAN	Mitogen-activated protein kinase 1 (MAP kinase 1) (MAPK 1) (EC 2.7.11.24) (ERT1) (Extracellular signal-regulated kinase 2) (ERK-2) (MAP kinase isoform p42) (p42-MAPK) (Mitogen-activated protein kinase 2) (MAP kinase 2) (MAPK 2)	MAPK1
975,45	974,959	975,935	975,460	0,013	R.STFSTNYR.S	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
975,55	975,064	976,039	975,460	0,092	R.STFSTNYR.S	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
976,46	975,968	976,944	976,456	0,000	K.AGFAGDDAPR.A	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			976,456	0,000	K.AGFAGDDAPR.A	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			976,456	0,000	K.AGFAGDDAPR.A	Q6S8J3	POTEE_HUMAN	POTE ankryrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
976,70	976,215	977,192	976,551	0,095	K.QLFDQVVK.T	P15311	EZRI_HUMAN	Ezrin (Cyto villin) (Villin-2) (p81)	EZR
			976,551	0,095	K.QLFDQVVK.T	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			976,456	0,248	K.AGFAGDDAPR.A	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
976,46	975,968	976,944	976,456	0,000	K.AGFAGDDAPR.A	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			976,456	0,000	K.AGFAGDDAPR.A	Q6S8J3	POTEE_HUMAN	POTE ankryrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			976,551	0,095	K.QLFDQVVK.T	P15311	EZRI_HUMAN	Ezrin (Cyto villin) (Villin-2) (p81)	EZR
976,70	976,215	977,192	976,551	0,153	K.QLFDQVVK.T	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			976,456	0,248	K.AGFAGDDAPR.A	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			976,456	0,248	K.AGFAGDDAPR.A	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
976,46	975,968	976,944	976,456	0,000	K.AGFAGDDAPR.A	Q6S8J3	POTEE_HUMAN	POTE ankryrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			976,551	0,095	K.QLFDQVVK.T	P15311	EZRI_HUMAN	Ezrin (Cyto villin) (Villin-2) (p81)	EZR
			976,551	0,095	K.QLFDQVVK.T	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
977,48	976,990	977,967	978,493	0,038	R.FSTPEQAAK.N	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
			978,499	0,043	R.MNGIMLRK.I	Q9UKD1	GMEB2_HUMAN	Glucocorticoid modulatory element-binding protein 2 (GMEB-2) (DNA-binding protein p79PIF) (Parvovirus initiation factor p79) (PIF p79)	GMEB2
			978,499	0,043	R.MNGIMLRK.I	Q9UKD1	GMEB2_HUMAN	Glucocorticoid modulatory element-binding protein 2 (GMEB-2) (DNA-binding protein p79PIF) (Parvovirus initiation factor p79) (PIF p79)	GMEB2
978,54	978,047	979,026	978,499	0,038	R.MNGIMLRK.I	Q9UKD1	GMEB2_HUMAN	Glucocorticoid modulatory element-binding protein 2 (GMEB-2) (DNA-binding protein p79PIF) (Parvovirus initiation factor p79) (PIF p79)	GMEB2
			978,499	0,043	R.FSTPEQAAK.N	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
			978,499	0,043	R.FSTPEQAAK.N	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL
979,52	979,028	980,008	979,506	0,012	R.DYLHYIR.K	P62280	RS11_HUMAN	40S ribosomal protein S11 (Small ribosomal subunit protein uS17)	RPS11
			979,502	0,016	K.AYGRIER.M	P14625	ENPL_HUMAN	Endoplasmic reticulum protein 94 kDa glucose-regulated protein (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			979,558	0,040	K.LLSYGASR.N	Q99728	BARD1_HUMAN	BRCA1-associated RING domain protein 1 (BARD-1) (EC 2.3.2.27) (RING-type E3 ubiquitin transferase BARD1)	BARD1
980,50	980,012	980,993	979,573	0,055	R.NVNPVALPR.A	P08311	CATG_HUMAN	Cathepsin G (CG) (EC 3.4.21.20)	CTSG
			980,497	0,005	K.YIQHTYR.K	P52565	GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)	ARHGDI1
			980,496	0,007	R.VGVVSGWGR.N	P00738	HPT_HUMAN	Haptoglobin (Zonulin) [Cleaved into: Haptoglobin alpha chain; Haptoglobin beta chain]	HP

981,44	980,952	981,934	981,471	0,028	R.MEFGTAGL.R.A	Q96G03	PGM2_HUMAN	Phosphoglucomutase-2 (PGM 2) (EC 5.4.2.2) (Glucose phosphomutase 2) (Phosphodeoxyribomutase) (Phosphopentomutase) (EC 5.4.2.7)	PGM2
981,54	981,049	982,031	981,471	0,069	R.MEFGTAGL.R.A	Q96G03	PGM2_HUMAN	Phosphoglucomutase-2 (PGM 2) (EC 5.4.2.2) (Glucose phosphomutase 2) (Phosphodeoxyribomutase) (Phosphopentomutase) (EC 5.4.2.7)	PGM2
982,51	982,016	982,999	982,524	0,017	R.HPFAQAVGR.N	O43837	IDH3B_HUMAN	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial (Isocitric dehydrogenase subunit beta) (NAD(+)-specific ICDH subunit beta)	IDH3B
983,53	983,040	984,024	983,538	0,007	R.HGSLGFLPR.K	P39023	RL3_HUMAN	60S ribosomal protein L3 (HIV-1 TAR RNA-binding protein B) (TARBP-B) (Large ribosomal subunit protein uL3)	RPL3
			983,470	0,061	R.QGSFQGGFR.S	P0C0L5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
984,09	983,595	984,579	983,620	0,088	R.ALILVGLER.V	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			984,499	0,411	K.TYETLEK.C	P02768	ALBU_HUMAN	Serum albumin	ALB
			984,523	0,435	K.GLEGERPAR.L	P46783	RS10_HUMAN	40S ribosomal protein S10 (Small ribosomal subunit protein eS10)	RPS10
			984,539	0,452	R.QAVDVSP.LR	P46782	R55_HUMAN	40S ribosomal protein S5 (Small ribosomal subunit protein uS7) [Cleaved into: 40S ribosomal protein S5, N-terminally processed]	RP55
984,52	984,027	985,012	983,620	0,468	R.ALILVGLER.V	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			984,523	0,003	K.GLEGERPAR.L	P46783	RS10_HUMAN	40S ribosomal protein S10 (Small ribosomal subunit protein eS10)	RPS10
			984,539	0,020	R.QAVDVSP.LR	P46782	R55_HUMAN	40S ribosomal protein S5 (Small ribosomal subunit protein uS7) [Cleaved into: 40S ribosomal protein S5, N-terminally processed]	RP55
			984,499	0,021	K.TYETLEK.C	P02768	ALBU_HUMAN	Serum albumin	ALB
985,56	985,070	986,056	984,610	0,091	R.GLVGEIKR.F	P22392	NDKB_HUMAN	Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (EC 2.7.4.6) (C-myc purine-binding transcription factor PUF) (Histidine protein kinase NDKB) (EC 2.7.13.3) (nm23-H2)	NME2
			985,509	0,054	R.EALPGSGQAR.F	Q96IU4	ABHEB_HUMAN	Protein ABHD14B (EC 3.-.-.-) (Alpha/beta hydrolase domain-containing protein 14B) (Abhydrolase domain-containing protein 14B) (CCG1-interacting factor B)	ABHD14B
986,48	985,987	986,974	985,433	0,130	K.GGPFDSYR.L	P00915	CAH1_HUMAN	Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase I) (Carbonic anhydrase B) (CAB) (Carbonic anhydrase I) (CA-I)	CA1
			986,608	0,128	R.DLPLLLFR.T	O43175	SERA_HUMAN	D-3-phosphoglycerate dehydrogenase (3-PGDH) (EC 1.1.1.95) (2-oxoglutarate reductase) (EC 1.1.1.399) (Malate dehydrogenase) (EC 1.1.1.37)	PHGDH
986,56	986,067	987,054	986,608	0,048	R.DLPLLLFR.T	O43175	SERA_HUMAN	D-3-phosphoglycerate dehydrogenase (3-PGDH) (EC 1.1.1.95) (2-oxoglutarate reductase) (EC 1.1.1.399) (Malate dehydrogenase) (EC 1.1.1.37)	PHGDH
			987,535	0,002	R.SQFKGPAPR.E	O15145	ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3 (Arp2/3 complex 21 kDa subunit) (p21-ARC)	ARPC3
987,54	987,043	988,030	987,608	0,071	R.RVPFSLR.G	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	HSPB1
988,52	988,021	989,010	988,542	0,027	R.SAINEVVTR.E	P62899	RL31_HUMAN	60S ribosomal protein L31 (Large ribosomal subunit protein eL31)	RPL31
			988,552	0,037	R.LQETGLLSK.C	Q9UQL6	HDAC5_HUMAN	Histone deacetylase 5 (HD5) (EC 3.5.1.98) (Antigen NY-CO-9)	HDAC5
989,54	989,041	990,031	989,529	0,007	R.LSKEDIER.M	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
			989,578	0,042	K.VFLENVIR.D	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
990,45 990,57 991,43	989,953 990,071 990,930	990,943 991,062 991,921	991,527	0,102	K.FHPIQGHR.V	Q13151	ROA0_HUMAN	Heterogeneous nuclear ribonucleoprotein A0 (hnRNP A0)	HNRNPA0
			991,531	0,106	K.HQNVQLPR.E	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
991,55	991,051	992,042	991,531	0,015	K.HQNVQLPR.E	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
			991,527	0,019	K.FHPIQGHR.V	Q13151	ROA0_HUMAN	Heterogeneous nuclear ribonucleoprotein A0 (hnRNP A0)	HNRNPA0
992,44	991,948	992,940	992,527	0,083	R.QVNEPHIR.V	P12109	CO6A1_HUMAN	Collagen alpha-1(VI) chain	COL6A1

992,56	992,066	993,058	992,527	0,035	R.QVNPHIR.V	P12109	CO6A1_HUMAN	Collagen alpha-1(VI) chain	COL6A1
993,47	992,977	993,970	993,597	0,124	R.LLIYGASTR.A	P01624	KV315_HUMAN	Immunoglobulin kappa variable 3-15 (Ig kappa chain V-III region CLL) (Ig kappa chain V-III region POM)	IGKV3-15
			993,674	0,200	K.IIVLGLLPR.G	P68402	PA1B2_HUMAN	Platelet-activating factor acetylhydrolase IB subunit beta (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH subunit beta) (PAFAH subunit beta)	PAFAH1B2
993,56	993,064	994,057	993,597	0,037	R.LLIYGASTR.A	P01624	KV315_HUMAN	Immunoglobulin kappa variable 3-15 (Ig kappa chain V-III region CLL) (Ig kappa chain V-III region POM)	IGKV3-15
			993,674	0,113	K.IIVLGLLPR.G	P68402	PA1B2_HUMAN	Platelet-activating factor acetylhydrolase IB subunit beta (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH subunit beta) (PAFAH subunit beta)	PAFAH1B2
994,47	993,974	994,969	994,505	0,033	R.LGLDYEER.V	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
994,58	994,079	995,074	994,505	0,072	R.LGLDYEER.V	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
995,54	995,039	996,034	995,563	0,026	K.IRIEDPPR.R	P61160	ARP2_HUMAN	Actin-related protein 2 (Actin-like protein 2)	ACTR2
996,53	996,028	997,025							
997,46	996,963	997,961							
997,52	997,021	998,018							
998,42	997,919	998,918	998,482	0,063	R.DLTDYLMK.I	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			998,482	0,063	R.DLTDYLMK.I	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			998,482	0,063	R.DLTDYLMK.I	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
998,55	998,048	999,047	998,482	0,066	R.DLTDYLMK.I	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			998,482	0,066	R.DLTDYLMK.I	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			998,482	0,066	R.DLTDYLMK.I	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
999,43	998,933	999,932	999,599	0,166	R.KVGIDNVVR.K	Q8WZ42	TITIN_HUMAN	Titin (EC 2.7.11.1) (Connectin) (Rhabdomyosarcoma antigen MU-RMS-40.14)	TTN
999,57	999,073	1000,073	999,599	0,026	R.KVGIDNVVR.K	Q8WZ42	TITIN_HUMAN	Titin (EC 2.7.11.1) (Connectin) (Rhabdomyosarcoma antigen MU-RMS-40.14)	TTN
999,91	999,407	1000,407	999,599	0,309	R.KVGIDNVVR.K	Q8WZ42	TITIN_HUMAN	Titin (EC 2.7.11.1) (Connectin) (Rhabdomyosarcoma antigen MU-RMS-40.14)	TTN
1000,06	999,556	1000,556	1000,494	0,439	K.YLGEEYVK.A	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			999,599	0,457	R.KVGIDNVVR.K	Q8WZ42	TITIN_HUMAN	Titin (EC 2.7.11.1) (Connectin) (Rhabdomyosarcoma antigen MU-RMS-40.14)	TTN
1000,54	1000,043	1001,044	1000,494	0,049	K.YLGEEYVK.A	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1000,612	0,069	K.QTALVELVK.H	P02768	ALBU_HUMAN	Serum albumin	ALB
1001,00	1000,504	1001,505	1000,612	0,392	K.QTALVELVK.H	P02768	ALBU_HUMAN	Serum albumin	ALB
1001,47	1000,967	1001,969	1001,531	0,063	R.VLNTNIDGR.R	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
			1001,579	0,111	K.EEELVKVR.E	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIa)	MYH9
			1001,600	0,131	K.VLTEIASR.T	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
1001,58	1001,077	1002,079	1001,579	0,001	K.EEELVKVR.E	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIa)	MYH9
			1001,600	0,021	K.VLTEIASR.T	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
			1001,531	0,047	R.VLNTNIDGR.R	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
1002,54	1002,038	1003,040							
1003,53	1003,032	1004,035	1003,543	0,009	R.LSKEEIER.M	P0DMV8	H571A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
			1003,513	0,021	R.SPYGGGRPGR.V	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RPS9
1004,53	1004,023	1005,027	1004,562	0,037	R.LQQNLFGGK.F	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1004,580	0,055	R.RFVEQVAR.R	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
			1004,614	0,088	R.TLIEFLLR.F	P28838	AMPL_HUMAN	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase 3) (LAP-3) (Leucyl aminopeptidase) (Peptidase 5) (Proline aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase)	LAP3

			1004,614	0,088	M.ELTIFILR.L	Q9H8H3	MET7A_HUMAN	Methyltransferase-like protein 7A (EC 2.1.1.-) (Protein AAM-B)	METTL7A
1005,48	1004,975	1005,980	1005,566	0,088	R.RDVYLSPR.D	P38159	RBMX_HUMAN	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX
1005,61	1005,106	1006,112	1005,566	0,043	R.RDVYLSPR.D	P38159	RBMX_HUMAN	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX
1006,47	1005,964	1006,970	1006,527	0,060	R.SEQFINLR.E	P07384	CAN1_HUMAN	Calpain-1 catalytic subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase 1) (CANP 1) (Calpain mu-type) (Calpain-1 large subunit) (Cell proliferation-inducing gene 30 protein) (Micromolar-calpain) (muCANP)	CAPN1
			1006,604	0,137	M.APEVLKPR.M	P09669	COX6C_HUMAN	Cytochrome c oxidase subunit 6C (Cytochrome c oxidase polypeptide Vic)	COX6C
1006,56	1006,057	1007,064	1006,527	0,033	R.SEQFINLR.E	P07384	CAN1_HUMAN	Calpain-1 catalytic subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase 1) (CANP 1) (Calpain mu-type) (Calpain-1 large subunit) (Cell proliferation-inducing gene 30 protein) (Micromolar-calpain) (muCANP)	CAPN1
			1006,604	0,044	M.APEVLKPR.M	P09669	COX6C_HUMAN	Cytochrome c oxidase subunit 6C (Cytochrome c oxidase polypeptide Vic)	COX6C
1007,60	1007,097	1008,104	1007,576	0,025	R.KIGGHGPTLK.A	Q16881	TRXR1_HUMAN	Thioredoxin reductase 1, cytoplasmic (TR) (EC 1.8.1.9) (Gene associated with retinoic and interferon-induced mortality 12 protein) (GRIM-12) (Gene associated with retinoic and IFN-induced mortality 12 protein) (KM-102-derived reductase-like factor) (Thioredoxin reductase TR1)	TXNRD1
			1007,576	0,025	R.LGLGHNQIR.M	P21810	PGS1_HUMAN	Biglycan (Bone/cartilage proteoglycan I) (PG-51)	BGN
			1007,514	0,087	R.DFSLEQLR.Q	O15173	PGRC2_HUMAN	Membrane-associated progesterone receptor component 2 (Progesterone membrane-binding protein) (Steroid receptor protein DG6)	PGRMC2
1008,58	1008,072	1009,081	1008,533	0,043	K.VFNDMKVR.K	P23528	COF1_HUMAN	Cofilin-1 (18 kDa phosphoprotein) (p18) (Cofilin, non-muscle isoform)	CFL1
1009,56	1009,056	1010,065	1009,547	0,014	M.GVPFFSSLR.C	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
1011,71	1011,205	1012,217	1011,574	0,137	K.GANPVEIRR.G	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
1012,59	1012,081	1013,093	1012,583	0,004	K.KAPALEDLR.Q	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-(1-242)]]	APOA1
1012,72	1012,212	1013,225	1012,583	0,136	K.KAPALEDLR.Q	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-(1-242)]]	APOA1
1013,50	1012,997	1014,011	1013,520	0,016	R.DGAAPTASAPR.G	Q6UX72	B3GN9_HUMAN	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9 (BGnT-9) (Beta-1,3-Gn-T9) (Beta-1,3-N-acetylglucosaminyltransferase 9) (Beta3Gn-T9) (EC 2.4.1.-)	B3GNT9
			1013,446	0,058	R.GGNFGFGDSR.G	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			1013,573	0,069	R.AELVGQLQR.L	Q9H008	LHPP_HUMAN	Phosphotyrosine phosphatase (hLHPP) (EC 3.1.3.-) (EC 3.6.1.1)	LHPP
			1013,573	0,069	R.QKGINGQLR.S	Q92609	TBCD5_HUMAN	TBC1 domain family member 5	TBC1D5
1013,68	1013,178	1014,192	1013,573	0,112	R.AELVGQLQR.L	Q9H008	LHPP_HUMAN	Phosphotyrosine phosphatase (hLHPP) (EC 3.1.3.-) (EC 3.6.1.1)	LHPP
			1013,573	0,112	R.QKGINGQLR.S	Q92609	TBCD5_HUMAN	TBC1 domain family member 5	TBC1D5
			1013,520	0,165	R.DGAAPTASAPR.G	Q6UX72	B3GN9_HUMAN	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9 (BGnT-9) (Beta-1,3-Gn-T9) (Beta-1,3-N-acetylglucosaminyltransferase 9) (Beta3Gn-T9) (EC 2.4.1.-)	B3GNT9
			1013,446	0,239	R.GGNFGFGDSR.G	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
1014,59	1014,079	1015,094	1014,530	0,057	R.QGANINEIR.Q	Q15365	PCBP1_HUMAN	Poly(rC)-binding protein 1 (Alpha-CP1) (Heterogeneous nuclear ribonucleoprotein E1) (hnRNP E1) (Nucleic acid-binding protein SUB2.3)	PCBP1
			1014,522	0,065	K.EAQMPAVIR.F	P19835	CEL_HUMAN	Bile salt-activated lipase (BAL) (EC 3.1.1.13) (EC 3.1.1.3) (Bile salt-stimulated lipase) (BSSL) (Bucelipase) (Carboxyl ester lipase) (Cholesterol esterase) (Pancreatic lysophospholipase) (Sterol esterase)	CEL
1015,60	1015,089	1016,105	1015,585	0,013	K.DVNAAIATIK.T	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B

			1015,481	0,116	R.GLFDEYGSK.K	P14625	ENPL_HUMAN	Endoplasmrin (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
1016,51	1015,997	1017,014							
1016,60	1016,088	1017,105							
1017,60	1017,096	1018,113							
1018,25	1017,740	1018,759	1018,526	0,277	R.SLQSVAEER.A	P61313	RL15_HUMAN	60S ribosomal protein L15 (Large ribosomal subunit protein eL15)	RPL15
			1018,577	0,328	R.LHPFHVIR.I	P27635	RL10_HUMAN	60S ribosomal protein L10 (Laminin receptor homolog) (Large ribosomal subunit protein uL16) (Protein QM) (Ribosomal protein L10) (Tumor suppressor QM)	RPL10
1018,53	1018,022	1019,040	1018,526	0,005	R.SLQSVAEER.A	P61313	RL15_HUMAN	60S ribosomal protein L15 (Large ribosomal subunit protein eL15)	RPL15
			1018,577	0,046	R.LHPFHVIR.I	P27635	RL10_HUMAN	60S ribosomal protein L10 (Laminin receptor homolog) (Large ribosomal subunit protein uL16) (Protein QM) (Ribosomal protein L10) (Tumor suppressor QM)	RPL10
1019,24	1018,727	1019,746	1019,497	0,261	K.NAGFTPQER.Q	P27695	APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase (EC 3.1.-.-) (EC 4.2.99.18) (APEX nuclease) (APEN) (Apyriminic-apyrimidinic endonuclease 1) (AP endonuclease 1) (APE-1) (REF-1) (Redox factor-1) [Cleaved into: DNA-(apurinic or apyrimidinic site) lyase, mitochondrial]	APEX1
			1019,576	0,339	R.AFKAWAVAR.L	P02768	ALBU_HUMAN	Serum albumin	ALB
1019,53	1019,020	1020,039	1019,497	0,032	K.NAGFTPQER.Q	P27695	APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase (EC 3.1.-.-) (EC 4.2.99.18) (APEX nuclease) (APEN) (Apyriminic-apyrimidinic endonuclease 1) (AP endonuclease 1) (APE-1) (REF-1) (Redox factor-1) [Cleaved into: DNA-(apurinic or apyrimidinic site) lyase, mitochondrial]	APEX1
			1019,576	0,046	R.AFKAWAVAR.L	P02768	ALBU_HUMAN	Serum albumin	ALB
1020,55	1020,035	1021,055							
1021,55	1021,042	1022,064							
1022,55	1022,043	1023,066							
1023,56	1023,043	1024,067	1023,571	0,016	R.AVIFDRFR.G	P35232	PHB_HUMAN	Prohibitin	PHB
1024,53	1024,018	1025,042	1024,546	0,016	R.VGDQVTHIR.I	P29350	PTN6_HUMAN	Tyrosine-protein phosphatase non-receptor type 6 (EC 3.1.3.48) (Hematopoietic cell protein-tyrosine phosphatase) (Protein-tyrosine phosphatase 1C) (PTP-1C) (Protein-tyrosine phosphatase SHP-1) (SH-PTP1)	PTPN6
			1024,554	0,023	R.FNALQYLRL	P51884	LUM_HUMAN	Lumican (Keratan sulfate proteoglycan lumican) (KSPG lumican)	LUM
1025,45	1024,935	1025,960	1025,542	0,094	R.DFVNYLVR.I	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A (EC 3.6.4.13) (DEAH box protein 9) (DExH-box helicase 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II) (RNA helicase A)	DHX9
			1025,586	0,138	K.YALPLVGHRR.K	P13667	PDIA4_HUMAN	Protein disulfide-isomerase A4 (EC 5.3.4.1) (Endoplasmic reticulum resident protein 70) (ER protein 70) (ERp70) (Endoplasmic reticulum resident protein 72) (ER protein 72) (ERp-72) (ERp72)	PDIA4
			1025,614	0,167	R.ALQSPALGLR.G	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
			1025,619	0,171	K.IGGIGTVPVGR.V	P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1
1025,58	1025,065	1026,091	1025,586	0,008	K.YALPLVGHRR.K	P13667	PDIA4_HUMAN	Protein disulfide-isomerase A4 (EC 5.3.4.1) (Endoplasmic reticulum resident protein 70) (ER protein 70) (ERp70) (Endoplasmic reticulum resident protein 72) (ER protein 72) (ERp-72) (ERp72)	PDIA4
			1025,542	0,036	R.DFVNYLVR.I	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A (EC 3.6.4.13) (DEAH box protein 9) (DExH-box helicase 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II) (RNA helicase A)	DHX9
			1025,614	0,036	R.ALQSPALGLR.G	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
			1025,619	0,040	K.IGGIGTVPVGR.V	P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1
1026,47	1025,960	1026,987	1026,592	0,118	K.AVDSLVPIGR.G	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
1026,59	1026,075	1027,101	1026,592	0,004	K.AVDSLVPIGR.G	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
1027,48	1026,965	1027,992							
1027,57	1027,054	1028,082	1028,535	0,037	K.TAVCDIPPR.G	P07437	TB85_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
1028,57	1028,058	1029,087	1028,535	0,037	K.TAVCDIPPR.G	P68371	TB84B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1028,508	0,065	K.NSLFEYQK.N	P02671	FIBA_HUMAN	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	FGA
1029,56	1029,044	1030,073	1029,586	0,028	K.KLGVSVSPSR.A	Q86VM9	ZCH18_HUMAN	Zinc finger CCH domain-containing protein 18 (Nuclear protein NHN1)	ZC3H18
			1029,600	0,042	R.VLDELTLAR.T	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
1030,55	1030,039	1031,070	1030,544	0,010	R.GVFHQTVSR.K	P12109	CO6A1_HUMAN	Collagen alpha-1(VI) chain	COL6A1
			1030,531	0,024	K.EAQMPAVIR.F	P19835	CEL_HUMAN	Bile salt-activated lipase (BAL) (EC 3.1.1.13) (EC 3.1.1.3) (Bile salt-stimulated lipase) (BSSL) (Bucelipase) (Carboxyl ester lipase) (Cholesterol esterase) (Pancreatic lysophospholipase) (Sterol esterase)	CEL
			1030,522	0,032	K.YEKPQSPPR.E	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1

1031,51	1030,998	1032,030	1031,540	0,026	K.SSAEVIAQAR.K	Q16555	DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) (Unc-33-like phosphoprotein 2) (ULIP-2)	DPYSL2
			1031,546	0,032	K.EGLVMVEVR.K	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
			1031,546	0,032	K.VLEGMEVVR.K	P23284	PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) (CYP-S1) (Cyclophilin B) (Rotamase B) (S-cyclophilin) (SCYLP)	PPIB
1031,54	1031,028	1032,060	1031,546	0,002	K.EGLVMVEVR.K	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
			1031,546	0,002	K.VLEGMEVVR.K	P23284	PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) (CYP-S1) (Cyclophilin B) (Rotamase B) (S-cyclophilin) (SCYLP)	PPIB
			1031,540	0,004	K.SSAEVIAQAR.K	Q16555	DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) (Unc-33-like phosphoprotein 2) (ULIP-2)	DPYSL2
1032,57	1032,058	1033,090	1032,566	0,008	K.IRPFFPQQ.-	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
			1032,557	0,017	R.AKWPEVVR.H	P15153	RAC2_HUMAN	Ras-related C3 botulinum toxin substrate 2 (GX) (Small G protein) (p21-Rac2)	RAC2
			1032,592	0,018	R.YRPGTVALR.E	P84243	H33_HUMAN	Histone H3.3	H3F3A; H3F3B
1033,58	1033,068	1034,101	1033,545	0,039	R.HGGPLPYHR.R	Q16853	AOC3_HUMAN	Membrane primary amine oxidase (EC 1.4.3.21) (Copper amine oxidase) (HPAO) (Semicarbazide-sensitive amine oxidase) (SSAO) (Vascular adhesion protein 1) (VAP-1)	AOC3
			1033,529	0,056	R.TLLEGESR.M	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
1034,59	1034,075	1035,110	1034,528	0,064	K.VGPEADKYR.L	P02679	FIBG_HUMAN	Fibrinogen gamma chain	FGG
1035,55	1035,033	1036,068	1035,530	0,021	K.WISIMTER.S	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1035,597	0,046	R.KFLPLFDR.V	P61604	CH10_HUMAN	10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperonin) (Chaperonin 10) (CPN10) (Early-pregnancy factor) (EPF)	HSPE1
1036,55	1036,028	1037,065	1036,552	0,005	R.HYELVRR.C	Q9NVA2	SEP11_HUMAN	Septin-11	SEPT11
			1036,536	0,010	R.VAVVQYSDR.T	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1036,651	0,104	K.IKIIAPPER.K	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			1036,651	0,104	K.IKIIAPPER.K	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1036,651	0,104	K.IKIIAPPER.K	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
1037,56	1037,041	1038,079	1037,542	0,018	R.GFTIPEAFR.G	O00299	CLIC1_HUMAN	Chloride intracellular channel protein 1 (Chloride channel ABP) (Nuclear chloride ion channel 27) (NCC27) (Regulatory nuclear chloride ion channel protein) (hRNCC)	CLIC1
			1037,536	0,023	K.GFLIDGYPR.E	P00568	KAD1_HUMAN	Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP-AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	AK1
			1037,606	0,046	M.EAAVAAPRPR.L	P36897	TGFR1_HUMAN	TGF-beta receptor type-1 (TGFR-1) (EC 2.7.11.30) (Activin A receptor type II-like protein kinase of 53kD) (Activin receptor-like kinase 5) (ALK-5) (ALK5) (Serine/threonine-protein kinase receptor R4) (SKR4) (TGF-beta type I receptor) (Transforming growth factor-beta receptor type I) (TGF-beta receptor type I) (TbetaR-I)	TGFBRI
1038,54	1038,020	1039,058	1038,565	0,026	R.SGQQIVGPPR.K	Q9UNZ2	NSF1C_HUMAN	NSF1 cofactor p47 (UBX domain-containing protein 2C) (p97 cofactor p47)	NSF1C
1039,56	1039,035	1040,075	1039,519	0,036	K.EGIQPDQQR.L	P62987	RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 (CEP52) (Ubiquitin A-52 residue ribosomal protein fusion product 1) [Cleaved into: Ubiquitin; 60S ribosomal protein L40 (Large ribosomal subunit protein eL40)]	UBA52
			1039,594	0,039	R.YLTVAAVFR.G	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1039,594	0,039	R.YLTVAAVFR.G	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1039,604	0,049	R.VVRDPQGIR.A	P61626	LYSC_HUMAN	Lysozyme C (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C)	LYZ
1040,54	1040,017	1041,057	1040,516	0,021	R.DFFLANASR.A	P07384	CAN1_HUMAN	Calpain-1 catalytic subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase 1) (CANP 1) (Calpain mu-type) (Calpain-1 large subunit) (Cell proliferation-inducing gene 30 protein) (Micromolar-calpain) (muCANP)	CAPN1
1041,49	1040,972	1042,013	1041,558	0,066	R.VEELVEAPR.A	Q9NZQ8	TRPM5_HUMAN	Transient receptor potential cation channel subfamily M member 5 (Long transient receptor potential channel 5) (LTpC-5) (LTpCS) (MLSN1-and TRP-related gene 1 protein)	TRPM5
			1041,602	0,110	R.IVLQIDNAR.L	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
			1041,602	0,110	R.IVLQIDNAR.L	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1041,607	0,114	R.AQQQAIALAK.E	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1041,607	0,114	K.LNTITPVVGK.K	Q9CHK8	CHD8_HUMAN	Chromodomain-helicase-DNA-binding protein 8 (CHD-8) (EC 3.6.4.12) (ATP-dependent helicase CHD8) (Helicase with SNF2 domain 1)	CHD8

1041,58	1041,058	1042,100	1041,645	0,152	R.ALVGKDLLGR.F	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1041,558	0,021	R.VEELVEAPR.A	Q9NZQ8	TRPM5_HUMAN	Transient receptor potential cation channel subfamily M member 5 (Long transient receptor potential channel 5) (LTrpC-5) (LTrpC5) (MLSN1- and TRP-related gene 1 protein)	TRPM5
			1041,602	0,024	R.IVLQIDNAR.L	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
			1041,602	0,024	R.IVLQIDNAR.L	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1041,607	0,028	R.AQQQAIALAK.E	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1041,607	0,028	K.LNTITPVVGK.K	Q9HCK8	CHD8_HUMAN	Chromodomain-helicase-DNA-binding protein 8 (CHD-8) (EC 3.6.4.12) (ATP-dependent helicase CHD8) (Helicase with SNF2 domain 1)	CHD8
			1041,645	0,066	R.ALVGKDLLGR.F	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1043,553	0,006	R.AGGTLGRAGAGR.G	Q9BYN0	SRXN1_HUMAN	Sulfiredoxin-1 (EC 1.8.98.2)	SRXN1
			1043,527	0,020	R.AFGYYGPLR.S	P84103	SRSF3_HUMAN	Serine/arginine-rich splicing factor 3 (Pre-mRNA-splicing factor SRP20) (Splicing factor, arginine/serine-rich 3)	SRSF3
			1043,625	0,078	R.ELTAVVQKR.F	P23396	RS3_HUMAN	40S ribosomal protein S3 (EC 4.2.99.18) (Small ribosomal subunit protein uS3)	RPS3
1044,55	1044,025	1045,069	1044,586	0,039	K.TTPATLAEK.I	Q8WZ42	TITIN_HUMAN	Titin (EC 2.7.11.1) (Connectin) (Rhabdomyosarcoma antigen MU-RMS-40.14)	TTN
			1044,634	0,087	R.ISVFRPGLR.D	Q04837	SSBP_HUMAN	Single-stranded DNA-binding protein, mitochondrial (Mt-SSB) (MTSSB) (PWP1-interacting protein 17)	SSBP1
1045,55	1045,027	1046,073	1046,553	0,010	K.VIDDTNITR.L	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
						P39656	OST48_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit (DDOST 48 kDa subunit) (Oligosaccharyl transferase 48 kDa subunit)	DDOST
1047,57	1047,049	1048,097	1050,551	0,037	R.VFDMLNRR.Y	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-I (eIF-4A-I) (eIF4A-I) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
						Q14240	IF4A2_HUMAN	Eukaryotic initiation factor 4A-II (eIF-4A-II) (eIF4A-II) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-2)	EIF4A2
						P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	PRKDC
						P50995	ANX11_HUMAN	Annexin A11 (56 kDa autoantigen) (Annexin XI) (Annexin-11) (Calcyclin-associated annexin 50) (CAP-50)	ANXA11
1051,57	1051,047	1052,099	1051,536	0,037	R.SIGEYDVL.R	P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	PRKDC
1052,55	1052,024	1053,077	1052,515	0,036	K.NTPAFFAER.L	P50995	ANX11_HUMAN	Annexin A11 (56 kDa autoantigen) (Annexin XI) (Annexin-11) (Calcyclin-associated annexin 50) (CAP-50)	ANXA11
1053,57	1053,046	1054,100	1053,606	0,033	R.EPSLEIPR.T	Q9UQL6	HDAC5_HUMAN	Histone deacetylase 5 (HD5) (EC 3.5.1.98) (Antigen NY-CO-9)	HDAC5
1054,57	1054,043	1055,098	1054,570	0,000	K.TPGGAQSALR.A	P62263	RS14_HUMAN	40S ribosomal protein S14 (Small ribosomal subunit protein uS11)	RPS14
			1054,613	0,043	K.IIDRRPER.R	Q8NC51	PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein (PAI1 RNA-binding protein 1) (PAI-RBP1) (SERPINE1 mRNA-binding protein 1)	SERBP1
			1054,513	0,058	K.GFGGQYGIQK.D	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
			1054,504	0,066	R.IDAYMAQSR.G	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
1055,60	1055,070	1056,126	1056,529	0,055	R.VYSTSVTGS.R	Q9H299	SH3L3_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 3 (SH3 domain-binding protein 1) (SH3BP-1)	SH3BGL3
						O60664	PLIN3_HUMAN	Perilipin-3 (47 kDa mannose 6-phosphate receptor-binding protein) (47 kDa MPR-binding protein) (Cargo selection protein TIP47) (Mannose-6-phosphate receptor-binding protein 1) (Placental protein 17) (PP17)	PLIN3
1057,58	1057,051	1058,109	1057,602	0,022	K.TLETVPLER.K	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			1057,605	0,025	K.LLPNMAVKR.N	Q99728	BARD1_HUMAN	BRCA1-associated RING domain protein 1 (BARD-1) (EC 2.3.2.27) (RING-type E3 ubiquitin transferase BARD1)	BARD1
			1057,536	0,044	K.GGVDHAAAFGR.I	Q9HC38	GLOD4_HUMAN	Glyoxalase domain-containing protein 4	GLOD4
1058,56	1058,032	1059,091	1058,645	0,083	R.IIVEKPFGR.D	P11413	G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	G6PD
1059,57	1059,040	1060,099	1060,554	0,004	K.IPDWF.LNR.Q	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
						P20774	MIME_HUMAN	Mimecan (Osteoglycin) (Osteoinductive factor) (OIF)	OGN
1061,58	1061,044	1062,106	1061,582	0,007	R.RPPEAAAPR.R	P98095	FBLN2_HUMAN	Fibulin-2 (FIBL-2)	FBLN2
1062,56	1062,033	1063,096	1062,509	0,056	K.ALTDMPQMR.M	P02671	FIBA_HUMAN	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	FGA
1063,56	1063,024	1064,088	1063,528	0,028	R.GVNTFSPEGR.L	P28066	PSA5_HUMAN	Proteasome subunit alpha type-5 (EC 3.4.25.1) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta chain) (Proteasome zeta chain)	PSMA5

1064,60	1064,071	1065,135	1064,613	0,010	R.LASYLDKVR.A	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1064,613	0,010	R.LASYLDKVR.A	P13645	K1C10_HUMAN	Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KRT10
			1064,585	0,018	K.SFPNLA FIR.L	P51888	PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	PRELP
			1064,583	0,020	R.LLIYDASNR.A	P04433	KV311_HUMAN	Immunoglobulin kappa variable 3-11 (Ig kappa chain V-III region VG)	IGKV3-11
			1064,556	0,048	R.ALYEAGERR.K	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
1065,60	1065,064	1066,130	1064,541	0,063	R.HFNAPSHVR.R	Q9UNX3	RL26L_HUMAN	60S ribosomal protein L26-like 1 (Large ribosomal subunit protein uL24-like 1)	RPL26L1
			1065,617	0,020	R.VVLGAHNLSR.R	P08246	ELNE_HUMAN	Neutrophil elastase (EC 3.4.21.37) (Bone marrow serine protease) (Elastase-2) (Human leukocyte elastase) (HLE) (Medullasin) (PMN elastase)	ELANE
			1065,456	0,141	R.RMNEAADSR.D	Q8IY92	SLX4_HUMAN	Structure-specific endonuclease subunit SLX4 (BTB/POZ domain-containing protein 12)	SLX4
			1065,617	0,456	R.VVLGAHNLSR.R	P08246	ELNE_HUMAN	Neutrophil elastase (EC 3.4.21.37) (Bone marrow serine protease) (Elastase-2) (Human leukocyte elastase) (HLE) (Medullasin) (PMN elastase)	ELANE
			1066,549	0,476	R.HPSFFLYR.S	P25774	CATS_HUMAN	Cathepsin S (EC 3.4.22.27)	CTSS
1066,17	1065,637	1066,703	1066,549	0,379	R.HPSFFLYR.S	P25774	CATS_HUMAN	Cathepsin S (EC 3.4.22.27)	CTSS
1066,58	1066,044	1067,111	1066,549	0,029	R.HPSFFLYR.S	P25774	CATS_HUMAN	Cathepsin S (EC 3.4.22.27)	CTSS
1067,13	1066,598	1067,665	1067,538	0,406	K.NTIVTSYNR.N	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
			1067,619	0,488	K.ESTLHLVLR.L	P62987	RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 (CEP52) (Ubiquitin A-52 residue ribosomal protein fusion product 1) [Cleaved into: Ubiquitin; 60S ribosomal protein L40 (Large ribosomal subunit protein eL40)]	UBA52
1067,46	1066,923	1067,990	1067,538	0,081	K.NTIVTSYNR.N	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
			1067,619	0,162	K.ESTLHLVLR.L	P62987	RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 (CEP52) (Ubiquitin A-52 residue ribosomal protein fusion product 1) [Cleaved into: Ubiquitin; 60S ribosomal protein L40 (Large ribosomal subunit protein eL40)]	UBA52
1067,59	1067,053	1068,120	1067,619	0,032	K.ESTLHLVLR.L	P62987	RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 (CEP52) (Ubiquitin A-52 residue ribosomal protein fusion product 1) [Cleaved into: Ubiquitin; 60S ribosomal protein L40 (Large ribosomal subunit protein eL40)]	UBA52
			1067,538	0,049	K.NTIVTSYNR.N	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
1068,60	1068,063	1069,131	1070,627	0,164	R.IAGQVAAANKK.H	P39019	RS19_HUMAN	40S ribosomal protein S19 (Small ribosomal subunit protein eS19)	RPS19
1069,59	1069,053	1070,123							
1070,79	1070,256	1071,327							
1071,57	1071,031	1072,103	1071,554	0,013	R.MFLSFPTTK.T	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			1071,532	0,036	R.RDDDP LNAR.V	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
			1071,604	0,036	R.VITIMQNPR.Q	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
			1071,477	0,090	R.FDSDVGEFR.A	P01911	2B1F_HUMAN	HLA class II histocompatibility antigen, DRB1-15 beta chain (DW2.2/DR2.2) (MHC class II antigen DRB1*15)	HLA-DRB1
1071,89	1071,356	1072,427	1071,604	0,288	R.VITIMQNPR.Q	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
			1071,554	0,338	R.MFLSFPTTK.T	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			1071,532	0,360	R.RDDDP LNAR.V	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
			1071,477	0,414	R.FDSDVGEFR.A	P01911	2B1F_HUMAN	HLA class II histocompatibility antigen, DRB1-15 beta chain (DW2.2/DR2.2) (MHC class II antigen DRB1*15)	HLA-DRB1
1072,61	1072,071	1073,144	1073,546	0,047	R.AFSYVGPLR.T	Q16629	SRSF7_HUMAN	Serine/arginine-rich splicing factor 7 (Splicing factor 9G8) (Splicing factor, arginine/serine-rich 7)	SRSF7
1073,59	1073,056	1074,129							
1074,58	1074,040	1075,115	1075,592	0,031	K.GGFIPGSLTAR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
				0,054	R.QLSSGVSEIR.H	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	HSPB1
			1075,543	0,080	K.MLQHIDYR.M	P14678	RSMB_HUMAN	Small nuclear ribonucleoprotein-associated proteins B and B' (snRNP-B) (Sm protein B/B') (Sm-B/B') (SmB/B')	SNRPB
				0,089	K.LAGESESNLR.K	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			1075,534	0,297	K.MLQHIDYR.M	P14678	RSMB_HUMAN	Small nuclear ribonucleoprotein-associated proteins B and B' (snRNP-B) (Sm protein B/B') (Sm-B/B') (SmB/B')	SNRPB
1075,84	1075,302	1076,378	1075,592	0,248	K.GGFIPGSLTAR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1075,569	0,271	R.QLSSGVSEIR.H	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	HSPB1
			1075,534	0,306	K.LAGESESNLR.K	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
1076,46	1075,919	1076,996	1076,514	0,057	R.YSVQTADHR.F	Q16658	FSCN1_HUMAN	Fascin (55 kDa actin-bundling protein) (Singed-like protein) (p55)	FSCN1

			1076,569	0,112	R.GPPASSPAPAK.F	Q15942	ZYX_HUMAN	Zyxin (Zyxin-2)	ZYX
			1076,595	0,138	R.LRAVDFAER.H	P62917	RL8_HUMAN	60S ribosomal protein L8 (Large ribosomal subunit protein uL2)	RPL8
1076,62	1076,085	1077,162	1076,595	0,029	R.LRAVDFAER.H	P62917	RL8_HUMAN	60S ribosomal protein L8 (Large ribosomal subunit protein uL2)	RPL8
			1076,569	0,055	R.GPPASSPAPAK.F	Q15942	ZYX_HUMAN	Zyxin (Zyxin-2)	ZYX
			1076,514	0,109	R.YSVQTDADHR.F	Q16658	FSCN1_HUMAN	Fascin (55 kDa actin-bundling protein) (Singed-like protein) (p55)	FSCN1
1077,60	1077,057	1078,134	1077,579	0,016	K.GHAVGDIPGVR.F	P62266	RS23_HUMAN	40S ribosomal protein S23 (Small ribosomal subunit protein uS12)	RPS23
			1077,568	0,028	R.DFHHLRPR.F	Q2TAZ0	ATG2A_HUMAN	Autophagy-related protein 2 homolog A	ATG2A
			1077,544	0,052	R.HYLFQVQR.N	P24539	AT5F1_HUMAN	ATP synthase F(0) complex subunit B1, mitochondrial (ATP synthase peripheral stalk-membrane subunit b) (ATP synthase proton-transporting mitochondrial F(0) complex subunit B1) (ATP synthase subunit b) (ATPase subunit b)	ATP5PB
			1077,537	0,059	K.IREEYPDR.I	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1077,537	0,059	K.IREEYPDR.I	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1077,516	0,079	R.LDHFNFER.F	Q9UHL4	DPP2_HUMAN	Dipeptidyl peptidase 2 (EC 3.4.14.2) (Dipeptidyl aminopeptidase II) (Dipeptidyl peptidase 7) (Dipeptidyl peptidase II) (DPP II) (Quiescent cell proline dipeptidase)	DPP7
1078,59	1078,051	1079,130	1078,565	0,026	R.HFNAPSHIR.R	P61254	RL26_HUMAN	60S ribosomal protein L26 (Large ribosomal subunit protein uL24)	RPL26
			1078,536	0,054	K.FLENEDRR.S	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiproteinase) (Serpine A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
			1078,526	0,065	K.RPMSSPEMK.S	P51610	HCFC1_HUMAN	Host cell factor 1 (HCF) (HCF-1) (C1 factor) (CFF) (VCAF) (VP16 accessory protein) [Cleaved into: HCF N-terminal chain 1; HCF N-terminal chain 2; HCF N-terminal chain 3; HCF N-terminal chain 4; HCF N-terminal chain 5; HCF N-terminal chain 6; HCF C-terminal chain 1; HCF C-terminal chain 2; HCF C-terminal chain 3; HCF C-terminal chain 4; HCF C-terminal chain 5; HCF C-terminal chain 6]	HCFC1
1079,58	1079,044	1080,124	1079,621	0,037	R.IGGGIDVPVPR.H	Q92945	FUBP2_HUMAN	Far upstream element-binding protein 2 (FUSE-binding protein 2) (KH type-splicing regulatory protein) (KSRP) (p75)	KHSRP
			1079,519	0,065	K.AQYEDIANR.S	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
1080,39	1079,846	1080,927	1080,479	0,092	K.YAYYDTER.I	O00303	EIF3F_HUMAN	Eukaryotic translation initiation factor 3 subunit F (eIF3f) (Deubiquitinating enzyme eIF3f) (EC 3.4.19.12) (Eukaryotic translation initiation factor 3 subunit 5) (eIF-3-epsilon) (eIF3 p47)	EIF3F
1080,60	1080,056	1081,137	1080,479	0,117	K.YAYYDTER.I	O00303	EIF3F_HUMAN	Eukaryotic translation initiation factor 3 subunit F (eIF3f) (Deubiquitinating enzyme eIF3f) (EC 3.4.19.12) (Eukaryotic translation initiation factor 3 subunit 5) (eIF-3-epsilon) (eIF3 p47)	EIF3F
1081,26	1080,721	1081,802	1081,538	0,276	K.FAFQAEVNR.M	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			1081,662	0,400	K.RPIKEVPSR.V	P49802	RG57_HUMAN	Regulator of G-protein signaling 7 (RG57)	RG57
1081,60	1081,057	1082,138	1081,538	0,060	K.FAFQAEVNR.M	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			1081,662	0,065	K.RPIKEVPSR.V	P49802	RG57_HUMAN	Regulator of G-protein signaling 7 (RG57)	RG57
1082,04	1081,498	1082,580	1081,662	0,377	K.RPIKEVPSR.V	P49802	RG57_HUMAN	Regulator of G-protein signaling 7 (RG57)	RG57
			1081,538	0,501	K.FAFQAEVNR.M	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			1082,551	0,512	R.LSEHATAPTR.G	P33316	DUT_HUMAN	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial (dUTPase) (EC 3.6.1.23) (dUTP pyrophosphatase)	DUT
1082,17	1081,628	1082,710	1082,551	0,382	R.LSEHATAPTR.G	P33316	DUT_HUMAN	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial (dUTPase) (EC 3.6.1.23) (dUTP pyrophosphatase)	DUT
			1082,607	0,437	K.FASFIDKVR.F	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
			1082,607	0,437	K.FASFIDKVR.F	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolelectin) (Type-II keratin Kb7)	KRT7
			1081,662	0,507	K.RPIKEVPSR.V	P49802	RG57_HUMAN	Regulator of G-protein signaling 7 (RG57)	RG57
1082,27	1081,731	1082,813	1082,551	0,279	R.LSEHATAPTR.G	P33316	DUT_HUMAN	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial (dUTPase) (EC 3.6.1.23) (dUTP pyrophosphatase)	DUT
			1082,607	0,334	K.FASFIDKVR.F	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
			1082,607	0,334	K.FASFIDKVR.F	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolelectin) (Type-II keratin Kb7)	KRT7
1082,57	1082,024	1083,107	1082,551	0,014	R.LSEHATAPTR.G	P33316	DUT_HUMAN	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial (dUTPase) (EC 3.6.1.23) (dUTP pyrophosphatase)	DUT
			1082,607	0,041	K.FASFIDKVR.F	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
			1082,607	0,041	K.FASFIDKVR.F	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolelectin) (Type-II keratin Kb7)	KRT7
1083,58	1083,036	1084,119	1083,598	0,020	K.YLYEIARR.H	P02768	ALBU_HUMAN	Serum albumin	ALB

1084,61	1084,064	1085,149	1083,557	0,021	K.GYTQQLAFR.Q	P01024	CO3_HUMAN	Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
			1083,649	0,072	R.ILKSPFIQR.A	P36578	RL4_HUMAN	60S ribosomal protein L4 (60S ribosomal protein L1) (Large ribosomal subunit protein uL4)	RPL4
			1084,634	0,028	K.LITPAVVSER.L	P62851	RS25_HUMAN	40S ribosomal protein S25 (Small ribosomal subunit protein eS25)	RPS25
1085,58	1085,037	1086,123	1086,550	0,035	K.IANPVEGSSGR.Q	Q15365	PCBP1_HUMAN	Poly(rC)-binding protein 1 (Alpha-CP1) (Heterogeneous nuclear ribonucleoprotein E1) (hnRNP E1) (Nucleic acid-binding protein SUB2.3)	PCBP1
1086,59	1086,042	1087,129				P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
						Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1087,57	1087,024	1088,112	1087,546	0,022	R.MFLSFPTTK.T	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			1087,624	0,056	K.LRVDPVNFK.L	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			1087,464	0,104	R.FDSDVGEYR.A	Q9TQE0	2B19_HUMAN	HLA class II histocompatibility antigen, DRB1-9 beta chain (MHC class II antigen DRB1*9) (DR-9) (DR9)	HLA-DRB1
1088,55	1088,011	1089,099	1089,566	0,007	R.SLETENAGLR.L	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
1089,57	1089,029	1090,118				O00264	PGRC1_HUMAN	Membrane-associated progesterone receptor component 1 (mPR) (Dap1) (IZA)	PGRMC1
						O15523	DDX3Y_HUMAN	ATP-dependent RNA helicase DDX3Y (EC 3.6.4.13) (DEAD box protein 3, Y-chromosomal)	DDX3Y
1090,61	1090,063	1091,154	1091,589	0,394	K.GLSQSALPYR.R	P62277	RS13_HUMAN	40S ribosomal protein S13 (Small ribosomal subunit protein uS15)	RPS13
1091,20	1090,650	1091,741				P62277	RS13_HUMAN	40S ribosomal protein S13 (Small ribosomal subunit protein uS15)	RPS13
1091,59	1091,043	1092,135				P52597	HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein F, N-terminally processed]	HNRNPF
1092,56	1092,010	1093,103	1092,581	0,025	R.VHIEIGPDGR.V	P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 (hnRNP H2) (FTP-3) (Heterogeneous nuclear ribonucleoprotein H') (hnRNP H') [Cleaved into: Heterogeneous nuclear ribonucleoprotein H2, N-terminally processed]	HNRNPH2
			1092,581	0,025	R.VHIEIGPDGR.V	P31943	HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H (hnRNP H) [Cleaved into: Heterogeneous nuclear ribonucleoprotein H, N-terminally processed]	HNRNPH1
			1093,571	0,016	R.AQYDELARK.N	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
1093,55	1093,008	1094,101	1093,526	0,029	R.IADGYEQAAR.V	P48643	TCPE_HUMAN	T-complex protein 1 subunit epsilon (TCP-1-epsilon) (CCT-epsilon)	CCT5
			1094,565	0,006	K.NTVVATGGYGR.T	P31040	SDHA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) (Flavoprotein subunit of complex II) (Fp)	SDHA
			1095,514	0,044	R.DTAFAANTR.A	O60240	PLIN1_HUMAN	Perilipin-1 (Lipid droplet-associated protein)	PLIN1
1095,56	1095,011	1096,106	1095,663	0,105	R.GLIENPALLR.W	O95168	NDUB4_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4 (Complex I-B15) (CI-B15) (NADH-ubiquinone oxidoreductase B15 subunit)	NDUF84
1096,56	1096,015	1097,111	1096,542	0,021	K.DNAMLEYLK.I	P15311	EZRI_HUMAN	Ezrin (Cytovillin) (Villinin-2) (p81)	EZR
			1096,651	0,088	R.QALAQISLPR.I	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
			1097,499	0,298	R.YYGYTGAFR.C	P02788	TRFL_HUMAN	Lactotransferrin (Lactoferrin) (EC 3.4.21.-) (Growth-inhibiting protein 12) (Talalectoferrin) [Cleaved into: Lactoferrin-H (Lfcin-H); Kaliocin-1; Lactoferroxin-A; Lactoferroxin-B; Lactoferroxin-C]	LTF
1097,20	1096,653	1097,750	1097,613	0,411	K.AKQGYVIYR.I	P61313	RL15_HUMAN	60S ribosomal protein L15 (Large ribosomal subunit protein eL15)	RPL15
			1097,671	0,469	K.GIIDPTKVVR.T	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
			1097,613	0,053	K.AKQGYVIYR.I	P61313	RL15_HUMAN	60S ribosomal protein L15 (Large ribosomal subunit protein eL15)	RPL15

1098,52 1098,55 1099,54	1097,966 1097,998 1098,989	1099,064 1099,096 1100,089	1097,499	0,061	R.YYGTYGAFRC	P02788	TRFL_HUMAN	Lactotransferrin (Lactoferrin) (EC 3.4.21.-) (Growth-inhibiting protein 12) (Talalectoferrin) [Cleaved into: Lactoferricin-H (Lfcin-H); Kaliocin-1; Lactoferroxin-A; Lactoferroxin-B; Lactoferroxin-C]	LTF
			1097,671	0,111	K.GIIDPTKVVR.T	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
			1099,504	0,035	R.STPEYFAER.L	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6
1100,57 1101,31	1100,018 1100,755	1101,119 1101,856	1099,605	0,065	R.GGIVDEGALLR.A	O43175	SERA_HUMAN	D-3-phosphoglycerate dehydrogenase (3-PGDH) (EC 1.1.1.95) (2-oxoglutarate reductase) (EC 1.1.1.399) (Malate dehydrogenase) (EC 1.1.1.37)	PHGDH
			1099,613	0,073	R.AVVIVDDRGR.S	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
			1101,590	0,284	R.SRFDRPPAR.R	Q16629	SRSF7_HUMAN	Serine/arginine-rich splicing factor 7 (Splicing factor 9G8) (Splicing factor, arginine/serine-rich 7)	SRSF7
1101,50	1100,952	1102,054	1101,590	0,087	R.SRFDRPPAR.R	Q16629	SRSF7_HUMAN	Serine/arginine-rich splicing factor 7 (Splicing factor 9G8) (Splicing factor, arginine/serine-rich 7)	SRSF7
1101,65	1101,095	1102,197	1101,590	0,056	R.SRFDRPPAR.R	Q16629	SRSF7_HUMAN	Serine/arginine-rich splicing factor 7 (Splicing factor 9G8) (Splicing factor, arginine/serine-rich 7)	SRSF7
1102,30	1101,752	1102,854	1102,600	0,297	K.TIQMVRAQR.S	P29350	PTN6_HUMAN	Tyrosine-protein phosphatase non-receptor type 6 (EC 3.1.3.48) (Hematopoietic cell protein-tyrosine phosphatase) (Protein-tyrosine phosphatase 1C) (PTP-1C) (Protein-tyrosine phosphatase SHP-1) (SH-PTP1)	PTPN6
1102,57	1102,020	1103,122	1102,600	0,029	K.TIQMVRAQR.S	P29350	PTN6_HUMAN	Tyrosine-protein phosphatase non-receptor type 6 (EC 3.1.3.48) (Hematopoietic cell protein-tyrosine phosphatase) (Protein-tyrosine phosphatase 1C) (PTP-1C) (Protein-tyrosine phosphatase SHP-1) (SH-PTP1)	PTPN6
1103,56	1103,010	1104,114	1103,655	0,093	R.ILVATNLFGR.G	Q13838	DX398_HUMAN	Spliceosome RNA helicase DDX398 (EC 3.6.4.13) (56 kDa UZAF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	DDX398
1104,56	1104,004	1105,108	1104,582	0,026	R.SAYGGPVGAGIR.E	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7)	KRT7
			1104,586	0,030	R.RDFTPAELR.R	O00264	PGRC1_HUMAN	Membrane-associated progesterone receptor component 1 (mPR) (Dap1) (IZA)	PGRMC1
			1104,586	0,030	K.IGFPWSEIR.N	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			1104,586 1104,619	0,030 0,063	K.IGFPWSEIR.N R.VSSFLPWIR.T	P15311 P08311	EZRI_HUMAN CATG_HUMAN	Ezrin (Cytovillin) (Villin-2) (p81) Cathepsin G (CG) (EC 3.4.21.20)	EZR CTSG
1105,56 1106,56	1105,007 1106,010	1106,113 1107,117	1106,586	0,023	R.SEIDLFNIR.K	P08758	ANXA5_HUMAN	Annexin A5 (Anchoring CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
1107,57	1107,012	1108,120	1106,512	0,052	R.NTDEMVELR.I	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
			1106,695	0,131	R.VVLPIEAPIR.M	P00403	COX2_HUMAN	Cytochrome c oxidase subunit 2 (Cytochrome c oxidase polypeptide II)	MT-CO2
			1107,563	0,003	K.ALAAGYDVEK.N	P16403	H12_HUMAN	Histone H1.2 (Histone H1c) (Histone H1d) (Histone H1s-1)	HIST1H1C
1108,57	1108,015	1109,124	1108,538	0,031	R.APFDLFENR.K	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
1109,57	1109,016	1110,126	1109,548	0,023	K.LLQDFFNGR.D	P0DMV8	HS71A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
1110,55	1109,998	1111,109	1110,562 1110,541	0,009 0,012	R.EAFAEQFLR.G R.STTDPITGYR.I	P01266 P02751	THYG_HUMAN FINC_HUMAN	Thyroglobulin (Tg) Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	TG FN1
1111,54	1110,983	1112,095	1111,553	0,014	R.QDIAFAYQR.R	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1111,623	0,083	K.IVDQIRPDR.Q	Q92841	DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.4.13) (DEAD box protein 17) (DEAD box protein p72) (DEAD box protein p82) (RNA-dependent helicase p72)	DDX17
			1111,649	0,110	K.TGAAPIIDVVR.S	P46776	RL27A_HUMAN	60S ribosomal protein L27a (Large ribosomal subunit protein uL15)	RPL27A

1111,57	1111,017	1112,129	1111,553	0,020	R.QDIAFAYQR.R	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1111,623	0,050	K.IVDQIRPDR.Q	Q92841	DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.4.13) (DEAD box protein 17) (DEAD box protein p72) (DEAD box protein p82) (RNA-dependent helicase p72)	DDX17
			1111,649	0,076	K.TGAAPIIDVVR.S	P46776	RL27A_HUMAN	60S ribosomal protein L27a (Large ribosomal subunit protein uL15)	RPL27A
1112,53	1111,972	1113,084	1112,608	0,080	K.TGQEIPVNV.R.F	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
1112,58	1112,027	1113,140	1112,608	0,024	K.TGQEIPVNV.R.F	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
1113,16	1112,599	1113,713	1112,608	0,548	K.TGQEIPVNV.R.F	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
1113,58	1113,026	1114,139	1114,684	0,121	R.VLUTDLLAR.G	Q14240	IF4A2_HUMAN	Eukaryotic initiation factor 4A-II (eIF-4A-II) (eIF4A-II) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-2)	EIF4A2
1114,56	1114,005	1115,120		0,121	R.VLUTDLLAR.G	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-I (eIF-4A-I) (eIF4A-I) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
1115,58	1115,018	1116,134	1117,533 1117,513	0,010	R.VELEDWNGR.T	P02679	FIBG_HUMAN	Fibrinogen gamma chain	FGG
1116,53	1115,976	1117,093		0,029	R.YGTCIYQGR.L	P59665	DEF1_HUMAN	Neutrophil defensin 1 (Defensin, alpha 1) (HNP-1) (HP-1) (HP1) [Cleaved into: HP 1-56; Neutrophil defensin 2 (HNP-2) (HP-2) (HP2)]	DEFA1; DEFA1B
1117,54	1116,984	1118,102		0,065	R.IIDTPQFQR.L	Q9Y3Z3	SAMH1_HUMAN	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 (dNTPase) (EC 3.1.5.-) (Dendritic cell-derived IFNG-induced protein) (DCIP) (Monocyte protein 5) (MOP-5) (SAM domain and HD domain-containing protein 1) (hSAMHD1)	SAMHD1
1118,56	1117,996	1119,114	1118,581	0,026	R.ESIESEIRR.E	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			1118,605	0,050	K.NKVMMVALGR.S	Q9UKD2	MRT4_HUMAN	mRNA turnover protein 4 homolog (Ribosome assembly factor MRT04)	MRT04
1119,57	1119,014	1120,134	1119,573	0,001	R.LFAYPDTHR.H	P04040	CATA_HUMAN	Catalase (EC 1.11.1.6)	CAT
1120,57	1120,006	1121,127	1120,564 1120,574	0,003 0,007	K.QRIDEFEAL.- K.STTTGHUVK.C	P15311 P68104	EZR1_HUMAN EF1A1_HUMAN	Ezrin (Cytovillin) (Villin-2) (p81) Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EZR EEF1A1
			1120,720	0,154	R.VGLKAPGIIP.R.I	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
1121,57	1121,012	1122,134	1121,612	0,039	K.SVNELIYKR.G	P18124	RL7_HUMAN	60S ribosomal protein L7 (Large ribosomal subunit protein uL30)	RPL7
1122,59	1122,031	1123,153	1122,641	0,049	K.EHVIALRR.A	P27635	RL10_HUMAN	60S ribosomal protein L10 (Laminin receptor homolog) (Large ribosomal subunit protein uL16) (Protein QM) (Ribosomal protein L10) (Tumor suppressor QM)	RPL10
			1122,504	0,088	R.MGESDDSLR.L	P63220	RS21_HUMAN	40S ribosomal protein S21 (Small ribosomal subunit protein eS21)	RP521
1123,42	1122,861	1123,984	1123,587	0,164	R.NRGPPPSWGR.R	P84103	SRSF3_HUMAN	Serine/arginine-rich splicing factor 3 (Pre-mRNA-splicing factor SRP20) (Splicing factor, arginine/serine-rich 3)	SRSF3
1123,59	1123,030	1124,154	1123,587	0,005	R.NRGPPPSWGR.R	P84103	SRSF3_HUMAN	Serine/arginine-rich splicing factor 3 (Pre-mRNA-splicing factor SRP20) (Splicing factor, arginine/serine-rich 3)	SRSF3
1124,54	1123,981	1125,106	1125,608	0,075	R.FANYIDKVR.F	P08670	VIME_HUMAN	Vimentin	VIM
1125,53	1124,969	1126,095		0,058	R.FANYIDKVR.F	P08670	VIME_HUMAN	Vimentin	VIM
1125,55	1124,987	1126,112	1125,608	0,015	K.LHVDPENFR.L	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
1126,55	1125,992	1127,118	1126,570	0,015	K.LHVDPENFR.L	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
1127,55	1126,990	1128,117	1127,610	0,056	R.WTGMIIIGPPR.T	Q13404	UB2V1_HUMAN	Ubiquitin-conjugating enzyme E2 variant 1 (UEV-1) (CROC-1) (TRAF6-regulated IKK activator 1 beta Uev1A)	UBE2V1
1128,56	1127,995	1129,124	1128,581	0,021	R.GLLEFEHQ.R.A	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			1128,584	0,025	K.YEKDIAAYR.A	P26583	HMGB2_HUMAN	High mobility group protein B2 (High mobility group protein 2) (HMG-2)	HMGB2
			1128,711	0,152	K.KQTALVELVK.H	P02768	ALBU_HUMAN	Serum albumin	ALB
1129,56	1129,000	1130,129	1130,548	0,017	R.GYSFVTTAER.E	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
1130,57	1130,000	1131,131							

			1130,597	0,031	R.FPGQLNADLR.K	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain)	TUBB4B
			1130,597	0,031	R.FPGQLNADLR.K	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1130,630	0,064	R.SINQPVAFVR.R	Q9GZT3	SLRP_HUMAN	SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLRP
			1130,667	0,102	R.AGLLPNHRPR.L	Q9NV52	RT18A_HUMAN	39S ribosomal protein S18a, mitochondrial (MRP-S18-a) (Mrps18a) (S18mt-a) (39S ribosomal protein S18-3, mitochondrial) (MRP-S18-3) (Mitochondrial large ribosomal subunit protein bS18a) (Mitochondrial large ribosomal subunit protein mL66)	MRPS18A
1131,56	1130,999	1132,130	1131,540	0,025	R.NGVMPSHFSR.G	P39019	RS19_HUMAN	40S ribosomal protein S19 (Small ribosomal subunit protein eS19)	RPS19
1132,54	1131,977	1133,109	1132,535	0,008	R.GYSFTTTAER.E	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
1133,56	1132,992	1134,125	1134,556	0,011	K.DVNQQEFVR.A	P39019	RS19_HUMAN	40S ribosomal protein S19 (Small ribosomal subunit protein eS19)	RPS19
1134,57	1133,999	1135,134	1134,546	0,021	R.DAVTYTEHAK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
			1134,616	0,049	M.AALRALCGFR.G	O75306	NDUS2_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial (EC 1.6.99.3) (EC 7.1.1.2) (Complex I-49kD) (CI-49kD) (NADH-ubiquinone oxidoreductase 49 kDa subunit)	NDUF52
1135,58	1135,008	1136,144	1135,580	0,004	R.RDYLYHYIR.K	P62280	RS11_HUMAN	40S ribosomal protein S11 (Small ribosomal subunit protein uS17)	RPS11
			1135,620	0,044	R.QFVTATDVVR.G	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LCG4P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
1136,57	1135,997	1137,134	1136,616	0,051	R.DIVQFVPYR.R	Q99829	CPNE1_HUMAN	Copine-1 (Chromobindin 17) (Copine I)	CPNE1
1137,57	1137,002	1138,140	1137,580	0,009	K.IAVAAQNCYK.V	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP1
			1137,549	0,022	K.ESYSVYYVK.V	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
1138,55	1137,983	1139,122	1138,522	0,030	R.DAGMQLQGYR.Y	P00505	AATM_HUMAN	Aspartate aminotransferase, mitochondrial (mAspAT) (EC 2.6.1.1) (EC 2.6.1.7) (Fatty acid-binding protein) (FABP-1) (Glutamate oxaloacetate transaminase 2) (Kynurenine aminotransferase 4) (Kynurenine aminotransferase IV) (Kynurenine--oxoglutarate transaminase 4) (Kynurenine--oxoglutarate transaminase IV) (Plasma membrane-associated fatty acid-binding protein) (FABPpm) (Transaminase A)	GOT2
			1138,503	0,050	K.CCTESLVNR.R	P02768	ALBU_HUMAN	Serum albumin	ALB
1139,56	1138,987	1140,126	1139,549	0,007	R.YYPTEVPR.K	Q02878	RL6_HUMAN	60S ribosomal protein L6 (Large ribosomal subunit protein eL6) (Neoplasm-related protein C140) (Tax-responsive enhancer element-binding protein 107) (TaxREB107)	RPL6
			1139,592	0,036	K.LGVIEDHSNR.T	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
1140,56	1139,994	1141,134	1140,584	0,020	R.WESQLPQPR.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1140,654	0,090	R.QAVDVSPLRR.V	P46782	RS5_HUMAN	40S ribosomal protein S5 (Small ribosomal subunit protein uS7) [Cleaved into: 40S ribosomal protein S5, N-terminally processed]	RP55
1141,58	1141,012	1142,153	1141,583	0,000	K.LGIHEDSTNR.R	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			1141,547	0,036	R.MICAGFLEGG.V	Q7Z410	TMP59_HUMAN	Transmembrane protease serine 9 (EC 3.4.21.-) (Polyserase-1) (Polyserine protease 1) (Polyserase-1) [Cleaved into: Serase-1; Serase-2; Serase-3]	TMPSR59
1142,57	1141,996	1143,138	1142,547	0,020	R.TFDEIASGFR.Q	P11166	GTR1_HUMAN	Solute carrier family 2, facilitated glucose transporter member 1 (Glucose transporter type 1, erythrocyte/brain) (GLUT-1) (HepG2 glucose transporter)	SLC2A1
			1142,621	0,054	R.IPACIAGERR.Y	P59665	DEF1_HUMAN	Neutrophil defensin 1 (Defensin, alpha 1) (HNP-1) (HP-1) (HP1) [Cleaved into: HP 1-56; Neutrophil defensin 2 (HNP-2) (HP-2) (HP2)]	DEFA1; DEFA1B
1143,57	1142,995	1144,139	1143,606	0,039	R.RALELEQER.K	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			1143,627	0,060	R.JGAEVYHNLK.N	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			1143,640	0,073	M.AATTGSGVKVPR.N	Q13404	UB2V1_HUMAN	Ubiquitin-conjugating enzyme E2 variant 1 (UEV-1) (CROC-1) (TRAF6-regulated IKK activator 1 beta Uev1A)	UBE2V1
			1143,640	0,073	K.LAVNMVFPFR.L	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1143,640	0,073	K.LAVNMVFPFR.L	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
1144,58	1144,009	1145,154	1144,600	0,018	R.VVHIMDFQR.G	P43243	MATR3_HUMAN	Matrin-3	MATR3

1145,52	1144,944	1146,090	1145,521	0,004	R.GYSDRDGYGR.D	P38159	RBMX_HUMAN	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX
			1145,648	0,130	R.SIRPGLSPYR.A	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1145,63	1145,062	1146,207	1145,648	0,013	R.SIRPGLSPYR.A	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			1145,521	0,114	R.GYSDRDGYGR.D	P38159	RBMX_HUMAN	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX
1146,58	1146,009	1147,156	1146,598	0,015	R.LSEGFSIHTR.D	P20618	PSB1_HUMAN	Proteasome subunit beta type-1 (EC 3.4.25.1) (Macropain subunit C5) (Multicatalytic endopeptidase complex subunit C5) (Proteasome component C5) (Proteasome gamma chain)	PSMB1
1147,51	1146,939	1148,087	1147,514	0,001	R.YQPMEPNPR.V	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
			1147,606	0,093	K.KNAGFTPQER.Q	P27695	APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase (EC 3.1.-.-) (EC 4.2.99.18) (APEX nuclease) (APEN) (Apyrimidinic endonuclease 1) (AP endonuclease 1) (APE-1) (REF-1) (Redox factor-1) [Cleaved into: DNA-(apurinic or apyrimidinic site) lyase, mitochondrial]	APEX1
1147,61	1147,037	1148,184	1147,606	0,004	K.KNAGFTPQER.Q	P27695	APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase (EC 3.1.-.-) (EC 4.2.99.18) (APEX nuclease) (APEN) (Apyrimidinic endonuclease 1) (AP endonuclease 1) (APE-1) (REF-1) (Redox factor-1) [Cleaved into: DNA-(apurinic or apyrimidinic site) lyase, mitochondrial]	APEX1
			1147,514	0,096	R.YQPMEPNPR.V	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
1148,52	1147,948	1149,096	1148,582	0,060	R.GTPQQIDYAR.Q	Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1) (DNA helicase V) (hDH V)	FUBP1
			1148,631	0,109	R.QGIPFFGQVR.L	P01023	A2MG_HUMAN	Alpha-2-macroglobulin (Alpha-2-M) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 5)	A2M
1148,62	1148,048	1149,197	1148,631	0,009	R.QGIPFFGQVR.L	P01023	A2MG_HUMAN	Alpha-2-macroglobulin (Alpha-2-M) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 5)	A2M
			1148,582	0,040	R.GTPQQIDYAR.Q	Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1) (DNA helicase V) (hDH V)	FUBP1
1149,57	1148,998	1150,148	1149,592	0,019	R.FDAGELITQR.E	P35232	PHB_HUMAN	Prohibitin	PHB
			1149,626	0,053	K.LVNEVTEFAK.T	P02768	ALBU_HUMAN	Serum albumin	ALB
			1149,680	0,107	K.VIEPKDIAK.C	Q13228	SBP1_HUMAN	Methanethiol oxidase (MTO) (EC 1.8.3.4) (56 kDa selenium-binding protein) (SBP56) (SP56) (Selenium-binding protein 1)	SELENBP1
			1149,680	0,107	K.VVAGVANALAHK.Y	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			1149,680	0,107	K.VVAGVANALAHK.Y	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
1150,58	1150,010	1151,160	1150,592	0,007	K.FAEAFEAIRP.A	P50990	TCPQ_HUMAN	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta) (Chaperonin containing T-complex polypeptide 1 subunit 8) (Renal carcinoma antigen NY-REN-15)	CCT8
			1150,570	0,015	K.CPFTGNVSIR.G	P62280	RS11_HUMAN	40S ribosomal protein S11 (Small ribosomal subunit protein uS17)	RPS11
			1150,545	0,040	K.EAESPFVER.L	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			1150,672	0,087	R.VLIAAHGNSLR.G	P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG-dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	PGAM1
1151,58	1151,008	1152,159	1151,556	0,027	R.FTNIGPDTMR.V	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
1152,61	1152,029	1153,182	1152,617	0,012	R.IANVFTNAFR.Y	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
			1152,686	0,081	R.AIRLELQGPR.G	P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL
1153,61	1153,037	1154,190	1153,602	0,012	R.ERPPEVAAR.L	Q16891	MIC60_HUMAN	MICOS complex subunit MIC60 (Cell proliferation-inducing gene 4/52 protein) (Mitochondrial inner membrane protein) (Mitofilin) (p87/89)	IMMT
			1153,537	0,077	R.GGDLMAYDRR.G	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
			1153,697	0,084	R.LALLVDTVGPR.L	Q9Y646	CBPQ_HUMAN	Carboxypeptidase Q (EC 3.4.17.-) (Lysosomal dipeptidase) (Plasma glutamate carboxypeptidase)	CPQ
1154,59	1154,010	1155,164	1154,621	0,034	R.AGGPTTPLSPTRL.L	P20700	LMNB1_HUMAN	Lamin-B1	LMNB1

			1154,512	0,075	K.QRIDEFESM.-	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
1155,60	1155,022	1156,177	1155,576	0,023	K.GAGTDDTLIR.V	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
			1155,656	0,056	R.RGDLFPVVPR.R	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
1156,60	1156,023	1157,180	1156,618	0,017	R.HITIFSEGR.L	P60900	PSA6_HUMAN	Proteasome subunit alpha type-6 (EC 3.4.25.1) (27 kDa prosomal protein) (PROS-27) (p27K) (Macropain iota chain) (Multicatalytic endopeptidase complex iota chain) (Proteasome iota chain)	PSMA6
			1156,643	0,041	R.AVLHVHGGGGPR.V	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
1157,52	1156,942	1158,099	1157,559	0,039	R.FPTTDGNHLR.I	Q96PE3	INP4A_HUMAN	Type I inositol 3,4-bisphosphate 4-phosphatase (EC 3.1.3.66) (Inositol polyphosphate 4-phosphatase type I)	INPP4A
			1157,559	0,039	K.SDPFLEFFR.Q	Q99829	CPNE1_HUMAN	Copine-1 (Chromobindin 17) (Copine I)	CPNE1
			1157,638	0,117	R.LEALKENGGAR.L	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
1157,66	1157,077	1158,235	1157,638	0,018	R.LEALKENGGAR.L	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
			1157,559	0,096	R.FPTTDGNHLR.I	Q96PE3	INP4A_HUMAN	Type I inositol 3,4-bisphosphate 4-phosphatase (EC 3.1.3.66) (Inositol polyphosphate 4-phosphatase type I)	INPP4A
			1157,559	0,096	K.SDPFLEFFR.Q	Q99829	CPNE1_HUMAN	Copine-1 (Chromobindin 17) (Copine I)	CPNE1
1158,62	1158,039	1159,197	1158,663	0,045	K.AIPQLQGYLR.S	Q02878	RL6_HUMAN	60S ribosomal protein L6 (Large ribosomal subunit protein eL6) (Neoplasm-related protein C140) (Tax-responsive enhancer element-binding protein 107) (TaxREB107)	RPL6
1159,63	1159,054	1160,214	1159,637	0,003	K.LAVNMVFPFR.L	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1159,637	0,003	K.LAVNMVFPFR.L	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
1160,58	1160,002	1161,163	1160,576	0,007	K.SMQNHAAVFR.V	P31040	SDHA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) (Flavoprotein subunit of complex II) (Fp)	SDHA
			1160,662	0,080	K.RLQQNLFGGK.F	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1161,62	1161,038	1162,199	1161,627	0,009	K.EITALAPSTMK.I	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1161,627	0,009	K.EITALAPSTMK.I	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
1162,64	1162,056	1163,219	1162,557	0,081	R.SHEGETAYIR.V	Q07955	SRSF1_HUMAN	Serine/arginine-rich splicing factor 1 (Alternative-splicing factor 1) (ASF-1) (Splicing factor, arginine/serine-rich 1) (pre-mRNA-splicing factor SF2, P33 subunit)	SRSF1
1163,48	1162,895	1164,058	1163,582	0,106	K.SAGEVLMTISR.H	Q8IZQ1	WDFY3_HUMAN	WD repeat and FYVE domain-containing protein 3 (Autophagy-linked FYVE protein) (Alfy)	WDFY3
			1163,629	0,153	R.LFDQAFGLPR.L	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	HSPB1
			1163,645	0,168	K.YGAIRDILK.N	Q07955	SRSF1_HUMAN	Serine/arginine-rich splicing factor 1 (Alternative-splicing factor 1) (ASF-1) (Splicing factor, arginine/serine-rich 1) (pre-mRNA-splicing factor SF2, P33 subunit)	SRSF1
1163,60	1163,016	1164,179	1163,582	0,015	K.SAGEVLMTISR.H	Q8IZQ1	WDFY3_HUMAN	WD repeat and FYVE domain-containing protein 3 (Autophagy-linked FYVE protein) (Alfy)	WDFY3
			1163,629	0,032	R.LFDQAFGLPR.L	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	HSPB1
			1163,645	0,047	K.YGAIRDILK.N	Q07955	SRSF1_HUMAN	Serine/arginine-rich splicing factor 1 (Alternative-splicing factor 1) (ASF-1) (Splicing factor, arginine/serine-rich 1) (pre-mRNA-splicing factor SF2, P33 subunit)	SRSF1
1164,58	1163,993	1165,157	1164,578	0,003	K.ATAVMPDQGFK.D	Q06830	PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
			1164,749	0,173	K.LLSPKQPLL.RA	Q8NAT1	PMGT2_HUMAN	Protein O-linked-mannose beta-1,4-N-acetylglucosaminyltransferase 2 (POMGnT2) (EC 2.4.1.312) (Extracellular O-linked N-acetylglucosamine transferase-like) (Glycosyltransferase-like domain-containing protein 2)	POMGNT2

1164,58	1164,001	1165,165	1164,578	0,005	K.KATAVMPDGGQFK.D	Q06830	PRDX1_HUMAN	Peroxisiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
			1164,749	0,166	K.LLSPKQPLLR.A	Q8NAT1	PMGT2_HUMAN	Protein O-linked-mannose beta-1,4-N-acetylglucosaminyltransferase 2 (POMGnT2) (EC 2.4.1.312) (Extracellular O-linked N-acetylglucosamine transferase-like) (Glycosyltransferase-like domain-containing protein 2)	POMGNT2
1165,59	1165,006	1166,172	1166,505	0,083	K.KYEMASHLR.R	P07737	PROF1_HUMAN	Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I)	PFN1
1166,59	1166,006	1167,172	1166,691	0,102	R.AVAQALEVIPR.T	P49368	TCPG_HUMAN	T-complex protein 1 subunit gamma (TCP-1-gamma) (CCT-gamma) (hTRICS)	CCT3
1167,53	1166,945	1168,112	1167,598	0,069	K.FHHTIGGSRR.A	P61313	RL15_HUMAN	60S ribosomal protein L15 (Large ribosomal subunit protein eL15)	RPL15
			1167,626	0,097	R.LQAVTDDHIR.M	P30043	BLVRB_HUMAN	Flavin reductase (NADPH) (FR) (EC 1.5.1.30) (Bliverdin reductase B) (BVR-B) (EC 1.3.1.24) (Bliverdin-IX beta-reductase) (Green heme-binding protein) (GHBP) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR)	BLVRB
			1167,626	0,097	K.HQCNKVLLR.V	Q9HCK8	CHD8_HUMAN	Chromodomain-helicase-DNA-binding protein 8 (CHD-8) (EC 3.6.4.12) (ATP-dependent helicase CHD8) (Helicase with SNF2 domain 1)	CHD8
			1167,667	0,139	R.VVPGYGHAVLR.K	O75390	CISY_HUMAN	Citrate synthase, mitochondrial (EC 2.3.3.1) (Citrate (Si)-synthase)	CS
1167,63	1167,047	1168,214	1167,626	0,005	R.LQAVTDDHIR.M	P30043	BLVRB_HUMAN	Flavin reductase (NADPH) (FR) (EC 1.5.1.30) (Bliverdin reductase B) (BVR-B) (EC 1.3.1.24) (Bliverdin-IX beta-reductase) (Green heme-binding protein) (GHBP) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR)	BLVRB
			1167,626	0,005	K.HQCNKVLLR.V	Q9HCK8	CHD8_HUMAN	Chromodomain-helicase-DNA-binding protein 8 (CHD-8) (EC 3.6.4.12) (ATP-dependent helicase CHD8) (Helicase with SNF2 domain 1)	CHD8
			1167,598	0,033	K.FHHTIGGSRR.A	P61313	RL15_HUMAN	60S ribosomal protein L15 (Large ribosomal subunit protein eL15)	RPL15
			1167,667	0,036	R.VVPGYGHAVLR.K	O75390	CISY_HUMAN	Citrate synthase, mitochondrial (EC 2.3.3.1) (Citrate (Si)-synthase)	CS
1168,67	1168,081	1169,250	1168,603	0,063	K.QVHPDTGSSK.A	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
			1168,603	0,063	K.QVHPDTGSSK.A	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
1169,49	1168,910	1170,079	1169,533	0,038	K.SADFTNFDPR.G	P00918	CAH2_HUMAN	Carbonic anhydrase 2 (EC 4.2.1.1) (Carbonate dehydratase II) (Carbonic anhydrase C) (CAC) (Carbonic anhydrase II) (CA-II)	CA2
			1169,716	0,222	R.FIPLARPEVK.W	Q9Y323	SAMH1_HUMAN	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 (dNTPase) (EC 3.1.5.-) (Dendritic cell-derived IFNG-induced protein) (DCIP) (Monocyte protein 5) (MOP-5) (SAM domain and HD domain-containing protein 1) (hSAMHD1)	SAMHD1
			1169,716	0,222	R.AMLRLIPSLR.T	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
1169,65	1169,069	1170,239	1169,716	0,062	R.FIPLARPEVK.W	Q9Y323	SAMH1_HUMAN	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 (dNTPase) (EC 3.1.5.-) (Dendritic cell-derived IFNG-induced protein) (DCIP) (Monocyte protein 5) (MOP-5) (SAM domain and HD domain-containing protein 1) (hSAMHD1)	SAMHD1
			1169,716	0,062	R.AMLRLIPSLR.T	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
			1169,533	0,122	K.SADFTNFDPR.G	P00918	CAH2_HUMAN	Carbonic anhydrase 2 (EC 4.2.1.1) (Carbonate dehydratase II) (Carbonic anhydrase C) (CAC) (Carbonic anhydrase II) (CA-II)	CA2
1170,53	1169,944	1171,115	1170,696	0,167	R.IALTDNALIAR.S	P18124	RL7_HUMAN	60S ribosomal protein L7 (Large ribosomal subunit protein uL30)	RPL7
			1170,697	0,168	R.EHPVPLPIR.Q	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
1170,68	1170,093	1171,264	1170,696	0,018	R.IALTDNALIAR.S	P18124	RL7_HUMAN	60S ribosomal protein L7 (Large ribosomal subunit protein uL30)	RPL7
			1170,697	0,019	R.EHPVPLPIR.Q	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
1171,54	1170,953	1172,125	1171,546	0,007	K.QEEASGGTAPK.A	P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP)	VASP
			1171,589	0,050	R.HQGVMMVGMGQK.D	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1171,589	0,050	R.HQGVMMVGMGQK.D	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1171,589	0,050	R.HQGVMMVGMGQK.D	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			1171,656	0,117	R.AGHYAASIIIR.R	P55263	ADK_HUMAN	Adenosine kinase (AK) (EC 2.7.1.20) (Adenosine 5'-phosphotransferase)	ADK
			1171,674	0,135	M.VLSPADKTNVK.A	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
1171,68	1171,089	1172,261	1171,674	0,002	M.VLSPADKTNVK.A	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			1171,656	0,019	R.AGHYAASIIIR.R	P55263	ADK_HUMAN	Adenosine kinase (AK) (EC 2.7.1.20) (Adenosine 5'-phosphotransferase)	ADK
			1171,589	0,086	R.HQGVMMVGMGQK.D	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1171,589	0,086	R.HQGVMMVGMGQK.D	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1171,589	0,086	R.HQGVMMVGMGQK.D	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			1171,546	0,130	K.QEEASGGTAPK.A	P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP)	VASP

1172,64	1172,056	1173,228	1172,656	0,014	K.TTGKPIEASIR.G	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6
			1172,547	0,095	K.FVMQEEFSR.D	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	PDIA3
1173,59	1173,006	1174,180	1173,664	0,071	R.AQLLELPYAR.K	P50453	SPB9_HUMAN	Serpin B9 (Cytoplasmic antiproteinase 3) (CAP-3) (CAP3) (Peptidase inhibitor 9) (PI-9)	SERPINB9
1174,52	1173,933	1175,107	1174,583	0,063	R.DNEKIEASLR.R	Q8NB16	MLKL_HUMAN	Mixed lineage kinase domain-like protein (hMLKL)	MLKL
			1174,627	0,107	R.FRIDELEPR.R	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1174,63	1174,043	1175,217	1174,627	0,003	R.FRIDELEPR.R	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			1174,583	0,047	R.DNEKIEASLR.R	Q8NB16	MLKL_HUMAN	Mixed lineage kinase domain-like protein (hMLKL)	MLKL
1175,61	1175,023	1176,199	1175,612	0,001	K.SSGVPPEVFTR.V	P08311	CATG_HUMAN	Cathepsin G (CG) (EC 3.4.21.20)	CTSG
			1175,602	0,009	R.KYVSQYYPK.L	Q5SSJ5	HP1B3_HUMAN	Heterochromatin protein 1-binding protein 3 (Protein HP1-BP74)	HP1BP3
			1175,623	0,012	R.KTGTQQELDR.V	O95229	ZWINT_HUMAN	ZW10 interactor (ZW10-interacting protein 1) (Zwint-1)	ZWINT
			1175,653	0,042	R.RFEKPLEEK.G	Q8NC51	PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein (PAI1 RNA-binding protein 1) (PAI-RBP1) (SERPINE1 mRNA-binding protein 1)	SERBP1
			1175,658	0,047	K.DRPFFPGLVK.Y	P22392	NDKB_HUMAN	Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (EC 2.7.4.6) (C-myc purine-binding transcription factor PUF) (Histidine protein kinase NDKB) (EC 2.7.13.3) (nm23-H2)	NME2
1176,60	1176,008	1177,184	1176,555	0,041	R.NQPQFQQMR.Q	P54727	RD23B_HUMAN	UV excision repair protein RAD23 homolog B (HR23B) (hHR23B) (XP-C repair-complementing complex 58 kDa protein) (p58)	RAD23B
			1176,676	0,080	R.FLAVQSVISGR.F	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1177,53	1176,943	1178,121	1177,646	0,115	K.NLQGISSFRR.G	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
1177,68	1177,092	1178,270	1177,646	0,035	K.NLQGISSFRR.G	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
1178,59	1178,003	1179,181							
1179,62	1179,034	1180,214	1179,599	0,025	K.AASNLRDNRYR.F	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	PDIA3
			1179,653	0,029	R.AGLLEQPGAAPR.D	A6NH11	GLTD2_HUMAN	Glycolipid transfer protein domain-containing protein 2	GLTPD2
			1179,684	0,060	R.IKLYESLAR.Y	P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
			1179,684	0,060	R.IKLYESLAR.Y	P31150	GDIA_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
1180,64	1180,051	1181,231	1180,626	0,015	R.ISGLIYEETR.G	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
			1180,666	0,025	K.RFNALQYLR.L	P51884	LUM_HUMAN	Lumican (Keratan sulfate proteoglycan lumican) (KSPG lumican)	LUM
			1180,679	0,038	R.GLAPEQPVTLR.A	Q86TX2	ACOT1_HUMAN	Acyl-coenzyme A thioesterase 1 (Acyl-CoA thioesterase 1) (EC 3.1.2.-) (CTE-I) (CTE-Ib) (Inducible cytosolic acyl-coenzyme A thioester hydrolase) (Long chain acyl-CoA thioester hydrolase) (Long chain acyl-CoA hydrolase) (Palmitoyl-coenzyme A thioesterase) (EC 3.1.2.2)	ACOT1
1181,63	1181,036	1182,218	1182,595	0,018	K.APDFVFYAPR.L	P15311	EZRI_HUMAN	Ezrin (Cytovillin) (Villin-2) (p81)	EZR
1182,61	1182,022	1183,204	1182,595	0,018	K.APDFVFYAPR.L	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
1183,60	1183,008	1184,192	1183,516	0,083	R.NYYGYQGYR.-	Q1KMD3	HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 2 (Scaffold-attachment factor A2) (SAF-A2)	HNRNPUL2

1184,32	1183,727	1184,911	1184,687	0,368	K.GGIVGMTLPIAR.D	Q99714	HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2 (EC 1.1.1.35) (17-beta-hydroxysteroid dehydrogenase 10) (17-beta-HSD 10) (EC 1.1.1.51) (2-methyl-3-hydroxybutyryl-CoA dehydrogenase) (MHBD) (3-hydroxy-2-methylbutyryl-CoA dehydrogenase) (EC 1.1.1.178) (3-hydroxyacyl-CoA dehydrogenase type II) (Endoplasmic reticulum-associated amyloid beta-peptide-binding protein) (Mitochondrial ribonuclease P protein 2) (Mitochondrial RNase P protein 2) (Short chain dehydrogenase/reductase family 5C member 1) (Short-chain type dehydrogenase/reductase XH98G2) (Type II HADH)	HSD17B10
			1184,710	0,391	R.IINDLLQSLR.S	Q92945	FUBP2_HUMAN	Far upstream element-binding protein 2 (FUSE-binding protein 2) (KH type-splicing regulatory protein) (KSRP) (p75)	KHSRP
1184,57	1183,976	1185,160	1184,687	0,118	K.GGIVGMTLPIAR.D	Q99714	HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2 (EC 1.1.1.35) (17-beta-hydroxysteroid dehydrogenase 10) (17-beta-HSD 10) (EC 1.1.1.51) (2-methyl-3-hydroxybutyryl-CoA dehydrogenase) (MHBD) (3-hydroxy-2-methylbutyryl-CoA dehydrogenase) (EC 1.1.1.178) (3-hydroxyacyl-CoA dehydrogenase type II) (Endoplasmic reticulum-associated amyloid beta-peptide-binding protein) (Mitochondrial ribonuclease P protein 2) (Mitochondrial RNase P protein 2) (Short chain dehydrogenase/reductase family 5C member 1) (Short-chain type dehydrogenase/reductase XH98G2) (Type II HADH)	HSD17B10
			1184,710	0,142	R.IINDLLQSLR.S	Q92945	FUBP2_HUMAN	Far upstream element-binding protein 2 (FUSE-binding protein 2) (KH type-splicing regulatory protein) (KSRP) (p75)	KHSRP
1185,39	1184,793	1185,979	1185,657	0,271	R.NRPAPYSRPK.Q	Q86V81	THOC4_HUMAN	THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Aly/REF export factor) (Transcriptional coactivator Aly/REF) (bZIP-enhancing factor BEF)	ALYREF
1185,62	1185,028	1186,213	1185,657	0,036	R.NRPAPYSRPK.Q	Q86V81	THOC4_HUMAN	THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Aly/REF export factor) (Transcriptional coactivator Aly/REF) (bZIP-enhancing factor BEF)	ALYREF
1186,41	1185,816	1187,003	1186,648	0,239	K.FRHFVGQPAK.A	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
1186,62	1186,029	1187,216	1186,648	0,026	K.FRHFVGQPAK.A	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
1187,52	1186,928	1188,115	1187,576	0,055	R.HQGMVMGGMGQK.D	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1187,576	0,055	R.HQGMVMGGMGQK.D	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			1187,576	0,055	R.HQGMVMGGMGQK.D	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1187,620	0,099	R.FQSLGVAFYR.G	P51149	RAB7A_HUMAN	Ras-related protein Rab-7a	RAB7A
			1187,655	0,133	K.GPLQSVQVFGGR.K	P62249	RS16_HUMAN	40S ribosomal protein S16 (Small ribosomal subunit protein uS9)	RPS16
			1187,684	0,162	K.SILFVPTSAPR.G	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
1187,66	1187,062	1188,249	1187,655	0,001	K.GPLQSVQVFGGR.K	P62249	RS16_HUMAN	40S ribosomal protein S16 (Small ribosomal subunit protein uS9)	RPS16
			1187,684	0,028	K.SILFVPTSAPR.G	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			1187,620	0,035	R.FQSLGVAFYR.G	P51149	RAB7A_HUMAN	Ras-related protein Rab-7a	RAB7A
			1187,576	0,079	R.HQGMVMGGMGQK.D	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1187,576	0,079	R.HQGMVMGGMGQK.D	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			1187,576	0,079	R.HQGMVMGGMGQK.D	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
1188,54	1187,947	1189,135	1188,615	0,074	R.MVPAGMGAGLER.M	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			1188,658	0,117	R.GAFGKPQGTVAR.V	P27635	RL10_HUMAN	60S ribosomal protein L10 (Laminin receptor homolog) (Large ribosomal subunit protein uL16) (Protein QM) (Ribosomal protein L10) (Tumor suppressor QM)	RPL10
			1188,686	0,145	R.RLFEGNALLR.R	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RPS9
			1188,691	0,150	R.ITAHLVHEL.R	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2
1188,67	1188,071	1189,260	1188,658	0,008	R.GAFGKPQGTVAR.V	P27635	RL10_HUMAN	60S ribosomal protein L10 (Laminin receptor homolog) (Large ribosomal subunit protein uL16) (Protein QM) (Ribosomal protein L10) (Tumor suppressor QM)	RPL10
			1188,686	0,021	R.RLFEGNALLR.R	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RPS9
			1188,691	0,026	R.ITAHLVHEL.R	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2
			1188,615	0,050	R.MVPAGMGAGLER.M	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM

1189,63	1189,033	1190,223	1189,623	0,005	R.QAFQIGSPWR.T	P00352	AL1A1_HUMAN	Retinal dehydrogenase 1 (RALDH 1) (RaIDH1) (EC 1.2.1.-) (EC 1.2.1.36) (ALDH-E1) (ALHDI1) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic)	ALDH1A1
1190,64 1191,63	1190,040 1191,039	1191,231 1192,230	1191,618	0,017	K.SLPFGAQSTQR.G	Q9UHL4	DPP2_HUMAN	Dipeptidyl peptidase 2 (EC 3.4.14.2) (Dipeptidyl aminopeptidase II) (Dipeptidyl peptidase 7) (Dipeptidyl peptidase II) (DPP II) (Quiescent cell proline dipeptidase)	DPP7
			1191,607	0,028	R.LAPEYEAATR.L	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	PDIA3
			1191,675	0,040	R.ELKQLYLER.V	P61160	ARP2_HUMAN	Actin-related protein 2 (Actin-like protein 2)	ACTR2
1192,64	1192,042	1193,235	1192,649	0,011	R.QINWTVLYR.R	P83731	RL24_HUMAN	60S ribosomal protein L24 (60S ribosomal protein L30) (Large ribosomal subunit protein eL24)	RPL24
			1192,570	0,069	R.DETNYGIPQR.A	P63244	RACK1_HUMAN	Receptor of activated protein C kinase 1 (Cell proliferation-inducing gene 21 protein) (Guanine nucleotide-binding protein subunit beta-2-like 1) (Guanine nucleotide-binding protein subunit beta-like protein 12.3) (Human lung cancer oncogene 7 protein) (HLC-7) (Receptor for activated C kinase) (Small ribosomal subunit protein RACK1) [Cleaved into: Receptor of activated protein C kinase 1, N-terminally processed (Guanine nucleotide-binding protein subunit beta-2-like 1, N-terminally processed)]	RACK1
1193,55	1192,958	1194,151	1193,584	0,029	R.MPLFEHYTR.Q	P28838	AMPL_HUMAN	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase 3) (LAP-3) (Leucyl aminopeptidase) (Peptidase 5) (Proline aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase)	LAP3
			1193,710	0,156	R.LVLVNAVYFR.G	P35237	SPB6_HUMAN	Serpin B6 (Cytoplasmic antiproteinase) (CAP) (Peptidase inhibitor 6) (PI-6) (Placental thrombin inhibitor)	SERPINB6
1193,64	1193,045	1194,238	1193,584	0,058	R.MPLFEHYTR.Q	P28838	AMPL_HUMAN	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase 3) (LAP-3) (Leucyl aminopeptidase) (Peptidase 5) (Proline aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase)	LAP3
			1193,710	0,069	R.LVLVNAVYFR.G	P35237	SPB6_HUMAN	Serpin B6 (Cytoplasmic antiproteinase) (CAP) (Peptidase inhibitor 6) (PI-6) (Placental thrombin inhibitor)	SERPINB6
1194,55	1193,954	1195,148	1194,576	0,025	K.GRPDYNGPR.E	P13667	PDIA4_HUMAN	Protein disulfide-isomerase A4 (EC 5.3.4.1) (Endoplasmic reticulum resident protein 70) (ER protein 70) (ERp70) (Endoplasmic reticulum resident protein 72) (ER protein 72) (ERp-72) (ERp72)	PDIA4
			1194,698	0,147	R.NLPLPPPPPR.G	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
1194,68	1194,086	1195,281	1194,698	0,015	R.NLPLPPPPPR.G	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
			1194,576	0,107	K.GRPDYNGPR.E	P13667	PDIA4_HUMAN	Protein disulfide-isomerase A4 (EC 5.3.4.1) (Endoplasmic reticulum resident protein 70) (ER protein 70) (ERp70) (Endoplasmic reticulum resident protein 72) (ER protein 72) (ERp-72) (ERp72)	PDIA4
1195,47	1194,871	1196,066	1195,556	0,087	K.DSGFQMQLR.G	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
1195,56	1194,963	1196,159	1195,556	0,005	K.DSGFQMQLR.G	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
1195,68	1195,082	1196,278	1195,556	0,124	K.DSGFQMQLR.G	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
1196,57 1196,67 1197,63	1195,969 1196,073 1197,028	1197,166 1197,270 1198,226	1197,642 1197,660	0,015 0,033	R.GGPPPPPPATGR.S R.LDIDSPPIAR.N	P42768 P14618	WASP_HUMAN KPYM_HUMAN	Wiskott-Aldrich syndrome protein (WASp) Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	WAS PKM
			1197,694	0,066	K.DAGVIAGLNVL.R	P0DMV8	HS71A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
			1197,701	0,074	R.LLLNNDNLL.R	P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (CapZ alpha-1)	CAPZA1
			1197,701	0,074	R.LLLNNDNLL.R	P47755	CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 (CapZ alpha-2)	CAPZA2
1198,49	1197,895	1199,093	1198,718	0,224	R.AVFPSIVGRPR.H	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1198,718	0,224	R.AVFPSIVGRPR.H	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1198,718	0,224	R.AVFPSIVGRPR.Q	Q6S8J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
1198,71	1198,110	1199,309	1198,718	0,009	R.AVFPSIVGRPR.H	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1

1198,91	1198,314	1199,513	1198,718	0,009	R.AVFPSIVGRPR.H	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1198,718	0,009	R.AVFPSIVGRPR.Q	Q6S8J3	POTEE_HUMAN	POTE ankryrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			1198,718	0,195	R.AVFPSIVGRPR.H	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1198,718	0,195	R.AVFPSIVGRPR.H	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
1198,91	1198,314	1199,513	1198,718	0,195	R.AVFPSIVGRPR.Q	Q6S8J3	POTEE_HUMAN	POTE ankryrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			1199,683	0,158	K.DAGTIAGLNVLR.I	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
			1199,683	0,028	K.DAGTIAGLNVLR.I	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
			1201,609	0,024	R.LGDNFHTNKR.V	P08708	RS17_HUMAN	40S ribosomal protein S17 (Small ribosomal subunit protein eS17)	RPS17
1201,70	1201,099	1202,300	1201,609	0,090	R.LGDNFHTNKR.V	P08708	RS17_HUMAN	40S ribosomal protein S17 (Small ribosomal subunit protein eS17)	RPS17
			1202,643	0,010	K.NVIGLQMGNTNR.G	P37802	TAGL2_HUMAN	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	TAGLN2
			1202,617	0,036	K.QQSELQSQVR.Y	Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 (LASP-1) (Metastatic lymph node gene 50 protein) (MLN 50)	LASP1
			1203,638	0,017	K.FAAATGATPIAGR.F	P08865	RSSA_HUMAN	40S ribosomal protein SA (37 kDa laminin receptor precursor) (37LRP) (37/67 kDa laminin receptor) (LRP/LR) (67 kDa laminin receptor) (67LR) (Colon carcinoma laminin-binding protein) (Laminin receptor 1) (LamR) (Laminin-binding protein precursor p40) (LBP/p40) (Multidrug resistance-associated protein MGR1-Ag) (NEM/1CHD4) (Small ribosomal subunit protein uS2)	RPSA
1204,64	1204,035	1205,240	1205,683	0,055	R.KGHAVGDIPGVR.F	P62266	RS23_HUMAN	40S ribosomal protein S23 (Small ribosomal subunit protein uS12)	RPS23
			1206,666	0,332	K.HLSVNDLPVGR.S	P30048	PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial (EC 1.11.1.15) (Antioxidant protein 1) (AOP-1) (HBC189) (Peroxiredoxin III) (Prx-III) (Peroxiredoxin-3) (Protein MERS homolog)	PRDX3
			1206,666	0,167	K.HLSVNDLPVGR.S	P30048	PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial (EC 1.11.1.15) (Antioxidant protein 1) (AOP-1) (HBC189) (Peroxiredoxin III) (Prx-III) (Peroxiredoxin-3) (Protein MERS homolog)	PRDX3
			1206,666	0,012	K.HLSVNDLPVGR.S	P30048	PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial (EC 1.11.1.15) (Antioxidant protein 1) (AOP-1) (HBC189) (Peroxiredoxin III) (Prx-III) (Peroxiredoxin-3) (Protein MERS homolog)	PRDX3
1207,62	1207,020	1208,228	1207,583	0,041	R.ASYAQQAESR.V	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
			1208,694	0,043	K.TIAFLPMFR.H	Q7L014	DDX46_HUMAN	Probable ATP-dependent RNA helicase DDX46 (EC 3.6.4.13) (DEAD box protein 46) (PRP5 homolog)	DDX46
			1208,526	0,126	K.EGALCEENMR.G	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
			1209,696	0,071	K.IVPNVLLEQ GK.A	O75390	CISY_HUMAN	Citrate synthase, mitochondrial (EC 2.3.3.1) (Citrate (Si)-synthase)	CS
1209,63	1209,021	1210,230	1209,696	0,071	R.VNPALAEINLR.S	P13489	RINI_HUMAN	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor) (Ribonuclease/angiogenin inhibitor 1) (RAI)	RNH1
			1210,740	0,181	K.LIGNMALLPIR.S	O15145	ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3 (Arp2/3 complex 21 kDa subunit) (p21-ARC)	ARPC3
			1210,740	0,056	K.LIGNMALLPIR.S	O15145	ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3 (Arp2/3 complex 21 kDa subunit) (p21-ARC)	ARPC3
			1211,587	0,208	K.NEPQNATGAPGR.N	P51148	RAB5C_HUMAN	Ras-related protein Rab-5C (L1880) (RAB5L)	RAB5C
1211,38	1210,774	1211,985	1211,642	0,262	K.HVIGLQMGSNR.G	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein WS3-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
			1211,682	0,303	R.QITVNDLPVGR.S	P32119	PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
			1211,682	0,303	R.QITVNDLPVGR.S	Q06830	PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
			1211,587	0,057	K.NEPQNATGAPGR.N	P51148	RAB5C_HUMAN	Ras-related protein Rab-5C (L1880) (RAB5L)	RAB5C

			1211,642	0,112	K.HVIGLQMGSNR.G	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein WS3-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
			1211,682	0,152	R.QITVNDLPVGR.S	P32119	PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
			1211,682	0,152	R.QITVNDLPVGR.S	Q06830	PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
1211,68	1211,075	1212,286	1211,682	0,001	R.QITVNDLPVGR.S	P32119	PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
			1211,682	0,001	R.QITVNDLPVGR.S	Q06830	PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
			1211,642	0,039	K.HVIGLQMGSNR.G	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein WS3-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
1212,38	1211,775	1212,988	1211,587	0,093	K.NEPQNATGAPGR.N	P51148	RAB5C_HUMAN	Ras-related protein Rab-5C (L1880) (RAB5L)	RAB5C
			1212,619	0,238	R.VNHFVPEAGSR.L	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1212,619	0,032	R.VNHFVPEAGSR.L	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1212,65	1212,045	1213,258	1212,619	0,032	R.VNHFVPEAGSR.L	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1213,64	1213,032	1214,246	1213,632	0,007	R.WLQGSQELPR.E	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
1214,58	1213,974	1215,189	1214,571	0,010	K.EFSIDVGYER.F	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
1214,63	1214,018	1215,233	1214,571	0,054	K.EFSIDVGYER.F	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
1215,49	1214,878	1216,093	1215,665	0,180	K.GIPHLVTHDAR.T	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein eS4)	RPS4X
			1215,696	0,210	R.TLMNLGGLAVAR.D	P37802	TAGL2_HUMAN	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	TAGLN2
			1215,717	0,232	K.NVTGRMLVGLR.W	Q9NYZ1	TV23B_HUMAN	Golgi apparatus membrane protein TVP23 homolog B	TVP23B
			1215,721	0,235	R.TIRYPDLIK.V	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein eS4)	RPS4X
			1215,665	0,024	K.GIPHLVTHDAR.T	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein eS4)	RPS4X
			1215,696	0,055	R.TLMNLGGLAVAR.D	P37802	TAGL2_HUMAN	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	TAGLN2
1215,64	1215,033	1216,249	1215,717	0,076	K.NVTGRMLVGLR.W	Q9NYZ1	TV23B_HUMAN	Golgi apparatus membrane protein TVP23 homolog B	TVP23B
			1215,721	0,080	R.TIRYPDLIK.V	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein eS4)	RPS4X
			1216,676	0,027	K.LIDRTESLNR.S	P33241	LSP1_HUMAN	Lymphocyte-specific protein 1 (47 kDa actin-binding protein) (52 kDa phosphoprotein) (pp52) (Lymphocyte-specific antigen WP34)	LSP1
1216,65	1216,041	1217,257	1216,608	0,041	R.IAEFAFEYAR.N	P50213	IDH3A_HUMAN	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial (EC 1.1.1.41) (Isocitric dehydrogenase subunit alpha) (NAD(+)-specific IDH subunit alpha)	IDH3A
			1217,631	0,200	R.NGPALQEAYVR.V	Q9UJU6	DBNL_HUMAN	Drebrin-like protein (Cervical SH3P7) (Cervical mucin-associated protein) (Drebrin-F) (HPK1-interacting protein of 55 kDa) (HIP-55) (SH3 domain-containing protein 7)	DBNL
			1217,644	0,213	K.DAGTIAGLNVMR.I	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
1217,43	1216,822	1218,039	1217,631	0,200	R.NGPALQEAYVR.V	Q9UJU6	DBNL_HUMAN	Drebrin-like protein (Cervical SH3P7) (Cervical mucin-associated protein) (Drebrin-F) (HPK1-interacting protein of 55 kDa) (HIP-55) (SH3 domain-containing protein 7)	DBNL
			1217,644	0,213	K.DAGTIAGLNVMR.I	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			1217,631	0,013	R.NGPALQEAYVR.V	Q9UJU6	DBNL_HUMAN	Drebrin-like protein (Cervical SH3P7) (Cervical mucin-associated protein) (Drebrin-F) (HPK1-interacting protein of 55 kDa) (HIP-55) (SH3 domain-containing protein 7)	DBNL
1217,64	1217,035	1218,252	1217,644	0,000	K.DAGTIAGLNVMR.I	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			1217,631	0,013	R.NGPALQEAYVR.V	Q9UJU6	DBNL_HUMAN	Drebrin-like protein (Cervical SH3P7) (Cervical mucin-associated protein) (Drebrin-F) (HPK1-interacting protein of 55 kDa) (HIP-55) (SH3 domain-containing protein 7)	DBNL
			1217,631	0,013	R.NGPALQEAYVR.V	Q9UJU6	DBNL_HUMAN	Drebrin-like protein (Cervical SH3P7) (Cervical mucin-associated protein) (Drebrin-F) (HPK1-interacting protein of 55 kDa) (HIP-55) (SH3 domain-containing protein 7)	DBNL
1218,65	1218,037	1219,256	1218,642	0,004	K.DANLYISGLPR.T	Q15717	ELAV1_HUMAN	ELAV-like protein 1 (Hu-antigen R) (HuR)	ELAVL1
			1218,687	0,040	R.LVREIAQDFK.T	P84243	H33_HUMAN	Histone H3.3	H3F3A; H3F3B
			1218,696	0,049	R.VAQLQEVYIR.G	P62318	SMD3_HUMAN	Small nuclear ribonucleoprotein Sm D3 (Sm-D3) (snRNP core protein D3)	SNRPD3
1219,40	1218,786	1220,005	1219,598	0,202	K.SLEDOQVEMLR.T	P14314	GLU2B_HUMAN	Glucosidase 2 subunit beta (80K-H protein) (Glucosidase II subunit beta) (Protein kinase C substrate 60.1 kDa protein heavy chain) (PKCSH)	PRKCSH
			1219,636	0,241	K.YELGRPAANTK.I	P62241	RS8_HUMAN	40S ribosomal protein S8 (Small ribosomal subunit protein eS8)	RPS8
			1219,636	0,241	K.YELGRPAANTK.I	P62241	RS8_HUMAN	40S ribosomal protein S8 (Small ribosomal subunit protein eS8)	RPS8
1219,67	1219,056	1220,276	1219,636	0,030	K.YELGRPAANTK.I	P62241	RS8_HUMAN	40S ribosomal protein S8 (Small ribosomal subunit protein eS8)	RPS8

			1219,598	0,068	K.SLEDQVEMLR.T	P14314	GLU2B_HUMAN	Glucosidase 2 subunit beta (80K-H protein) (Glucosidase II subunit beta) (Protein kinase C substrate 60.1 kDa protein heavy chain) (PKCSH)	PRKCSH
1220,49	1219,880	1221,100	1220,610 1220,683	0,120 0,193	K.NFPSVDAAFR.Q K.FMLGKQEVIR.G	P02790 P62942	HEMO_HUMAN FKB1A_HUMAN	Hemopexin (Beta-1B-glycoprotein) Peptidyl-prolyl cis-trans isomerase FKBP1A (PPIase FKBP1A) (EC 5.2.1.8) (12 kDa FK506-binding protein) (12 kDa FKBP) (FKBP-12) (Calstabin-1) (FK506-binding protein 1A) (FKBP-1A) (Immunophilin FKBP12) (Rotamase)	HPX FKBP1A
			1220,694	0,203	K.KLSSWVLLMK.Y	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiproteinase) (Serpine A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
1220,68	1220,069	1221,290	1220,683	0,003	K.FMLGKQEVIR.G	P62942	FKB1A_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP1A (PPIase FKBP1A) (EC 5.2.1.8) (12 kDa FK506-binding protein) (12 kDa FKBP) (FKBP-12) (Calstabin-1) (FK506-binding protein 1A) (FKBP-1A) (Immunophilin FKBP12) (Rotamase)	FKBP1A
			1220,694	0,014	K.KLSSWVLLMK.Y	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiproteinase) (Serpine A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
			1220,610	0,070	K.NFPSVDAAFR.Q	P02790	HEMO_HUMAN	Hemopexin (Beta-1B-glycoprotein)	HPX
1221,67	1221,060	1222,282	1221,632	0,039	R.GHLENNPALEK.L	P05388	RLA0_HUMAN	60S acidic ribosomal protein P0 (60S ribosomal protein L10E) (Large ribosomal subunit protein uL10)	RPLP0
			1221,562	0,109	R.QEMQEVQSSR.S	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
1221,67	1221,060	1222,282	1221,632	0,040	R.GHLENNPALEK.L	P05388	RLA0_HUMAN	60S acidic ribosomal protein P0 (60S ribosomal protein L10E) (Large ribosomal subunit protein uL10)	RPLP0
			1221,562	0,109	R.QEMQEVQSSR.S	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
1222,63	1222,016	1223,238	1222,624	0,004	R.FEPYANPTKR.Y	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			1222,647	0,020	R.TKFETEQALR.M	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeatin-19) (CK-19) (Keratin-19) (K19)	KRT19
1222,66	1222,052	1223,275	1222,647	0,016	R.TKFETEQALR.M	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeatin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1222,624	0,040	R.FEPYANPTKR.Y	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
1223,64 1224,65 1225,65	1223,026 1224,034 1225,039	1224,249 1225,259 1226,265	1225,679	0,027	R.VLANPGNSQVAR.V	Q14974	IMB1_HUMAN	Importin subunit beta-1 (Importin-90) (Karyopherin subunit beta-1) (Nuclear factor p97) (Pore targeting complex 97 kDa subunit) (PTAC97)	KPNB1
			1225,694	0,042	R.QITLNDLPVGR.S	Q13162	PRDX4_HUMAN	Peroxisomal protein 4 (EC 1.11.1.15) (Antioxidant enzyme AOE372) (AOE37-2) (Peroxisomal protein IV) (Prx-IV) (Thioredoxin peroxidase AOE372) (Thioredoxin-dependent peroxide reductase AOE372)	PRDX4
1226,66 1227,64	1226,044 1227,025	1227,271 1228,253	1227,601	0,038	K.EHFAQGHVLR.R	Q9GZT3	SLIRP_HUMAN	SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP
			1227,549	0,090	R.EVCGFAPYER.R	Q9Y3U8	RL36_HUMAN	60S ribosomal protein L36 (Large ribosomal subunit protein eL36)	RPL36
1228,67	1228,055	1229,283	1228,643	0,026	K.VEIIANDQGNR.T	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
			1228,643	0,026	R.VEIIANDQGNR.I	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (immunoglobulin heavy chain-binding protein)	HSPA5
			1228,643	0,026	K.VEIIANDQGNR.T	P0DMV8	H571A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
			1228,639	0,030	R.AAPGAEFAPNKR.R	Q15233	NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrb)) (p54nrb)	NONO
			1228,706	0,038	R.SEIDLNIRR.E	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6
1229,56	1228,948	1230,178	1229,593 1229,603	0,030 0,040	R.NNLTSSAGYR.A R.ISEQFTAMFR.R	P12111 P68371	CO6A3_HUMAN TBB4B_HUMAN	Collagen alpha-3(VI) chain Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	COL6A3 TUBB4B
			1229,603 1229,708	0,040 0,146	R.ISEQFTAMFR.R R.SARAGVIFPVGR.L	P07437 Q9P0M6	TBB5_HUMAN H2AW_HUMAN	Tubulin beta chain (Tubulin beta-5 chain) Core histone macro-H2A.2 (Histone macroH2A2) (mH2A2)	TUBB H2AFY2
1229,69	1229,073	1230,302	1229,708	0,021	R.SARAGVIFPVGR.L	Q9P0M6	H2AW_HUMAN	Core histone macro-H2A.2 (Histone macroH2A2) (mH2A2)	H2AFY2
			1229,603	0,084	R.ISEQFTAMFR.R	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1229,603 1229,593	0,084 0,094	R.ISEQFTAMFR.R R.NNLTSSAGYR.A	P07437 P12111	TBB5_HUMAN CO6A3_HUMAN	Tubulin beta chain (Tubulin beta-5 chain) Collagen alpha-3(VI) chain	TUBB COL6A3
1230,65 1231,63	1230,032 1231,010	1231,263 1232,242	1231,614	0,012	R.SLGTADVHFER.K	Q86V81	THOC4_HUMAN	THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Aly/REF export factor) (Transcriptional coactivator Aly/REF) (bZIP-enhancing factor BEF)	ALYREF

			1231,677	0,051	K.GIVEFSGKPAAR.K	Q15233	NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrb)) (p54nrb)	NONO
1232,59	1231,974	1233,207	1232,652	0,061	R.VAYVSGPHAGK.L	P50914	RL14_HUMAN	60S ribosomal protein L14 (CAG-ISL 7) (Large ribosomal subunit protein eL14)	RPL14
			1232,686	0,096	K.GVLFASGQNLAR.Q	P28838	AMPL_HUMAN	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase 3) (LAP-3) (Leucyl aminopeptidase) (Peptidase 5) (Proline aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase)	LAP3
1232,67	1232,053	1233,286	1232,686	0,016	K.GVLFASGQNLAR.Q	P28838	AMPL_HUMAN	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase 3) (LAP-3) (Leucyl aminopeptidase) (Peptidase 5) (Proline aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase)	LAP3
			1232,652	0,018	R.VAYVSGPHAGK.L	P50914	RL14_HUMAN	60S ribosomal protein L14 (CAG-ISL 7) (Large ribosomal subunit protein eL14)	RPL14
1233,63	1233,018	1234,251	1233,622	0,012	R.FGGPVVHHQAQR.F	Q15717	ELAV1_HUMAN	ELAV-like protein 1 (Hu-antigen R) (HuR)	ELAVL1
			1233,652	0,017	K.TVFGVEPDLTR.E	Q96KP4	CNDP2_HUMAN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Carnosine dipeptidase II) (Epididymis secretory protein Li 13) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	CNDP2
			1233,612	0,022	R.IQVWHEHR.G	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			1233,661	0,027	R.ARSEQFINLR.E	P07384	CAN1_HUMAN	Calpain-1 catalytic subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase 1) (CANP 1) (Calpain mu-type) (Calpain-1 large subunit) (Cell proliferation-inducing gene 30 protein) (Micromolar-calpain) (muCANP)	CAPN1
1234,66	1234,047	1235,281	1234,684	0,020	R.SEIDLFNIRK.E	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
			1234,688	0,024	R.LKYENEVALR.Q	P13645	K1C10_HUMAN	Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KRT10
1235,61	1234,988	1236,224	1235,599	0,007	K.DQVANSAFVER.L	P07900	H590A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
			1235,625	0,019	R.AAQDRDQIYR.R	P62995	TRA2B_HUMAN	Transformer-2 protein homolog beta (TRA-2 beta) (TRA2-beta) (hTRA2-beta) (Splicing factor, arginine/serine-rich 10) (Transformer-2 protein homolog B)	TRA2B
			1235,631	0,025	K.QVAEQFLNMR.G	P22695	QCR2_HUMAN	Cytochrome b-c1 complex subunit 2, mitochondrial (Complex III subunit 2) (Core protein II) (Ubiquinol-cytochrome-c reductase complex core protein 2)	UQCRC2
			1235,539	0,067	R.FSSSSGYGGSSSR.V	P35527	K1C9_HUMAN	Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9) (Keratin-9) (K9)	KRT9
1236,62	1235,998	1237,234	1236,629	0,013	K.KEMQPTHPIR.L	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
			1236,629	0,013	K.KEMQPTHPIR.L	P31946	1433B_HUMAN	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHAH
			1236,710	0,094	R.LNIPVSQVNP.R.D	P13637	AT1A3_HUMAN	Sodium/potassium-transporting ATPase subunit alpha-3 (Na(+)/K(+) ATPase alpha-3 subunit) (EC 7.2.2.13) (Na(+)/K(+) ATPase alpha(III) subunit) (Sodium pump subunit alpha-3)	ATP1A3
			1236,768	0,151	K.ILITVPPNLR.K	Q12905	ILF2_HUMAN	Interleukin enhancer-binding factor 2 (Nuclear factor of activated T-cells 45 kDa)	ILF2
1237,62	1237,006	1238,243	1237,669	0,045	R.EFEVYGPIKR.I	P08621	RU17_HUMAN	U1 small nuclear ribonucleoprotein 70 kDa (U1 snRNP 70 kDa) (U1-70K) (snRNP70)	SNRNP70
			1237,546	0,079	R.QEMQEVSQSSR.S	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
1238,63	1238,011	1239,250	1238,599	0,031	K.FFEHFIEGGR.T	Q96FW1	OTUB1_HUMAN	Ubiquitin thioesterase OTUB1 (EC 3.4.19.12) (Deubiquitinating enzyme OTUB1) (OTU domain-containing ubiquitin aldehyde-binding protein 1) (Otubain-1) (hOTU1) (Ubiquitin-specific-processing protease OTUB1)	OTUB1
1239,61	1238,988	1240,228	1239,624	0,017	K.FDGILGMAYPR.I	P07339	CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD
			1239,652	0,044	R.VKYETELAMR.Q	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
1240,45	1239,834	1241,075	1240,566	0,111	K.INFDDNAEFR.Q	Q96I99	SUCB2_HUMAN	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial (EC 6.2.1.4) (GTP-specific succinyl-CoA synthetase subunit beta) (G-SCS) (GTPSCS) (Succinyl-CoA synthetase beta-G chain) (SCS-betaG)	SUCLG2
1240,52	1239,905	1241,145	1240,566	0,041	K.INFDDNAEFR.Q	Q96I99	SUCB2_HUMAN	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial (EC 6.2.1.4) (GTP-specific succinyl-CoA synthetase subunit beta) (G-SCS) (GTPSCS) (Succinyl-CoA synthetase beta-G chain) (SCS-betaG)	SUCLG2
1240,64	1240,021	1241,261	1240,566	0,075	K.INFDDNAEFR.Q	Q96I99	SUCB2_HUMAN	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial (EC 6.2.1.4) (GTP-specific succinyl-CoA synthetase subunit beta) (G-SCS) (GTPSCS) (Succinyl-CoA synthetase beta-G chain) (SCS-betaG)	SUCLG2

1241,53	1240,910	1242,152	1241,654	0,123	K.STFVLDEFKR.K	P26641	EF1G_HUMAN	Elongation factor 1-gamma (EF-1-gamma) (eEF-18 gamma)	EEF1G
			1241,671	0,140	K.GKLEEQRP.R.V	P13693	TCTP_HUMAN	Translationally-controlled tumor protein (TCTP) (Fortilin) (Histamine-releasing factor) (HRF) (p23)	TPT1
			1241,682	0,151	K.GGGHVAQYAIR.Q	P62249	RS16_HUMAN	40S ribosomal protein S16 (Small ribosomal subunit protein uS9)	RPS16
1241,68	1241,060	1242,301	1241,682	0,002	K.GGGHVAQYAIR.Q	P62249	RS16_HUMAN	40S ribosomal protein S16 (Small ribosomal subunit protein uS9)	RPS16
			1241,671	0,009	K.GKLEEQRP.R.V	P13693	TCTP_HUMAN	Translationally-controlled tumor protein (TCTP) (Fortilin) (Histamine-releasing factor) (HRF) (p23)	TPT1
			1241,654	0,026	K.STFVLDEFKR.K	P26641	EF1G_HUMAN	Elongation factor 1-gamma (EF-1-gamma) (eEF-18 gamma)	EEF1G
1242,52	1241,897	1243,139	1242,688	0,170	K.AGNLGGGVVTIER.S	P35268	RL22_HUMAN	60S ribosomal protein L22 (EBER-associated protein) (EAP) (Epstein-Barr virus small RNA-associated protein) (Heparin-binding protein HBp15) (Large ribosomal subunit protein eL22)	RPL22
1242,68	1242,056	1243,298	1242,688	0,011	K.AGNLGGGVVTIER.S	P35268	RL22_HUMAN	60S ribosomal protein L22 (EBER-associated protein) (EAP) (Epstein-Barr virus small RNA-associated protein) (Heparin-binding protein HBp15) (Large ribosomal subunit protein eL22)	RPL22
1243,53	1242,912	1244,156	1243,657	0,123	K.LLEGEERLR.L	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
			1243,674	0,140	K.HGVVPLATYMR.I	P46778	RL21_HUMAN	60S ribosomal protein L21 (Large ribosomal subunit protein eL21)	RPL21
1243,65	1243,033	1244,276	1243,657	0,002	K.LLEGEERLR.L	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
			1243,674	0,020	K.HGVVPLATYMR.I	P46778	RL21_HUMAN	60S ribosomal protein L21 (Large ribosomal subunit protein eL21)	RPL21
1244,62	1243,996	1245,241	1244,634	0,016	R.TNQLQEINR.V	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
1244,65	1244,026	1245,270	1244,634	0,014	R.TNQLQEINR.V	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
1245,51	1244,887	1246,133	1245,697	0,187	K.GIVEFASKPAAR.K	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
1245,66	1245,038	1246,283	1245,697	0,037	K.GIVEFASKPAAR.K	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
1246,65	1246,024	1247,271	1246,651	0,003	R.LVEDMENKIR.S	P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta (CapZ beta)	CAPZB
			1246,629	0,019	R.VNEAREELMR.M	P61204	ARF3_HUMAN	ADP-ribosylation factor 3	ARF3
1247,65	1247,029	1248,277	1247,684	0,031	K.GLSQSALPYRR.S	P62277	RS13_HUMAN	40S ribosomal protein S13 (Small ribosomal subunit protein uS15)	RPS13
			1247,588	0,065	R.AGELTEDEVER.V	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
1248,64	1248,017	1249,266	1248,690	0,049	R.GLKTVFDEAIR.A	P15153	RAC2_HUMAN	Ras-related C3 botulinum toxin substrate 2 (GX) (Small G protein) (p21-Rac2)	RAC2
1249,65	1249,025	1250,275	1249,626	0,024	K.EQVANSAFVER.V	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			1249,690	0,039	R.NRNVNPVALPR.A	P08311	CATG_HUMAN	Cathepsin G (CG) (EC 3.4.21.20)	CTSG
1250,65	1250,023	1251,273	1250,670	0,022	R.DQLLPSPNNR.I	P12109	CO6A1_HUMAN	Collagen alpha-1(VI) chain	COL6A1
			1250,615	0,033	R.LTQVMKEETR.A	Q6NUQ1	RINT1_HUMAN	RAD50-interacting protein 1 (RAD50 interactor 1) (HsRINT-1) (RINT-1)	RINT1
			1250,578	0,070	R.EVQQGEEFER.R	P00568	KAD1_HUMAN	Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	AK1
			1250,720	0,072	R.YQKSTELLIR.K	P84243	H33_HUMAN	Histone H3.3	H3F3A; H3F3B
1251,64	1251,011	1252,263	1252,641	0,065	R.LSFDKDMVAR.A	P37837	TALDO_HUMAN	Transaldolase (EC 2.2.1.2)	TALDO1
1252,58	1251,949	1253,202	1252,713	0,137	R.VHIGQVIMSIR.T	P27635	RL10_HUMAN	60S ribosomal protein L10 (Laminin receptor homolog) (Large ribosomal subunit protein uL16) (Protein QM) (Ribosomal protein L10) (Tumor suppressor QM)	RPL10
1252,69	1252,065	1253,318	1252,713	0,022	R.VHIGQVIMSIR.T	P27635	RL10_HUMAN	60S ribosomal protein L10 (Laminin receptor homolog) (Large ribosomal subunit protein uL16) (Protein QM) (Ribosomal protein L10) (Tumor suppressor QM)	RPL10
			1252,641	0,050	R.LSFDKDMVAR.A	P37837	TALDO_HUMAN	Transaldolase (EC 2.2.1.2)	TALDO1
1253,62	1252,992	1254,245	1253,628	0,010	R.FEELNADLFR.G	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8

1253,67	1253,044	1254,298	1253,628	0,043	R.FEELNADLFR.G	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
1254,55	1253,923	1255,178	1254,572	0,021	R.LGDLYEEEMR.E	P08670	VIME_HUMAN	Vimentin	VIM
1254,70	1254,072	1255,327	1254,572	0,128	R.LGDLYEEEMR.E	P08670	VIME_HUMAN	Vimentin	VIM
1255,57	1254,938	1256,194	1255,607	0,041	-MPEPSKSAPAPK.K	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
			1255,607	0,041	-MPEPSKSAPAPK.K	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
			1255,647	0,080	K.AIGYLTGYQR.Q	P01023	A2MG_HUMAN	Alpha-2-macroglobulin (Alpha-2-M) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 5)	A2M
1255,71	1255,079	1256,334	1255,647	0,060	K.AIGYLTGYQR.Q	P01023	A2MG_HUMAN	Alpha-2-macroglobulin (Alpha-2-M) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 5)	A2M
			1255,607	0,099	-MPEPSKSAPAPK.K	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
			1255,607	0,099	-MPEPSKSAPAPK.K	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
1256,58	1255,950	1257,207	1256,621	0,042	R.GMQLMHANAQR.T	P13284	GILT_HUMAN	Gamma-interferon-inducible lysosomal thiol reductase (EC 1.8.-.-) (Gamma-interferon-inducible protein IP-30) (Legumaturain)	IFI30
			1256,675	0,096	R.AQADLALEKAAR.A	Q14980	NUMA1_HUMAN	Nuclear mitotic apparatus protein 1 (Nuclear matrix protein-22) (NMP-22) (Nuclear mitotic apparatus protein) (NuMA protein) (SP-H antigen)	NUMA1
			1256,675	0,096	K.VNVDAVGGEALGR.L	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
			1256,701	0,122	R.IYVGNLPPDIR.T	Q07955	SRSF1_HUMAN	Serine/arginine-rich splicing factor 1 (Alternative-splicing factor 1) (ASF-1) (Splicing factor, arginine/serine-rich 1) (pre-mRNA-splicing factor SF2, P33 subunit)	SRSF1
1256,70	1256,072	1257,329	1256,701	0,000	R.IYVGNLPPDIR.T	Q07955	SRSF1_HUMAN	Serine/arginine-rich splicing factor 1 (Alternative-splicing factor 1) (ASF-1) (Splicing factor, arginine/serine-rich 1) (pre-mRNA-splicing factor SF2, P33 subunit)	SRSF1
			1256,675	0,026	R.AQADLALEKAAR.A	Q14980	NUMA1_HUMAN	Nuclear mitotic apparatus protein 1 (Nuclear matrix protein-22) (NMP-22) (Nuclear mitotic apparatus protein) (NuMA protein) (SP-H antigen)	NUMA1
			1256,675	0,026	K.VNVDAVGGEALGR.L	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
			1256,621	0,079	R.GMQLMHANAQR.T	P13284	GILT_HUMAN	Gamma-interferon-inducible lysosomal thiol reductase (EC 1.8.-.-) (Gamma-interferon-inducible protein IP-30) (Legumaturain)	IFI30
1257,63	1257,006	1258,263	1257,632	0,002	R.ALSTGEKGFYK.G	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
1258,64	1258,014	1259,273	1258,677	0,034	K.GGETIKQLQER.A	Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1) (DNA helicase V) (hDH V)	FUBP1
			1258,677	0,034	K.GGETIKQLQER.A	Q92945	FUBP2_HUMAN	Far upstream element-binding protein 2 (FUSE-binding protein 2) (KH type-splicing regulatory protein) (KSRP) (p75)	KHSRP
			1258,681	0,038	R.DLALAIRDSER.Q	P40121	CAPG_HUMAN	Macrophage-capping protein (Actin regulatory protein CAP-G)	CAPG
			1258,594	0,050	R.VTGGQPACESPR.C	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1259,66	1259,025	1260,285	1259,619	0,037	R.YQYFKDFQR.R	Q13838	DX39B_HUMAN	Spliceosome RNA helicase DDX39B (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	DDX39B
			1259,574	0,081	R.VGFYESDVMGR.G	P01023	A2MG_HUMAN	Alpha-2-macroglobulin (Alpha-2-M) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 5)	A2M
1260,61	1259,977	1261,238	1260,656	0,048	K.LDEREAGITEK.V	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP1I
			1260,672	0,064	R.TEHINIHQLR.N	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
1260,67	1260,035	1261,296	1260,672	0,006	R.TEHINIHQLR.N	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
			1260,656	0,010	K.LDEREAGITEK.V	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP1I
1261,65	1261,019	1262,281	1261,661	0,011	R.RVSPGVYPACR.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1261,721	0,071	K.AFLTLAEDILR.K	P61026	RAB10_HUMAN	Ras-related protein Rab-10	RAB10
1262,64	1262,013	1263,275	1262,651	0,007	R.TIAMDGTGELVR.G	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			1262,627	0,017	R.KVYDQMPEPR.Y	O75251	NDUS7_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial (EC 1.6.99.3) (EC 7.1.1.2) (Complex I-20kD) (CI-20kD) (NADH-ubiquinone oxidoreductase 20 kDa subunit) (PSST subunit)	NDUF57
1262,65	1262,021	1263,283	1262,651	0,001	R.TIAMDGTGELVR.G	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			1262,627	0,025	R.KVYDQMPEPR.Y	O75251	NDUS7_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial (EC 1.6.99.3) (EC 7.1.1.2) (Complex I-20kD) (CI-20kD) (NADH-ubiquinone oxidoreductase 20 kDa subunit) (PSST subunit)	NDUF57
1263,68	1263,052	1264,316							
1264,63	1263,995	1265,259	1264,637	0,010	R.ASGAPSAGPEPAPR.L	O60240	PLIN1_HUMAN	Perilipin-1 (Lipid droplet-associated protein)	PLIN1

			1264,649	0,022	R.RAPDFLFENR.K	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
1265,53	1264,894	1266,159	1265,653	0,126	R.KESYSVVYVK.V	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
1265,67	1265,040	1266,306	1265,653	0,020	R.KESYSVVYVK.V	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
1266,64	1266,009	1267,276	1267,666	0,005	R.QDIAFAYQRR.T	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
1267,66	1267,028	1268,295							
			1267,742	0,081	R.IAAAILNTPDLR.K	P00505	AATM_HUMAN	Aspartate aminotransferase, mitochondrial (mAspAT) (EC 2.6.1.1) (EC 2.6.1.7) (Fatty acid-binding protein) (FABP-1) (Glutamate oxaloacetate transaminase 2) (Kynurenine aminotransferase 4) (Kynurenine aminotransferase IV) (Kynurenine--oxoglutarate transaminase 4) (Kynurenine--oxoglutarate transaminase IV) (Plasma membrane-associated fatty acid-binding protein) (FABPpm) (Transaminase A)	GOT2
			1267,776	0,115	R.LLVSTRASAPPR.R	A4D2P6	GRD2I_HUMAN	Delphilin (Glutamate receptor, ionotropic, delta 2-interacting protein 1)	GRD2IP
1268,67	1268,037	1269,306	1270,632	0,063	K.VFMQEFKEGR.R	O15144	ARPC2_HUMAN	Actin-related protein 2/3 complex subunit 2 (Arp2/3 complex 34 kDa subunit) (p34-ARC)	ARPC2
1269,68	1269,049	1270,319							
1270,69	1270,059	1271,330							
1271,68	1271,042	1272,313	1271,719	0,042	K.VIFDANAPVAVR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1271,734	0,056	R.KLAVNMVFPRL.L	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1271,734	0,056	R.KLAVNMVFPRL.L	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1271,752	0,074	K.QVVNIPSFIVR.L	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RP59
1271,69	1271,050	1272,322	1271,719	0,033	K.VIFDANAPVAVR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1271,734	0,047	R.KLAVNMVFPRL.L	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1271,734	0,047	R.KLAVNMVFPRL.L	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1271,752	0,066	K.QVVNIPSFIVR.L	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RP59
1271,86	1271,222	1272,493	1271,752	0,105	K.QVVNIPSFIVR.L	P46781	RS9_HUMAN	40S ribosomal protein S9 (Small ribosomal subunit protein uS4)	RP59
			1271,734	0,124	R.KLAVNMVFPRL.L	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1271,734	0,124	R.KLAVNMVFPRL.L	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1271,719	0,138	K.VIFDANAPVAVR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1272,42	1271,785	1273,057	1273,628	0,371	R.GNDVAFHFNPR.F	P17931	LEG3_HUMAN	Galectin-3 (Gal-3) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Galactose-specific lectin 3) (Galactoside-binding protein) (GALBP) (IgE-binding protein) (L-31) (Laminin-binding protein) (Lectin L-29) (Mac-2 antigen)	LGALS3
1272,69	1272,049	1273,322							
1272,87	1272,229	1273,502							
1273,26	1272,621	1273,894							
			1273,730	0,473	R.ECLPLIIFLR.N	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein eS4)	RP54X
1273,53	1272,894	1274,167	1273,628	0,097	R.GNDVAFHFNPR.F	P17931	LEG3_HUMAN	Galectin-3 (Gal-3) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Galactose-specific lectin 3) (Galactoside-binding protein) (GALBP) (IgE-binding protein) (L-31) (Laminin-binding protein) (Lectin L-29) (Mac-2 antigen)	LGALS3
			1273,730	0,200	R.ECLPLIIFLR.N	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein eS4)	RP54X
1273,71	1273,078	1274,352	1273,730	0,015	R.ECLPLIIFLR.N	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein eS4)	RP54X
			1273,628	0,087	R.GNDVAFHFNPR.F	P17931	LEG3_HUMAN	Galectin-3 (Gal-3) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Galactose-specific lectin 3) (Galactoside-binding protein) (GALBP) (IgE-binding protein) (L-31) (Laminin-binding protein) (Lectin L-29) (Mac-2 antigen)	LGALS3
1274,00	1273,364	1274,638	1273,730	0,270	R.ECLPLIIFLR.N	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein eS4)	RP54X
			1273,628	0,373	R.GNDVAFHFNPR.F	P17931	LEG3_HUMAN	Galectin-3 (Gal-3) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Galactose-specific lectin 3) (Galactoside-binding protein) (GALBP) (IgE-binding protein) (L-31) (Laminin-binding protein) (Lectin L-29) (Mac-2 antigen)	LGALS3
1274,72	1274,079	1275,354	1274,702	0,014	R.SSRAGLOFPVGR.V	P16104	H2AX_HUMAN	Histone H2AX (H2a/x) (Histone H2A.X)	H2AFX
			1274,702	0,014	R.SSRAGLOFPVGR.V	Q6F113	H2A2A_HUMAN	Histone H2A type 2-A (Histone H2A.2) (Histone H2A/o)	HIST2H2AA3; HIST2H2AA4
			1274,702	0,014	R.SSRAGLOFPVGR.V	Q93077	H2A1C_HUMAN	Histone H2A type 1-C (Histone H2A/I)	HIST1H2AC
			1274,702	0,014	R.SSRAGLOFPVGR.V	Q8IU66	H2A2B_HUMAN	Histone H2A type 2-B	HIST2H2AB
			1274,739	0,023	R.LLVVYPWTQR.F	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
			1274,739	0,023	R.LLVVYPWTQR.F	P69892	HBG2_HUMAN	Hemoglobin subunit gamma-2 (Gamma-2-globin) (Hb F Ggamma) (Hemoglobin gamma-2 chain) (Hemoglobin gamma-G chain)	HBG2
			1274,739	0,023	R.LLVVYPWTQR.F	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB

			1274,690	0,027	K.QQISLATQMVR.M	P48643	TCPE_HUMAN	T-complex protein 1 subunit epsilon (TCP-1-epsilon) (CCT-epsilon)	CCT5
1275,72	1275,081	1276,357	1275,726	0,006	K.HVVPNEVVQR.L	P06396	GELS_HUMAN	Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF) (Brevin)	GSN
			1275,615	0,104	K.NFGGHRDYGPR.T	Q92804	RBP56_HUMAN	TATA-binding protein-associated factor 2N (68 kDa TATA-binding protein-associated factor) (TAFII68) (TAFII68) (RNA-binding protein 56)	TAF15
1276,54	1275,904	1277,180							
1276,72	1276,083	1277,360							
1277,57	1276,931	1278,209	1277,627	0,057	R.QQPGPSEHIER.R	P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP)	VASP
1277,73	1277,092	1278,370	1277,627	0,104	R.QQPGPSEHIER.R	P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP)	VASP
1278,57	1277,927	1279,206	1278,580	0,014	K.EGMNIVEAMER.F	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
			1278,615	0,048	R.RMGESDDSLR.L	P63220	RS21_HUMAN	40S ribosomal protein S21 (Small ribosomal subunit protein eS21)	RPS21
			1278,647	0,081	R.KEAESSPFVER.L	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			1278,722	0,155	R.EPETPLAVGLR.V	Q02388	CO7A1_HUMAN	Collagen alpha-1(VII) chain (Long-chain collagen) (LC collagen)	COL7A1
1278,73	1278,089	1279,368	1278,722	0,007	R.EPETPLAVGLR.V	Q02388	CO7A1_HUMAN	Collagen alpha-1(VII) chain (Long-chain collagen) (LC collagen)	COL7A1
			1278,647	0,082	R.KEAESSPFVER.L	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			1278,615	0,114	R.RMGESDDSLR.L	P63220	RS21_HUMAN	40S ribosomal protein S21 (Small ribosomal subunit protein eS21)	RPS21
			1278,580	0,149	K.EGMNIVEAMER.F	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
1279,49	1278,849	1280,129	1279,653	0,164	R.KESYSIVYK.V	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
			1279,653	0,164	R.KESYSIVYK.V	Q6DRA6	H2B2D_HUMAN	Putative histone H2B type 2-D	HIST2H2BD
1279,58	1278,942	1280,221	1279,653	0,071	R.KESYSIVYK.V	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
			1279,653	0,071	R.KESYSIVYK.V	Q6DRA6	H2B2D_HUMAN	Putative histone H2B type 2-D	HIST2H2BD
1279,73	1279,091	1280,370	1279,653	0,078	R.KESYSIVYK.V	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
			1279,653	0,078	R.KESYSIVYK.V	Q6DRA6	H2B2D_HUMAN	Putative histone H2B type 2-D	HIST2H2BD
1280,66	1280,018	1281,299							
1281,67	1281,027	1282,309	1281,673	0,005	K.NIVLSGGSTMFR.D	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
1282,70	1282,055	1283,338	1282,681	0,015	R.AIRHPQYNQR.T	P08311	CATG_HUMAN	Cathepsin G (CG) (EC 3.4.21.20)	CTSG
1283,57	1282,924	1284,208	1283,575	0,009	K.EGYGYTGAFR.C	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1283,579	0,013	K.WQEEMELYR.Q	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
			1283,649	0,083	K.FIHDQTSNPK.Y	P53007	TXTP_HUMAN	Tricarboxylate transport protein, mitochondrial (Citrate transport protein) (CTP) (Solute carrier family 25 member 1) (Tricarboxylate carrier protein)	SLC25A1
			1283,674	0,108	R.KLGQSESQGPFR.A	O00233	PSMD9_HUMAN	26S proteasome non-ATPase regulatory subunit 9 (26S proteasome regulatory subunit p27)	PSMD9
			1283,699	0,133	R.TKTPGGAQSALR.A	P62263	RS14_HUMAN	40S ribosomal protein S14 (Small ribosomal subunit protein uS11)	RPS14
			1283,717	0,151	R.LSPQAVNSIAKR.Y	P30626	SORCN_HUMAN	Sorcin (22 kDa protein) (CP-22) (CP22) (V19)	SRI
1283,68	1283,042	1284,326	1283,674	0,009	R.KLGQSESQGPFR.A	O00233	PSMD9_HUMAN	26S proteasome non-ATPase regulatory subunit 9 (26S proteasome regulatory subunit p27)	PSMD9
			1283,699	0,015	R.TKTPGGAQSALR.A	P62263	RS14_HUMAN	40S ribosomal protein S14 (Small ribosomal subunit protein uS11)	RPS14
			1283,717	0,034	R.LSPQAVNSIAKR.Y	P30626	SORCN_HUMAN	Sorcin (22 kDa protein) (CP-22) (CP22) (V19)	SRI
			1283,649	0,034	K.FIHDQTSNPK.Y	P53007	TXTP_HUMAN	Tricarboxylate transport protein, mitochondrial (Citrate transport protein) (CTP) (Solute carrier family 25 member 1) (Tricarboxylate carrier protein)	SLC25A1
			1283,579	0,105	K.WQEEMELYR.Q	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
			1283,575	0,109	K.EGYGYTGAFR.C	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
1284,68	1284,036	1285,321	1284,694	0,016	R.ARPAEVGGMQLR.F	P33316	DUT_HUMAN	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial (dUTPase) (EC 3.6.1.23) (dUTP pyrophosphatase)	DUT
			1284,635	0,043	K.QGGGGGGGSGVPIER.M	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			1284,631	0,047	K.YLGQDYEQLR.V	P07384	CAN1_HUMAN	Calpain-1 catalytic subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase 1) (CANP 1) (Calpain mu-type) (Calpain-1 large subunit) (Cell proliferation-inducing gene 30 protein) (Micromolar-calpain) (muCANP)	CAPN1
1285,60	1284,952	1286,238	1285,664	0,068	K.QAKVLENAEGAR.T	P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9
			1285,664	0,068	K.QVAQQEAERAR.F	P35232	PHB_HUMAN	Prohibitin	PHB

1285,71	1285,069	1286,354	1285,664	0,048	K.QAKVLENAEGAR.T	P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9
			1285,664	0,048	K.QVAQQEAERAR.F	P35232	PHB_HUMAN	Prohibitin	PHB
1286,67	1286,026	1287,313	1286,687	0,018	R.EPQVYTLPPSR.E	P01860	IGHG3_HUMAN	Immunoglobulin heavy constant gamma 3 (HDC) (Heavy chain disease protein) (Ig gamma-3 chain C region)	IGHG3
			1286,647	0,022	K.LAEQEAHYAVR.Q	Q9NUV9	GIMA4_HUMAN	GTPase IMAP family member 4 (Immunity-associated nucleotide 1 protein) (IAN-1) (hIAN1) (Immunity-associated protein 4)	GIMAP4
1287,67	1287,025	1288,313	1287,678	0,008	R.QVDQLTNDKAR.V	P08670	VIME_HUMAN	Vimentin	VIM
			1287,658	0,011	K.GPSVFPLAPCSR.S	P01860	IGHG3_HUMAN	Immunoglobulin heavy constant gamma 3 (HDC) (Heavy chain disease protein) (Ig gamma-3 chain C region)	IGHG3
			1287,628	0,041	R.NWMNSLGVNPR.V	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LCG4P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
			1287,789	0,120	R.GLFIIDGKGVLR.Q	P32119	PRDX2_HUMAN	Peroxisedoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
1288,71	1288,062	1289,350	1288,651	0,055	R.ELDESILQVAER.L	P10909	CLUS_HUMAN	Clusterin (Aging-associated gene 4 protein) (Apolipoprotein J) (Apo-J) (Complement cytotoxicity inhibitor) (CLI) (Complement-associated protein SP-40,40) (Ku70-binding protein 1) (NA1/NA2) (Sulfated glycoprotein 2) (SGP-2) (Testosterone-repressed prostate message 2) (TRPM-2) [Cleaved into: Clusterin beta chain (ApoJalpha) (Complement cytotoxicity inhibitor a chain); Clusterin alpha chain (ApoJbeta) (Complement cytotoxicity inhibitor b chain)]	CLU
			1288,612	0,094	R.INISEGNCPCR.I	Q15365	PCBP1_HUMAN	Poly(rC)-binding protein 1 (Alpha-CP1) (Heterogeneous nuclear ribonucleoprotein E1) (hnRNP E1) (Nucleic acid-binding protein SUB2.3)	PCBP1
1289,68	1289,040	1290,330	1289,725	0,041	R.VISSIEQKTER.N	P31946	1433B_HUMAN	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHA8
			1289,616	0,069	K.SGSDEVQVGGQQR.T	P01024	CO3_HUMAN	Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
1290,70	1290,056	1291,346	1290,712	0,011	-MAATTGSGVKVPR.N	Q13404	UB2V1_HUMAN	Ubiquitin-conjugating enzyme E2 variant 1 (UEV-1) (CROC-1) (TRAF6-regulated IKK activator 1 beta Uev1A)	UBE2V1
			1290,642	0,059	R.DAVTYTEHAKR.K	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
1291,62	1290,971	1292,263							
1291,73	1291,080	1292,371							
1292,49	1291,841	1293,134	1292,719	0,231	R.DIVQFVPYRR.F	Q99829	CPNE1_HUMAN	Copine-1 (Chromobindin 17) (Copine I)	CPNE1
1292,67	1292,019	1293,311	1292,719	0,054	R.DIVQFVPYRR.F	Q99829	CPNE1_HUMAN	Copine-1 (Chromobindin 17) (Copine I)	CPNE1
1293,49	1292,839	1294,132							
1293,71	1293,062	1294,355							
1294,57	1293,922	1295,216	1294,711	0,142	R.MVIPGGIDVHTR.F	Q16555	DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) (Unc-33-like phosphoprotein 2) (ULIP-2)	DPYSL2
1294,71	1294,059	1295,354	1294,711	0,005	R.MVIPGGIDVHTR.F	Q16555	DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) (Unc-33-like phosphoprotein 2) (ULIP-2)	DPYSL2
1295,62	1294,970	1296,266							
1295,64	1294,995	1296,291							
1295,66	1295,013	1296,308							
1296,65	1296,002	1297,299							
1296,73	1296,083	1297,380							
1297,63	1296,981	1298,279	1297,720	0,090	R.EAPVDVLTQIGR.S	Q9BVC6	TM109_HUMAN	Transmembrane protein 109 (Mitsugumin-23) (Mg23)	TMEM109
1298,63	1297,985	1299,283	1298,617	0,017	R.YYGGGSEGGRAPK.R	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNP L
			1298,693	0,059	R.MLAQAQGVDPGLAR.A	P19971	TYPH_HUMAN	Thymidine phosphorylase (TP) (EC 2.4.2.4) (Gliostatin) (Platelet-derived endothelial cell growth factor) (PD-ECGF) (TdRpase)	TYMP
1299,62	1298,968	1300,267	1299,643	0,026	R.GVDLQENNPASR.S	P51148	RAB5C_HUMAN	Ras-related protein Rab-5C (L1880) (RAB5L)	RAB5C

1299,65	1299,000	1300,300	1299,660	0,043	R.EVSAAREEVPR.R	P21281	VATB2_HUMAN	V-type proton ATPase subunit B, brain isoform (V-ATPase subunit B 2) (Endomembrane proton pump 58 kDa subunit) (HO57) (Vacuolar proton pump subunit B 2)	ATP6V1B2
			1299,694	0,076	K.KVSSTNNTVPVPR.L	A2RUB1	MEIOC_HUMAN	Meiosis-specific coiled-coil domain-containing protein MEIOC (Meiosis-specific with coiled-coil domain protein)	MEIOC
			1299,643	0,007	R.GVDLQENNPASR.S	P51148	RAB5C_HUMAN	Ras-related protein Rab-5C (L1880) (RAB5L)	RAB5C
			1299,660	0,010	R.EVSAAREEVPR.R	P21281	VATB2_HUMAN	V-type proton ATPase subunit B, brain isoform (V-ATPase subunit B 2) (Endomembrane proton pump 58 kDa subunit) (HO57) (Vacuolar proton pump subunit B 2)	ATP6V1B2
1300,57	1299,921	1301,222	1299,694	0,044	K.KVSSTNNTVPVPR.L	A2RUB1	MEIOC_HUMAN	Meiosis-specific coiled-coil domain-containing protein MEIOC (Meiosis-specific with coiled-coil domain protein)	MEIOC
			1300,618	0,047	R.YHSLAPMYR.G	P51148	RAB5C_HUMAN	Ras-related protein Rab-5C (L1880) (RAB5L)	RAB5C
			1300,658	0,086	R.RLPDAHSDYAR.Y	Q96PK6	RBM14_HUMAN	RNA-binding protein 14 (Paraspeckle protein 2) (PSP2) (RNA-binding motif protein 14) (RRM-containing coactivator activator/modulator) (Synaptotagmin-interacting protein) (SYT-interacting protein)	RBM14
			1300,697	0,125	R.NDEELNKLGR.V	Q93077	H2A1C_HUMAN	Histone H2A type 1-C (Histone H2A/I)	HIST1H2AC
1300,69	1300,044	1301,345	1300,697	0,003	R.NDEELNKLGR.V	Q93077	H2A1C_HUMAN	Histone H2A type 1-C (Histone H2A/I)	HIST1H2AC
			1300,658	0,037	R.RLPDAHSDYAR.Y	Q96PK6	RBM14_HUMAN	RNA-binding protein 14 (Paraspeckle protein 2) (PSP2) (RNA-binding motif protein 14) (RRM-containing coactivator activator/modulator) (Synaptotagmin-interacting protein) (SYT-interacting protein)	RBM14
			1300,618	0,076	R.YHSLAPMYR.G	P51148	RAB5C_HUMAN	Ras-related protein Rab-5C (L1880) (RAB5L)	RAB5C
			1301,659	0,009	R.THLAPYSDEL.R.Q	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
1301,67	1301,017	1302,318	1301,658	0,010	R.SHGQDSPAVYLK.K	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1301,641	0,027	R.ISVYYNEATGGK.Y	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1301,801	0,133	K.ILCAAKFIPL.R.S	Q5V579	OBSCN_HUMAN	Obscurin (EC 2.7.11.1) (Obscurin-RhoGEF) (Obscurin-myosin light chain kinase) (Obscurin-MLCK)	OBSCN
			1302,658	0,001	K.LSPLGEEMRDR.A	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
1302,66	1302,008	1303,311	1302,685	0,026	K.TVSSHEVFLQR.L	Q9Y5X3	SNX5_HUMAN	Sorting nexin-5	SNX5
			1304,673	0,056	R.GPQVQQPPPSNR.F	Q15436	SC23A_HUMAN	Protein transport protein Sec23A (hSec23A) (SEC23-related protein A)	SEC23A
			1306,758	0,153	R.FILNLPTFSVR.I	P49721	PSB2_HUMAN	Proteasome subunit beta type-2 (EC 3.4.25.1) (Macropain subunit C7-I) (Multicatalytic endopeptidase complex subunit C7-I) (Proteasome component C7-I)	PSMB2
			1306,758	0,056	R.FILNLPTFSVR.I	P49721	PSB2_HUMAN	Proteasome subunit beta type-2 (EC 3.4.25.1) (Macropain subunit C7-I) (Multicatalytic endopeptidase complex subunit C7-I) (Proteasome component C7-I)	PSMB2
1307,68	1307,024	1308,331	1307,691	0,014	R.IKFEMEQLNR.Q	P35527	K1C9_HUMAN	Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9) (Keratin-9) (K9)	KRT9
			1307,644	0,033	R.SVQAGNPGGPGGGR.G	Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1) (DNA helicase V) (hDH V)	FUBP1
			1308,619	0,007	R.YGRPPDSHHSR.R	Q01130	SRSF2_HUMAN	Serine/arginine-rich splicing factor 2 (Protein PR264) (Splicing component, 35 kDa) (Splicing factor SC35) (SC-35) (Splicing factor, arginine/serine-rich 2)	SRSF2
			1308,636	0,010	K.EAETRAEFAER.T	P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	TPM4
1308,72	1308,070	1309,379	1308,636	0,089	K.EAETRAEFAER.T	P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	TPM4
			1308,619	0,106	R.YGRPPDSHHSR.R	Q01130	SRSF2_HUMAN	Serine/arginine-rich splicing factor 2 (Protein PR264) (Splicing component, 35 kDa) (Splicing factor SC35) (SC-35) (Splicing factor, arginine/serine-rich 2)	SRSF2
			1309,649	0,022	K.DVLSVAFSSDNR.Q	P63244	RACK1_HUMAN	Receptor of activated protein C kinase 1 (Cell proliferation-inducing gene 21 protein) (Guanine nucleotide-binding protein subunit beta-2-like 1) (Guanine nucleotide-binding protein subunit beta-like protein 12.3) (Human lung cancer oncogene 7 protein) (HLC-7) (Receptor for activated C kinase) (Small ribosomal subunit protein RACK1) [Cleaved into: Receptor of activated protein C kinase 1, N-terminally processed (Guanine nucleotide-binding protein subunit beta-2-like 1, N-terminally processed)]	RACK1
			1309,549	0,122	R.GYDDRDRYYSR.S	P62995	TRA2B_HUMAN	Transformer-2 protein homolog beta (TRA-2 beta) (TRA2-beta) (hTRA2-beta) (Splicing factor, arginine/serine-rich 10) (Transformer-2 protein homolog B)	TRA2B
1310,64	1309,982	1311,293	1309,820	0,149	R.ALTLGALTPLAR.L	Q9BSJ8	ESYT1_HUMAN	Extended synaptotagmin-1 (E-Syt1) (Membrane-bound C2 domain-containing protein)	ESYT1
			1310,692	0,055	K.KAPDFVFYAPR.L	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			1310,692	0,055	K.KAPDFVFYAPR.L	P15311	EZR_HUMAN	Ezrin (Cytovillin) (Villin-2) (p81)	EZR
			1310,692	0,010	K.KAPDFVFYAPR.L	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN

1311,67	1311,013	1312,324	1310,692	0,010	K.KAPDFVYAPR.L	P15311	EZRI_HUMAN	Ezrin (Cytovillin) (Villin-2) (p81)	EZR
			1311,666	0,003	R.TGYTLDVTTGQR.K	O43390	HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R)	HNRNPR
			1311,750	0,081	R.HPDYSVVLRL.L	P02768	ALBU_HUMAN	Serum albumin	ALB
1312,69 1313,66	1312,030 1313,006	1313,342 1314,319	1313,612	0,050	R.SGRGGNFGFGDSR.G	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			1313,612	0,050	K.WARDHGESLDK.A	Q8WZ42	TITIN_HUMAN	Titin (EC 2.7.11.1) (Connectin) (Rhabdomyosarcoma antigen MU-RMS-40.14)	TTN
1314,66	1314,000	1315,315	1314,667	0,010	K.VNVDEVGGEALGR.L	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			1314,686	0,029	R.RVDTVDPYPYR.S	P04004	VTNC_HUMAN	Vitronectin (VN) (S-protein) (Serum-spreading factor) (V75) [Cleaved into: Vitronectin V65 subunit; Vitronectin V10 subunit; Somatomedin-B]	VTN
			1314,727	0,070	K.LGELPSWILMR.D	P56134	ATPK_HUMAN	ATP synthase subunit f, mitochondrial (ATP synthase membrane subunit f)	ATP5MF
1315,66 1316,67	1315,006 1316,010	1316,322 1317,327	1316,677	0,008	K.LQIWDTAGQER.F	P61106	RAB14_HUMAN	Ras-related protein Rab-14	RAB14
			1316,677	0,008	K.LQIWDTAGQER.F	Q9H0U4	RAB18_HUMAN	Ras-related protein Rab-18	RAB18
			1316,677	0,008	K.LQIWDTAGQER.F	P61026	RAB10_HUMAN	Ras-related protein Rab-10	RAB10
			1316,657	0,012	K.VNVEDAGGETLGR.L	P69892	HBG2_HUMAN	Hemoglobin subunit gamma-2 (Gamma-2-globin) (Hb F Ggamma) (Hemoglobin gamma-2 chain) (Hemoglobin gamma-G chain)	HBG2
			1316,741	0,072	K.VAASVLNPYVKR.S	P48047	ATPO_HUMAN	ATP synthase subunit O, mitochondrial (ATP synthase peripheral stalk subunit OSCP) (Oligomycin sensitivity conferral protein) (OSCP)	ATP5PO
1317,68 1318,64 1318,67 1319,67	1317,025 1317,976 1318,012 1319,006	1318,342 1319,294 1319,331 1320,326	1319,689	0,023	R.SGGMERPFVLAR.A	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			1319,690	0,024	K.DRPHGTRPVR.A	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
			1319,717	0,051	R.ATGQRPHHFLR.R	P23381	SYWC_HUMAN	Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleaved into: T1-TrpRS; T2-TrpRS]	WARS
			1319,757	0,090	K.GIVKDIHDPGR.G	P62917	RL8_HUMAN	60S ribosomal protein L8 (Large ribosomal subunit protein uL2)	RPL8
			1320,691	0,042	K.GSAPPGPVPEGSI.R.I	P78417	GSTO1_HUMAN	Glutathione S-transferase omega-1 (GSTO-1) (EC 2.5.1.18) (Glutathione S-transferase omega 1-1) (GSTO 1-1) (Glutathione-dependent dehydroascorbate reductase) (EC 1.8.5.1) (Monomethylarsonic acid reductase) (MMA(V) reductase) (EC 1.20.4.2) (S-(Phenacyl)glutathione reductase) (SPG-R)	GSTO1
			1320,707	0,059	R.KAGNFYVPAEPK.L	P18124	RL7_HUMAN	60S ribosomal protein L7 (Large ribosomal subunit protein uL30)	RPL7
			1320,742	0,094	R.LFLAEFQSIPR.V	P08575	PTPRC_HUMAN	Receptor-type tyrosine-protein phosphatase C (EC 3.1.3.48) (Leukocyte common antigen) (L-CA) (T200) (CD antigen CD45)	PTPRC
1321,65 1322,67	1320,994 1322,005	1322,315 1323,328	1322,671	0,004	R.KGRPYDYNGPRE	P13667	PDIA4_HUMAN	Protein disulfide-isomerase A4 (EC 5.3.4.1) (Endoplasmic reticulum resident protein 70) (ER protein 70) (ERp70) (Endoplasmic reticulum resident protein 72) (ER protein 72) (ERp72)	PDIA4
			1323,727	0,061	K.LGVRPSQGGGEAPR.E	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
1324,63 1325,56	1323,972 1324,893	1325,296 1326,219	1325,686	0,130	R.NKVSEHDVLR.K	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
			1325,761	0,205	R.DNIQGITKPAIR.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
1325,57	1324,909	1326,234	1325,686	0,114	R.NKVSEHDVLR.K	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
			1325,761	0,189	R.DNIQGITKPAIR.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4

1325,73	1325,062	1326,388	1325,761	0,036	R.DNIQGITKPAIR.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
			1325,686	0,039	R.NKVSEHDVLR.K	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
1326,58	1325,916	1327,243	1326,700	0,120	R.NPHNDRFVLSK.G	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
1326,73	1326,071	1327,398	1326,700	0,035	R.NPHNDRFVLSK.G	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
1327,59 1327,74 1328,71	1326,921 1327,076 1328,048	1328,249 1328,404 1329,377	1328,661	0,052	K.FGYQFTQQGPR.T	Q9NYL9	TMOD3_HUMAN	Tropomodulin-3 (Ubiquitous tropomodulin) (U-Tmod)	TMOD3
1329,64	1328,977	1330,306	1329,666	0,024	K.GFAFVQYVNER.N	P07910	HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1/C2)	HNRNPC
			1329,681	0,040	R.RCEPIAMTVPR.K	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
1329,72	1329,060	1330,389	1329,681	0,043	R.RCEPIAMTVPR.K	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
			1329,666	0,059	K.GFAFVQYVNER.N	P07910	HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1/C2)	HNRNPC
1330,45 1330,70 1331,42	1329,789 1330,037 1330,758	1331,119 1331,368 1332,089	1331,701	0,278	R.GAPAAATAPAPTAHK.A	Q92522	H1X_HUMAN	Histone H1x	H1FX
1331,67	1331,007	1332,339	1331,701	0,028	R.GAPAAATAPAPTAHK.A	Q92522	H1X_HUMAN	Histone H1x	H1FX
1331,72	1331,051	1332,383	1331,701	0,016	R.GAPAAATAPAPTAHK.A	Q92522	H1X_HUMAN	Histone H1x	H1FX
1332,72	1332,053	1333,386	1332,740	0,021	R.FVFDRLPVS.R.L	P25786	PSA1_HUMAN	Proteasome subunit alpha type-1 (EC 3.4.25.1) (30 kDa prosomal protein) (PROS-30) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome component C2) (Proteasome nu chain)	PSMA1
			1332,697	0,022	K.HGRPGIGATHSSR.F	P62841	RS15_HUMAN	40S ribosomal protein S15 (RIG protein) (Small ribosomal subunit protein uS19)	RPS15
			1332,659	0,061	R.HAQAQYVPGAR.F	Q14112	NID2_HUMAN	Nidogen-2 (NID-2) (Osteonidogen)	NID2
1333,33	1332,664	1333,997	1332,740	0,591	R.FVFDRLPVS.R.L	P25786	PSA1_HUMAN	Proteasome subunit alpha type-1 (EC 3.4.25.1) (30 kDa prosomal protein) (PROS-30) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome component C2) (Proteasome nu chain)	PSMA1
			1332,697	0,634	K.HGRPGIGATHSSR.F	P62841	RS15_HUMAN	40S ribosomal protein S15 (RIG protein) (Small ribosomal subunit protein uS19)	RPS15
1333,72 1334,69 1335,69	1333,055 1334,025 1335,018	1334,389 1335,360 1336,354	1335,702	0,017	R.EIAQDFKTDLR.F	P84243	H33_HUMAN	Histone H3.3	H3F3A; H3F3B
1336,70	1336,028	1337,365	1336,726	0,030	K.RISGLIYEETR.G	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
			1336,739	0,043	R.IGGNEGIDVPIPR.F	Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1) (DNA helicase V) (hDH V)	FUBP1
			1336,616	0,081	R.DAQELYAAGENR.L	P50995	ANX11_HUMAN	Annexin A11 (56 kDa autoantigen) (Annexin XI) (Annexin-11) (Calcyclin-associated annexin 50) (CAP-50)	ANXA11
1337,67	1337,006	1338,343	1337,734	0,060	M.PPYTVVVFVPR.G	P09211	GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1)	GSTP1
1338,69	1338,024	1339,362	1338,732	0,039	R.NVHGINFVSPVR.N	P53634	CATC_HUMAN	Dipeptidyl peptidase 1 (EC 3.4.14.1) (Cathepsin C) (Cathepsin J) (Dipeptidyl peptidase I) (DPP-I) (DPPi) (Dipeptidyl transferase) [Cleaved into: Dipeptidyl peptidase 1 exclusion domain chain (Dipeptidyl peptidase I exclusion domain chain); Dipeptidyl peptidase 1 heavy chain (Dipeptidyl peptidase I heavy chain); Dipeptidyl peptidase 1 light chain (Dipeptidyl peptidase I light chain)]	CTSC
1339,70 1340,66	1339,034 1339,992	1340,374 1341,333							

1341,66	1340,984	1342,326	1341,672	0,017	R.FQGGAGPVGQGQGR.G	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
			1341,688	0,033	K.IMQYFSHFIR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1341,778	0,123	R.DLLGETLAQLIR.Q	P36269	GGT5_HUMAN	Glutathione hydrolase 5 proenzyme (EC 3.4.19.13) (Gamma-glutamyl transpeptidase-related enzyme) (GGT-rel) (Gamma-glutamyltransferase 5) (GGT 5) (EC 2.3.2.2) (Gamma-glutamyltransferase-like activity 1) (Gamma-glutamyltranspeptidase 5) (Leukotriene-C4 hydrolase) (EC 3.4.19.14) [Cleaved into: Glutathione hydrolase 5 heavy chain; Glutathione hydrolase 5 light chain]	GGT5
1342,67	1341,999	1343,342	1342,665	0,005	R.HLIEQDFPGMR.I	Q9H4M9	EHD1_HUMAN	EH domain-containing protein 1 (PAST homolog 1) (hPAST1) (Testilin)	EHD1
1343,67	1343,003	1344,347	1344,719	0,028	R.TVIEQSWGSPK.V	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
1344,69	1344,018	1345,363							
1345,69	1345,022	1346,367	1347,710	0,005	K.RLAPEYEAATR.L	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (S8 kDa glucose-regulated protein) (S8 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	PDIA3
1346,67	1346,001	1347,348							
1347,71	1347,031	1348,379							
1348,71	1348,035	1349,384	1348,672	0,038	K.HFSVEGQLEFR.A	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			1348,672	0,038	K.HFSVEGQLEFR.A	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
1349,69	1349,019	1350,369	1349,648	0,046	R.YIETDPANRDR.R	P06396	GELS_HUMAN	Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF) (Brevin)	GSN
			1349,617	0,078	R.YQEYGGAEASPQR.T	Q9UJU6	DBNL_HUMAN	Drebrin-like protein (Cervical SH3P7) (Cervical mucin-associated protein) (Drebrin-F) (HPK1-interacting protein of 55 kDa) (HIP-55) (SH3 domain-containing protein 7)	DBNL
1350,69	1350,020	1351,370	1350,712	0,017	R.YLENGKETLQR.A	P30492	1B54_HUMAN	HLA class I histocompatibility antigen, B-54 alpha chain (Bw-22) (Bw-54) (MHC class I antigen B*54)	HLA-B
			1350,712	0,017	R.YLENGKETLQR.T	P13746	1A11_HUMAN	HLA class I histocompatibility antigen, A-11 alpha chain (MHC class I antigen A*11)	HLA-A
1351,71	1351,031	1352,383	1351,656	0,050	K.YQEGGVESAFHK.T	P40121	CAPG_HUMAN	Macrophage-capping protein (Actin regulatory protein CAP-G)	CAPG
1352,71	1352,033	1353,386	1352,641	0,069	K.GISQEQMQEFR.A	O43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
1353,21	1352,533	1353,886	1353,726	0,516	K.EAPPMEKPEVVK.T	P62841	RS15_HUMAN	40S ribosomal protein S15 (RIG protein) (Small ribosomal subunit protein uS19)	RPS15
			1352,641	0,569	K.GISQEQMQEFR.A	O43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
1353,66	1352,984	1354,337	1353,726	0,065	K.EAPPMEKPEVVK.T	P62841	RS15_HUMAN	40S ribosomal protein S15 (RIG protein) (Small ribosomal subunit protein uS19)	RPS15
1353,75	1353,075	1354,429	1353,726	0,026	K.EAPPMEKPEVVK.T	P62841	RS15_HUMAN	40S ribosomal protein S15 (RIG protein) (Small ribosomal subunit protein uS19)	RPS15
1354,22	1353,546	1354,900	1354,616	0,393	R.SQYEVMAEQNR.K	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cyokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1354,637	0,414	K.DSYVGDEAQSKR.G	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1354,637	0,414	K.DSYVGDEAQSKR.G	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1353,726	0,497	K.EAPPMEKPEVVK.T	P62841	RS15_HUMAN	40S ribosomal protein S15 (RIG protein) (Small ribosomal subunit protein uS19)	RPS15
1354,37	1353,688	1355,042	1354,616	0,251	R.SQYEVMAEQNR.K	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cyokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1354,637	0,271	K.DSYVGDEAQSKR.G	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1354,637	0,271	K.DSYVGDEAQSKR.G	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1353,726	0,639	K.EAPPMEKPEVVK.T	P62841	RS15_HUMAN	40S ribosomal protein S15 (RIG protein) (Small ribosomal subunit protein uS19)	RPS15
1354,66	1353,986	1355,340	1354,637	0,027	K.DSYVGDEAQSKR.G	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1354,637	0,027	K.DSYVGDEAQSKR.G	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1354,616	0,047	R.SQYEVMAEQNR.K	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cyokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
1354,71	1354,032	1355,387	1354,637	0,073	K.DSYVGDEAQSKR.G	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1354,637	0,073	K.DSYVGDEAQSKR.G	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1354,616	0,093	R.SQYEVMAEQNR.K	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cyokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19

1355,65 1355,75 1356,72	1354,969 1355,073 1356,040	1356,324 1356,429 1357,396	1356,656	0,062	R.HHPEHFSGRPR.E	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
1357,73	1357,052	1358,410	1357,738	0,007	R.QLGTVQQVISER.V	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1358,71	1358,029	1359,388	1358,760	0,051	R.ISVREPMQTGIK.A	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
1359,35	1358,674	1360,033	1359,685	0,331	R.YLHDESLNRR.H	Q15019	SEPT2_HUMAN	Septin-2 (Neural precursor cell expressed developmentally down-regulated protein 5) (NEDD-5)	SEPT2
			1359,702	0,349	R.SGAQASSTPLSPTR.I	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
			1359,803	0,449	R.GLFIDDKGILR.Q	Q13162	PRDX4_HUMAN	Peroxiredoxin-4 (EC 1.11.1.15) (Antioxidant enzyme AOE372) (AOE37-2) (Peroxiredoxin IV) (Prx-IV) (Thioredoxin peroxidase AO372) (Thioredoxin-dependent peroxide reductase A0372)	PRDX4
			1359,803	0,449	R.GLFIDDKGILR.Q	Q06830	PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
			1358,760	0,594	R.ISVREPMQTGIK.A	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
1359,70	1359,023	1360,383	1359,702	0,001	R.SGAQASSTPLSPTR.I	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
			1359,685	0,018	R.YLHDESLNRR.H	Q15019	SEPT2_HUMAN	Septin-2 (Neural precursor cell expressed developmentally down-regulated protein 5) (NEDD-5)	SEPT2
			1359,803	0,100	R.GLFIDDKGILR.Q	Q13162	PRDX4_HUMAN	Peroxiredoxin-4 (EC 1.11.1.15) (Antioxidant enzyme AOE372) (AOE37-2) (Peroxiredoxin IV) (Prx-IV) (Thioredoxin peroxidase AO372) (Thioredoxin-dependent peroxide reductase A0372)	PRDX4
			1359,803	0,100	R.GLFIDDKGILR.Q	Q06830	PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
1360,73	1360,046	1361,407	1360,716	0,010	K.ELSAVTFPDIIR.N	P42224	STAT1_HUMAN	Signal transducer and activator of transcription 1-alpha/beta (Transcription factor ISGF-3 components p91/p84)	STAT1
1361,64	1360,957	1362,319	1361,672	0,034	R.FLQGDHFGTSPR.T	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1361,67	1360,986	1362,348	1361,672	0,005	R.FLQGDHFGTSPR.T	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1361,80	1361,123	1362,485	1361,672	0,132	R.FLQGDHFGTSPR.T	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1362,67	1361,992	1363,354	1362,667	0,006	R.NNRFSTPEQAAK.N	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNP L
1362,81	1362,125	1363,488	1362,667	0,140	R.NNRFSTPEQAAK.N	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNP L
1363,10	1362,416	1363,779	1362,667	0,431	R.NNRFSTPEQAAK.N	P14866	HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNP L
1363,70 1363,82 1364,72	1363,016 1363,140 1364,041	1364,380 1364,503 1365,406	1364,755	0,031	K.IHFRPELPAER.N	P21397	AOFA_HUMAN	Amine oxidase [flavin-containing] A (EC 1.4.3.4) (Monoamine oxidase type A) (MAO-A)	MAOA
1365,73	1365,048	1366,414	1365,712	0,019	K.DLGTESQIFISR.T	P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDIB
1366,69 1367,69 1368,68 1369,67	1366,011 1367,003 1367,992 1368,983	1367,378 1368,371 1369,360 1370,353	1369,766	0,098	R.HLEIIVAINQR.H	P11216	PYGB_HUMAN	Glycogen phosphorylase, brain form (EC 2.4.1.1)	PYGB
			1369,783	0,115	R.IKIGDPLLEDTR.M	P49189	AL9A1_HUMAN	4-trimethylaminobutyraldehyde dehydrogenase (TMABADH) (EC 1.2.1.47) (Aldehyde dehydrogenase E3 isozyme) (Aldehyde dehydrogenase family 9 member A1) (EC 1.2.1.3) (Gamma-aminobutyraldehyde dehydrogenase) (EC 1.2.1.19) (R-aminobutyraldehyde dehydrogenase) [Cleaved into: 4-trimethylaminobutyraldehyde dehydrogenase, N-terminally processed]	ALDH9A1
			1369,791	0,123	K.VNTLIRPDGEKK.A	P62750	RL23A_HUMAN	60S ribosomal protein L23a (Large ribosomal subunit protein uL23)	RPL23A
1369,77	1369,085	1370,455	1369,766	0,004	R.HLEIIVAINQR.H	P11216	PYGB_HUMAN	Glycogen phosphorylase, brain form (EC 2.4.1.1)	PYGB
			1369,783	0,013	R.IKIGDPLLEDTR.M	P49189	AL9A1_HUMAN	4-trimethylaminobutyraldehyde dehydrogenase (TMABADH) (EC 1.2.1.47) (Aldehyde dehydrogenase E3 isozyme) (Aldehyde dehydrogenase family 9 member A1) (EC 1.2.1.3) (Gamma-aminobutyraldehyde dehydrogenase) (EC 1.2.1.19) (R-aminobutyraldehyde dehydrogenase) [Cleaved into: 4-trimethylaminobutyraldehyde dehydrogenase, N-terminally processed]	ALDH9A1
			1369,791	0,021	K.VNTLIRPDGEKK.A	P62750	RL23A_HUMAN	60S ribosomal protein L23a (Large ribosomal subunit protein uL23)	RPL23A

1370,75	1370,061	1371,432	1370,698	0,049	R.ELSDFISYLQR.E	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	PDIA3
1371,28	1370,592	1371,963	1370,698	0,580	R.ELSDFISYLQR.E	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	PDIA3
1371,72 1372,22	1371,039 1371,534	1372,411 1372,906	1372,742	0,521	R.SIVEEIDLVAR.L	P04844	RPN2_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 (Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit) (RIBIIR) (Ribophorin II) (RPN-II) (Ribophorin-2)	RPN2
1372,71	1372,023	1373,396	1372,742	0,032	R.SIVEEIDLVAR.L	P04844	RPN2_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 (Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit) (RIBIIR) (Ribophorin II) (RPN-II) (Ribophorin-2)	RPN2
1373,72 1374,65 1374,74 1375,66 1375,76 1376,72	1373,030 1373,963 1374,056 1374,971 1375,071 1376,035	1374,404 1375,338 1375,430 1376,346 1376,447 1377,412	1376,679	0,045	R.GHTPTQP GALNQR.Q	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
1377,68	1376,986	1378,364	1377,643	0,032	R.GGGGNFGPGPSNFR.G	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			1377,762	0,086	K.AQAAPASVPAQAPK.R	P47914	RL29_HUMAN	60S ribosomal protein L29 (Cell surface heparin-binding protein HIP) (Large ribosomal subunit protein eL29)	RPL29
1378,68	1377,987	1379,365	1378,717	0,041	K.EFTPPVQAAYQK.V	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
1379,71	1379,018	1380,398	1379,594	0,114	R.FDDGAGGDNEVQR.T	P35998	PRS7_HUMAN	26S proteasome regulatory subunit 7 (26S proteasome AAA-ATPase subunit RPT1) (Proteasome 26S subunit ATPase 2) (Protein MSS1)	P5MC2
1380,72	1380,025	1381,406	1380,717	0,002	K.VQPYLDDFQKK.W	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
1380,85	1380,164	1381,545	1380,717	0,137	K.VQPYLDDFQKK.W	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
1381,66 1381,81 1382,63	1380,969 1381,123 1381,943	1382,350 1382,504 1383,325	1382,655	0,021	R.ATVMLYDDGNKR.W	P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP)	VASP
1382,76	1382,070	1383,453	1382,655	0,106	R.ATVMLYDDGNKR.W	P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP)	VASP
1383,65	1382,955	1384,339	1383,619	0,028	R.GASQAGMTGYGMPR.Q	P37802	TAGL2_HUMAN	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	TAGLN2
1383,77	1383,073	1384,457	1383,619	0,146	R.GASQAGMTGYGMPR.Q	P37802	TAGL2_HUMAN	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	TAGLN2
1384,72	1384,030	1385,415	1384,738 1384,654	0,016 0,068	R.LAAQSTLSFYQR.R R.SGSMDPGSAHPSVR.Q	P01266 Q07666	THYG_HUMAN KHDR1_HUMAN	Thyroglobulin (Tg) KH domain-containing, RNA-binding, signal transduction-associated protein 1 (GAP-associated tyrosine phosphoprotein p62) (Src-associated in mitosis 68 kDa protein) (Sam68) (p21 Ras GTPase-activating protein-associated p62) (p68)	TG KHDRBS1
1384,85	1384,161	1385,546	1384,738 1384,654	0,115 0,199	R.LAAQSTLSFYQR.R R.SGSMDPGSAHPSVR.Q	P01266 Q07666	THYG_HUMAN KHDR1_HUMAN	Thyroglobulin (Tg) KH domain-containing, RNA-binding, signal transduction-associated protein 1 (GAP-associated tyrosine phosphoprotein p62) (Src-associated in mitosis 68 kDa protein) (Sam68) (p21 Ras GTPase-activating protein-associated p62) (p68)	TG KHDRBS1
1385,76	1385,072	1386,458	1385,769 1385,746 1385,704 1385,704	0,005 0,018 0,061 0,061	R.GPSPWGFRLVGGRL.D R.AKQEELEAALQR.G R.ISEQFTAMFRR.K R.ISEQFTAMFRR.K	P50479 P08729 P68371 P07437	PDLI4_HUMAN K2C7_HUMAN TBB4B_HUMAN TBB5_HUMAN	PDZ and LIM domain protein 4 (LIM protein RIL) (Reversion-induced LIM protein) Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7) Tubulin beta-4B chain (Tubulin beta-2 chain) Tubulin beta chain (Tubulin beta-5 chain)	PDLIM4 KRT7 TUBB4B TUBB
1386,75	1386,061	1387,448	1386,761 1386,801	0,007 0,047	R.YGFIEGHVVIPI.R R.VGWEQLTTIAR.T	P16070 O43707	CD44_HUMAN ACTN4_HUMAN	CD44 antigen (CDw44) (Epican) (Extracellular matrix receptor III) (ECMR-III) (GP90 lymphocyte homing/adhesion receptor) (HUTCH-I) (Heparan sulfate proteoglycan) (Hermes antigen) (Hyaluronate receptor) (Phagocytic glycoprotein 1) (PGP-1) (Phagocytic glycoprotein I) (PGP-I) (CD antigen CD44) Alpha-actinin-4 (Non-muscle alpha-actinin 4)	CD44 ACTN4
1387,75	1387,059	1388,447							

1388,73	1388,038	1389,427	1388,756	0,024	R.ASGQAFELIUSP.R.S	P16949	STMN1_HUMAN	Stathmin (Leukemia-associated phosphoprotein p18) (Metablastin) (Oncoprotein 18) (Op18) (Phosphoprotein p19) (pp19) (Prosolin) (Protein Pr22) (pp17)	STMN1
			1388,688	0,045	R.QREEEIEAQEK.A	O75937	DNJC8_HUMAN	DnaJ homolog subfamily C member 8 (Splicing protein spf31)	DNJC8
1389,75	1389,055	1390,444	1389,756	0,006	R.EVPLNTIIFMGR.V	P01008	ANT3_HUMAN	Antithrombin-III (ATIII) (Serpin C1)	SERPINC1
			1389,759	0,010	R.QAALQVAEGFISR.M	P40121	CAPG_HUMAN	Macrophage-capping protein (Actin regulatory protein CAP-G)	CAPG
			1389,665	0,084	R.QAHLTNQYMQR.M	P11940	PABP1_HUMAN	Polyadenylate-binding protein 1 (PABP-1) (Poly(A)-binding protein 1)	PABPC1
1390,75	1390,058	1391,449							
1391,76	1391,063	1392,455							
1392,72	1392,028	1393,421							
1393,73	1393,032	1394,426	1393,726	0,003	R.DVRQQYESVAAK.N	P08670	VIME_HUMAN	Vimentin	VIM
			1393,710	0,019	K.FVEGLPINDFS.R.E	P40925	MDHC_HUMAN	Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) (Cytosolic malate dehydrogenase) (Diiodophenylpyruvate reductase) (EC 1.1.1.96)	MDH1
1394,72	1394,023	1395,417	1394,725	0,005	R.VVANSKESYELR.Y	P35268	RL22_HUMAN	60S ribosomal protein L22 (EBER-associated protein) (EAP) (Epstein-Barr virus small RNA-associated protein) (Heparin-binding protein HBp15) (Large ribosomal subunit protein el22)	RPL22
			1394,730	0,010	R.FVFGTTPEDILR.N	P07996	TSP1_HUMAN	Thrombospondin-1 (Glycoprotein G)	THBS1
			1394,782	0,062	K.IISKIENHEGVR.R	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
1395,74	1395,040	1396,435	1395,737	0,000	R.QSVENDIHLGRK.V	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
1396,73	1396,033	1397,430	1396,846	0,115	R.IILFRPVASQLPR.I	P35232	PHB_HUMAN	Prohibitin	PHB
1397,73	1397,030	1398,428							
1397,74	1397,040	1398,438							
1398,77	1398,072	1399,471	1398,739	0,032	K.TTPDVIFVFGFR.T	P62847	RS24_HUMAN	40S ribosomal protein S24 (Small ribosomal subunit protein eS24)	RPS24
			1398,831	0,060	K.DVALLVTSGLALAR.C	P46092	CCR10_HUMAN	C-C chemokine receptor type 10 (C-C CKR-10) (CC-CKR-10) (CCR-10) (G-protein coupled receptor 2)	CCR10
1399,64	1398,940	1400,340							
1399,77	1399,071	1400,471							
1400,67	1399,966	1401,367	1400,675	0,008	R.STDYGIFQNSR.Y	P61626	LYSC_HUMAN	Lysozyme C (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C)	LYZ
1400,80	1400,095	1401,496	1400,675	0,121	R.STDYGIFQNSR.Y	P61626	LYSC_HUMAN	Lysozyme C (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C)	LYZ
1401,70	1400,997	1402,399							
1402,71	1402,006	1403,408	1402,689	0,018	K.QDKIYFMAGSSR.K	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			1402,632	0,075	K.TANDMIHAENMR.L	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
1403,67	1402,971	1404,375	1403,793	0,120	K.LSDAGITPLFLTR.Q	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1403,80	1403,097	1404,501	1403,793	0,006	K.LSDAGITPLFLTR.Q	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1404,63	1403,925	1405,330	1404,679	0,052	R.FSDSAASPRGEPR.A	P30492	1B54_HUMAN	HLA class I histocompatibility antigen, B-54 alpha chain (Bw-22) (Bw-54) (MHC class I antigen B*54)	HLA-B
1404,78	1404,075	1405,480	1404,679	0,098	R.FSDSAASPRGEPR.A	P30492	1B54_HUMAN	HLA class I histocompatibility antigen, B-54 alpha chain (Bw-22) (Bw-54) (MHC class I antigen B*54)	HLA-B
1405,76	1405,053	1406,458	1405,772	0,016	K.EIKDILIQYDR.T	P62249	RS16_HUMAN	40S ribosomal protein S16 (Small ribosomal subunit protein uS9)	RPS16
			1405,674	0,081	R.FFDEESYSLLR.K	P51571	SSRD_HUMAN	Translocon-associated protein subunit delta (TRAP-delta) (Signal sequence receptor subunit delta) (SSR-delta)	SSR4
1406,74	1406,040	1407,447	1406,702	0,041	R.FSPDDASAGASALLR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1406,689	0,055	K.AHGGYSVFAGVGER.T	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
1407,74	1407,034	1408,442	1407,694	0,044	K.VYNYNHLMPT.R.Y	P61353	RL27_HUMAN	60S ribosomal protein L27 (Large ribosomal subunit protein el27)	RPL27
1408,74	1408,032	1409,441	1408,695	0,042	R.AVFDEYTPDPVR.V	P49588	SYAC_HUMAN	Alanine--tRNA ligase, cytoplasmic (EC 6.1.1.7) (Alanyl-tRNA synthetase) (AlaRS) (Renal carcinoma antigen NY-REN-42)	AARS
			1408,694	0,043	M.GHQQLYWSHPR.K	P62273	RS29_HUMAN	40S ribosomal protein S29 (Small ribosomal subunit protein uS14)	RPS29
			1408,653	0,083	R.NVEAMNFIADIER.T	P36957	ODO2_HUMAN	Dihydrolipoilysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex) (E2K)	DLST
1409,74	1409,035	1410,445	1409,792	0,051	R.DITYFIQQLLR.D	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
1410,73	1410,028	1411,438	1410,696	0,037	K.YHTINGHNAEVR.K	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			1410,782	0,049	R.QLFHEPQLITGK.E	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B

1411,73 1412,75	1411,027 1412,046	1412,438 1413,459	1412,592	0,161	R.DGMDNQGGYGSVGR.M	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNPH3
1413,66	1412,952	1414,366	1413,767	0,108	R.QTPSRQPPLPHR.S	Q07666	KHDR1_HUMAN	KH domain-containing, RNA-binding, signal transduction-associated protein 1 (GAP-associated tyrosine phosphoprotein p62) (Src-associated in mitosis 68 kDa protein) (Sam68) (p21 Ras GTPase-activating protein-associated p62) (p68)	KHDRBS1
1413,77	1413,067	1414,480	1413,767	0,006	R.QTPSRQPPLPHR.S	Q07666	KHDR1_HUMAN	KH domain-containing, RNA-binding, signal transduction-associated protein 1 (GAP-associated tyrosine phosphoprotein p62) (Src-associated in mitosis 68 kDa protein) (Sam68) (p21 Ras GTPase-activating protein-associated p62) (p68)	KHDRBS1
1414,69 1414,78 1415,75 1416,75 1417,77	1413,986 1414,075 1415,038 1416,041 1417,063	1415,401 1415,490 1416,454 1417,458 1418,481	1417,776	0,004	K.SGYLAGDKLLPQR.V	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
1418,75	1418,046	1419,464	1418,737	0,018	K.GFSVVADTPELQR.I	Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 (LASP-1) (Metastatic lymph node gene 50 protein) (MLN 50)	LASP1
1419,75 1420,73 1421,75	1419,040 1420,017 1421,042	1420,460 1421,437 1422,464	1421,704	0,049	K.ETVVRLEEFGR.F	P01903	DRA_HUMAN	HLA class II histocompatibility antigen, DR alpha chain (MHC class II antigen DRA)	HLA-DRA
1422,74	1422,025	1423,448	1422,738	0,001	R.GGGHILPYDQPLR.A	Q9H3G5	CPVL_HUMAN	Probable serine carboxypeptidase CPVL (EC 3.4.16.-) (Carboxypeptidase, vitellogenic-like) (Vitellogenic carboxypeptidase-like protein) (VCP-like protein) (hVLP)	CPVL
1423,74	1423,027	1424,451	1423,760 1423,718 1423,763	0,021 0,021 0,023	K.MALDIEIATYRK.L R.ATAPQQTQHVSPMR.Q K.ATEPVIAFYEKR.G	P08670 P29692 P00568	VIME_HUMAN EF1D_HUMAN KAD1_HUMAN	Vimentin Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO-4) Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	VIM EEF1D AK1
			1423,681	0,059	R.ELAEDGYSVGEVR.V	P23396	RS3_HUMAN	40S ribosomal protein S3 (EC 4.2.99.18) (Small ribosomal subunit protein uS3)	RPS3
1424,72	1424,008	1425,433	1424,691	0,030	R.KWEAAHAAEQQR.A	P13746	1A11_HUMAN	HLA class I histocompatibility antigen, A-11 alpha chain (MHC class I antigen A*11)	HLA-A
1425,68 1425,75 1426,77	1424,966 1425,033 1426,059	1426,392 1426,459 1427,486	1426,775	0,003	R.QKPANVLNDAQTK.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1427,75	1427,038	1428,466	1427,729	0,023	K.WAAVVVPSGEEQR.Y	P30492	1B54_HUMAN	HLA class I histocompatibility antigen, B-54 alpha chain (Bw-22) (Bw-54) (MHC class I antigen B*54)	HLA-B
			1427,729	0,023	K.WAAVVVPSGEEQR.Y	P13746	1A11_HUMAN	HLA class I histocompatibility antigen, A-11 alpha chain (MHC class I antigen A*11)	HLA-A
			1427,729	0,023	K.WAAVVVPSGEEQR.Y	P30460	1B08_HUMAN	HLA class I histocompatibility antigen, B-8 alpha chain (MHC class I antigen B*8)	HLA-B
			1427,728	0,025	R.MGPAMGALGAGIER.M	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
1428,72	1428,007	1429,436	1428,724 1428,697	0,002 0,025	R.SLYASSPGGVYATR.S R.DFSPSGIFGAFQR.G	P08670 P56134	VIME_HUMAN ATPK_HUMAN	Vimentin ATP synthase subunit f, mitochondrial (ATP synthase membrane subunit f)	VIM ATPSMF
1429,73	1429,014	1430,444	1429,726	0,003	K.AFGPLGQGSAGSPAR.F	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			1429,770	0,041	R.TINEVENQILTR.D	O43707	ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	ACTN4
1430,74	1430,022	1431,453	1430,632	0,106	R.SGNPNYPYEFSR.K	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1431,74 1432,75	1431,027 1432,032	1432,458 1433,465	1432,794	0,046	R.MGPLINRPHLER.V	P49189	AL9A1_HUMAN	4-trimethylaminobutylaldehyde dehydrogenase (TMABADH) (EC 1.2.1.47) (Aldehyde dehydrogenase E3 isozyme) (Aldehyde dehydrogenase family 9 member A1) (EC 1.2.1.3) (Gamma-aminobutylaldehyde dehydrogenase) (EC 1.2.1.19) (R-aminobutylaldehyde dehydrogenase) [Cleaved into: 4-trimethylaminobutylaldehyde dehydrogenase, N-terminally processed]	ALDH9A1
1433,75	1433,036	1434,470	1433,732	0,021	R.QQGPSEHIERR.V	P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP)	VASP
1434,74	1434,019	1435,454	1434,689	0,048	K.HIMGQNVADYMR.Y	P46777	RL5_HUMAN	60S ribosomal protein L5 (Large ribosomal subunit protein uL18)	RPL5
1435,76 1436,77	1435,046 1436,054	1436,481 1437,490	1436,774	0,002	R.QLFRPWDTVTK.L	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
1437,77	1437,052	1438,489	1437,748	0,023	R.EDSQRPGAHLTVK.K	P09651	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	HNRNPA1
1438,76 1439,69 1440,10	1438,041 1438,969 1439,384	1439,480 1440,409 1440,824	1440,656	0,552	R.NIDEHANEDVER.M	P61026	RAB10_HUMAN	Ras-related protein Rab-10	RAB10

1440,97	1440,251	1441,692	1440,656	0,316	R.NIDEHANEDEV.R.M	P61026	RAB10_HUMAN	Ras-related protein Rab-10	RAB10
1441,74	1441,022	1442,464	1441,742	0,001	R.MGPGAASGGERPNLK.I	Q9H0U4	RAB1B_HUMAN	Ras-related protein Rab-1B	RAB1B
1442,21	1441,486	1442,928	1441,742	0,465	R.MGPGAASGGERPNLK.I	Q9H0U4	RAB1B_HUMAN	Ras-related protein Rab-1B	RAB1B
			1442,710	0,503	R.AGQSAAGAAPGGGVDT.R.D	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			1442,810	0,603	R.LPDIFEAQIAGLR.G	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcoleictin) (Type-II keratin Kb7)	KRT7
1442,77	1442,051	1443,494	1442,810	0,037	R.LPDIFEAQIAGLR.G	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcoleictin) (Type-II keratin Kb7)	KRT7
			1442,710	0,063	R.AGQSAAGAAPGGGVDT.R.D	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
1443,77	1443,051	1444,495	1443,806	0,033	R.LKQSELQSQVR.Y	Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 (LASP-1) (Metastatic lymph node gene 50 protein) (MLN 50)	LASP1
			1443,642	0,131	R.VDCDQHSIDIAQR.Y	Q9B526	ERP44_HUMAN	Endoplasmic reticulum resident protein 44 (ER protein 44) (ERp44) (Thioredoxin domain-containing protein 4)	ERP44
1444,78	1444,055	1445,500	1444,796	0,018	R.QLYVLGHEAMKR.L	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
1445,76	1445,038	1446,484	1445,749	0,012	R.QLPPPTPANEER.R	P42768	WASP_HUMAN	Wiskott-Aldrich syndrome protein (WASp)	WAS
1446,76	1446,038	1447,485	1446,745	0,017	R.AHLVAVFNEYQR.M	P50995	ANX11_HUMAN	Annexin A11 (56 kDa autoantigen) (Annexin XI) (Annexin-11) (Calcyclin-associated annexin 50) (CAP-50)	ANXA11
1447,76	1447,038	1448,486							
1448,76	1448,033	1449,482							
1449,47	1448,748	1450,197	1449,747	0,274	R.SNAQRQEISAAFK.T	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
			1449,807	0,335	R.FVTVQTISGTGALR.I	P00505	AATM_HUMAN	Aspartate aminotransferase, mitochondrial (mAspAT) (EC 2.6.1.1) (EC 2.6.1.7) (Fatty acid-binding protein) (FABP-1) (Glutamate oxaloacetate transaminase 2) (Kynurenine aminotransferase 4) (Kynurenine aminotransferase IV) (Kynurenine--oxoglutarate transaminase 4) (Kynurenine--oxoglutarate transaminase IV) (Plasma membrane-associated fatty acid-binding protein) (FABPpm) (Transaminase A)	GOT2
1449,75	1449,030	1450,480	1449,747	0,008	R.SNAQRQEISAAFK.T	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
			1449,807	0,053	R.FVTVQTISGTGALR.I	P00505	AATM_HUMAN	Aspartate aminotransferase, mitochondrial (mAspAT) (EC 2.6.1.1) (EC 2.6.1.7) (Fatty acid-binding protein) (FABP-1) (Glutamate oxaloacetate transaminase 2) (Kynurenine aminotransferase 4) (Kynurenine aminotransferase IV) (Kynurenine--oxoglutarate transaminase 4) (Kynurenine--oxoglutarate transaminase IV) (Plasma membrane-associated fatty acid-binding protein) (FABPpm) (Transaminase A)	GOT2
1450,33	1449,603	1451,053	1449,807	0,521	R.FVTVQTISGTGALR.I	P00505	AATM_HUMAN	Aspartate aminotransferase, mitochondrial (mAspAT) (EC 2.6.1.1) (EC 2.6.1.7) (Fatty acid-binding protein) (FABP-1) (Glutamate oxaloacetate transaminase 2) (Kynurenine aminotransferase 4) (Kynurenine aminotransferase IV) (Kynurenine--oxoglutarate transaminase 4) (Kynurenine--oxoglutarate transaminase IV) (Plasma membrane-associated fatty acid-binding protein) (FABPpm) (Transaminase A)	GOT2
			1449,747	0,582	R.SNAQRQEISAAFK.T	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
1450,49	1449,762	1451,213	1449,807	0,680	R.FVTVQTISGTGALR.I	P00505	AATM_HUMAN	Aspartate aminotransferase, mitochondrial (mAspAT) (EC 2.6.1.1) (EC 2.6.1.7) (Fatty acid-binding protein) (FABP-1) (Glutamate oxaloacetate transaminase 2) (Kynurenine aminotransferase 4) (Kynurenine aminotransferase IV) (Kynurenine--oxoglutarate transaminase 4) (Kynurenine--oxoglutarate transaminase IV) (Plasma membrane-associated fatty acid-binding protein) (FABPpm) (Transaminase A)	GOT2
1450,73	1450,009	1451,460							
1451,31	1450,581	1452,033							
1451,75	1451,020	1452,471							
1452,71	1451,988	1453,441	1452,770	0,056	R.GLLEFEHQRAPR.V	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB

[illegible]

			1466,720	0,649	K.TATPQQAQEVHEK.L	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP1
1467,68	1466,950	1468,417	1467,801	0,117	K.VEPLRAELQEGAR.Q	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
			1467,851	0,167	R.RHPDYSVLLRL.L	P02768	ALBU_HUMAN	Serum albumin	ALB
1468,34	1467,606	1469,074	1467,851	0,489	R.RHPDYSVLLRL.L	P02768	ALBU_HUMAN	Serum albumin	ALB
			1467,801	0,539	K.VEPLRAELQEGAR.Q	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1
1468,71	1467,974	1469,442							
1469,64	1468,902	1470,372							
1469,71	1468,972	1470,442							
1470,37	1469,635	1471,106	1470,752	0,381	R.SSFYVNGLTGGQK.C	P07737	PROF1_HUMAN	Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I)	PFN1
			1470,778	0,407	R.QNQIADVDEIRER.L	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
			1470,779	0,408	R.WLQGSQELPREK.Y	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
1470,71	1469,971	1471,441	1470,752	0,046	R.SSFYVNGLTGGQK.C	P07737	PROF1_HUMAN	Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I)	PFN1
			1470,778	0,072	R.QNQIADVDEIRER.L	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
			1470,779	0,073	R.WLQGSQELPREK.Y	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
1470,71	1469,971	1471,442	1470,752	0,045	R.SSFYVNGLTGGQK.C	P07737	PROF1_HUMAN	Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I)	PFN1
			1470,778	0,071	R.QNQIADVDEIRER.L	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
			1470,779	0,072	R.WLQGSQELPREK.Y	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
1471,44	1470,701	1472,173	1470,779	0,658	R.WLQGSQELPREK.Y	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
			1470,778	0,659	R.QNQIADVDEIRER.L	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
			1470,752	0,685	R.SSFYVNGLTGGQK.C	P07737	PROF1_HUMAN	Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I)	PFN1
1471,71	1470,975	1472,447							
1472,40	1471,667	1473,139	1472,694	0,290	K.FVMQEEFSRDGK.A	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (Erp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (Erp60)	PDIA3
			1472,740	0,337	K.FYGPAGPYGIFAGR.D	O15173	PGRC2_HUMAN	Membrane-associated progesterone receptor component 2 (Progesterone membrane-binding protein) (Steroid receptor protein DG6)	PGRMC2
1472,75	1472,019	1473,491	1472,740	0,015	K.FYGPAGPYGIFAGR.D	O15173	PGRC2_HUMAN	Membrane-associated progesterone receptor component 2 (Progesterone membrane-binding protein) (Steroid receptor protein DG6)	PGRMC2
			1472,694	0,061	K.FVMQEEFSRDGK.A	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (Erp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (Erp60)	PDIA3
1473,25	1472,515	1473,988	1472,740	0,511	K.FYGPAGPYGIFAGR.D	O15173	PGRC2_HUMAN	Membrane-associated progesterone receptor component 2 (Progesterone membrane-binding protein) (Steroid receptor protein DG6)	PGRMC2
			1472,694	0,558	K.FVMQEEFSRDGK.A	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (Erp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (Erp60)	PDIA3
1473,90	1473,162	1474,636							
1474,73	1473,988	1475,463	1474,759	0,034	R.LFGGNFAHQASVAR.V	O14773	TPP1_HUMAN	Tripeptidyl-peptidase 1 (TPP-1) (EC 3.4.14.9) (Cell growth-inhibiting gene 1 protein) (Lysosomal pepstatin-insensitive protease) (LPIC) (Tripeptidyl aminopeptidase) (Tripeptidyl-peptidase I) (TPP-I)	TPP1

1475,76	1475,022	1476,498	1475,801	0,041	K.GLVQALGLSNFNSR.Q	P14550	AK1A1_HUMAN	Aldo-keto reductase family 1 member A1 (EC 1.1.1.2) (EC 1.1.1.372) (EC 1.1.1.54) (Alcohol dehydrogenase [NADP(+)]) (Aldehyde reductase) (Glucuronate reductase) (EC 1.1.1.19) (Glucuronolactone reductase) (EC 1.1.1.20)	AKR1A1
1476,75	1476,015	1477,492	1476,770	0,017	R.VHRDGPALSGPQSR.A	P19971	TYPH_HUMAN	Thymidine phosphorylase (TP) (EC 2.4.2.4) (Gliostatin) (Platelet-derived endothelial cell growth factor) (PD-ECGF) (TdRpase)	TYMP
			1476,842	0,088	R.LEGVEGVAHIIDPK.A	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
1477,74	1477,001	1478,478	1477,760	0,020	R.APLPDLYPFGTMR.G	Q92841	DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.4.13) (DEAD box protein 17) (DEAD box protein p72) (DEAD box protein p82) (RNA-dependent helicase p72)	DDX17
1478,06	1477,325	1478,803	1477,760	0,305	R.APLPDLYPFGTMR.G	Q92841	DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.4.13) (DEAD box protein 17) (DEAD box protein p72) (DEAD box protein p82) (RNA-dependent helicase p72)	DDX17
			1478,749	0,684	K.MYLGYEYVTAIR.N	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
1478,75	1478,007	1479,486	1478,749	0,002	K.MYLGYEYVTAIR.N	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
1479,11	1478,374	1479,853	1478,749	0,364	K.MYLGYEYVTAIR.N	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1479,773	0,660	R.QYKIPDWFLNR.Q	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
1479,75	1479,013	1480,493	1479,773	0,020	R.QYKIPDWFLNR.Q	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
1480,76	1480,020	1481,500	1480,758	0,002	R.ARFEELNADLFR.G	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
1481,73	1480,992	1482,474	1481,735	0,002	R.AFYVNVNLEEQR.K	P04040	CATA_HUMAN	Catalase (EC 1.11.1.6)	CAT
			1481,816	0,083	K.SQIHDIVLVGGSTR.I	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
			1481,864	0,131	R.VLDSPPSPVNLTR.E	Q8WZ42	TITIN_HUMAN	Titin (EC 2.7.11.1) (Connectin) (Rhabdomyosarcoma antigen MU-RMS-40.14)	TTN
1482,74	1481,999	1483,482	1482,718	0,022	R.SQYEVMAEQNRK.D	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			1482,804	0,064	K.TVTAMDVVYALKR.Q	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
1483,73	1482,984	1484,468	1483,734	0,008	K.GSFSEQGINEFLR.E	Q15084	PDI A6_HUMAN	Protein disulfide-isomerase A6 (EC 5.3.4.1) (Endoplasmic reticulum protein 5) (ER protein 5) (ERp5) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)	PDI A6
			1483,867	0,142	R.SANLVAATLGAILNR.L	P19367	HXK1_HUMAN	Hexokinase-1 (EC 2.7.1.1) (Brain form hexokinase) (Hexokinase type I) (HK I)	HK1
			1483,898	0,172	K.ISGSILNELIGLVR.S	Q86VP6	CAND1_HUMAN	Cullin-associated NEDD8-dissociated protein 1 (Cullin-associated and neddylation-dissociated protein 1) (TBP-interacting protein of 120 kDa A) (TBP-interacting protein 120A) (p120 CAND1)	CAND1
1484,67	1483,930	1485,414							
1484,76	1484,020	1485,505							
1485,75	1485,007	1486,492	1485,769	0,020	K.GVVSDDDLNVSR.E	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
			1485,939	0,190	R.VVQVVKPHPLIR.F	P82909	RT36_HUMAN	28S ribosomal protein S36, mitochondrial (MRP-S36) (S36mt)	MRPS36
1486,76	1486,017	1487,504							
1487,73	1486,985	1488,473	1487,709	0,021	R.TTPSVVAFDTTER.L	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
			1487,709	0,021	R.TTPSVVAFDTTER.L	P0DMV8	H571A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
			1487,806	0,077	R.RGAPAAATAPARTAHK.A	Q92522	H1X_HUMAN	Histone H1x	H1FX
			1487,879	0,150	R.LISQVSSITASLR.F	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
1488,72	1487,977	1489,466	1488,780	0,058	R.RKPDIEVQQMK.A	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			1488,780	0,058	R.RKPDIEVQQMK.A	P15311	EZRI_HUMAN	Ezrin (Cytovillin) (Villin-2) (p81)	EZR
1489,68	1488,937	1490,427	1489,664	0,019	R.MGPSGGEGMEPERR.D	Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 (LASP-1) (Metastatic lymph node gene 50 protein) (MLN 50)	LASP1
1489,85	1489,101	1490,591	1489,664	0,182	R.MGPSGGEGMEPERR.D	Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 (LASP-1) (Metastatic lymph node gene 50 protein) (MLN 50)	LASP1

1490,69	1489,942	1491,432	1490,804	0,117	R.ADFLEQPLVIGFVRL	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
			1490,827	0,140	R.ELPAAVAPAGPASLAR.W	O95336	6PGL_HUMAN	6-phosphogluconolactonase (6PGL) (EC 3.1.1.31)	PGL5
1490,84	1490,096	1491,587	1490,827	0,014	R.ELPAAVAPAGPASLAR.W	O95336	6PGL_HUMAN	6-phosphogluconolactonase (6PGL) (EC 3.1.1.31)	PGL5
			1490,804	0,038	R.ADFLEQPLVIGFVRL	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
1491,71	1490,963	1492,455	1491,753	0,044	K.FGGAAVFPNQEQR.E	P19971	TYPH_HUMAN	Thymidine phosphorylase (TP) (EC 2.4.2.4) (Gliostatin) (Platelet-derived endothelial cell growth factor) (PD-ECGF) (TdRPase)	TYMP
1491,84	1491,097	1492,589	1491,753	0,090	K.FGGAAVFPNQEQR.E	P19971	TYPH_HUMAN	Thymidine phosphorylase (TP) (EC 2.4.2.4) (Gliostatin) (Platelet-derived endothelial cell growth factor) (PD-ECGF) (TdRPase)	TYMP
1492,78	1492,037	1493,530	1492,711	0,073	K.KYEEIDNAPEER.A	P49411	EFTU_HUMAN	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	TUFM
			1492,904	0,121	K.AVAEQIPLLVQGVR.G	Q9Y490	TLN1_HUMAN	Talin-1	TLN1
1493,74	1492,989	1494,483	1493,741	0,005	R.SQYEQLAEQNRK.D	P13645	K1C10_HUMAN	Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KRT10
			1493,726	0,010	R.HNYGVGESFTVQR.R	Q9TQE0	2B19_HUMAN	HLA class II histocompatibility antigen, DRB1-9 beta chain (MHC class II antigen DRB1*9) (DR-9) (DR9)	HLA-DRB1
1494,73	1493,987	1495,481	1493,694	0,042	R.FNTANDDNVTQVR.A	P04040	CATA_HUMAN	Catalase (EC 1.11.1.6)	CAT
			1494,726	0,008	K.MYLGVEYVTAIR.N	P02787	TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF
			1494,753	0,019	R.EAEYFELPLVR.R	Q96CX2	KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 (Pfetin) (Predominantly fetal expressed T1 domain)	KCTD12
			1494,709	0,025	R.MFGGPGTASRPSSSR.S	P08670	VIME_HUMAN	Vimentin	VIM
			1494,793	0,059	K.INVNEIFYDLVR.Q	P61224	RAP1B_HUMAN	Ras-related protein Rap-1b (GTP-binding protein smg p21B)	RAP1B
1495,75	1494,999	1496,495	1494,793	0,059	K.GAVDGGLSIPHSTKR.F	P46777	RLS_HUMAN	60S ribosomal protein L5 (Large ribosomal subunit protein uL18)	RPL5
			1495,758	0,012	K.YGYTHLSTGDLR.S	P00568	KAD1_HUMAN	Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	AK1
1496,75 1497,75 1498,74	1496,006 1496,999 1497,992	1497,503 1498,497 1499,491	1495,786	0,040	R.TYSLGSALRPSTSR.S	P08670	VIME_HUMAN	Vimentin	VIM
			1498,775	0,033	K.QADLYISEGLHPR.I	Q92526	TCPW_HUMAN	T-complex protein 1 subunit zeta-2 (TCP-1-zeta-2) (CCT-zeta-2) (CCT-zeta-like) (TCP-1-zeta-like) (Testis-specific Tcp20) (Testis-specific protein TSA303)	CCT6B
			1499,707	0,030	K.EVYQQQQYSGGR.G	Q99729	ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein A/B (hnRNP A/B) (APOBEC1-binding protein 1) (ABBP-1)	HNRNPAB
1500,74	1499,993	1501,494	1500,723	0,020	K.QEYDEAGPSIVHR.K	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
1501,74 1502,74	1500,990 1501,991	1502,491 1503,494	1502,759	0,017	K.MINLSVPDTIDER.T	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
1503,76 1504,75	1503,006 1504,000	1504,509 1505,505	1504,760	0,007	R.GYPIYTPFFMR.K	P49591	SYSC_HUMAN	Serine--tRNA ligase, cytoplasmic (EC 6.1.1.11) (Seryl-tRNA synthetase) (SerRS) (Seryl-tRNA(Ser/Sec) synthetase)	SARS
1505,79	1505,034	1506,540	1505,781	0,006	R.QFPFLASIQNQGR.H	P20160	CAP7_HUMAN	Azurocidin (Cationic antimicrobial protein CAP37) (Heparin-binding protein) (HBP) (hHBP)	AZU1
			1505,747	0,040	K.VKEGMNIVEAMER.F	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
			1505,864	0,077	R.KVDGQLLLMAVYR.W	Q5T4F7	SFRP5_HUMAN	Secreted frizzled-related protein 5 (sFRP-5) (Frizzled-related protein 1b) (FRP-1b) (Secreted apoptosis-related protein 3) (SARP-3)	SFRP5
1505,84	1505,087	1506,593	1505,864	0,024	R.KVDGQLLLMAVYR.W	Q5T4F7	SFRP5_HUMAN	Secreted frizzled-related protein 5 (sFRP-5) (Frizzled-related protein 1b) (FRP-1b) (Secreted apoptosis-related protein 3) (SARP-3)	SFRP5
			1505,781	0,059	R.QFPFLASIQNQGR.H	P20160	CAP7_HUMAN	Azurocidin (Cationic antimicrobial protein CAP37) (Heparin-binding protein) (HBP) (hHBP)	AZU1
			1505,747	0,093	K.VKEGMNIVEAMER.F	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
1506,71	1505,959	1507,466	1506,749	0,037	R.TVQSLEIDLDSMR.N	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
1506,84	1506,084	1507,591	1506,749	0,088	R.TVQSLEIDLDSMR.N	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
1507,80	1507,044	1508,552	1507,816	0,018	R.EHQALQDLVDLAR.E	Q8IY92	SLX4_HUMAN	Structure-specific endonuclease subunit SLX4 (BTB/POZ domain-containing protein 12)	SLX4

1508,70	1507,943	1509,452	1508,855	0,157	K.VLKQVHPDTGISSK.A	Q99877 P33778	H2B1N_HUMAN H2B1B_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d) Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BN HIST1H2BB
			1508,855	0,157	K.VLKQVHPDTGISSK.A				
1509,71	1508,952	1510,462	1509,769	0,062	R.YGHTLIQPFMFR.L	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
1510,70	1509,946	1511,457	1510,703	0,002	R.MFGGPGTASRPSSSR.S	P08670	VIME_HUMAN	Vimentin	VIM
1511,75	1510,995	1512,506	1511,820	0,069	R.LVAYYTLIGASGQR.E	P01024	CO3_HUMAN	Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3b-c); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
1512,76	1512,008	1513,521	1512,752	0,013	R.AKFEELNMDLFR.S	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BIP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
1513,77	1513,013	1514,527	1513,794	0,024	R.GVVDESLPLNISR.E	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			1513,794	0,024	R.GVVDESLPLNISR.E	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
1514,75 1515,73	1513,990 1514,970	1515,505 1516,485	1513,712	0,058	R.YLQEIYNSNNQK.I	P02679	FIBG_HUMAN	Fibrinogen gamma chain	FGG
			1513,861	0,091	R.LLLREEATHIYR.K	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1515,73	1514,970	1516,485	1515,757	0,029	K.IWHHTFYNELR.V	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1515,757	0,029	K.IWHHTFYNELR.V	Q6S8J3	POTEE_HUMAN	POTE ankryrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
1516,71	1515,950	1517,467	1515,757	0,029	K.IWHHTFYNELR.V	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1515,764	0,037	R.FLQDYFDGNLKR.Y	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	PDIA3
1516,71	1515,950	1517,467	1516,696	0,013	K.QEYDESGPSIVHR.K	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1516,696	0,013	K.QEYDESGPSIVHR.K	Q6S8J3	POTEE_HUMAN	POTE ankryrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
1516,74	1515,979	1517,496	1516,727	0,018	K.FYGPEGPYGVFAGR.D	O00264	PGRC1_HUMAN	Membrane-associated progesterone receptor component 1 (mPR) (Dap1) (IZA)	PGRMC1
			1516,727	0,010	K.FYGPEGPYGVFAGR.D	O00264	PGRC1_HUMAN	Membrane-associated progesterone receptor component 1 (mPR) (Dap1) (IZA)	PGRMC1
1517,75	1516,989	1518,507	1516,696	0,041	K.QEYDESGPSIVHR.K	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1516,696	0,041	K.QEYDESGPSIVHR.K	Q6S8J3	POTEE_HUMAN	POTE ankryrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
1517,75	1516,989	1518,507	1517,774	0,026	K.GAYQDRDKPAQIR.F	P50991	TCPD_HUMAN	T-complex protein 1 subunit delta (TCP-1-delta) (CCT-delta) (Stimulator of TAR RNA-binding)	CCT4
			1517,884	0,136	R.LLYPPETGLFLVR.E	P41240	CSK_HUMAN	Tyrosine-protein kinase CSK (EC 2.7.10.2) (C-Src kinase) (Protein-tyrosine kinase CYL)	CSK
1518,75 1519,77	1517,991 1519,012	1519,510 1520,532	1519,828	0,056	R.NILHQGQEAILQR.Y	Q96C86	DCPS_HUMAN	m7GpppX diphosphatase (EC 3.6.1.59) (DCS-1) (Decapping scavenger enzyme) (Hint-related 7meGMP-directed hydrolase) (Histidine triad nucleotide-binding protein 5) (Histidine triad protein member 5) (HINT-5) (Scavenger mRNA-decapping enzyme Dcp5)	DCPS
1520,77 1521,76 1522,75 1523,75	1520,014 1520,997 1521,994 1522,989	1521,535 1522,519 1523,516 1524,512	1523,783	0,033	K.IQDKEGIPPDQQR.L	P62987	RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 (CEP52) (Ubiquitin A-S2 residue ribosomal protein fusion product 1) [Cleaved into: Ubiquitin; 60S ribosomal protein L40 (Large ribosomal subunit protein eL40)]	UBA52
1524,71	1523,952	1525,477	1523,819	0,068	K.LAPVPFFSLQYE.-	P07741	APT_HUMAN	Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	APRT

1525,73	1524,968	1526,493	1525,768	0,038	K.LAQANGWGVMSVSHR.S	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			1525,939	0,209	R.ASITPGTILULTGR.H	Q02878	RL6_HUMAN	60S ribosomal protein L6 (Large ribosomal subunit protein eL6) (Neoplasm-related protein C140) (Tax-responsive enhancer element-binding protein 107) (TaxREB107)	RPL6
1526,74	1525,979	1527,506	1527,786	0,086	K.QGAAGIPYFTAYR.A	Q08257	QOR_HUMAN	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-crystallin)	CRYZ
1527,70	1526,936	1528,464	1527,839	0,139	R.HLREYQDLLNVK.M	P08670	VIME_HUMAN	Vimentin	VIM
			1527,839	0,140	K.SLQALGEVIEAELR.S	Q9Y285	SYFA_HUMAN	Phenylalanine--tRNA ligase alpha subunit (EC 6.1.1.20) (CML33) (Phenylalanyl-tRNA synthetase alpha subunit) (PheRS)	FARSA
			1527,850	0,150	K.LAAVDATVNQVLASR.Y	Q15084	PDIA6_HUMAN	Protein disulfide-isomerase A6 (EC 5.3.4.1) (Endoplasmic reticulum protein 5) (ER protein 5) (ERp5) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)	PDIA6
1527,80	1527,038	1528,566	1527,786	0,016	K.QGAAGIPYFTAYR.A	Q08257	QOR_HUMAN	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-crystallin)	CRYZ
			1527,839	0,036	R.HLREYQDLLNVK.M	P08670	VIME_HUMAN	Vimentin	VIM
			1527,839	0,037	K.SLQALGEVIEAELR.S	Q9Y285	SYFA_HUMAN	Phenylalanine--tRNA ligase alpha subunit (EC 6.1.1.20) (CML33) (Phenylalanyl-tRNA synthetase alpha subunit) (PheRS)	FARSA
			1527,850	0,048	K.LAAVDATVNQVLASR.Y	Q15084	PDIA6_HUMAN	Protein disulfide-isomerase A6 (EC 5.3.4.1) (Endoplasmic reticulum protein 5) (ER protein 5) (ERp5) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)	PDIA6
1528,74	1527,972	1529,500	1529,732	0,033	K.VGAHAGEYGAEALER.M	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
1529,70	1528,934	1530,464	1529,919	0,220	R.ALPLALVHELGAAGR.S	P19971	TYPH_HUMAN	Thymidine phosphorylase (TP) (EC 2.4.2.4) (Gliostatin) (Platelet-derived endothelial cell growth factor) (PD-ECGF) (TdrPase)	TYMP
1530,70	1529,930	1531,461	1530,806	0,111	R.VPTANVSVDLTCR.L	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
1531,70	1530,938	1532,470	1533,728	0,048	R.GWEEGVAQMMSGVQR.A	P62942	FKB1A_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP1A (PPIase FKBP1A) (EC 5.2.1.8) (12 kDa FK506-binding protein) (12 kDa FKBP) (FKBP-12) (Calstabin-1) (FK506-binding protein 1A) (FKBP-1A) (Immunophilin FKBP12) (Rotamase)	FKBP1A
1532,67	1531,904	1533,437	1533,769	0,089	R.AEAGVPAEFSIWTR.E	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
1532,70	1531,930	1533,463							
1533,68	1532,913	1534,446	1535,760	0,066	R.HNYGVVESFTVQR.R	P01911	2B1F_HUMAN	HLA class II histocompatibility antigen, DRB1-15 beta chain (DW2.2/DR2.2) (MHC class II antigen DRB1*15)	HLA-DRB1
1534,68	1533,914	1535,449	1536,902	0,181	R.ILSGRPPLGLNPR.L	Q14773	TPP1_HUMAN	Tripeptidyl-peptidase 1 (TPP-1) (EC 3.4.14.9) (Cell growth-inhibiting gene 1 protein) (Lysosomal pepstatin-insensitive protease) (LPIC) (Tripeptidyl aminopeptidase) (Tripeptidyl-peptidase I) (TPP-I)	TPP1
1535,69	1534,926	1536,462	1538,777	0,047	K.YHTINGHNAEVRK.A	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
1536,72	1535,952	1537,489	1538,670	0,060	R.MGQMAMGGAMGINNR.G	Q15233	NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrb)) (p54nrb)	NONO
1537,71	1536,943	1538,481	1538,835	0,105	R.SLMPFYFLTQAVR.T	O43242	PSMD3_HUMAN	26S proteasome non-ATPase regulatory subunit 3 (26S proteasome regulatory subunit RPN3) (26S proteasome regulatory subunit S3) (Proteasome subunit p58)	PSMD3
1538,73	1537,961	1539,499	1539,912	0,176	K.ILLAELEQLKGQGK.S	P08670	VIME_HUMAN	Vimentin	VIM
1539,74	1538,966	1540,505	1540,801	0,110	R.IFDSEEILAGYKR.E	O43776	SYNC_HUMAN	Asparagine--tRNA ligase, cytoplasmic (EC 6.1.1.22) (Asparaginyl-tRNA synthetase) (AsnRS)	NARS
1540,69	1539,921	1541,462	1540,801	0,023	R.IFDSEEILAGYKR.E	O43776	SYNC_HUMAN	Asparagine--tRNA ligase, cytoplasmic (EC 6.1.1.22) (Asparaginyl-tRNA synthetase) (AsnRS)	NARS
1540,78	1540,008	1541,549	1541,909	0,216	R.VLDPFTIKPLDRK.L	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
1541,69	1540,922	1542,463	1541,909	0,125	R.VLDPFTIKPLDRK.L	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
1541,78	1541,013	1542,555	1542,739	0,017	R.HSEAATAQREEWK.M	Q14103	HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1)	HNRNPD
1542,76	1541,985	1543,528	1542,858	0,102	K.GVDEVTVNILTNR.S	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
1543,75	1542,983	1544,526	1543,834	0,079	K.QVEILNRYPHFK.T	P07099	HYEP_HUMAN	Epoxide hydrolase 1 (EC 3.3.2.9) (Epoxide hydratase) (Microsomal epoxide hydrolase) (mEH)	EPHX1
			1543,873	0,119	K.GVDEATIIDIILTKR.N	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1

1544,76	1543,992	1545,537	1544,778	0,014	R.TIPDGNFFTYTR.H	P00352	AL1A1_HUMAN	Retinal dehydrogenase 1 (RALDH 1) (RaldDH1) (EC 1.2.1.-) (EC 1.2.1.36) (ALDH-E1) (ALHDI) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic)	ALDH1A1
			1544,819	0,055	K.LQAEAPHVIVGTPGR.V	Q14240	IF4A2_HUMAN	Eukaryotic initiation factor 4A-II (eIF-4A-II) (eIF4A-II) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-2)	EIF4A2
			1544,850	0,086	R.TIQNDIMLLQLSR.R	P08311	CATG_HUMAN	Cathepsin G (CG) (EC 3.4.21.20)	CTSG
1545,75	1544,979	1546,525							
1546,76	1545,984	1547,531							
1546,76	1545,991	1547,538							
1547,33	1546,556	1548,103	1547,817	0,487	K.APGTPHSHTKPYVR.S	Q07020	RL18_HUMAN	60S ribosomal protein L18 (Large ribosomal subunit protein eL18)	RPL18
1547,77	1546,995	1548,543	1547,817	0,048	K.APGTPHSHTKPYVR.S	Q07020	RL18_HUMAN	60S ribosomal protein L18 (Large ribosomal subunit protein eL18)	RPL18
1548,33	1547,554	1549,102	1548,729	0,401	K.SVTEQGAELSNEER.N	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
			1548,749	0,421	R.FPDADFVTFSSFOR.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1548,780	0,452	R.MQKEITALAPSTMK.I	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1548,780	0,452	R.MQKEITALAPSTMK.I	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1547,817	0,511	K.APGTPHSHTKPYVR.S	Q07020	RL18_HUMAN	60S ribosomal protein L18 (Large ribosomal subunit protein eL18)	RPL18
1548,77	1547,996	1549,544	1548,780	0,010	R.MQKEITALAPSTMK.I	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1548,780	0,010	R.MQKEITALAPSTMK.I	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1548,749	0,021	R.FPDADFVTFSSFOR.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1548,729	0,041	K.SVTEQGAELSNEER.N	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
1549,38	1548,608	1550,158	1549,850	0,467	K.AAVHLEGKIEQAQR.W	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL
			1549,871	0,488	K.NLMQLNLAHNILR.K	P51888	PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	PRELP
			1548,780	0,603	R.MQKEITALAPSTMK.I	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1548,780	0,603	R.MQKEITALAPSTMK.I	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1548,749	0,634	R.FPDADFVTFSSFOR.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1548,729	0,654	K.SVTEQGAELSNEER.N	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
1549,61	1548,839	1550,389	1549,850	0,236	K.AAVHLEGKIEQAQR.W	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL
			1549,871	0,257	K.NLMQLNLAHNILR.K	P51888	PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	PRELP
1549,77	1548,996	1550,546	1549,850	0,078	K.AAVHLEGKIEQAQR.W	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL
			1549,871	0,100	K.NLMQLNLAHNILR.K	P51888	PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	PRELP
1550,65	1549,872	1551,423	1550,816	0,169	K.GTDVNVFNTILTTR.S	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
			1550,878	0,230	R.VVVGAPQIEVAANQR.G	P11215	ITAM_HUMAN	Integrin alpha-M (CD11 antigen-like family member B) (CR-3 alpha chain) (Cell surface glycoprotein MAC-1 subunit alpha) (Leukocyte adhesion receptor MO1) (Neutrophil adherence receptor) (CD antigen CD11b)	ITGAM
			1550,895	0,248	R.ALIAGGGAPEIELALR.L	P50991	TCPD_HUMAN	T-complex protein 1 subunit delta (TCP-1-delta) (CCT-delta) (Stimulator of TAR RNA-binding)	CCT4
1550,79	1550,016	1551,567	1550,816	0,025	K.GTDVNVFNTILTTR.S	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
			1550,878	0,086	R.VVVGAPQIEVAANQR.G	P11215	ITAM_HUMAN	Integrin alpha-M (CD11 antigen-like family member B) (CR-3 alpha chain) (Cell surface glycoprotein MAC-1 subunit alpha) (Leukocyte adhesion receptor MO1) (Neutrophil adherence receptor) (CD antigen CD11b)	ITGAM
			1550,895	0,103	R.ALIAGGGAPEIELALR.L	P50991	TCPD_HUMAN	T-complex protein 1 subunit delta (TCP-1-delta) (CCT-delta) (Stimulator of TAR RNA-binding)	CCT4
1551,72	1550,948	1552,500							
1552,72	1551,943	1553,496	1552,845	0,125	R.VISKHDLGHFMLR.C	P30043	BLVRB_HUMAN	Flavin reductase (NADPH) (FR) (EC 1.5.1.30) (Biliverdin reductase B) (BVR-B) (EC 1.3.1.24) (Biliverdin-IX beta-reductase) (Green heme-binding protein) (GHBP) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR)	BLVRB
1553,73	1552,956	1554,509	1553,747	0,015	R.EAYPGDVFLYHSR.L	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
1554,33	1553,557	1555,112	1554,872	0,537	K.NREPVQLETLSIR.G	P62314	SMD1_HUMAN	Small nuclear ribonucleoprotein Sm D1 (Sm-D1) (Sm-D autoantigen) (snRNP core protein D1)	SNRPD1
			1553,747	0,587	R.EAYPGDVFLYHSR.L	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
1554,64	1553,866	1555,421	1554,872	0,228	K.NREPVQLETLSIR.G	P62314	SMD1_HUMAN	Small nuclear ribonucleoprotein Sm D1 (Sm-D1) (Sm-D autoantigen) (snRNP core protein D1)	SNRPD1
1554,78	1553,998	1555,553	1554,872	0,096	K.NREPVQLETLSIR.G	P62314	SMD1_HUMAN	Small nuclear ribonucleoprotein Sm D1 (Sm-D1) (Sm-D autoantigen) (snRNP core protein D1)	SNRPD1
1555,33	1554,549	1556,104	1555,714	0,387	K.MFVLDEADEMLSR.G	Q14240	IF4A2_HUMAN	Eukaryotic initiation factor 4A-II (eIF-4A-II) (eIF4A-II) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-2)	EIF4A2

1555,74	1554,961	1556,516	1555,714	0,387	K.MFVLDEADEMLSR.G	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-I (eIF-4A-I) (eIF4A-I) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
			1554,872	0,455	K.NREPVLQETLSIR.G	P62314	SMD1_HUMAN	Small nuclear ribonucleoprotein Sm D1 (Sm-D1) (Sm-D autoantigen) (snRNP core protein D1)	SNRPD1
			1555,798	0,471	R.FLTAGRTDPAHDVR.V	P12109	CO6A1_HUMAN	Collagen alpha-1(VI) chain	COL6A1
			1555,714	0,024	K.MFVLDEADEMLSR.G	Q14240	IF4A2_HUMAN	Eukaryotic initiation factor 4A-II (eIF-4A-II) (eIF4A-II) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-2)	EIF4A2
			1555,714	0,024	K.MFVLDEADEMLSR.G	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-I (eIF-4A-I) (eIF4A-I) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
1556,67	1555,895	1557,451	1555,798	0,059	R.FLTAGRTDPAHDVR.V	P12109	CO6A1_HUMAN	Collagen alpha-1(VI) chain	COL6A1
			1556,792	0,119	R.QQEGESRLNLVQR.N	P00338	LDHA_HUMAN	L-lactate dehydrogenase A chain (LDH-A) (EC 1.1.1.27) (Cell proliferation-inducing gene 19 protein) (LDH muscle subunit) (LDH-M) (Renal carcinoma antigen NY-REN-59)	LDHA
			1556,828	0,155	R.MAAPIDRVGQTIER.M	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			1556,867	0,194	K.QLDDLKVELSQLR.V	P42766	RL35_HUMAN	60S ribosomal protein L35 (Large ribosomal subunit protein uL29)	RPL35
			1556,792	0,001	R.QQEGESRLNLVQR.N	P00338	LDHA_HUMAN	L-lactate dehydrogenase A chain (LDH-A) (EC 1.1.1.27) (Cell proliferation-inducing gene 19 protein) (LDH muscle subunit) (LDH-M) (Renal carcinoma antigen NY-REN-59)	LDHA
1556,79	1556,012	1557,569	1556,828	0,037	R.MAAPIDRVGQTIER.M	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			1556,867	0,077	K.QLDDLKVELSQLR.V	P42766	RL35_HUMAN	60S ribosomal protein L35 (Large ribosomal subunit protein uL29)	RPL35
			1557,742	0,008	R.QEMTMSAELKMR.A	Q96CN5	LRC45_HUMAN	Leucine-rich repeat-containing protein 45	LRR45
			1557,669	0,081	R.DQGGFGDRNEYGSR.I	Q92945	FUBP2_HUMAN	Far upstream element-binding protein 2 (FUSE-binding protein 2) (KH type-splicing regulatory protein) (KSRP) (p75)	KHSRP
			1558,745	0,012	R.MFNGEKINYTEGR.A	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
1559,75	1558,974	1560,534	1560,803	0,040	K.VDFPDQQLTALTGR.I	P40926	MDHM_HUMAN	Malate dehydrogenase, mitochondrial (EC 1.1.1.37)	MDH2
			1560,929	0,166	R.GALINVPPFLGLPR.F	P26640	SYVC_HUMAN	Valine--tRNA ligase (EC 6.1.1.9) (Protein G7a) (Valyl-tRNA synthetase) (ValRS)	VAR5
			1561,786	0,015	K.MVGVPAAALDMMMLTGR.S	P40939	ECHA_HUMAN	Trifunctional enzyme subunit alpha, mitochondrial (78 kDa gastrin-binding protein) (TP-alpha) [Includes: Long-chain enoyl-CoA hydratase (EC 4.2.1.17); Long chain 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.211)]	HADHA
			1561,727	0,044	R.TATSEYQTFNPR.T	P00734	THRB_HUMAN	Prothrombin (EC 3.4.21.5) (Coagulation factor II) [Cleaved into: Activation peptide fragment 1; Activation peptide fragment 2; Thrombin light chain; Thrombin heavy chain]	F2
			1562,779	0,008	K.LTRDETNYGIPQR.A	P63244	RACK1_HUMAN	Receptor of activated protein C kinase 1 (Cell proliferation-inducing gene 21 protein) (Guanine nucleotide-binding protein subunit beta-2-like 1) (Guanine nucleotide-binding protein subunit beta-like protein 12.3) (Human lung cancer oncogene 7 protein) (HLC-7) (Receptor for activated C kinase) (Small ribosomal subunit protein RACK1) [Cleaved into: Receptor of activated protein C kinase 1, N-terminally processed (Guanine nucleotide-binding protein subunit beta-2-like 1, N-terminally processed)]	RACK1
1563,75	1562,973	1564,536	1562,798	0,027	R.RFSPDDSGAGASALLR.S	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1562,818	0,047	K.MFGIDRDIAQAVR.G	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
			1563,751	0,004	R.ERLQEMLMGLEAK.Q	Q98V73	CP250_HUMAN	Centrosome-associated protein CEP250 (250 kDa centrosomal protein) (Cep250) (Centrosomal Nek2-associated protein 1) (C-Nap1) (Centrosomal protein 2)	CEP250
			1563,751	0,025	R.ERLQEMLMGLEAK.Q	Q98V73	CP250_HUMAN	Centrosome-associated protein CEP250 (250 kDa centrosomal protein) (Cep250) (Centrosomal Nek2-associated protein 1) (C-Nap1) (Centrosomal protein 2)	CEP250
			1564,768	0,013	K.ALAAGGYDVEKNNSR.I	P16401	H15_HUMAN	Histone H1.5 (Histone H1a) (Histone H1b) (Histone H1s-3)	HIST1H1B
1565,77	1564,984	1566,549	1565,79	0,011	R.ITPSYVAFTPEGER.L	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			1566,78	0,011	R.ITPSYVAFTPEGER.L	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			1567,744	0,014	R.SQSAAVTPSTTSSTR.A	Q16186	ADRM1_HUMAN	Proteasomal ubiquitin receptor ADRM1 (110 kDa cell membrane glycoprotein) (Gp110) (Adhesion-regulating molecule 1) (ARM-1) (Proteasome regulatory particle non-ATPase 13) (hRpn13) (Rpn13 homolog)	ADRM1
			1567,831	0,073	R.VGRRPDQLQEGEGK.I	Q8NC51	PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein (PAI1 RNA-binding protein 1) (PAI-RBP1) (SERPINE1 mRNA-binding protein 1)	SERP1
			1568,949	0,462	K.IPAFLNVVDIAGLVK.G	Q9NTK5	OLA1_HUMAN	Odg-like ATPase 1 (DNA damage-regulated overexpressed in cancer 45) (DOC45) (GTP-binding protein 9)	OLA1

			1567,831	0,656	R.VGRRPDQQLQEGEK.I	Q8NC51	PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein (PAI1 RNA-binding protein 1) (PAI-RBP1) (SERPINE1 mRNA-binding protein 1)	SERP1
			1567,744	0,743	R.SQSAAVPTSSSTTSSTR.A	Q16186	ADRM1_HUMAN	Proteasomal ubiquitin receptor ADRM1 (110 kDa cell membrane glycoprotein) (Gp110) (Adhesion-regulating molecule 1) (ARM-1) (Proteasome regulatory particle non-ATPase 13) (hRpn13) (Rpn13 homolog)	ADRM1
			1568,949	0,189	K.IPAFLNVVDIAGLVK.G	Q9NTK5	OLA1_HUMAN	Obg-like ATPase 1 (DNA damage-regulated overexpressed in cancer 45) (DOC45) (GTP-binding protein 9)	OLA1
1568,76	1567,976	1569,544	1568,949	0,409	K.IPAFLNVVDIAGLVK.G	Q9NTK5	OLA1_HUMAN	Obg-like ATPase 1 (DNA damage-regulated overexpressed in cancer 45) (DOC45) (GTP-binding protein 9)	OLA1
1569,36	1568,573	1570,142	1569,772	0,415	K.KAEAGAGSATEFQFR.G	P46783	RS10_HUMAN	40S ribosomal protein S10 (Small ribosomal subunit protein eS10)	RPS10
1569,54	1568,757	1570,327	1569,772	0,230	K.KAEAGAGSATEFQFR.G	P46783	RS10_HUMAN	40S ribosomal protein S10 (Small ribosomal subunit protein eS10)	RPS10
			1568,949	0,593	K.IPAFLNVVDIAGLVK.G	Q9NTK5	OLA1_HUMAN	Obg-like ATPase 1 (DNA damage-regulated overexpressed in cancer 45) (DOC45) (GTP-binding protein 9)	OLA1
1569,76	1568,980	1570,550	1569,772	0,007	K.KAEAGAGSATEFQFR.G	P46783	RS10_HUMAN	40S ribosomal protein S10 (Small ribosomal subunit protein eS10)	RPS10
1570,49	1569,702	1571,273	1570,898	0,411	R.ISLPLPNFSSLNLR.E	P08670	VIME_HUMAN	Vimentin	VIM
			1569,772	0,715	K.KAEAGAGSATEFQFR.G	P46783	RS10_HUMAN	40S ribosomal protein S10 (Small ribosomal subunit protein eS10)	RPS10
1570,73	1569,949	1571,519	1570,898	0,164	R.ISLPLPNFSSLNLR.E	P08670	VIME_HUMAN	Vimentin	VIM
1570,87	1570,082	1571,653	1570,898	0,031	R.ISLPLPNFSSLNLR.E	P08670	VIME_HUMAN	Vimentin	VIM
1571,33	1570,544	1572,116	1570,898	0,432	R.ISLPLPNFSSLNLR.E	P08670	VIME_HUMAN	Vimentin	VIM
			1571,865	0,535	K.VSHLLGINVDTFTR.G	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
1571,77	1570,985	1572,556	1571,865	0,095	K.VSHLLGINVDTFTR.G	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
1571,84	1571,055	1572,626	1571,865	0,025	K.VSHLLGINVDTFTR.G	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
1572,70	1571,915	1573,488	1572,800	0,099	K.DLAAFDKSHDQAVR.T	P09960	LKHA4_HUMAN	Leukotriene A-4 hydrolase (LTA-4 hydrolase) (EC 3.3.2.6) (Leukotriene A(4) hydrolase)	LTA4H
1572,85	1572,063	1573,636	1572,800	0,049	K.DLAAFDKSHDQAVR.T	P09960	LKHA4_HUMAN	Leukotriene A-4 hydrolase (LTA-4 hydrolase) (EC 3.3.2.6) (Leukotriene A(4) hydrolase)	LTA4H
1573,68	1572,889	1574,463							
1573,84	1573,052	1574,626							
1574,77	1573,979	1575,554	1574,772	0,005	R.QAGEVTYADAHKER.T	Q13247	SRSF6_HUMAN	Serine/arginine-rich splicing factor 6 (Pre-mRNA-splicing factor SRP55) (Splicing factor, arginine/serine-rich 6)	SRSF6
1575,77	1574,980	1576,556							
1576,71	1575,919	1577,496	1576,746	0,038	R.MNTNPSRGPYHFR.A	P40429	RL13A_HUMAN	60S ribosomal protein L13a (23 kDa highly basic protein) (Large ribosomal subunit protein uL13)	RPL13A
1576,77	1575,981	1577,557	1576,746	0,023	R.MNTNPSRGPYHFR.A	P40429	RL13A_HUMAN	60S ribosomal protein L13a (23 kDa highly basic protein) (Large ribosomal subunit protein uL13)	RPL13A
1577,77	1576,984	1578,562	1577,896	0,123	R.ISGLIYEETRGVLK.V	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
1578,78	1577,989	1579,568	1578,786	0,008	R.SLADIAREEASNFR.S	P25788	PSA3_HUMAN	Proteasome subunit alpha type-3 (EC 3.4.25.1) (Macropain subunit C8) (Multicatalytic endopeptidase complex subunit C8) (Proteasome component C8)	PSMA3
			1578,794	0,016	K.ALAAAGYDVKEKNSNR.I	P16403	H12_HUMAN	Histone H1.2 (Histone H1c) (Histone H1d) (Histone H1s-1)	HIST1H1C
1579,77	1578,980	1580,560							
1580,75	1579,958	1581,539	1580,801	0,053	K.ESISVSSEQLAQFR.S	P00915	CAH1_HUMAN	Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase I) (Carbonic anhydrase B) (CAB) (Carbonic anhydrase I) (CA-I)	CA1
1581,76	1580,968	1582,550							
1582,77	1581,979	1583,562	1582,916	0,146	K.LVRPPVQYQYIEGR.Y	P48047	ATPO_HUMAN	ATP synthase subunit O, mitochondrial (ATP synthase peripheral stalk subunit OSCP) (Oligomycin sensitivity conferral protein) (OSCP)	ATP5PO

1583,77	1582,982	1584,565	1583,885	0,111	K.GQLVPLETVLDMLR.D	P00568	KAD1_HUMAN	Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	AK1
			1583,938	0,165	R.VTPTRTEIILATR.T	P23396	RS3_HUMAN	40S ribosomal protein S3 (EC 4.2.99.18) (Small ribosomal subunit protein uS3)	RPS3
1584,77	1583,976	1585,560	1584,724	0,044	R.GPYESGSGHSSGLGHR.E	Q86Y23	HORN_HUMAN	Hornerin	HRNR
			1584,624	0,144	K.DSDMGSRPESMGCR.K	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1584,956	0,188	R.LSAKPAPPKPEPKPK.K	P05204	HMG2_HUMAN	Non-histone chromosomal protein HMG-17 (High mobility group nucleosome-binding domain-containing protein 2)	HMG2
1585,75	1584,958	1586,544	1585,802	0,050	R.THLAPYSDELRLR.L	P02647	APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-1(1-242))]	APOA1
			1585,816	0,065	R.WEAQNGQDLTPAK.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1586,75	1585,959	1587,546	1586,759	0,007	K.AVQAQGGESQEAQR.L	Q14980	NUMA1_HUMAN	Nuclear mitotic apparatus protein 1 (Nuclear matrix protein-22) (NMP-22) (Nuclear mitotic apparatus protein) (NuMa protein) (SP-H antigen)	NUMA1
1587,76	1586,962	1588,549	1587,767	0,011	R.ELPTAFDYVEFTR.S	Q13813	SPTN1_HUMAN	Spectrin alpha chain, non-erythrocytic 1 (Alpha-II spectrin) (Fodrin alpha chain) (Spectrin, non-erythroid alpha subunit)	SPTAN1
			1587,808	0,052	R.TNEKVELQLNDR.F	P08670	VIME_HUMAN	Vimentin	VIM
1588,76	1587,969	1589,558	1588,847	0,083	K.QMADTGKLTLLQR.A	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNP
1589,74	1588,944	1590,534	1589,821	0,081	K.EAINVEQAFQTIAR.N	P51149	RAB7A_HUMAN	Ras-related protein Rab-7a	RAB7A
			1589,879	0,140	R.FRPAAGAARPPPKPM.-	P62854	RS26_HUMAN	40S ribosomal protein S26 (Small ribosomal subunit protein eS26)	RPS26
1589,83	1589,035	1590,625	1589,821	0,009	K.EAINVEQAFQTIAR.N	P51149	RAB7A_HUMAN	Ras-related protein Rab-7a	RAB7A
			1589,879	0,049	R.FRPAAGAARPPPKPM.-	P62854	RS26_HUMAN	40S ribosomal protein S26 (Small ribosomal subunit protein eS26)	RPS26
1590,71	1589,915	1591,505	1590,893	0,183	K.LENLLLLDLQHNR.L	P51888	PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	PRELP
1590,83	1590,035	1591,626	1590,893	0,063	K.LENLLLLDLQHNR.L	P51888	PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	PRELP
1591,73	1590,930	1592,522	1591,705	0,021	R.NTDQASMPDNTAAQK.V	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
1591,86	1591,061	1592,652	1591,705	0,151	R.NTDQASMPDNTAAQK.V	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
1592,71	1591,917	1593,510							
1592,84	1592,039	1593,632							
1593,80	1593,005	1594,599	1593,852	0,050	R.EGTIQVQGQALFFR.E	Q96IU4	ABHEB_HUMAN	Protein ABHD14B (EC 3.-.-.-) (Alpha/beta hydrolase domain-containing protein 14B) (Abhydrolase domain-containing protein 14B) (CCG1-interacting factor B)	ABHD14B
			1593,732	0,070	R.WYQMGAYQPFR.FA	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1593,81	1593,013	1594,607	1593,852	0,042	R.EGTIQVQGQALFFR.E	Q96IU4	ABHEB_HUMAN	Protein ABHD14B (EC 3.-.-.-) (Alpha/beta hydrolase domain-containing protein 14B) (Abhydrolase domain-containing protein 14B) (CCG1-interacting factor B)	ABHD14B
			1593,732	0,078	R.WYQMGAYQPFR.FA	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1594,80	1594,007	1595,602	1594,904	0,099	K.KLEFVPTNLHIQR.M	Q96PE3	INP4A_HUMAN	Type I inositol 3,4-bisphosphate 4-phosphatase (EC 3.1.3.66) (Inositol polyphosphate 4-phosphatase type I)	INPP4A
1595,75	1594,957	1596,553							
1595,83	1595,028	1596,624							
1596,81	1596,009	1597,606							
1597,83	1597,033	1598,631	1597,846	0,014	R.KLDYGQHVAVGTPGR.V	P38919	IF4A3_HUMAN	Eukaryotic initiation factor 4A-III (eIF-4A-III) (eIF4A-III) (EC 3.6.4.13) (ATP-dependent RNA helicase DDX48) (ATP-dependent RNA helicase eIF4A-3) (DEAD box protein 48) (Eukaryotic initiation factor 4A-like NUK-34) (Eukaryotic translation initiation factor 4A isoform 3) (Nuclear matrix protein 265) (NMP 265) (hNMP 265) [Cleaved into: Eukaryotic initiation factor 4A-III, N-terminally processed]	EIF4A3
1598,80	1598,003	1599,602	1598,758	0,045	K.AVTEQGHLSNEER.N	P31946	1433B_HUMAN	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHA
			1598,748	0,054	R.IIPGFMCQGGDFTR.H	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
1599,82	1599,019	1600,619	1599,928	0,109	R.ALLKDQQPGTFLLR.F	P42224	STAT1_HUMAN	Signal transducer and activator of transcription 1-alpha/beta (Transcription factor ISGF-3 components p91/p84)	STAT1

1600,80	1600,004	1601,604	1600,786	0,018	K.YVTSAPMPEQPAPGR.Y	P01871	IGHM_HUMAN	Immunoglobulin heavy constant mu (Ig mu chain C region) (Ig mu chain C region BOT) (Ig mu chain C region GAL) (Ig mu chain C region OU)	IGHM
1601,81	1601,011	1602,613	1601,808	0,004	K.VALVYGQMNPPGAR.A	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			1601,802	0,010	R.NAVTQEFQVPDTR.Y	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
			1601,822	0,011	R.AVLVDLEPGTMDSVR.S	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1601,796	0,016	K.IDKTDYMGVSGYGR.A	P52565	GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)	ARHGDI1A
			1601,893	0,081	K.IVAPISDSPKPPQR.V	O95336	6PGL_HUMAN	6-phosphogluconolactonase (6PGL) (EC 3.1.1.31)	PGLS
1602,79	1601,984	1603,587	1602,774	0,011	K.YNEQHVPQSPFTAR.V	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			1602,762	0,023	K.TFHFNTVEEVHSR.F	P30740	ILEU_HUMAN	Leukocyte elastase inhibitor (LEI) (Monocyte/neutrophil elastase inhibitor) (EI) (M/NEI) (Peptidase inhibitor 2) (PI-2) (Serin B1)	SERPINB1
1603,79	1602,993	1604,597	1603,740	0,055	R.SMQGFPHYDKPMR.I	P09012	SNRPA_HUMAN	U1 small nuclear ribonucleoprotein A (U1 snRNP A) (U1-A) (U1A)	SNRPA
			1603,858	0,063	R.GPVYIGELPQDFLR.I	Q9H0E2	TOLIP_HUMAN	Toll-interacting protein	TOLLIP
1604,81	1604,005	1605,610	1604,817	0,009	R.LYQQHAGLFDVTR.G	O14773	TPP1_HUMAN	Tripeptidyl-peptidase 1 (TPP-1) (EC 3.4.14.9) (Cell growth-inhibiting gene 1 protein) (Lysosomal pepstatin-insensitive protease) (LPIC) (Tripeptidyl aminopeptidase) (Tripeptidyl-peptidase I) (TPP-I)	TPP1
			1604,969	0,162	K.ILPEIPILEEGLR.S	Q92616	GCN1_HUMAN	eIF-2-alpha kinase activator GCN1 (GCN1 eIF-2-alpha kinase activator homolog) (GCN1-like protein 1) (General control of amino-acid synthesis 1-like protein 1) (Translational activator GCN1) (HsGCN1)	GCN1
1605,82	1605,012	1606,618	1605,819	0,004	R.VAVEEDVEEGKVR.L	P02545	LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA
			1605,860	0,044	R.FRPAGAAPRPPKPM.-	P62854	RS26_HUMAN	40S ribosomal protein S26 (Small ribosomal subunit protein eS26)	RPS26
			1605,968	0,152	K.ALTHGLEEVLLALK.T	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
1606,81	1606,007	1607,614	1606,791	0,019	K.AVPKEDIYSGGGGGSRS.S	Q13151	ROA0_HUMAN	Heterogeneous nuclear ribonucleoprotein A0 (hnRNP A0)	HNRNPA0
			1606,705	0,106	R.MTGSEFDPEEMKR.K	P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
1607,78	1606,974	1608,582	1607,769	0,009	R.DVSELTGFPEMLGGR.V	P31939	PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH [Cleaved into: Bifunctional purine biosynthesis protein PURH, N-terminally processed] [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (5-aminimidazole-4-carboxamide ribonucleotide formyltransferase) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (ATIC) (IMP synthase) (Inosinase)]	ATIC
			1607,809	0,030	R.LGGPEAGLGEYLFER.L	P02792	FRIL_HUMAN	Ferritin light chain (Ferritin L subunit)	FTL
			1607,824	0,045	R.YNVLGAETVLNQMR.M	Q1KMD3	HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 2 (Scaffold-attachment factor A2) (SAF-A2)	HNRNPUL2
			1607,862	0,084	R.QYNVGPSVSKYPLR.N	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
1608,76	1607,955	1609,564	1608,777	0,018	R.YNFPVEVEVPMER.K	P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	PRKDC
			1608,782	0,023	K.QSFTMVADTPENLR.L	Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 (LASP-1) (Metastatic lymph node gene 50 protein) (MLN 50)	LASP1
			1608,839	0,079	R.ASYVAPLTAQPATYR.A	Q96PK6	RBM14_HUMAN	RNA-binding protein 14 (Paraspeckle protein 2) (PSP2) (RNA-binding motif protein 14) (RRM-containing coactivator activator/modulator) (Synaptotagmin-interacting protein) (SYT-interacting protein)	RBM14
1608,80	1607,993	1609,602	1608,782	0,016	K.QSFTMVADTPENLR.L	Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 (LASP-1) (Metastatic lymph node gene 50 protein) (MLN 50)	LASP1
			1608,777	0,020	R.YNFPVEVEVPMER.K	P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	PRKDC
			1608,839	0,041	R.ASYVAPLTAQPATYR.A	Q96PK6	RBM14_HUMAN	RNA-binding protein 14 (Paraspeckle protein 2) (PSP2) (RNA-binding motif protein 14) (RRM-containing coactivator activator/modulator) (Synaptotagmin-interacting protein) (SYT-interacting protein)	RBM14
1609,80	1608,993	1610,602	1609,871	0,073	R.LAQQGSDLVPAQGGR.T	P53367	ARFP1_HUMAN	Arfaptin-1 (ADP-ribosylation factor-interacting protein 1)	ARFP1
1610,81	1610,009	1611,619	1610,842	0,028	R.DLTDYLMKILTER.G	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1610,842	0,028	R.DLTDYLMKILTER.G	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1610,842	0,028	R.DLTDYLMKILTER.G	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
1611,79	1610,985	1612,596	1611,885	0,094	R.LGAPQQPGPGPPPSRR.G	Q96CX2	KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 (Pfetin) (Predominantly fetal expressed T1 domain)	KCTD12

1612,82	1612,010	1613,623	1612,889	0,073	R.YIYGKPVQGVAYVR.F	P0COL5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
			1612,943	0,127	R.LSAKPAPPKPEPKPR.K	Q15651	HMGN3_HUMAN	High mobility group nucleosome-binding domain-containing protein 3 (Thyroid receptor-interacting protein 7) (TR-interacting protein 7) (TRIP-7)	HMGN3
1613,82	1613,014	1614,628	1613,812	0,008	R.YIEVKSSQEEVR.S	P52597	HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein F, N-terminally processed]	HNRNPF
			1613,851	0,030	K.SLDEISQPAQLKR.S	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1613,774	0,047	R.MGPLGLDHMASSIER.M	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			1613,749	0,072	K.YHTVNGHNCEVR.K.A	P09651	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	HNRNPA1
			1613,903	0,082	K.LVINGNPITIFQER.D	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
			1613,738	0,083	R.GYAFNHSADFETVR.M	P61160	ARP2_HUMAN	Actin-related protein 2 (Actin-like protein 2)	ACTR2
1614,78	1613,975	1615,590	1614,800	0,017	K.VHACGVNPVETYIR.S	Q08257	QOR_HUMAN	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-crystallin)	CRY2
			1614,838	0,055	R.RHVFGESEDLGQK.V	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP1
1614,83	1614,025	1615,639	1614,838	0,006	R.RHVFGESEDLGQK.V	P60174	TPIS_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	TP1
			1614,800	0,032	K.VHACGVNPVETYIR.S	Q08257	QOR_HUMAN	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-crystallin)	CRY2
1615,82	1615,009	1616,624	1615,823	0,006	R.IMGPEEEQMGLLR.V	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIa)	MYH9
			1615,843	0,026	R.AILVDLEPGTMSDVR.S	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1615,775	0,041	K.TGTITTFEAHANMR.V	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
			1615,738	0,079	K.VMEGTVAAQDEFYR.S	P41240	CSK_HUMAN	Tyrosine-protein kinase CSK (EC 2.7.10.2) (C-Src kinase) (Protein-tyrosine kinase CYL)	CSK
1616,80	1615,993	1617,610							
1617,77	1616,964	1618,581	1617,949	0,177	R.AAPLQGMPLGLAPLR.T	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1617,90	1617,089	1618,707	1617,949	0,051	R.AAPLQGMPLGLAPLR.T	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1618,77	1617,957	1619,576	1618,883	0,116	K.LQMEAPHIIVGTPGR.V	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-1 (eIF-4A-1) (eIF4A-1) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
1618,89	1618,077	1619,696	1618,883	0,004	K.LQMEAPHIIVGTPGR.V	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-1 (eIF-4A-1) (eIF4A-1) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
1619,77	1618,958	1620,578							
1620,78	1619,968	1621,589	1620,780	0,001	R.GEEGHDPKEPEQLR.K	P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3
			1620,842	0,064	R.LHFFMPGFAPLTSR.G	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1620,842	0,064	R.LHFFMPGFAPLTSR.G	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
1621,79	1620,980	1622,602							
1622,80	1621,993	1623,616							
1623,78	1622,973	1624,597	1623,793	0,008	K.DVFLGMFLYEYAR.R	P02768	ALBU_HUMAN	Serum albumin	ALB
			1623,837	0,052	R.QGFPNRRVVFQEFR.Q	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIa)	MYH9
			1623,863	0,078	R.LDLAGRDLTDYLMK.I	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			1623,863	0,078	R.LDLAGRDLTDYLMK.I	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1623,863	0,078	R.LDLAGRDLTDYLMK.I	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
1624,81	1623,999	1625,624							
1625,80	1624,986	1626,612	1625,747	0,052	R.DSLLQDGEFSMDLR.T	P07737	PROF1_HUMAN	Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I)	PFN1
			1625,859	0,060	R.JRHHPEHFSGRPR.E	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			1625,942	0,142	R.QATKDAGVIAGLVNLR.I	P0DMV8	HS71A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
1626,78	1625,968	1627,595	1626,834	0,052	R.VIKDFMIQGGDFTR.G	P23284	PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) (CYP-S1) (Cyclophilin B) (Rotamase B) (S-cyclophilin) (SCYLP)	PPIB
1627,78	1626,964	1628,591	1627,846	0,068	R.GYSFVTTAREIVR.D	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1627,921	0,144	R.QATKDAGTIAGLVNLR.I	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8

1628,78	1627,968	1629,596	1628,793	0,011	R.SSGPYGGGGQYFAKPR.N	P09651	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	HNRNPA1
1629,82	1629,002	1630,631	1629,818	0,001	R.KYEMFAQTLQQSR.G	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (155 Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			1629,825	0,009	R.FIAVGYYDDTQFVR.F	P13746	1A11_HUMAN	HLA class I histocompatibility antigen, A-11 alpha chain (MHC class I antigen A*11)	HLA-A
			1629,825	0,009	R.FIAVGYYDDTQFVR.F	P30492	1B54_HUMAN	HLA class I histocompatibility antigen, B-54 alpha chain (Bw-22) (Bw-54) (MHC class I antigen B*54)	HLA-B
			1629,836	0,019	R.GYSFTTTAEREIVR.D	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1629,896	0,080	R.LEPKPQPVAEATPR.S	Q9UHD8	SEPT9_HUMAN	Septin-9 (MLL septin-like fusion protein MSF-A) (MLL septin-like fusion protein) (Ovarian/Breast septin) (Ov/Br septin) (Septin D1)	SEPT9
			1629,695	0,121	R.YGEDNRYGGSGQGGR.G	Q92804	RBP56_HUMAN	TATA-binding protein-associated factor 2N (68 kDa TATA-binding protein-associated factor) (TAF(II)68) (TAFII68) (RNA-binding protein 56)	TAF15
1630,83	1630,011	1631,642	1630,968	0,142	R.HLVPGAPFLQLQVR.E	P0C0L5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
1631,83	1631,014	1632,646	1631,823	0,007	R.AILVDLEPGTMDSVR.S	P07437	TB85_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
1632,90	1632,080	1633,713							
1633,85	1633,036	1634,670							
1634,86	1634,043	1635,678	1634,800	0,061	K.LGDVYVNDAFGTAHR.A	P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1
1635,83	1635,015	1636,651							
1636,84	1636,024	1637,661	1636,834	0,008	R.SELDMLDIREIFR.T	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6
			1636,834	0,008	R.LHFFMPGFAPLTSR.G	P07437	TB85_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1636,834	0,008	R.LHFFMPGFAPLTSR.G	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
1637,83	1637,010	1638,648	1637,771	0,058	R.ESSSHHPGIAEFPSR.G	P02671	FIBA_HUMAN	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	FGA
			1637,934	0,106	R.VFAIPPSFASIFLK.S	P01871	IGHM_HUMAN	Immunoglobulin heavy constant mu (Ig mu chain C region) (Ig mu chain C region BOT) (Ig mu chain C region GAL) (Ig mu chain C region OU)	IGHM
1638,83	1638,008	1639,647	1638,860	0,032	K.SLNNQFASFIDKVR.F	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
1639,85	1639,030	1640,670	1639,837	0,013	R.LDLAGRDLDYLMK.I	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1639,837	0,013	R.LDLAGRDLDYLMK.I	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1639,837	0,013	R.LDLAGRDLDYLMK.I	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			1639,778	0,072	K.DVFLGMFLYEYAR.R	P02768	ALBU_HUMAN	Serum albumin	ALB
			1639,946	0,097	K.KVPQVSTPTLVEVSR.N	P02768	ALBU_HUMAN	Serum albumin	ALB
1640,88	1640,055	1641,696	1640,786	0,089	R.DLAKDITSDTSGDFR.N	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
			1641,684	0,809	R.DYGHSSSRDDYPSR.G	P38159	RBMX_HUMAN	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX
1641,83	1641,004	1642,646	1641,867	0,042	K.ITPNLAEFAFSLYR.Q	P01009	A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiproteinase) (Serp1 A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1
			1641,769	0,056	K.AGDFLEANYMNLQR.S	P01024	CO3_HUMAN	Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
			1641,744	0,081	R.DSLLDQGEFSMDLR.T	P07737	PROF1_HUMAN	Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I)	PFN1
			1641,684	0,141	R.DYGHSSSRDDYPSR.G	P38159	RBMX_HUMAN	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX
1642,81	1641,992	1643,635							
1643,81	1642,984	1644,628	1643,843	0,037	R.AQLGGPEAAKSDETAAK.-	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	HSPB1
1644,83	1644,005	1645,650	1644,823	0,005	R.KFYGPEGPYGVFAGR.D	O00264	PGRC1_HUMAN	Membrane-associated progesterone receptor component 1 (mPR) (Dap1) (IPA)	PGRMC1

1645,77	1644,947	1646,592	1644,817	0,011	K.QEYDESGPSIVHRK.C	Q658J3	POTEE_HUMAN	POTE ankryrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			1644,817	0,011	K.QEYDESGPSIVHRK.C	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1645,784	0,015	R.LDNRYQPMEPNPR.V	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
			1645,816	0,046	R.IFVEESIYDEFVR.R	P00352	AL1A1_HUMAN	Retinal dehydrogenase 1 (RALDH 1) (Raldh1) (EC 1.2.1.-) (EC 1.2.1.36) (ALDH-E1) (ALHDI) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic)	ALDH1A1
			1645,858	0,088	R.FISVGYVDDTQFVR.F	P30460	1B08_HUMAN	HLA class I histocompatibility antigen, B-8 alpha chain (MHC class I antigen B*8)	HLA-B
1645,85	1645,027	1646,673	1645,858	0,008	R.FISVGYVDDTQFVR.F	P30460	1B08_HUMAN	HLA class I histocompatibility antigen, B-8 alpha chain (MHC class I antigen B*8)	HLA-B
			1645,816	0,034	R.IFVEESIYDEFVR.R	P00352	AL1A1_HUMAN	Retinal dehydrogenase 1 (RALDH 1) (Raldh1) (EC 1.2.1.-) (EC 1.2.1.36) (ALDH-E1) (ALHDI) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic)	ALDH1A1
			1645,784	0,065	R.LDNRYQPMEPNPR.V	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
1646,82	1645,992	1647,639	1646,816	0,001	R.DVWGIEGPIDAAFR.I	P04004	VTNC_HUMAN	Vitronectin (VN) (S-protein) (Serum-spreading factor) (V75) [Cleaved into: Vitronectin V65 subunit; Vitronectin V10 subunit; Somatomedin-B]	VTN
			1646,818	0,003	R.LQSIGTENTENRR.F	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
1647,86	1647,035	1648,682	1647,834	0,025	R.NFILDQTNVSAQAQR.R	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
1648,83	1648,009	1649,658	1648,810	0,023	K.ALSRQEMQEVQSSR.S	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
1649,82	1648,994	1650,644	1649,818	0,001	R.HNYGVGESFTVQRR.V	Q9TQE0	2B19_HUMAN	HLA class II histocompatibility antigen, DRB1-9 beta chain (MHC class II antigen DRB1*9) (DR-9) (DR9)	HLA-DRB1
			1649,836	0,017	K.TQAYQDQKPGTSGLR.K	P36871	PGM1_HUMAN	Phosphoglucomutase-1 (PGM 1) (EC 5.4.2.2) (Glucose phosphomutase 1)	PGM1
			1649,855	0,035	K.VAVNDAHLQVNH.R	P17931	LEG3_HUMAN	Galectin-3 (Gal-3) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Galactose-specific lectin 3) (Galactoside-binding protein) (GALBP) (IgE-binding protein) (L-31) (Laminin-binding protein) (Lectin L-29) (Mac-2 antigen)	LGALS3
1650,83	1650,008	1651,659	1649,855	0,035	R.GLKYQEGGVESAFAHK.T	P40121	CAPG_HUMAN	Macrophage-capping protein (Actin regulatory protein CAP-G)	CAPG
			1650,853	0,020	R.EAEYFELPELVRR.L	Q96CX2	KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 (Pfetin) (Predominantly fetal expressed T1 domain)	KCTD12
			1650,920	0,086	R.LVLEVAQHLGESTVR.T	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
1651,77	1650,946	1652,598	1651,787	0,015	R.TVPFCSTFAAFTR.A	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
			1651,755	0,017	R.SSFDEMLPGTHFQR.V	Q02218	ODO1_HUMAN	2-oxoglutarate dehydrogenase, mitochondrial (EC 1.2.4.2) (2-oxoglutarate dehydrogenase complex component E1) (OGDC-E1) (Alpha-ketoglutarate dehydrogenase)	OGDH
			1651,859	0,086	K.NMQNVEHVPLSLDR.A	P20618	PSB1_HUMAN	Proteasome subunit beta type-1 (EC 3.4.25.1) (Macropain subunit C5) (Multicatalytic endopeptidase complex subunit C5) (Proteasome component C5) (Proteasome gamma chain)	PSMB1
1651,86	1651,037	1652,689	1651,859	0,004	K.NMQNVEHVPLSLDR.A	P20618	PSB1_HUMAN	Proteasome subunit beta type-1 (EC 3.4.25.1) (Macropain subunit C5) (Multicatalytic endopeptidase complex subunit C5) (Proteasome component C5) (Proteasome gamma chain)	PSMB1
			1651,787	0,075	R.TVPFCSTFAAFTR.A	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
			1651,755	0,108	R.SSFDEMLPGTHFQR.V	Q02218	ODO1_HUMAN	2-oxoglutarate dehydrogenase, mitochondrial (EC 1.2.4.2) (2-oxoglutarate dehydrogenase complex component E1) (OGDC-E1) (Alpha-ketoglutarate dehydrogenase)	OGDH
1652,84	1652,010	1653,663	1652,794	0,043	R.LGDLYEEMRELR.R	P08670	VIME_HUMAN	Vimentin	VIM
			1652,885	0,048	R.GQAAVQQLQAEGLSPR.F	P16152	CBR1_HUMAN	Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (15-hydroxyprostaglandin dehydrogenase [NADP(+)]) (EC 1.1.1.197) (NADPH-dependent carbonyl reductase 1) (Prostaglandin 9-ketoreductase) (Prostaglandin-E(2) 9-reductase) (EC 1.1.1.189) (Short chain dehydrogenase/reductase family 21C member 1)	CBR1
			1652,762	0,075	K.IFRDGEAGAYDGRP.T	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (Erp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (Erp60)	PDIA3
1653,83	1652,998	1654,652							
1654,84	1654,014	1655,669							

1655,80	1654,968	1656,624	1655,783	0,013	K.HEERQDEHGYSR.C	P04792	HSPB1_HUMAN	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	HSPB1
			1655,953	0,156	R.VLTVINQTKENLR.K	P42766	RL35_HUMAN	60S ribosomal protein L35 (Large ribosomal subunit protein uL29)	RPL35
1656,82	1655,987	1657,644							
1657,82	1656,995	1658,653							
1658,82	1657,995	1659,654	1658,915	0,090	R.AAVENLPTFLVELSR.V	Q14974	IMB1_HUMAN	Importin subunit beta-1 (Importin-90) (Karyopherin subunit beta-1) (Nuclear factor p97) (Pore targeting complex 97 kDa subunit) (PTAC97)	KPNB1
1659,81	1658,978	1660,638	1659,793	0,015	R.LYGSSVSFADDFVR.S	P50454	SERPH_HUMAN	Serpin H1 (47 kDa heat shock protein) (Arsenic-transactivated protein 3) (AsTP3) (Cell proliferation-inducing gene 14 protein) (Collagen-binding protein) (Colligin) (Rheumatoid arthritis-related antigen RA-A47)	SERPINH1
			1659,824	0,016	R.AGEAGKLEEVQMQLR.A	Q9BR76	COR1B_HUMAN	Coronin-1B (Coronin-2)	CORO1B
			1659,894	0,087	R.ATSFLLALEPELEAR.L	P04843	RPN1_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 (Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit) (Ribophorin I) (RPN-I) (Ribophorin-1)	RPN1
1660,83	1659,999	1661,660							
1661,85	1661,015	1662,677							
1662,84	1662,012	1663,675							
1663,75	1662,921	1664,585	1663,817	0,064	K.TPAQFDADELRAAMK.G	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
1663,86	1663,029	1664,692	1663,817	0,043	K.TPAQFDADELRAAMK.G	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
1664,81	1663,975	1665,640	1664,761	0,046	K.MDATANDVSPYEVVR.G	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	PDIA3
1665,82	1664,984	1666,650	1665,825	0,009	R.YEDFSNLGTTLLR.L	P22695	QCR2_HUMAN	Cytochrome b-c1 complex subunit 2, mitochondrial (Complex III subunit 2) (Core protein II) (Ubiquinol-cytochrome-c reductase complex core protein 2)	UQCRC2
1666,83	1665,992	1667,659	1666,785	0,041	R.DWHGVPGQVDAAMAGR.I	P04004	VTNC_HUMAN	Vitronectin (VN) (S-protein) (Serum-spreading factor) (V75) [Cleaved into: Vitronectin V65 subunit; Vitronectin V10 subunit; Somatomedin-B]	VTN
1667,82	1666,990	1668,658	1667,835	0,012	R.SNAQRQDIAFAYQR.R	P07355	ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	ANXA2
			1667,803	0,021	K.IFQKGESVVDYDGGRT.T	Q15084	PDIA6_HUMAN	Protein disulfide-isomerase A6 (EC 5.3.4.1) (Endoplasmic reticulum protein 5) (ER protein 5) (ERp5) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)	PDIA6
1668,80	1667,967	1669,635	1668,859	0,058	K.SLEYDLISFNQIAR.L	P51884	LUM_HUMAN	Lumican (Keratan sulfate proteoglycan lumican) (KSPG lumican)	LUM
1669,85	1669,012	1670,682	1669,893	0,046	K.VLGAFSGLAHLNLK.G	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
			1669,893	0,046	K.VLGAFSGLAHLNLK.G	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			1669,913	0,066	R.VAGGPQMIQLSLDGKR.L	Q13228	SBP1_HUMAN	Methanethiol oxidase (MTO) (EC 1.8.3.4) (56 kDa selenium-binding protein) (SBP56) (SP56) (Selenium-binding protein 1)	SELENBP1
1670,79	1669,957	1671,627	1670,826	0,034	R.SAPPTRGPPPSYGGSSR.Y	P38159	RBMX_HUMAN	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX
1671,81	1670,969	1672,641							
1672,81	1671,976	1673,649							
1673,84	1673,001	1674,675	1673,898	0,060	K.VQQTQVDLFGRAPSK.A	P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9
1674,85	1674,011	1675,685	1674,847	0,001	K.LQPLDFKENAQSR.A	P01008	ANT3_HUMAN	Antithrombin-III (ATIII) (Serpin C1)	SERPINC1
1675,83	1674,995	1676,671	1675,856	0,023	K.FSHEEIAMATVTLAR.R	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
			1675,801	0,032	K.GAEEMETVIPVDVMR.R	Q99497	PARK7_HUMAN	Protein/nucleic acid deglycase DJ-1 (EC 3.1.2.-) (EC 3.5.1.-) (EC 3.5.1.124) (Maillard deglycase) (Oncogene DJ1) (Parkinson disease protein 7) (Parkinsonism-associated deglycase) (Protein DJ-1) (DJ-1)	PARK7
			1675,747	0,086	K.ATAGDTHLGGEDFDNR.L	P0DMV8	H571A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
1676,84	1675,998	1677,675							
1677,82	1676,983	1678,660	1677,900	0,079	M.VLLESEQFLTELTR.L	P37108	SRP14_HUMAN	Signal recognition particle 14 kDa protein (SRP14) (18 kDa Alu RNA-binding protein)	SRP14
1678,85	1678,009	1679,688	1678,818	0,031	K.QMEQISQFLQAAER.Y	P37802	TAGL2_HUMAN	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	TAGLN2
			1678,816	0,032	R.RTVQSLEILDLSMR.N	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18

			1678,918	0,069	R.KGTDVNVFNTILTR.S	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
1679,83	1678,991	1680,671	1679,929	0,098	K.EMVELPLRHPALFK.A	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (155 Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
1680,76	1679,919	1681,600	1680,949	0,189	R.YRVPDVLVADPPPIAR.L	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			1679,929	0,830	K.EMVELPLRHPALFK.A	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (155 Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
1680,89	1680,048	1681,728	1680,949	0,061	R.YRVPDVLVADPPPIAR.L	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1681,83	1680,986	1682,668	1681,905	0,078	M.APSVPAAEPEYKGI.R.A	P54819	KAD2_HUMAN	Adenylate kinase 2, mitochondrial (AK 2) (EC 2.7.4.3) (ATP-AMP transphosphorylase 2) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) [Cleaved into: Adenylate kinase 2, mitochondrial, N-terminally processed]	AK2
1682,78	1681,937	1683,620	1682,961	0,183	K.IHLUSTQSAIPYALR.V	P02679	FIBG_HUMAN	Fibrinogen gamma chain	FGG
1682,91	1682,065	1683,748	1682,961	0,055	K.IHLUSTQSAIPYALR.V	P02679	FIBG_HUMAN	Fibrinogen gamma chain	FGG
1683,85	1683,012	1684,696	1684,695	0,840	R.YDDYSSSRDGYGGS.R.D	P38159	RBMX_HUMAN	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX
1684,84	1684,002	1685,686	1684,775	0,070	K.HTGPNSPDTANDGFVR.L	P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 (hnRNP H2) (FTP-3) (Heterogeneous nuclear ribonucleoprotein H') (hnRNP H') [Cleaved into: Heterogeneous nuclear ribonucleoprotein H2, N-terminally processed]	HNRNPH2
			1684,775	0,070	K.HTGPNSPDTANDGFVR.L	P31943	HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H (hnRNP H) [Cleaved into: Heterogeneous nuclear ribonucleoprotein H, N-terminally processed]	HNRNPH1
			1684,695	0,149	R.YDDYSSSRDGYGGS.R.D	P38159	RBMX_HUMAN	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX
1685,84	1685,001	1686,687	1685,865	0,020	K.HSGNITFDEIVNIAR.Q	P30050	RL12_HUMAN	60S ribosomal protein L12 (Large ribosomal subunit protein uL11)	RPL12
1686,83	1685,982	1687,669	1686,828	0,002	R.QNLFQEAEEFLYR.F	Q9UL46	PSME2_HUMAN	Proteasome activator complex subunit 2 (11S regulator complex subunit beta) (REG-beta) (Activator of multicatalytic protease subunit 2) (Proteasome activator 28 subunit beta) (PA28b) (PA28beta)	PSME2
1687,84	1686,995	1688,683	1687,785	0,053	K.GTVRPANDFNPDADAK.A	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6
			1687,917	0,079	R.IIINEPTAAAIAYGLDR.T	P0DMV8	HS71A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
1688,84	1687,995	1689,684	1688,832	0,008	R.VEVERDNLAEDIMR.L	P08670	VIME_HUMAN	Vimentin	VIM
			1688,893	0,053	R.QVLLSEPEEAALYR.G	P13798	ACPH_HUMAN	Acylamino-acid-releasing enzyme (AARE) (EC 3.4.19.1) (Acyl-peptide hydrolase) (APH) (Acylaminoacyl-peptidase) (Oxidized protein hydrolase) (OPH)	APEH
1689,86 1690,83 1691,85	1689,017 1689,984 1690,999	1690,707 1691,675 1692,691	1691,891	0,046	K.YNQLLRIEEELGSK.A	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
1692,39	1691,541	1693,233	1691,891	0,496	K.YNQLLRIEEELGSK.A	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			1692,902	0,515	R.HLQLAIRNDEELNK.L	Q6FI13	H2A2A_HUMAN	Histone H2A type 2-A (Histone H2A.2) (Histone H2A/o)	HIST2H2AA3; HIST2H2AA4
			1692,902	0,515	R.HLQLAIRNDEELNK.L	Q93077	H2A1C_HUMAN	Histone H2A type 1-C (Histone H2A/I)	HIST1H2AC
			1692,902	0,515	R.HLQLAIRNDEELNK.L	P16104	H2AX_HUMAN	Histone H2AX (H2a/x) (Histone H2A.X)	H2AFX
1692,85	1692,001	1693,694	1692,902	0,055	R.HLQLAIRNDEELNK.L	Q6FI13	H2A2A_HUMAN	Histone H2A type 2-A (Histone H2A.2) (Histone H2A/o)	HIST2H2AA3; HIST2H2AA4
			1692,902	0,055	R.HLQLAIRNDEELNK.L	Q93077	H2A1C_HUMAN	Histone H2A type 1-C (Histone H2A/I)	HIST1H2AC
			1692,902	0,055	R.HLQLAIRNDEELNK.L	P16104	H2AX_HUMAN	Histone H2AX (H2a/x) (Histone H2A.X)	H2AFX
1693,47	1692,621	1694,314	1692,902	0,565	R.HLQLAIRNDEELNK.L	Q6FI13	H2A2A_HUMAN	Histone H2A type 2-A (Histone H2A.2) (Histone H2A/o)	HIST2H2AA3; HIST2H2AA4
			1692,902	0,565	R.HLQLAIRNDEELNK.L	Q93077	H2A1C_HUMAN	Histone H2A type 1-C (Histone H2A/I)	HIST1H2AC
			1692,902	0,565	R.HLQLAIRNDEELNK.L	P16104	H2AX_HUMAN	Histone H2AX (H2a/x) (Histone H2A.X)	H2AFX
1693,85 1694,85	1693,007 1694,000	1694,701 1695,694	1694,862	0,015	K.NAVITVPAYFNDSQR.Q	P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9

			1694,707	0,140	R.NQGGYGGSSSSSYGSGR.R	P09651	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	HNRNPA1
1695,83	1694,979	1696,675	1695,755	0,071	R.FAQPGSFYEYAMR.W	Q15233	NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrb)) (p54nrb)	NONO
1696,84	1695,993	1697,690	1696,844	0,002	R.KLEVEANNAFDQYR.D	P47756	CAPZB_HUMAN	F-actin-capping protein subunit beta (CapZ beta)	CAPZB
			1696,823	0,019	R.YFTWDPSTRFPQPR.T	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1697,84	1696,993	1698,691	1697,789	0,053	R.GYFEYIEENKYSR.A	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
1698,83 1699,86 1700,85	1697,983 1699,011 1700,711 1699,998 1701,698		1700,757	0,091	K.FNADEFEDMVAEKR.L	P27635	RL10_HUMAN	60S ribosomal protein L10 (Laminin receptor homolog) (Large ribosomal subunit protein uL16) (Protein QM) (Ribosomal protein L10) (Tumor suppressor QM)	RPL10
1701,72	1700,866	1702,568	1701,912	0,195	R.AVFVDLEPTVIDEVR.T	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
1701,89	1701,042	1702,744	1701,912	0,019	R.AVFVDLEPTVIDEVR.T	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
1702,73	1701,874	1703,577	1702,936 1701,912	0,210 0,814	K.VKEEIEAFVQELR.K R.AVFVDLEPTVIDEVR.T	P50552 P68363	VASP_HUMAN TBA1B_HUMAN	Vasodilator-stimulated phosphoprotein (VASP) Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	VASP TUBA1B
1702,89	1702,035	1703,737	1702,936	0,049	K.VKEEIEAFVQELR.K	P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP)	VASP
1703,76	1702,909	1704,613	1703,817	0,056	R.SDSFENPVLQHFHR.N	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	XRCC6
			1703,842	0,082	K.TQEQLALEMAELTAR.I	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			1703,944	0,184	M.ASAVSPANLPAVLLQPR.W	P51610	HCFC1_HUMAN	Host cell factor 1 (HCF) (HCF-1) (C1 factor) (CFF) (VCAF) (VP16 accessory protein) [Cleaved into: HCF N-terminal chain 1; HCF N-terminal chain 2; HCF N-terminal chain 3; HCF N-terminal chain 4; HCF N-terminal chain 5; HCF N-terminal chain 6; HCF C-terminal chain 1; HCF C-terminal chain 2; HCF C-terminal chain 3; HCF C-terminal chain 4; HCF C-terminal chain 5; HCF C-terminal chain 6]	HCFC1
			1703,944	0,184	R.EMKPVIFLDVFLPR.V	P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	PRKDC
			1703,957	0,197	K.IILLANFLAQTEALMR.G	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
			1702,936	0,825	K.VKEEIEAFVQELR.K	P50552	VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP)	VASP
1703,85	1702,997	1704,701	1703,842	0,007	K.TQEQLALEMAELTAR.I	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			1703,817	0,033	R.SDSFENPVLQHFHR.N	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	XRCC6
			1703,944	0,095	M.ASAVSPANLPAVLLQPR.W	P51610	HCFC1_HUMAN	Host cell factor 1 (HCF) (HCF-1) (C1 factor) (CFF) (VCAF) (VP16 accessory protein) [Cleaved into: HCF N-terminal chain 1; HCF N-terminal chain 2; HCF N-terminal chain 3; HCF N-terminal chain 4; HCF N-terminal chain 5; HCF N-terminal chain 6; HCF C-terminal chain 1; HCF C-terminal chain 2; HCF C-terminal chain 3; HCF C-terminal chain 4; HCF C-terminal chain 5; HCF C-terminal chain 6]	HCFC1
			1703,944	0,095	R.EMKPVIFLDVFLPR.V	P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	PRKDC

			1703,957	0,108	K.ILLANFLAQTEALMR.G	P06744	G6PI_HUMAN	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	GPI
1704,86 1705,86	1704,004 1705,008	1705,709 1706,714	1705,924	0,062	K.GATYGKPVHHGVNQLK.F	P61313	RL15_HUMAN	60S ribosomal protein L15 (Large ribosomal subunit protein eL15)	RPL15
1706,75	1705,900	1707,607	1706,780 1705,924	0,027 0,830	K.HSGQFTDEYLPEQR.S K.GATYGKPVHHGVNQLK.F	Q14112 P61313	NID2_HUMAN RL15_HUMAN	Nidogen-2 (NID-2) (Osteonidogen) 60S ribosomal protein L15 (Large ribosomal subunit protein eL15)	NID2 RPL15
1707,78	1706,924	1708,631	1707,822	0,044	K.YVMLPVADQDQCIR.H	P00738	HPT_HUMAN	Haptoglobin (Zonulin) [Cleaved into: Haptoglobin alpha chain; Haptoglobin beta chain]	HP
			1707,874	0,096	R.VLSAPPHFHFGQTNR.T	P26641	EF1G_HUMAN	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma)	EEF1G
1708,77 1709,54	1707,918 1708,684	1709,627 1710,394	1709,925	0,386	K.SKINVNEIFYDLVR.Q	P61224	RAP1B_HUMAN	Ras-related protein Rap-1b (GTP-binding protein smg p21B)	RAP1B
1709,80	1708,943	1710,653	1709,925	0,128	K.SKINVNEIFYDLVR.Q	P61224	RAP1B_HUMAN	Ras-related protein Rap-1b (GTP-binding protein smg p21B)	RAP1B
1710,56	1709,710	1711,420	1709,925	0,640	K.SKINVNEIFYDLVR.Q	P61224	RAP1B_HUMAN	Ras-related protein Rap-1b (GTP-binding protein smg p21B)	RAP1B
1710,83 1711,83	1709,979 1710,970	1711,690 1712,682	1711,773	0,053	K.SYSCQVTHEGSTVEK.T	P0DOY3	IGLC3_HUMAN	Immunoglobulin lambda constant 3 (Ig lambda chain C region DOT) (Ig lambda chain C region NEWM) (Ig lambda-3 chain C regions)	IGLC3
			1711,902	0,076	K.HVLFTGVGPEHTYR.S	P04216	THY1_HUMAN	Thy-1 membrane glycoprotein (CDw90) (Thy-1 antigen) (CD antigen CD90)	THY1
1712,82	1711,961	1713,674	1712,865	0,048	K.FLVVYANFDEKDPR.T	P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GD12
			1712,881	0,063	K.EVNKFQMAYSNLLR.A	P37108	SRP14_HUMAN	Signal recognition particle 14 kDa protein (SRP14) (18 kDa Alu RNA-binding protein)	SRP14
1713,82	1712,962	1714,676	1713,785	0,034	R.SEYDRGVNTFSPEGRL	P28066	PSA5_HUMAN	Proteasome subunit alpha type-5 (EC 3.4.25.1) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta chain) (Proteasome zeta chain)	PSMA5
			1714,667	0,848	K.MGGMEGPFGGGMENMGR.F	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
1714,83	1713,974	1715,689	1714,667	0,164	K.MGGMEGPFGGGMENMGR.F	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
1715,73 1715,86 1716,83 1717,69 1717,85 1718,88	1714,871 1715,000 1715,968 1716,827 1716,989 1718,018	1716,587 1716,716 1717,685 1718,545 1718,707 1719,737	1718,877	0,000	R.NLDIERPTYNLNR.L	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
1719,49	1718,629	1720,349	1719,913	0,424	K.VYVGNLGTGAGKGELER.A	Q16629	SRSF7_HUMAN	Serine/arginine-rich splicing factor 7 (Splicing factor 9G8) (Splicing factor, arginine/serine-rich 7)	SRSF7
			1718,877	0,612	R.NLDIERPTYNLNR.L	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
1719,85	1718,985	1720,705	1719,913	0,068	K.VYVGNLGTGAGKGELER.A	Q16629	SRSF7_HUMAN	Serine/arginine-rich splicing factor 7 (Splicing factor 9G8) (Splicing factor, arginine/serine-rich 7)	SRSF7
1720,84	1719,984	1721,705	1720,775	0,069	R.AYYEFREEAYHSR.S	Q1KMD3	HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 2 (Scaffold-attachment factor A2) (SAF-A2)	HNRNPUL2
1721,83 1722,85	1720,971 1721,988	1722,693 1723,711	1722,860	0,011	R.VFDKEGNGTVMGAEIR.H	P60660	MYL6_HUMAN	Myosin light polypeptide 6 (17 kDa myosin light chain) (LC17) (Myosin light chain 3) (MLC-3) (Myosin light chain alkali 3) (Myosin light chain A3) (Smooth muscle and nonmuscle myosin light chain alkali 6)	MYL6
			1722,824	0,026	R.GLGGEVPGSHQPDOPYR.Q	Q6UW68	TM205_HUMAN	Transmembrane protein 205	TMEM205
1723,76	1722,897	1724,621	1723,917	0,158	R.IPWFAQPIIYDIR.A	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
1723,90	1723,036	1724,760	1723,917	0,020	R.IPWFAQPIIYDIR.A	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
1724,77	1723,905	1725,630	1724,885	0,117	R.QAVTNPNNTFYATKR.L	P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9
			1723,917	0,850	R.IPWFAQPIIYDIR.A	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
1724,92	1724,059	1725,784	1724,885	0,037	R.QAVTNPNNTFYATKR.L	P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9
1725,46	1724,598	1726,323	1724,885	0,575	R.QAVTNPNNTFYATKR.L	P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9

1725,71	1724,851	1726,576	1724,885	0,829	R.QAVTNPNNTFYATKRL	P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9
1725,88 1726,65	1725,014 1725,792	1726,740 1727,518	1726,766 1726,942	0,111 0,287	R.FGGNPGGFGNQGGFGNSR.G R.EVLEKQPVLVSQTEAR.D	Q13148 P28070	TADBP_HUMAN PSB4_HUMAN	TAR DNA-binding protein 43 (TDP-43) Proteasome subunit beta type-4 (EC 3.4.25.1) (26 kDa prosomal protein) (HsBPROS26) (PROS-26) (Macropain beta chain) (Multicatalytic endopeptidase complex beta chain) (Proteasome beta chain) (Proteasome chain 3) (HsN3)	TARDBP PSMB4
1726,85	1725,988	1727,715	1726,766 1726,942	0,086 0,091	R.FGGNPGGFGNQGGFGNSR.G R.EVLEKQPVLVSQTEAR.D	Q13148 P28070	TADBP_HUMAN PSB4_HUMAN	TAR DNA-binding protein 43 (TDP-43) Proteasome subunit beta type-4 (EC 3.4.25.1) (26 kDa prosomal protein) (HsBPROS26) (PROS-26) (Macropain beta chain) (Multicatalytic endopeptidase complex beta chain) (Proteasome beta chain) (Proteasome chain 3) (HsN3)	TARDBP PSMB4
1727,84	1726,977	1728,705	1727,845	0,004	R.TERFGQGGAGPVGQGQPR.G	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
1728,74	1727,879	1729,608	1728,886	0,142	R.ALVHERDEAAYGELR.A	Q9UL46	PSME2_HUMAN	Proteasome activator complex subunit 2 (11S regulator complex subunit beta) (REG-beta) (Activator of multicatalytic protease subunit 2) (Proteasome activator 28 subunit beta) (PA28b) (PA28beta)	PSME2
1728,82	1727,952	1729,681	1728,886	0,069	R.ALVHERDEAAYGELR.A	Q9UL46	PSME2_HUMAN	Proteasome activator complex subunit 2 (11S regulator complex subunit beta) (REG-beta) (Activator of multicatalytic protease subunit 2) (Proteasome activator 28 subunit beta) (PA28b) (PA28beta)	PSME2
1729,36	1728,498	1730,227	1728,886	0,477	R.ALVHERDEAAYGELR.A	Q9UL46	PSME2_HUMAN	Proteasome activator complex subunit 2 (11S regulator complex subunit beta) (REG-beta) (Activator of multicatalytic protease subunit 2) (Proteasome activator 28 subunit beta) (PA28b) (PA28beta)	PSME2
1729,82 1730,85	1728,951 1729,984	1730,681 1731,715	1730,755 1730,737	0,095 0,113	R.YYDSRPGGYGYGYGR.S R.GDFSSANNRDNTYNR.V	P98179 P02671	RBM3_HUMAN FIBA_HUMAN	RNA-binding protein 3 (RNA-binding motif protein 3) (RNPL) Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	RBM3 FGA
1731,74 1731,93 1732,74 1732,88 1734,00	1730,874 1731,063 1731,869 1732,014 1733,747	1732,605 1732,795 1733,602 1733,747 1734,868	1733,973 1734,825	0,027 0,825	R.LRNEDLGLPLFPPE.R R.LQDEIQNMKEEMAR.H	P01266 P08670	THYG_HUMAN VIME_HUMAN	Thyroglobulin (Tg) Vimentin	TG VIM
1734,99	1734,126	1735,861	1734,825	0,168	R.LQDEIQNMKEEMAR.H	P08670	VIME_HUMAN	Vimentin	VIM
1735,78	1734,914	1736,650	1735,881 1735,922	0,099 0,139	K.ARPEYMLPVHFYGR.V K.TATPQQAQEVHEKLR.G	P11216 P60174	PYGB_HUMAN TPIS_HUMAN	Glycogen phosphorylase, brain form (EC 2.4.1.1) Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	PYGB TPI1
1735,96	1735,097	1736,833	1735,922 1735,881	0,043 0,083	K.TATPQQAQEVHEKLR.G K.ARPEYMLPVHFYGR.V	P60174 P11216	TPIS_HUMAN PYGB_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase) Glycogen phosphorylase, brain form (EC 2.4.1.1)	TPI1 PYGB
1736,37	1735,501	1737,238	1735,922 1735,881	0,448 0,488	K.TATPQQAQEVHEKLR.G K.ARPEYMLPVHFYGR.V	P60174 P11216	TPIS_HUMAN PYGB_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase) Glycogen phosphorylase, brain form (EC 2.4.1.1)	TPI1 PYGB
1736,80 1736,93 1737,83 1737,91 1738,82	1735,927 1736,060 1736,962 1737,039 1737,947	1737,663 1737,797 1738,700 1738,777 1739,686	1738,953	0,137	R.WVGGEPEIELIAITGGR.I	P48643	TCPE_HUMAN	T-complex protein 1 subunit epsilon (TCP-1-epsilon) (CCT-epsilon)	CCT5
1739,81	1738,938	1740,678	1739,838 1738,953	0,030 0,855	R.YFDTAMSRPRGGEPR.F R.WVGGEPEIELIAITGGR.I	P30460 P48643	1B08_HUMAN TCPE_HUMAN	HLA class I histocompatibility antigen, B-8 alpha chain (MHC class I antigen B*8) T-complex protein 1 subunit epsilon (TCP-1-epsilon) (CCT-epsilon)	HLA-B CCT5
1740,83	1739,959	1741,700	1740,835 1740,920 1740,955	0,005 0,090 0,126	K.DLFVPACLETGEYAR.L R.LSFQHDPETSVLVLR.K R.AIVAIENPADVSVISSR.N	P01266 Q14697 P08865	THYG_HUMAN GANAB_HUMAN RSSA_HUMAN	Thyroglobulin (Tg) Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha) 40S ribosomal protein SA (37 kDa laminin receptor precursor) (37LRP) (37/67 kDa laminin receptor) (LRP/LR) (67 kDa laminin receptor) (67LR) (Colon carcinoma laminin-binding protein) (Laminin receptor 1) (LamR) (Laminin-binding protein precursor p40) (LBP/p40) (Multidrug resistance-associated protein MGR1-Ag) (NEM/1CHD4) (Small ribosomal subunit protein uS2)	TG GANAB RPSA
1741,85 1742,76	1740,976 1741,891	1742,717 1743,634	1742,842 1742,905 1743,030	0,080 0,142 0,267	R.YLAEKYWDVAEAR.K R.HPYFYAPELLFFAK.R R.LQPVVLQPLSPGVGGKR.D	P13639 P02768 P12111	EF2_HUMAN ALBU_HUMAN CO6A3_HUMAN	Elongation factor 2 (EF-2) Serum albumin Collagen alpha-3(VI) chain	EEF2 ALB COL6A3

1743,77	1742,899	1744,643	1743,819	0,048	K.AMGIMNSFVNDIFER.I	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
			1743,819	0,048	K.AMGIMNSFVNDIFER.I	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
			1743,030	0,741	R.LQPVLQPLPSPGVGGKR.D	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			1742,905	0,867	R.HPYFYAPELLFFAK.R	P02768	ALBU_HUMAN	Serum albumin	ALB
1743,80	1742,925	1744,669	1743,819	0,022	K.AMGIMNSFVNDIFER.I	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
			1743,819	0,022	K.AMGIMNSFVNDIFER.I	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
			1743,030	0,767	R.LQPVLQPLPSPGVGGKR.D	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
1744,79	1743,916	1745,661	1744,882	0,093	K.ILTERGYSFTTTAER.E	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
1745,78	1744,910	1746,656							
1745,81	1744,933	1746,678							
1746,82	1745,948	1747,695	1746,913	0,091	R.IAQSDYIPTQQDVL.R	P04899	GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2 (Adenylate cyclase-inhibiting G alpha protein)	GNAI2
1747,84	1746,967	1748,715	1747,888	0,046	R.IMEGPAFNFLDAPAVR.V	P11177	ODPB_HUMAN	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial (PDHE1-B) (EC 1.2.4.1)	PDHB
			1747,945	0,103	K.AIKVEQATKPSFESGR.R	P38159	RBMX_HUMAN	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX
1748,85	1747,975	1749,724	1748,732	0,117	R.SGGGYGGDRSGGGYSGDR.S	Q92804	RBP56_HUMAN	TATA-binding protein-associated factor 2N (68 kDa TATA-binding protein-associated factor) (TAF(II)68) (TAFII68) (RNA-binding protein 56)	TAF15
1749,86	1748,983	1750,733							
1750,85	1749,979	1751,729							
1751,83	1750,956	1752,707							
1752,34	1751,464	1753,216	1752,841	0,501	R.FTQDTQPHYIYSPR.E	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
			1752,959	0,619	R.YVGGQEHFAHLLIUR.D	P02763	A1AG1_HUMAN	Alpha-1-acid glycoprotein 1 (AGP 1) (Orosomucoid-1) (OMD 1)	ORM1
1752,84	1751,960	1753,713	1752,841	0,005	R.FTQDTQPHYIYSPR.E	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
			1752,959	0,122	R.YVGGQEHFAHLLIUR.D	P02763	A1AG1_HUMAN	Alpha-1-acid glycoprotein 1 (AGP 1) (Orosomucoid-1) (OMD 1)	ORM1
1753,36	1752,482	1754,235	1752,959	0,399	R.YVGGQEHFAHLLIUR.D	P02763	A1AG1_HUMAN	Alpha-1-acid glycoprotein 1 (AGP 1) (Orosomucoid-1) (OMD 1)	ORM1
			1752,841	0,517	R.FTQDTQPHYIYSPR.E	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
1753,85	1752,978	1754,731							
1754,83	1753,949	1755,704	1754,839	0,013	R.SYQDPSNAQFLESIR.R	Q9UNZ2	NSF1C_HUMAN	NSFL1 cofactor p47 (UBX domain-containing protein 2C) (p97 cofactor p47)	NSFL1C
			1754,886	0,060	R.VFDKDGNGYISAAELR.H	P0DP23	CALM1_HUMAN	Calmodulin-1	CALM1
1754,85	1753,968	1755,723	1754,839	0,006	R.SYQDPSNAQFLESIR.R	Q9UNZ2	NSF1C_HUMAN	NSFL1 cofactor p47 (UBX domain-containing protein 2C) (p97 cofactor p47)	NSFL1C
			1754,886	0,041	R.VFDKDGNGYISAAELR.H	P0DP23	CALM1_HUMAN	Calmodulin-1	CALM1
1755,81	1754,933	1756,689							
1755,91	1755,034	1756,790							
1756,78	1755,905	1757,662							
1756,93	1756,050	1757,807							
1757,95	1757,074	1758,832	1757,940	0,013	K.IFVGGLSPDTPPEKIR.E	Q14103	HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1)	HNRNPD
			1758,783	0,830	R.STAYEDYHHPPPR.M	O43390	HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R)	HNRNPR
1758,91	1758,033	1759,792	1758,783	0,129	R.STAYEDYHHPPPR.M	O43390	HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R)	HNRNPR
1758,95	1758,074	1759,833	1758,783	0,170	R.STAYEDYHHPPPR.M	O43390	HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R)	HNRNPR
			1759,816	0,863	K.AMGIMNSFVNDIFER.I	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
			1759,816	0,863	K.AMGIMNSFVNDIFER.I	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
1759,94	1759,055	1760,815	1759,816	0,119	K.AMGIMNSFVNDIFER.I	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
			1759,816	0,119	K.AMGIMNSFVNDIFER.I	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
			1760,795	0,860	K.YFQFQEEGKEGENR.A	O15144	ARPC2_HUMAN	Actin-related protein 2/3 complex subunit 2 (Arp2/3 complex 34 kDa subunit) (p34-ARC)	ARPC2
1760,90	1760,016	1761,777	1760,795	0,102	K.YFQFQEEGKEGENR.A	O15144	ARPC2_HUMAN	Actin-related protein 2/3 complex subunit 2 (Arp2/3 complex 34 kDa subunit) (p34-ARC)	ARPC2
1761,43	1760,545	1762,306	1760,795	0,630	K.YFQFQEEGKEGENR.A	O15144	ARPC2_HUMAN	Actin-related protein 2/3 complex subunit 2 (Arp2/3 complex 34 kDa subunit) (p34-ARC)	ARPC2
1761,85	1760,971	1762,732							
1762,57	1761,692	1763,455	1762,780	0,207	R.FAQHGTFEYYSQR.W	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
1762,90	1762,019	1763,782	1762,780	0,120	R.FAQHGTFEYYSQR.W	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ

1763,88	1762,995	1764,759	1763,804	0,072	K.LISWYDNEFGYSNR.V	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
1764,72	1763,841	1765,606	1765,880	0,049	R.AVGRLEAVSHTSDMHR.G	Q01518	CAP1_HUMAN	Adenylyl cyclase-associated protein 1 (CAP 1)	CAP1
1764,90	1764,014	1765,779							
1765,83	1764,948	1766,714							
1766,81	1765,929	1767,696	1768,910	0,062	K.GLGTDDETDIITHR.S	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6
1767,82	1766,936	1768,704							
1768,85	1767,964	1769,733							
			1768,924	0,076	R.DREVGIPPEQSLetak.A	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
			1768,992	0,143	K.ALESERPFLAILGGAK.V	P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1
1769,87	1768,985	1770,755	1768,992	0,878	K.ALESERPFLAILGGAK.V	P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1
1770,89	1770,004	1771,775	1771,998	0,090	R.NALGPGLSPELGPLPALR.V	Q8N1G4	LRC47_HUMAN	Leucine-rich repeat-containing protein 47	LRRC47
1771,91	1771,022	1772,794							
1772,89	1772,007	1773,779							
1773,88	1772,998	1774,771	1773,827	0,057	K.AMGIMNSFLNIDIFER.I	Q6DRA6	H2B2D_HUMAN	Putative histone H2B type 2-D	HIST2H2BD
			1773,994	0,109	K.GVALHRPDVYLPPAR.E	P01871	IGHM_HUMAN	Immunoglobulin heavy constant mu (lg mu chain C region) (lg mu chain C region BOT) (lg mu chain C region GAL) (lg mu chain C region OU)	IGHM
1774,88	1773,997	1775,772	1775,937	0,076	R.AQQLLSAGHPGEQIIR.L	P11277	SPTB1_HUMAN	Spectrin beta chain, erythrocytic (Beta-I spectrin)	SPTB
1775,86	1774,973	1776,749							
1775,88	1774,990	1776,766							
			1775,937	0,058	R.AQQLLSAGHPGEQIIR.L	P11277	SPTB1_HUMAN	Spectrin beta chain, erythrocytic (Beta-I spectrin)	SPTB
1776,87	1775,986	1777,763	1776,874	0,001	K.FADLSEANRNNDALR.Q	P08670	VIME_HUMAN	Vimentin	VIM
			1776,878	0,003	R.VFVGEEDEPEAESVTLR.V	Q86UX7	URP2_HUMAN	Fermitin family homolog 3 (Kindlin-3) (MIG2-like protein) (Unc-112-related protein 2)	FERMT3
1777,87	1776,978	1778,755	1777,802	0,065	R.FDIEMSMRGDIFER.I	Q9BYT8	NEUL_HUMAN	Neurolysin, mitochondrial (EC 3.4.24.16) (Angiotensin-binding protein) (Microsomal endopeptidase) (MEP) (Mitochondrial oligopeptidase M) (Neurotensin endopeptidase)	NLN
1778,93	1778,040	1779,819	1778,961	0,031	K.QGGLGPMNIPLVSPKRT	Q06830	PRDX1_HUMAN	Peroxioredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1
			1778,823	0,106	R.QFEDEKANWEAQQR.I	Q16181	SEPT7_HUMAN	Septin-7 (CDC10 protein homolog)	SEPT7
			1778,817	0,113	R.NQYDNDVTWVSPQGR.I	P25786	PSA1_HUMAN	Proteasome subunit alpha type-1 (EC 3.4.25.1) (30 kDa prosomal protein) (PROS-30) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome component C2) (Proteasome nu chain)	PSMA1
1779,94	1779,054	1780,834	1780,812	0,868	R.TDYNASVSVPDSSGPER.I	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
1780,92	1780,030	1781,811	1780,853	0,067	K.VDATEESDLAQYGVGR.G	P07237	PDIA1_HUMAN	Protein disulfide-isomerase (PDI) (EC 5.3.4.1) (Cellular thyroid hormone-binding protein) (Prolyl 4-hydroxylase subunit beta) (p55)	P4HB
			1780,812	0,109	R.TDYNASVSVPDSSGPER.I	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
1781,86	1780,973	1782,755	1782,957	0,096	K.HLEINPDHPIVETLR.Q	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90A81
1782,86	1781,970	1783,753							
1783,87	1782,973	1784,757							
1784,90	1784,008	1785,793	1784,902	0,002	K.LFIGGLSFETTDESLR.S	P09651	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	HNRNPA1
			1784,919	0,019	K.SNYNFEKPFLWLAR.K	P62826	RAN_HUMAN	GTP-binding nuclear protein Ran (Androgen receptor-associated protein 24) (GTPase Ran) (Ras-like protein TC4) (Ras-related nuclear protein)	RAN
			1784,872	0,028	R.YDYQRQRPDSGSISSR.S	P04843	RPN1_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 (Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit) (Ribophorin I) (RPN-I) (Ribophorin-1)	RPN1
1785,91	1785,013	1786,799	1785,924	0,018	R.VMLGETNPADSKPGTIR.G	P22392	NDKB_HUMAN	Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (EC 2.7.4.6) (C-myc purine-binding transcription factor PUF) (Histidine protein kinase NDKB) (EC 2.7.13.3) (nm23-H2)	NME2
			1785,886	0,020	K.FETLQAQAKHGDDLR.N	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7)	KRT7
1786,91	1786,014	1787,801	1786,952	0,044	K.HLEINPDHSIETLR.Q	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
1787,88	1786,989	1788,777							
1788,87	1787,971	1789,760							

1789,86	1788,967	1790,756	1789,819	0,042	R.TFVQEDIYDEFVER.S	P05091	ALDH2_HUMAN	Aldehyde dehydrogenase, mitochondrial (EC 1.2.1.3) (ALDH class 2) (ALDH-E2) (ALDH1)	ALDH2
1790,88	1789,982	1791,773	1790,897 1790,897	0,020 0,020	R.SYELPDGQVITIGNER.F K.SYELPDGQVITIGNER.F	Q562R1 Q6S8J3	ACTBL_HUMAN POTEE_HUMAN	Beta-actin-like protein 2 (Kappa-actin) POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	ACTBL2 POTEE
			1790,897	0,020	K.SYELPDGQVITIGNER.F	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			1790,897	0,020	K.SYELPDGQVITIGNER.F	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1790,899	0,022	R.SEAAHQGVITWNPQR.S	P08575	PTPRC_HUMAN	Receptor-type tyrosine-protein phosphatase C (EC 3.1.3.48) (Leukocyte common antigen) (L-CA) (T200) (CD antigen CD45)	PTPRC
			1791,724	0,847	R.GGSGGSYGSGSGGGYGGSGSR.G	P35527	K1C9_HUMAN	Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9) (Keratin-9) (K9)	KRT9
1791,88	1790,983	1792,775	1791,724	0,155	R.GGSGGSYGSGSGGGYGGSGSR.G	P35527	K1C9_HUMAN	Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9) (Keratin-9) (K9)	KRT9
1792,88 1793,89 1794,92 1795,92 1796,89 1797,89 1798,89 1799,90	1791,986 1792,996 1794,026 1795,021 1795,996 1796,989 1797,986 1798,997	1793,779 1794,790 1795,821 1796,817 1797,793 1798,787 1799,785 1800,797							
1800,91 1801,87	1800,009 1800,973	1801,810 1802,775	1799,904 1801,905	0,007 0,030	K.AYLPVNESFGFTADLR.S R.IFVEESYDEFVRR.S	P13639 P00352	EF2_HUMAN AL1A1_HUMAN	Elongation factor 2 (EF-2) Retinal dehydrogenase 1 (RALDH 1) (RALDH1) (EC 1.2.1.-) (EC 1.2.1.36) (ALDH-E1) (ALDH1) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic)	EEF2 ALDH1A1
			1801,814	0,061	R.LVAGEMGQNEPDQGGQR.G	Q99714	HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2 (EC 1.1.1.35) (17-beta-hydroxysteroid dehydrogenase 10) (17-beta-HSD 10) (EC 1.1.1.51) (2-methyl-3-hydroxybutyryl-CoA dehydrogenase) (MHBD) (3-hydroxy-2-methylbutyryl-CoA dehydrogenase) (EC 1.1.1.178) (3-hydroxyacyl-CoA dehydrogenase type II) (Endoplasmic reticulum-associated amyloid beta-peptide-binding protein) (Mitochondrial ribonuclease P protein 2) (Mitochondrial RNase P protein 2) (Short chain dehydrogenase/reductase family 5C member 1) (Short-chain type dehydrogenase/reductase XH98G2) (Type II HADH)	HSD17B10
			1801,981	0,107	R.NGKPVTTGVSETVFLPR.E	P01903	DRA_HUMAN	HLA class II histocompatibility antigen, DR alpha chain (MHC class II antigen DRA)	HLA-DRA
1801,92	1801,023	1802,825	1801,905	0,019	R.IFVEESYDEFVRR.S	P00352	AL1A1_HUMAN	Retinal dehydrogenase 1 (RALDH 1) (RALDH1) (EC 1.2.1.-) (EC 1.2.1.36) (ALDH-E1) (ALDH1) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic)	ALDH1A1
			1801,981	0,057	R.NGKPVTTGVSETVFLPR.E	P01903	DRA_HUMAN	HLA class II histocompatibility antigen, DR alpha chain (MHC class II antigen DRA)	HLA-DRA
			1801,814	0,110	R.LVAGEMGQNEPDQGGQR.G	Q99714	HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2 (EC 1.1.1.35) (17-beta-hydroxysteroid dehydrogenase 10) (17-beta-HSD 10) (EC 1.1.1.51) (2-methyl-3-hydroxybutyryl-CoA dehydrogenase) (MHBD) (3-hydroxy-2-methylbutyryl-CoA dehydrogenase) (EC 1.1.1.178) (3-hydroxyacyl-CoA dehydrogenase type II) (Endoplasmic reticulum-associated amyloid beta-peptide-binding protein) (Mitochondrial ribonuclease P protein 2) (Mitochondrial RNase P protein 2) (Short chain dehydrogenase/reductase family 5C member 1) (Short-chain type dehydrogenase/reductase XH98G2) (Type II HADH)	HSD17B10
1802,91 1803,89	1802,011 1802,988	1803,814 1804,792	1803,948	0,058	R.NFILDQTNVSAQAQR.K	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
1804,75	1803,843	1805,647	1804,946	0,200	R.AAVPSGASTGIYALELR.D	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			1803,948	0,797	R.NFILDQTNVSAQAQR.K	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
1804,90	1804,000	1805,805	1804,946	0,043	R.AAVPSGASTGIYALELR.D	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
1805,76	1804,859	1806,665	1805,909	0,147	K.NQVAMNPTNTVFDAKR.L	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
			1804,946	0,816	R.AAVPSGASTGIYALELR.D	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
1805,91	1805,005	1806,811	1805,909	0,000	K.NQVAMNPTNTVFDAKR.L	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8

1806,79	1805,883	1807,690	1805,909	0,877	K.NQVAMNPNTNVDKRL	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
1806,93	1806,022	1807,829	1807,790	0,865	R.NSYVAGQYDDAASYQR.L	P11413	G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	G6PD
1807,90	1806,994	1808,802	1807,790	0,107	R.NSYVAGQYDDAASYQR.L	P11413	G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	G6PD
1808,90	1807,992	1809,801	1810,872	0,072	K.YGPIADVSIVYDQQR.R	P62995	TRA2B_HUMAN	Transformer-2 protein homolog beta (TRA-2 beta) (TRA2-beta) (hTRA2-beta) (Splicing factor, arginine/serine-rich 10) (Transformer-2 protein homolog B)	TRA2B
1809,85	1808,942	1810,752		0,206	R.LKVPPAINQFTQALDR.Q	P62424	RL7A_HUMAN	60S ribosomal protein L7a (Large ribosomal subunit protein eL8) (PLA-X polypeptide) (Surfeit locus protein 3)	RPL7A
1809,96	1809,053	1810,863		0,051	R.LKVPPAINQFTQALDR.Q	P62424	RL7A_HUMAN	60S ribosomal protein L7a (Large ribosomal subunit protein eL8) (PLA-X polypeptide) (Surfeit locus protein 3)	RPL7A
1810,80	1809,894	1811,705		0,083	K.YGPIADVSIVYDQQR.R	P62995	TRA2B_HUMAN	Transformer-2 protein homolog beta (TRA-2 beta) (TRA2-beta) (hTRA2-beta) (Splicing factor, arginine/serine-rich 10) (Transformer-2 protein homolog B)	TRA2B
1811,81	1810,907	1812,719	1811,006	0,807	R.LKVPPAINQFTQALDR.Q	P62424	RL7A_HUMAN	60S ribosomal protein L7a (Large ribosomal subunit protein eL8) (PLA-X polypeptide) (Surfeit locus protein 3)	RPL7A
1811,96	1811,054	1812,865	1812,834	0,875	K.LAEQAEYDDMAAAMK.A	P31946	1433B_HUMAN	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHA8
1812,90	1811,990	1813,803	1812,834	0,062	K.LAEQAEYDDMAAAMK.A	P31946	1433B_HUMAN	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHA8
1813,87	1812,962	1814,776	1814,961	0,103	K.NQVALNPQNTVDFDKRL	P0DMV8	H571A_HUMAN	Heat shock 70 kDa protein 1A (Heat shock 70 kDa protein 1) (HSP70-1) (HSP70.1)	HSPA1A
1814,86	1813,951	1815,766		0,004	R.IJMDPNIVGSEHYDVAR.G	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
1815,89	1814,979	1816,795	1815,909	0,022	K.IAQLEEQLDNETKER.Q	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIa)	MYH9
			1816,008	0,121	R.IINEPTAAAIYGLDKR.E	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
1816,85	1815,943	1817,759	1816,008	0,843	R.IINEPTAAAIYGLDKR.E	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
1817,86	1816,948	1818,765	1821,923	0,042	R.RFDEILEASDGMVAR.G	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
1818,86	1817,953	1819,772		0,006	R.AGGENYKEFSELLPNR.Q	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1819,87	1818,956	1820,776		0,512	R.AGGENYKEFSELLPNR.Q	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1820,88	1819,972	1821,793		0,540	R.ETNLSLPLVDTHSKR.T	P08670	VIME_HUMAN	Vimentin	VIM
1821,88	1820,970	1822,792		0,050	R.ETNLSLPLVDTHSKR.T	P08670	VIME_HUMAN	Vimentin	VIM
				0,425	R.ETNLSLPLVDTHSKR.T	P08670	VIME_HUMAN	Vimentin	VIM
1822,87	1821,959	1823,782	1826,850	0,025	K.EVYQQQQYSGSGRGNR.N	Q99729	ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein A/B (hnRNP A/B) (APOBEC1-binding protein 1) (ABBP-1)	HNRNPAB
1823,89	1822,979	1824,802		0,172	R.GIYAYGFEKPSAIQQR.A	P38919	IF4A3_HUMAN	Eukaryotic initiation factor 4A-III (eIF-4A-III) (eIF4A-III) (EC 3.6.4.13) (ATP-dependent RNA helicase DDX48) (ATP-dependent RNA helicase eIF4A-3) (DEAD box protein 48) (Eukaryotic initiation factor 4A-like NUK-34) (Eukaryotic translation initiation factor 4A isoform 3) (Nuclear matrix protein 265) (NMP 265) (hNMP 265) [Cleaved into: Eukaryotic initiation factor 4A-III, N-terminally processed]	EIF4A3
1824,41	1823,496	1825,321		0,172	R.GIYAYGFEKPSAIQQR.A	Q14240	IF4A2_HUMAN	Eukaryotic initiation factor 4A-II (eIF-4A-II) (eIF4A-II) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-2)	EIF4A2
1824,90	1823,986	1825,810		0,172	R.GIYAYGFEKPSAIQQR.A	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-I (eIF-4A-I) (eIF4A-I) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
1825,37	1824,460	1826,286							
1825,90	1824,984	1826,810							
1826,87	1825,961	1827,788							
1827,77	1826,852	1828,679	1827,937	0,172	R.GIYAYGFEKPSAIQQR.A				
			1827,937	0,172	R.GIYAYGFEKPSAIQQR.A				
			1827,937	0,172	R.GIYAYGFEKPSAIQQR.A				

1827,91	1826,995	1828,823	1827,937	0,028	R.GIYAYGFEKPSAIQQR.A	P38919	IF4A3_HUMAN	Eukaryotic initiation factor 4A-III (eIF-4A-III) (eIF4A-III) (EC 3.6.4.13) (ATP-dependent RNA helicase DDX48) (ATP-dependent RNA helicase eIF4A-3) (DEAD box protein 48) (Eukaryotic initiation factor 4A-like NUK-34) (Eukaryotic translation initiation factor 4A isoform 3) (Nuclear matrix protein 265) (NMP 265) (hNMP 265) [Cleaved into: Eukaryotic initiation factor 4A-III, N-terminally processed]	EIF4A3
			1827,937	0,028	R.GIYAYGFEKPSAIQQR.A	Q14240	IF4A2_HUMAN	Eukaryotic initiation factor 4A-II (eIF-4A-II) (eIF4A-II) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-2)	EIF4A2
			1827,937	0,028	R.GIYAYGFEKPSAIQQR.A	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-I (eIF-4A-I) (eIF4A-I) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
1828,88 1829,89 1830,90	1827,963 1828,980 1829,980	1829,792 1830,810 1831,811	1830,871	0,024	R.QLEAEAEQAQRANASR.R	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
1831,89	1830,977	1832,809	1831,917	0,024	K.GAEEMETVIPVDMVRR.A	Q99497	PARK7_HUMAN	Protein/nucleic acid deglycase DJ-1 (EC 3.1.2.-) (EC 3.5.1.-) (EC 3.5.1.124) (Maillard deglycase) (Oncogene DJ1) (Parkinson disease protein 7) (Parkinsonism-associated deglycase) (Protein DJ-1) (DJ-1)	PARK7
			1831,918	0,025	K.SIYGKFEFENFILK.H	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
			1831,970	0,077	K.KTQEQLALEMAELTAR.I	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
1832,83	1831,916	1833,748	1831,970	0,862	K.KTQEQLALEMAELTAR.I	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			1831,918	0,914	K.SIYGKFEFENFILK.H	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
			1831,917	0,915	K.GAEEMETVIPVDMVRR.A	Q99497	PARK7_HUMAN	Protein/nucleic acid deglycase DJ-1 (EC 3.1.2.-) (EC 3.5.1.-) (EC 3.5.1.124) (Maillard deglycase) (Oncogene DJ1) (Parkinson disease protein 7) (Parkinsonism-associated deglycase) (Protein DJ-1) (DJ-1)	PARK7
1832,85	1831,930	1833,763	1831,970	0,876	K.KTQEQLALEMAELTAR.I	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
1833,86	1832,940	1834,774	1833,898	0,041	K.NQLTSNPENTVFDAKR.L	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			1833,903	0,046	K.TYFPHFDLSHGSAQVK.G	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
1834,85 1834,86 1835,86	1833,932 1833,942 1834,947	1835,766 1835,777 1836,783	1835,952	0,088	R.QEPSQGTTFVAVTSILR.V	P01876	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1
1836,87	1835,951	1837,788	1836,797 1835,952	0,073 0,917	R.DGQVINETSQHDDLE.- R.QEPSQGTTFVAVTSILR.V	P08670 P01876	VIME_HUMAN IGHA1_HUMAN	Vimentin Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	VIM IGHA1
1837,87 1838,86	1836,949 1837,941	1838,787 1839,780	1838,957	0,096	K.AQAGEGVRPSPMQLELR.M	O00764	PDXK_HUMAN	Pyridoxal kinase (EC 2.7.1.35) (Pyridoxine kinase)	PDXK
1839,86	1838,940	1840,779	1838,957	0,903	K.AQAGEGVRPSPMQLELR.M	O00764	PDXK_HUMAN	Pyridoxal kinase (EC 2.7.1.35) (Pyridoxine kinase)	PDXK
1840,44 1840,87 1841,38	1839,523 1839,949 1840,462	1841,364 1841,790 1842,303	1841,901	0,518	K.IVYGLDDPASQEIER.G	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
1841,88	1840,961	1842,803	1841,901	0,019	K.IVYGLDDPASQEIER.G	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
1842,88	1841,961	1843,804	1842,885	0,003	K.HEEAPGHRPTTNPASK.F	P21291	CSR1_HUMAN	Cysteine and glycine-rich protein 1 (Cysteine-rich protein 1) (CRP) (CRP1) (Epididymis luminal protein 141) (HEL-141)	CSR1
			1843,089	0,207	R.ILSISADIETIGELKK.I	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
1843,90	1842,978	1844,822	1843,940	0,040	R.INVYNEATGGKYVPR.A	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
			1843,089	0,811	R.ILSISADIETIGELKK.I	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
1844,77	1843,846	1845,691	1843,940	0,828	R.INVYNEATGGKYVPR.A	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
1844,92 1845,82 1845,90 1846,74 1846,92	1844,002 1844,893 1844,973 1845,813 1846,001	1845,846 1846,738 1846,819 1847,659 1847,848							

1847,89	1846,968	1848,815	1847,959	0,068	R.QGFGELLQAVPLADSF.R.H	P27695	APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase (EC 3.1.-.-) (EC 4.2.99.18) (APEX nuclease) (APEN) (Apyrimidinic endonuclease 1) (AP endonuclease 1) (APE-1) (REF-1) (Redox factor-1) [Cleaved into: DNA-(apurinic or apyrimidinic site) lyase, mitochondrial]	APEX1
1848,89 1849,95	1847,967 1849,022	1849,816 1850,872	1849,910	0,037	K.TEFLSFMNTELAFTK.N	P31949	S10AB_HUMAN	Protein S100-A11 (Calgizzarin) (Metastatic lymph node gene 70 protein) (MLN 70) (Protein S100-C) (S100 calcium-binding protein A11) [Cleaved into: Protein S100-A11, N-terminally processed]	S100A11
1850,90	1849,975	1851,825	1850,983	0,083	R.AVSREDSQRPGAHLTVK.K	P09651	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	HNRNPA1
1851,85	1850,926	1852,778	1851,886 1850,983	0,035 0,869	R.FSTVAGESGSADTVRDPR.G R.AVSREDSQRPGAHLTVK.K	P04040 P09651	CATA_HUMAN ROA1_HUMAN	Catalase (EC 1.11.1.6) Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	CAT HNRNPA1
1851,92	1850,991	1852,843	1851,886	0,031	R.FSTVAGESGSADTVRDPR.G	P04040	CATA_HUMAN	Catalase (EC 1.11.1.6)	CAT
1852,86 1853,89	1851,936 1852,967	1853,789 1854,821	1853,996	0,102	R.IGGVQQDTILAEGLHFR.I	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
1854,86	1853,930	1855,785	1853,996	0,861	R.IGGVQQDTILAEGLHFR.I	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
1855,87 1856,88 1857,89 1858,86 1859,90 1860,89 1861,84 1861,99	1854,941 1855,952 1856,958 1857,931 1858,974 1859,963 1860,910 1861,063	1856,797 1857,809 1858,816 1859,790 1860,833 1861,824 1862,772 1862,925	1862,918	0,924	R.QYYTLLNQAPDMLHR.F	Q13283	G3BP1_HUMAN	Ras GTPase-activating protein-binding protein 1 (G3BP-1) (EC 3.6.4.12) (EC 3.6.4.13) (ATP-dependent DNA helicase VIII) (hDH VIII) (GAP SH3 domain-binding protein 1)	G3BP1
1862,93	1862,000	1863,863	1862,918	0,013	R.QYYTLLNQAPDMLHR.F	Q13283	G3BP1_HUMAN	Ras GTPase-activating protein-binding protein 1 (G3BP-1) (EC 3.6.4.12) (EC 3.6.4.13) (ATP-dependent DNA helicase VIII) (hDH VIII) (GAP SH3 domain-binding protein 1)	G3BP1
1863,94 1864,91 1865,95	1863,010 1863,978 1865,021	1864,873 1865,843 1866,887	1865,992	0,038	R.AVLMGGSALSAAVISH.R.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1866,19	1865,261	1867,127	1865,992	0,202	R.AVLMGGSALSAAVISH.R.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1866,95 1867,19 1868,02 1868,95	1866,021 1866,256 1867,085 1868,017	1867,888 1868,123 1868,953 1869,886	1869,021	0,070	R.QFVPIKVEQIEAGTPGR.L	Q16881	TRXR1_HUMAN	Thioredoxin reductase 1, cytoplasmic (TR) (EC 1.8.1.9) (Gene associated with retinoic and interferon-induced mortality 12 protein) (GRIM-12) (Gene associated with retinoic and IFN-induced mortality 12 protein) (KM-102-derived reductase-like factor) (Thioredoxin reductase TR1)	TXNRD1
1869,87	1868,937	1870,807	1869,965	0,092	K.ANLQIDQINTDLNLR.S	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
			1869,021	0,851	R.QFVPIKVEQIEAGTPGR.L	Q16881	TRXR1_HUMAN	Thioredoxin reductase 1, cytoplasmic (TR) (EC 1.8.1.9) (Gene associated with retinoic and interferon-induced mortality 12 protein) (GRIM-12) (Gene associated with retinoic and IFN-induced mortality 12 protein) (KM-102-derived reductase-like factor) (Thioredoxin reductase TR1)	TXNRD1
1870,86	1869,929	1871,800	1869,965	0,900	K.ANLQIDQINTDLNLR.S	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
1871,88 1872,90 1873,92	1870,946 1871,964 1872,981	1872,818 1873,837 1874,855	1873,988	0,070	K.LFDSDPITVTPVEVSR.K	P10909	CLUS_HUMAN	Clusterin (Aging-associated gene 4 protein) (Apolipoprotein J) (Apo-J) (Complement cytotoxicity inhibitor) (CLI) (Complement-associated protein SP-40,40) (Ku70-binding protein 1) (NA1/NA2) (Sulfated glycoprotein 2) (SGP-2) (Testosterone-repressed prostate message 2) (TRPM-2) [Cleaved into: Clusterin beta chain (Apolalpha) (Complement cytotoxicity inhibitor a chain); Clusterin alpha chain (Apolbeta) (Complement cytotoxicity inhibitor b chain)]	CLU
1874,93	1873,994	1875,869	1874,887	0,045	K.ATEDEGSEQIKPEATNR.R	P01008	ANT3_HUMAN	Antithrombin-III (ATIII) (Serpin C1)	SERPINC1

1875,94	1875,004	1876,880	1875,940	0,002	K.VYAEVTHQGLSSPVTK.S	P01834	IGKC_HUMAN	Immunoglobulin kappa constant (Ig kappa chain C region) (Ig kappa chain C region AG) (Ig kappa chain C region CUM) (Ig kappa chain C region EU) (Ig kappa chain C region OU) (Ig kappa chain C region ROY) (Ig kappa chain C region TI)	IGKC
			1875,958	0,016	K.GLIDEVNDQDFTNRINK.L	P02671	FIBA_HUMAN	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	FGA
			1875,909	0,033	K.FGVEQDVLMVMFASFIR.K	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
1876,90	1875,962	1877,839	1877,041	0,141	R.LQEAAELEAVELPVPIR.F	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
1877,91	1876,971	1878,849	1877,912	0,002	R.AASAGQEPLHNEELAGAGR.V	Q96HY6	DDRKG_HUMAN	DDRKG domain-containing protein 1 (Dashurin) (UFM1-binding and PCI domain-containing protein 1)	DDRKG1
			1877,041	0,869	R.LQEAAELEAVELPVPIR.F	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
1878,92	1877,977	1879,856							
1879,93	1878,986	1880,866							
1880,93	1879,987	1881,868							
1881,94	1880,996	1882,878	1881,988	0,050	K.STLINSFLDTLYPER.V	Q15019	SEPT2_HUMAN	Septin-2 (Neural precursor cell expressed developmentally down-regulated protein 5) (NEDD-5)	SEPT2
1882,93	1881,989	1883,872	1883,781	0,850	R.YGDFRADDADFEFGYSR.-	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
1883,95	1883,007	1884,891	1883,956	0,007	K.FQDGLTLYQSNTILR.H	P09211	GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pI) (GSTP1-1)	GSTP1
			1883,935	0,014	R.NEEDAAELVALAQAVNAR.A	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
			1883,901	0,048	R.LNFSHGTHEYHAETIK.N	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
			1883,781	0,168	R.YGDFRADDADFEFGYSR.-	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
1884,96	1884,015	1885,900							
1885,86	1884,917	1886,803	1885,944	0,084	R.QLVHELDEAEYRDIR.L	Q06323	PSME1_HUMAN	Proteasome activator complex subunit 1 (11S regulator complex subunit alpha) (REG-alpha) (Activator of multicatalytic protease subunit 1) (Interferon gamma up-regulated I-5111 protein) (IGUP I-5111) (Proteasome activator 28 subunit alpha) (PA28a) (PA28alpha)	PSME1
1885,98	1885,040	1886,926	1885,944	0,039	R.QLVHELDEAEYRDIR.L	Q06323	PSME1_HUMAN	Proteasome activator complex subunit 1 (11S regulator complex subunit alpha) (REG-alpha) (Activator of multicatalytic protease subunit 1) (Interferon gamma up-regulated I-5111 protein) (IGUP I-5111) (Proteasome activator 28 subunit alpha) (PA28a) (PA28alpha)	PSME1
1886,91	1885,969	1887,856							
1887,96	1887,013	1888,901	1887,989	0,033	K.VTHAVVTPAYFNDAGR.Q	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BIP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			1887,917	0,039	R.NFGKEFTPQMQAAYQK.V	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
			1888,012	0,055	K.VLDFEHFLPMLQTVAK.N	P60660	MYL6_HUMAN	Myosin light polypeptide 6 (17 kDa myosin light chain) (LC17) (Myosin light chain 3) (MLC-3) (Myosin light chain alkali 3) (Myosin light chain A3) (Smooth muscle and nonmuscle myosin light chain alkali 6)	MYL6
1888,93	1887,988	1889,877	1888,960	0,028	R.EQHLYYDQLLPVSR.I	Q98Z13	TRYD_HUMAN	Tryptase delta (EC 3.4.21.59) (Delta-tryptase) (HmMCP-3-like tryptase III) (Mast cell mMCP-7-like) (Tryptase-3)	TPSD1
			1888,969	0,037	R.VLSRPNAQELPSMYQRL	Q99623	PHB2_HUMAN	Prohibitin-2 [B-cell receptor-associated protein BAP37] (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
			1888,012	0,920	K.VLDFEHFLPMLQTVAK.N	P60660	MYL6_HUMAN	Myosin light polypeptide 6 (17 kDa myosin light chain) (LC17) (Myosin light chain 3) (MLC-3) (Myosin light chain alkali 3) (Myosin light chain A3) (Smooth muscle and nonmuscle myosin light chain alkali 6)	MYL6
			1887,989	0,943	K.VTHAVVTPAYFNDAGR.Q	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BIP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
1889,92	1888,976	1890,866							
1890,92	1889,979	1891,870							
1891,94	1890,991	1892,883							
1892,91	1891,964	1893,857							
1893,86	1892,911	1894,805							
1893,99	1893,043	1894,937							

1894,94 1895,95 1896,96 1897,96	1893,990 1895,003 1896,012 1897,014	1895,885 1896,899 1897,909 1898,912	1897,983	0,021	R.AFYAELYHIISNLEK.I	Q9UL46	PSME2_HUMAN	Proteasome activator complex subunit 2 (11S regulator complex subunit beta) (REG-beta) (Activator of multicatalytic protease subunit 2) (Proteasome activator 28 subunit beta) (PA28b) (PA28beta)	PSME2
1898,96	1898,012	1899,911	1899,000	0,038	R.RHPYFYAPELLFFAK.R	P02768	ALBU_HUMAN	Serum albumin	ALB
1899,97	1899,017	1900,917	1899,928	0,039	R.GFAFVTFESPADAKDAAR.D	P38159	RBMX_HUMAN	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX
1900,95	1899,996	1901,897	1901,831	0,885	K.LAEQAERYDDMAACMK.S	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
1901,96	1901,007	1902,909	1901,958	0,000	R.ADGYVLEKLEFYLR.K	P62241	RS8_HUMAN	40S ribosomal protein S8 (Small ribosomal subunit protein e58)	RPS8
			1901,831	0,127	K.LAEQAERYDDMAACMK.S	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
			1902,887	0,929	R.IMLFTNEDNPHGNDSAKA	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	XRCC6
1902,96	1902,006	1903,909	1902,887	0,071	R.IMLFTNEDNPHGNDSAKA	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	XRCC6
1903,96 1904,96	1903,007 1904,008	1904,911 1905,913	1904,950	0,011	R.EPQVYTLPPSREEMTK.N	P01860	IGHG3_HUMAN	Immunoglobulin heavy constant gamma 3 (HDC) (Heavy chain disease protein) (Ig gamma-3 chain C region)	IGHG3
1905,97 1906,98 1907,97 1908,97 1909,96	1905,017 1906,025 1907,016 1908,016 1909,001	1906,923 1907,932 1908,924 1909,925 1910,911	1910,783	0,827	R.SSGSPYGGGYSGGGSGGYGSR.R	P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3
1910,89	1909,935	1911,846	1910,783	0,108	R.SSGSPYGGGYSGGGSGGYGSR.R	P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3
1910,98	1910,022	1911,933	1910,783	0,195	R.SSGSPYGGGYSGGGSGGYGSR.R	P51991	ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3
1911,96	1911,001	1912,913	1912,026	0,069	R.QAIKELPQFATGENLPR.V	Q98Z25	API5_HUMAN	Apoptosis inhibitor 5 (API-5) (Antiapoptosis clone 11 protein) (AAC-11) (Cell migration-inducing gene 8 protein) (Fibroblast growth factor 2-interacting factor) (FIF) (Protein XAGL)	API5
1912,97	1912,013	1913,926	1913,005	0,035	R.SSPVIDASTAIDAPSNL.R.F	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			1912,026	0,943	R.QAIKELPQFATGENLPR.V	Q98Z25	API5_HUMAN	Apoptosis inhibitor 5 (API-5) (Antiapoptosis clone 11 protein) (AAC-11) (Cell migration-inducing gene 8 protein) (Fibroblast growth factor 2-interacting factor) (FIF) (Protein XAGL)	API5
1913,97 1914,97 1915,99 1916,95	1913,017 1914,016 1915,031 1915,994	1914,931 1915,931 1916,947 1917,911	1916,980	0,027	R.YGPVIVDVVPLDFYTR.R	Q75494	SRS10_HUMAN	Serine/arginine-rich splicing factor 10 (40 kDa SR-repressor protein) (SRp40) (FUS-interacting serine-arginine-rich protein 1) (Splicing factor SRp38) (Splicing factor, arginine/serine-rich 13A) (TLS-associated protein with Ser-Arg repeats) (TASR) (TLS-associated protein with SR repeats) (TLS-associated serine-arginine protein) (TLS-associated SR protein)	SRSF10
			1917,910	0,957	R.ATQQQHDFLTQTADGR.S	P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	PRKDC
1917,96	1917,001	1918,919	1917,910	0,050	R.ATQQQHDFLTQTADGR.S	P78527	PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	PRKDC
			1918,868	0,908	R.EVQGNESDLFMSYFPR.G	P40121	CAPG_HUMAN	Macrophage-capping protein (Actin regulatory protein CAP-G)	CAPG
1918,98	1918,016	1919,935	1918,868	0,108	R.EVQGNESDLFMSYFPR.G	P40121	CAPG_HUMAN	Macrophage-capping protein (Actin regulatory protein CAP-G)	CAPG
1919,99 1921,00	1919,029 1920,039	1920,949 1921,960	1921,875	0,876	R.YNEEERAQQEAEAAQR.L	Q99426	TBCB_HUMAN	Tubulin-folding cofactor 8 (Cytoskeleton-associated protein 1) (Cytoskeleton-associated protein CKAP1) (Tubulin-specific chaperone B)	TBCB

1921,97	1921,006	1922,928	1921,875	0,092	R.YNEEERAQQEAEAAQR.L	Q99426	TBCB_HUMAN	Tubulin-folding cofactor B (Cytoskeleton-associated protein 1) (Cytoskeleton-associated protein CKAP1) (Tubulin-specific chaperone B)	TBCB
1922,95 1923,98	1921,992 1923,021	1923,914 1924,945	1923,962	0,021	R.QAAPCVLFFDELDSIAK.A	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
1924,95 1926,01 1927,02	1923,985 1925,045 1926,054	1925,910 1926,971 1927,981	1927,107	0,090	K.LQSRPAAPPAPGPGQLTLR.L	Q99536	VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog (EC 1.-.-.-)	VAT1
			1927,867	0,850	K.MMDYLQSGSETPQTDVR.W	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1927,52	1926,556	1928,483	1927,867	0,348	K.MMDYLQSGSETPQTDVR.W	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			1927,107	0,412	K.LQSRPAAPPAPGPGQLTLR.L	Q99536	VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog (EC 1.-.-.-)	VAT1
1928,01	1927,050	1928,978	1927,867	0,147	K.MMDYLQSGSETPQTDVR.W	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			1927,107	0,907	K.LQSRPAAPPAPGPGQLTLR.L	Q99536	VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog (EC 1.-.-.-)	VAT1
			1928,934	0,920	R.SLGYAYVNFQKPADAER.A	P11940	PABP1_HUMAN	Polyadenylate-binding protein 1 (PABP-1) (Poly(A)-binding protein 1)	PABPC1
			1928,956	0,942	R.LSEIDYGVLTDEGIAYR.G	P32119	PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
1928,45	1927,489	1929,417	1928,934	0,481	R.SLGYAYVNFQKPADAER.A	P11940	PABP1_HUMAN	Polyadenylate-binding protein 1 (PABP-1) (Poly(A)-binding protein 1)	PABPC1
			1928,956	0,503	R.LSEIDYGVLTDEGIAYR.G	P32119	PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
			1927,867	0,586	K.MMDYLQSGSETPQTDVR.W	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
1929,01	1928,041	1929,970	1928,956	0,049	R.LSEIDYGVLTDEGIAYR.G	P32119	PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
			1928,934	0,072	R.SLGYAYVNFQKPADAER.A	P11940	PABP1_HUMAN	Polyadenylate-binding protein 1 (PABP-1) (Poly(A)-binding protein 1)	PABPC1
			1929,921	0,916	K.SGVYQHVTEGMMGGHAIR.I	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
1929,90	1928,931	1930,861	1929,921	0,025	K.SGVYQHVTEGMMGGHAIR.I	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
			1928,956	0,940	R.LSEIDYGVLTDEGIAYR.G	P32119	PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	PRDX2
			1928,934	0,963	R.SLGYAYVNFQKPADAER.A	P11940	PABP1_HUMAN	Polyadenylate-binding protein 1 (PABP-1) (Poly(A)-binding protein 1)	PABPC1
1930,00	1929,036	1930,966	1929,921	0,080	K.SGVYQHVTEGMMGGHAIR.I	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
1930,99	1930,020	1931,951	1931,172	0,186	K.VTIAQGGVLPNIQAVLLPK.K	Q6F113	H2A2A_HUMAN	Histone H2A type 2-A (Histone H2A.2) (Histone H2A/o)	HIST2H2AA3; HIST2H2AA4
			1931,172	0,186	R.VTIAQGGVLPNIQAVLLPK.K	Q93077	H2A1C_HUMAN	Histone H2A type 1-C (Histone H2A/l)	HIST1H2AC
1932,06	1931,094	1933,026	1932,012	0,048	R.LEDIPVASLPDLHDIER.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1932,127	0,067	R.LLDVDNRVLPLEAPIR.M	P00403	COX2_HUMAN	Cytochrome c oxidase subunit 2 (Cytochrome c oxidase polypeptide II)	MT-CO2
			1931,985	0,075	R.EAEAAIYHLQFEEELR.R	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
			1932,939	0,879	R.VEPADASGTEKAFEPATGR.V	P49189	AL9A1_HUMAN	4-trimethylaminobutyraldehyde dehydrogenase (TMABADH) (EC 1.2.1.47) (Aldehyde dehydrogenase E3 isozyme) (Aldehyde dehydrogenase family 9 member A1) (EC 1.2.1.3) (Gamma-aminobutyraldehyde dehydrogenase) (EC 1.2.1.19) (R-aminobutyraldehyde dehydrogenase) [Cleaved into: 4-trimethylaminobutyraldehyde dehydrogenase, N-terminally processed]	ALDH9A1
			1931,172	0,888	K.VTIAQGGVLPNIQAVLLPK.K	Q6F113	H2A2A_HUMAN	Histone H2A type 2-A (Histone H2A.2) (Histone H2A/o)	HIST2H2AA3; HIST2H2AA4
			1931,172	0,888	R.VTIAQGGVLPNIQAVLLPK.K	Q93077	H2A1C_HUMAN	Histone H2A type 1-C (Histone H2A/l)	HIST1H2AC
			1933,015	0,955	R.VLVDMDGVLDADFAGLLR.G	Q87CD5	NTSC_HUMAN	5'(3')-deoxyribonucleotidase, cytosolic type (EC 3.1.3.-) (Cytosolic 5',3'-pyrimidine nucleotidase) (Deoxy-5'-nucleotidase 1) (dNT-1)	NTSC
1933,06	1932,094	1934,027	1933,102	0,041	R.LPVTLSAGPVAPRDLIAR.G	Q9ULE6	PALD_HUMAN	Paladin	PALD1
			1933,015	0,045	R.VLVDMDGVLDADFAGLLR.G	Q87CD5	NTSC_HUMAN	5'(3')-deoxyribonucleotidase, cytosolic type (EC 3.1.3.-) (Cytosolic 5',3'-pyrimidine nucleotidase) (Deoxy-5'-nucleotidase 1) (dNT-1)	NTSC

			1932,939	0,122	R.VEPADASGTKEKAFEPATGR.V	P49189	AL9A1_HUMAN	4-trimethylaminobutyraldehyde dehydrogenase (TMABADH) (EC 1.2.1.47) (Aldehyde dehydrogenase E3 isozyme) (Aldehyde dehydrogenase family 9 member A1) (EC 1.2.1.3) (Gamma-aminobutyraldehyde dehydrogenase) (EC 1.2.1.19) (R-aminobutyraldehyde dehydrogenase) [Cleaved into: 4-trimethylaminobutyraldehyde dehydrogenase, N-terminally processed]	ALDH9A1
			1932,127	0,934	R.LLDVDNRVVLPKEAPIR.M	P00403	COX2_HUMAN	Cytochrome c oxidase subunit 2 (Cytochrome c oxidase polypeptide II)	MT-CO2
			1934,021	0,960	K.HQTLQGLAFLPQPEAQR.A	Q6IBS0	TWF2_HUMAN	Twinfilin-2 (A6-related protein) (hA6RP) (Protein tyrosine kinase 9-like) (Twinfilin-1-like protein)	TWF2
1934,04	1933,077	1935,011	1934,021	0,023	K.HQTLQGLAFLPQPEAQR.A	Q6IBS0	TWF2_HUMAN	Twinfilin-2 (A6-related protein) (hA6RP) (Protein tyrosine kinase 9-like) (Twinfilin-1-like protein)	TWF2
			1934,964	0,920	K.FMSVQRPGPYDRPGTAR.R	P52597	HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein F, N-terminally processed]	HNRNPF
			1933,102	0,942	R.LPVTLSAGPVAPRDLIAR.G	Q9ULE6	PALD_HUMAN	Paladin	PALD1
1934,99	1934,024	1935,959	1934,964	0,028	K.FMSVQRPGPYDRPGTAR.R	P52597	HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein F, N-terminally processed]	HNRNPF
1935,04	1934,075	1936,010	1934,964	0,079	K.FMSVQRPGPYDRPGTAR.R	P52597	HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein F, N-terminally processed]	HNRNPF
1936,03	1935,061	1936,997	1936,982	0,953	R.QGFSYQCPQGQVIVAVR.S	Q07507	DERM_HUMAN	Dermatopontin (Tyrosine-rich acidic matrix protein) (TRAMP)	DPT
1937,02	1936,054	1937,991	1937,061	0,039	R.ALPAVQNNLNDEDURK.L	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
			1936,982	0,041	R.QGFSYQCPQGQVIVAVR.S	Q07507	DERM_HUMAN	Dermatopontin (Tyrosine-rich acidic matrix protein) (TRAMP)	DPT
1938,02	1937,051	1938,989	1938,961	0,941	R.QQPPDLVEFAVEYFTR.L	P13861	KAP2_HUMAN	cAMP-dependent protein kinase type II-alpha regulatory subunit	PRKAR2A
			1937,061	0,959	R.ALPAVQNNLNDEDURK.L	P22314	UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 (EC 6.2.1.45) (Protein A159) (Ubiquitin-activating enzyme E1)	UBA1
1938,96	1937,992	1939,931	1938,961	0,001	R.QQPPDLVEFAVEYFTR.L	P13861	KAP2_HUMAN	cAMP-dependent protein kinase type II-alpha regulatory subunit	PRKAR2A
1939,97 1940,98 1941,98	1938,999 1940,007 1941,948 1941,013 1942,955	1940,939 1941,948 1942,955	1942,040	0,056	K.NITLNFQGPQHPAAHGVLRL.L	O75306	NDUS2_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial (EC 1.6.99.3) (EC 7.1.1.2) (Complex I-49kD) (CI-49kD) (NADH-ubiquinone oxidoreductase 49 kDa subunit)	NDUFS2
1942,56	1941,584	1943,526	1942,040	0,515	K.NITLNFQGPQHPAAHGVLRL.L	O75306	NDUS2_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial (EC 1.6.99.3) (EC 7.1.1.2) (Complex I-49kD) (CI-49kD) (NADH-ubiquinone oxidoreductase 49 kDa subunit)	NDUFS2
1943,03 1943,55 1943,96 1945,00	1942,058 1942,577 1942,985 1944,025 1945,970	1944,001 1944,520 1944,929	1945,909	0,912	K.SGVYQHVTEGMMGGHAIR.I	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
1945,99	1945,018	1946,964	1945,997	0,007	M.VNPTVFFDIADVGEPLGR.V	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
			1945,909	0,081	K.SGVYQHVTEGMMGGHAIR.I	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
1946,93	1945,960	1947,907	1945,997	0,937	M.VNPTVFFDIADVGEPLGR.V	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA
			1947,906	0,973	R.QSLGHGQHGGSGGQSPSPSR.G	Q86Y23	HORN_HUMAN	Hornerin	HRNR
1946,99	1946,014	1947,961	1947,906	0,919	R.QSLGHGQHGGSGGQSPSPSR.G	Q86Y23	HORN_HUMAN	Hornerin	HRNR
1947,97	1946,993	1948,941	1947,906	0,061	R.QSLGHGQHGGSGGQSPSPSR.G	Q86Y23	HORN_HUMAN	Hornerin	HRNR
1948,89 1949,01	1947,918 1948,039	1949,867 1949,988	1949,935	0,921	K.MIDERQQELTHQEHR.V	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL
1949,99	1949,017	1950,967	1949,935 1950,052	0,058 0,060	K.MIDERQQELTHQEHR.V R.LENYPIPEPGPNEVLLR.M	P18206 Q00796	VINC_HUMAN DHSO_HUMAN	Vinculin (Metavinculin) (MV) Sorbitol dehydrogenase (SDH) (EC 1.1.1.-) ((R,R)-butanediol dehydrogenase) (EC 1.1.1.4) (L-iditol 2-dehydrogenase) (EC 1.1.1.14) (Polyol dehydrogenase) (Ribitol dehydrogenase) (RDH) (EC 1.1.1.56) (Xylitol dehydrogenase) (XDH) (EC 1.1.1.9)	VCL SORD
			1950,067	0,075	R.HLQLAIRGDEELDSLIIK.A	Q71UI9	H2AV_HUMAN	Histone H2A.V (H2A.F/Z)	H2AFV
1950,99	1950,014	1951,965	1951,009	0,020	R.EEAPSLRPAPPISGGGYR.A	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
			1950,067 1950,052	0,922 0,938	R.HLQLAIRGDEELDSLIIK.A R.LENYPIPEPGPNEVLLR.M	Q71UI9 Q00796	H2AV_HUMAN DHSO_HUMAN	Histone H2A.V (H2A.F/Z) Sorbitol dehydrogenase (SDH) (EC 1.1.1.-) ((R,R)-butanediol dehydrogenase) (EC 1.1.1.4) (L-iditol 2-dehydrogenase) (EC 1.1.1.14) (Polyol dehydrogenase) (Ribitol dehydrogenase) (RDH) (EC 1.1.1.56) (Xylitol dehydrogenase) (XDH) (EC 1.1.1.9)	H2AFV SORD

1951,97	1950,996	1952,948	1951,987	0,015	R.GGVDTAAAPAGGAPPAHAPGPR.D	Q14657	LAGE3_HUMAN	EKC/KEOPS complex subunit LAGE3 (L antigen family member 3) (Protein ESO-3) (Protein ITBA2)	LAGE3
			1951,009	0,962	R.EEAPSLRPAPPPIGGGGYR.A	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
1953,13	1952,157	1954,110	1953,980	0,846	K.NLEGYVGAFANLPNQVYR.K	Q16181	SEPT7_HUMAN	Septin-7 (CDC10 protein homolog)	SEPT7
			1954,076	0,942	R.VAPEEHPVLLTEAPLNPK.A	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
1954,11	1953,132	1955,086	1954,076	0,942	R.VAPDEHPILLTEAPLNPK.I	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			1954,076	0,033	R.VAPEEHPVLLTEAPLNPK.A	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
1954,12	1953,145	1955,099	1954,076	0,046	R.VAPDEHPILLTEAPLNPK.I	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			1953,980	0,130	K.NLEGYVGAFANLPNQVYR.K	Q16181	SEPT7_HUMAN	Septin-7 (CDC10 protein homolog)	SEPT7
1955,10	1954,125	1956,080	1955,006	0,897	R.SP5SGGAAGPLLTSPQSLDGSR.R	Q96CX2	KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 (Pftetin) (Predominantly fetal expressed T1 domain)	KCTD12
			1954,076	0,046	R.VAPEEHPVLLTEAPLNPK.A	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
1955,10	1954,125	1956,080	1954,076	0,046	R.VAPDEHPILLTEAPLNPK.I	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			1953,980	0,143	K.NLEGYVGAFANLPNQVYR.K	Q16181	SEPT7_HUMAN	Septin-7 (CDC10 protein homolog)	SEPT7
1955,10	1954,125	1956,080	1955,006	0,884	R.SP5SGGAAGPLLTSPQSLDGSR.R	Q96CX2	KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 (Pftetin) (Predominantly fetal expressed T1 domain)	KCTD12
			1955,006	0,096	R.SP5SGGAAGPLLTSPQSLDGSR.R	Q96CX2	KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 (Pftetin) (Predominantly fetal expressed T1 domain)	KCTD12
1956,08	1955,101	1957,057	1956,051	0,949	R.VAPEEHPVLLTEAPLNPK.A	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			1956,051	0,027	R.VAPEEHPVLLTEAPLNPK.A	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
1957,05	1956,070	1958,027	1957,71	0,267	K.GHYTEGAELVDSVLDVVR.K	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1957,99	0,267	K.GHYTEGAELVDSVLDVVR.K	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
1958,97	1957,994	1959,953	1958,985	0,011	K.GHYTEGAELVDSVLDVVR.K	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			1958,985	0,011	K.GHYTEGAELVDSVLDVVR.K	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
1959,99	1959,014	1960,974	1960,95	0,089	K.TIEGSGRTEHINIHLQLR.N	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
			1961,987	0,015	R.GHVFEESQVAGTPMFVVK.A	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
1961,97	1960,990	1962,952	1962,028	0,057	K.IADEGRFLAEFQSIPIR.V	P08575	PTPRC_HUMAN	Receptor-type tyrosine-protein phosphatase C (EC 3.1.3.48) (Leukocyte common antigen) (L-CA) (T200) (CD antigen CD45)	PTPRC
			1961,044	0,927	K.TIEGSGRTEHINIHLQLR.N	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
1963,00	1962,021	1963,984	1962,028	0,975	K.IADEGRFLAEFQSIPIR.V	P08575	PTPRC_HUMAN	Receptor-type tyrosine-protein phosphatase C (EC 3.1.3.48) (Leukocyte common antigen) (L-CA) (T200) (CD antigen CD45)	PTPRC
			1963,97	0,052	R.LFVGNLPAIDTEDEFKRL	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
1965,01	1964,024	1965,989	1966,00	0,953	R.AASQPPNSSEAGRPKWER.S	Q9UI08	EVL_HUMAN	Ena/VASP-like protein (Ena/vasodilator-stimulated phosphoprotein-like)	EVL
			1967,02	0,046	R.AASQPPNSSEAGRPKWER.S	Q9UI08	EVL_HUMAN	Ena/VASP-like protein (Ena/vasodilator-stimulated phosphoprotein-like)	EVL
1968,02	1967,032	1969,000	1968,912	0,895	K.HKELAPYDENWFYTRA	P39019	RS19_HUMAN	40S ribosomal protein S19 (Small ribosomal subunit protein eS19)	RPS19
			1968,912	0,026	K.HKELAPYDENWFYTRA	P39019	RS19_HUMAN	40S ribosomal protein S19 (Small ribosomal subunit protein eS19)	RPS19
1968,89	1967,901	1969,870	1967,970	0,916	R.AASQPPNSSEAGRPKWER.S	Q9UI08	EVL_HUMAN	Ena/VASP-like protein (Ena/vasodilator-stimulated phosphoprotein-like)	EVL
			1968,912	0,160	K.HKELAPYDENWFYTRA	P39019	RS19_HUMAN	40S ribosomal protein S19 (Small ribosomal subunit protein eS19)	RPS19
1969,07	1968,088	1970,057	1968,912	0,978	K.HKELAPYDENWFYTRA	P39019	RS19_HUMAN	40S ribosomal protein S19 (Small ribosomal subunit protein eS19)	RPS19
			1968,912	0,957	K.QVDOFLGVPIAAPLAER.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
1970,08	1969,092	1971,062	1971,034	0,038	K.QVDOFLGVPIAAPLAER.R	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			1971,07	0,803	K.IDASKNEEDEGHSSNSPR.H	Q14103	HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1)	HNRNPD
1972,05	1971,068	1973,040	1971,875	0,179	K.IDASKNEEDEGHSSNSPR.H	Q14103	HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1)	HNRNPD
			1972,46	0,589	K.IDASKNEEDEGHSSNSPR.H	Q14103	HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1)	HNRNPD

[illegible]

			1988,892	0,898	R.DAQDVQASQAEADQQQTRL	Q9P2E9	RRBP1_HUMAN	Ribosome-binding protein 1 (180 kDa ribosome receptor homolog) (RRp) (ES/130-related protein) (Ribosome receptor protein)	RRBP1
1989,00	1988,003	1989,992	1988,995	0,003	K.VNPFPRPGDSEPPAPGAQR.A	Q15942	ZYX_HUMAN	Zyxin (Zyxin-2)	ZYX
			1988,892	0,106	R.DAQDVQASQAEADQQQTRL	Q9P2E9	RRBP1_HUMAN	Ribosome-binding protein 1 (180 kDa ribosome receptor homolog) (RRp) (ES/130-related protein) (Ribosome receptor protein)	RRBP1
			1989,943	0,945	R.FFD5FGNLSSASAIMGNPK.V	P69892	HBG2_HUMAN	Hemoglobin subunit gamma-2 (Gamma-2-globin) (Hb F Ggamma) (Hemoglobin gamma-2 chain) (Hemoglobin gamma-G chain)	HBG2
			1988,033	0,964	R.AIAELGIYPAVDPLDSTR.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
1990,00	1989,009	1990,999	1989,943	0,061	R.FFD5FGNLSSASAIMGNPK.V	P69892	HBG2_HUMAN	Hemoglobin subunit gamma-2 (Gamma-2-globin) (Hb F Ggamma) (Hemoglobin gamma-2 chain) (Hemoglobin gamma-G chain)	HBG2
			1990,136	0,132	K.APIRPDIVNFVHTNLRK.N	P36578	RL4_HUMAN	60S ribosomal protein L4 (60S ribosomal protein L1) (Large ribosomal subunit protein uL4)	RPL4
1991,02	1990,023	1992,014	1990,136	0,882	K.APIRPDIVNFVHTNLRK.N	P36578	RL4_HUMAN	60S ribosomal protein L4 (60S ribosomal protein L1) (Large ribosomal subunit protein uL4)	RPL4
1992,01	1991,016	1993,008							
1993,01	1992,016	1994,009	1993,972	0,960	R.THNLEPYFESFINNLR.R	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
1994,01	1993,013	1995,007	1993,972	0,038	R.THNLEPYFESFINNLR.R	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
1995,01	1994,010	1996,005	1995,806	0,798	R.SSGGSYRDSYDSYATHNE.-	Q14011	CIRBP_HUMAN	Cold-inducible RNA-binding protein (A18 hnRNP) (Glycine-rich RNA-binding protein CIRP)	CIRBP
			1995,958	0,950	R.NDEYENLFNMIVEIPR.W	Q9H2U2	IPYR2_HUMAN	Inorganic pyrophosphatase 2, mitochondrial (EC 3.6.1.1) (Pyrophosphatase SID6-306) (Pyrophosphate phospho-hydrolase 2) (PPase 2)	PPA2
1996,00	1995,004	1997,000	1995,958	0,044	R.NDEYENLFNMIVEIPR.W	Q9H2U2	IPYR2_HUMAN	Inorganic pyrophosphatase 2, mitochondrial (EC 3.6.1.1) (Pyrophosphatase SID6-306) (Pyrophosphate phospho-hydrolase 2) (PPase 2)	PPA2
			1995,806	0,196	R.SSGGSYRDSYDSYATHNE.-	Q14011	CIRBP_HUMAN	Cold-inducible RNA-binding protein (A18 hnRNP) (Glycine-rich RNA-binding protein CIRP)	CIRBP
			1996,944	0,941	R.NECFLQHKDDNPNLPR.L	P02768	ALBU_HUMAN	Serum albumin	ALB
			1996,987	0,985	R.ATENDIYNFFSPLNPVR.V	P31943	HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H (hnRNP H) [Cleaved into: Heterogeneous nuclear ribonucleoprotein H, N-terminally processed]	HNRNPH1
			1996,987	0,985	K.ATENDIYNFFSPLNPVR.V	P52597	HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein F, N-terminally processed]	HNRNPF
1996,99	1995,987	1997,984	1996,987	0,002	R.ATENDIYNFFSPLNPVR.V	P31943	HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H (hnRNP H) [Cleaved into: Heterogeneous nuclear ribonucleoprotein H, N-terminally processed]	HNRNPH1
			1996,987	0,002	K.ATENDIYNFFSPLNPVR.V	P52597	HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein F, N-terminally processed]	HNRNPF
			1997,024	0,038	R.LQAYHTQTTPLEYR.K	P54819	KAD2_HUMAN	Adenylate kinase 2, mitochondrial (AK 2) (EC 2.7.4.3) (ATP-AMP transphosphorylase 2) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) [Cleaved into: Adenylate kinase 2, mitochondrial, N-terminally processed]	AK2
			1996,944	0,042	R.NECFLQHKDDNPNLPR.L	P02768	ALBU_HUMAN	Serum albumin	ALB
1997,99	1996,996	1998,993	1997,024	0,971	R.LQAYHTQTTPLEYR.K	P54819	KAD2_HUMAN	Adenylate kinase 2, mitochondrial (AK 2) (EC 2.7.4.3) (ATP-AMP transphosphorylase 2) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) [Cleaved into: Adenylate kinase 2, mitochondrial, N-terminally processed]	AK2
1999,00	1997,999	1999,998	1999,972	0,973	R.EPQDTHYLPFSLPHR.R	P10909	CLUS_HUMAN	Clusterin (Aging-associated gene 4 protein) (Apolipoprotein J) (Apo-J) (Complement cytotoxic inhibitor) (CLI) (Complement-associated protein SP-40,40) (Ku70-binding protein 1) (NA1/NA2) (Sulfated glycoprotein 2) (SGP-2) (Testosterone-repressed prostate message 2) (TRPM-2) [Cleaved into: Clusterin beta chain (Apolalpha) (Complement cytotoxic inhibitor a chain); Clusterin alpha chain (Apolbeta) (Complement cytotoxic inhibitor b chain)]	CLU
2000,00	1999,002	2001,002	2000,004	0,001	R.GGHFAAFEEPPELLAQDIR.K	P07099	HYEP_HUMAN	Epoxide hydrolase 1 (EC 3.3.2.9) (Epoxide hydratase) (Microsomal epoxide hydrolase) (mEH)	EPHX1
			1999,972	0,030	R.EPQDTHYLPFSLPHR.R	P10909	CLUS_HUMAN	Clusterin (Aging-associated gene 4 protein) (Apolipoprotein J) (Apo-J) (Complement cytotoxic inhibitor) (CLI) (Complement-associated protein SP-40,40) (Ku70-binding protein 1) (NA1/NA2) (Sulfated glycoprotein 2) (SGP-2) (Testosterone-repressed prostate message 2) (TRPM-2) [Cleaved into: Clusterin beta chain (Apolalpha) (Complement cytotoxic inhibitor a chain); Clusterin alpha chain (Apolbeta) (Complement cytotoxic inhibitor b chain)]	CLU
2001,01	2000,005	2002,006							

2002,02	2001,014	2003,016	2002,065	0,049	K.SPVPVPGAPPLQFYFQGGPR.F	Q16853	AOC3_HUMAN	Membrane primary amine oxidase (EC 1.4.3.21) (Copper amine oxidase) (HPAO) (Semicarbazide-sensitive amine oxidase) (SSAO) (Vascular adhesion protein 1) (VAP-1)	AOC3
2003,02	2002,018	2004,021	2002,065	0,955	K.SPVPVPGAPPLQFYFQGGPR.F	Q16853	AOC3_HUMAN	Membrane primary amine oxidase (EC 1.4.3.21) (Copper amine oxidase) (HPAO) (Semicarbazide-sensitive amine oxidase) (SSAO) (Vascular adhesion protein 1) (VAP-1)	AOC3
2003,98	2002,977	2004,981	2004,077	0,097	K.GTVVAEKDRPHEGTRPVR.A	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
2004,98	2003,973	2005,978	2004,077	0,899	K.GTVVAEKDRPHEGTRPVR.A	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
2005,98	2004,977	2006,983	2005,979	0,002	K.NGPVEGAFSVSYDFLLYK.S	P07858	CATB_HUMAN	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
			2006,019	0,039	R.FAHYVVTSQVVNTANEAR.E	P19827	ITIH1_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H1 (ITI heavy chain H1) (ITI-HC1) (Inter-alpha-inhibitor heavy chain 1) (Inter-alpha-trypsin inhibitor complex component III) (Serum-derived hyaluronan-associated protein) (SHAP)	ITIH1
			2006,072	0,091	R.LLAEPVPGIKAEPDESNA.R.Y	P61088	UBE2N_HUMAN	Ubiquitin-conjugating enzyme E2 N (EC 2.3.2.23) (Bendless-like ubiquitin-conjugating enzyme) (E2 ubiquitin-conjugating enzyme N) (Ubc13) (UbCH13) (Ubiquitin carrier protein N) (Ubiquitin-protein ligase N)	UBE2N
2006,99	2005,988	2007,995	2006,072	0,920	R.LLAEPVPGIKAEPDESNA.R.Y	P61088	UBE2N_HUMAN	Ubiquitin-conjugating enzyme E2 N (EC 2.3.2.23) (Bendless-like ubiquitin-conjugating enzyme) (E2 ubiquitin-conjugating enzyme N) (Ubc13) (UbCH13) (Ubiquitin carrier protein N) (Ubiquitin-protein ligase N)	UBE2N
			2006,019	0,973	R.FAHYVVTSQVVNTANEAR.E	P19827	ITIH1_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H1 (ITI heavy chain H1) (ITI-HC1) (Inter-alpha-inhibitor heavy chain 1) (Inter-alpha-trypsin inhibitor complex component III) (Serum-derived hyaluronan-associated protein) (SHAP)	ITIH1
2007,44	2006,437	2008,445							
2007,61	2006,607	2008,614							
2007,99	2006,985	2008,993							
2008,54	2007,532	2009,540							
2009,00	2007,994	2010,003							
2009,99	2008,982	2010,992							
2011,00	2009,999	2012,010	2011,920	0,915	R.FPGYDSESKFNAEVHR.K	P46777	RL5_HUMAN	60S ribosomal protein L5 (Large ribosomal subunit protein uL18)	RPL5
2012,01	2011,004	2013,016	2011,920	0,090	R.FPGYDSESKFNAEVHR.K	P46777	RL5_HUMAN	60S ribosomal protein L5 (Large ribosomal subunit protein uL18)	RPL5
2013,01	2012,003	2014,016							
2014,00	2012,997	2015,011	2014,053	0,050	K.MSATFIGNSTAIQELFKR.I	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
2015,00	2013,991	2016,006	2015,051	0,053	K.VILHLKEDQTEYLEER.R	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
			2015,051	0,053	K.VILHLKEDQTEYLEER.R	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			2014,053	0,945	K.MSATFIGNSTAIQELFKR.I	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B
2015,99	2014,985	2017,001	2015,051	0,942	K.VILHLKEDQTEYLEER.R	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
			2015,051	0,942	K.VILHLKEDQTEYLEER.R	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
2017,00	2015,994	2018,011	2017,052	0,049	R.GGPPPPPPPHNSGPPPPPAR.G	O00401	WASL_HUMAN	Neural Wiskott-Aldrich syndrome protein (N-WASP)	WASL
2017,99	2016,980	2018,998	2017,052	0,937	R.GGPPPPPPPHNSGPPPPPAR.G	O00401	WASL_HUMAN	Neural Wiskott-Aldrich syndrome protein (N-WASP)	WASL
2019,00	2017,987	2020,006	2019,144	0,147	K.QVKPYVEEGLHPQIIIR.A	Q99832	TCPH_HUMAN	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein) [Cleaved into: T-complex protein 1 subunit eta, N-terminally processed]	CCT7
			2019,935	0,938	R.HVFGQPAKADQCYEDVR.V	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
2020,02	2019,012	2021,032	2020,075	0,053	K.ILATPPQEDAPSVDIANIR.M	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
			2019,935	0,087	R.HVFGQPAKADQCYEDVR.V	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
			2019,144	0,878	K.QVKPYVEEGLHPQIIIR.A	Q99832	TCPH_HUMAN	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein) [Cleaved into: T-complex protein 1 subunit eta, N-terminally processed]	CCT7
2021,03	2020,015	2022,036	2021,955	0,929	R.SISLYYTGEKGQNQDYR.G	P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL
			2020,075	0,951	K.ILATPPQEDAPSVDIANIR.M	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
2021,49	2020,483	2022,505	2021,955	0,460	R.SISLYYTGEKGQNQDYR.G	P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL
2022,02	2021,009	2023,031	2021,955	0,066	R.SISLYYTGEKGQNQDYR.G	P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL
			2023,013	0,993	R.FLSQPFQVAEFTGHMGK.L	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
2022,45	2021,436	2023,458	2021,955	0,492	R.SISLYYTGEKGQNQDYR.G	P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL

			2023,013	0,566	R.FLSQPFQVAEVFTGHMGK.L	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
2023,03	2022,015	2024,039	2023,013	0,014	R.FLSQPFQVAEVFTGHMGK.L	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
2024,02	2023,004	2025,028	2024,975	0,959	K.AEGGGGGRRPGAPAAGDGKTEQK.G	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
			2023,013	1,003	R.FLSQPFQVAEVFTGHMGK.L	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
2025,03	2024,015	2026,040	2024,975	0,052	K.AEGGGGGRRPGAPAAGDGKTEQK.G	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
			2026,028	1,001	R.GAQAAIVVYDITNTDTFAR.A	P51148	RAB5C_HUMAN	Ras-related protein Rab-5C (L1880) (RAB5L)	RAB5C
2026,04	2025,023	2027,049	2026,028	0,008	R.GAQAAIVVYDITNTDTFAR.A	P51148	RAB5C_HUMAN	Ras-related protein Rab-5C (L1880) (RAB5L)	RAB5C
			2026,092	0,056	K.MAVTFIGNSTAIQELFKR.I	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
			2027,033	0,997	K.HGNRGETGPSGPVGPAGAVGPR.G	P08123	CO1A2_HUMAN	Collagen alpha-2(I) chain (Alpha-2 type I collagen)	COL1A2
2027,07	2026,057	2028,084	2027,033	0,037	K.HGNRGETGPSGPVGPAGAVGPR.G	P08123	CO1A2_HUMAN	Collagen alpha-2(I) chain (Alpha-2 type I collagen)	COL1A2
			2026,092	0,978	K.MAVTFIGNSTAIQELFKR.I	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB
2028,11	2027,091	2029,119	2028,115	0,010	R.ALKEASMVITESPAALQLR.Y	P27105	STOM_HUMAN	Erythrocyte band 7 integral membrane protein (Protein 7.2b) (Stomatin)	STOM
			2028,953	0,848	R.ATENDIYNFFSPLNPMR.V	P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 (hnRNP H2) (FTP-3) (Heterogeneous nuclear ribonucleoprotein H') (hnRNP H') [Cleaved into: Heterogeneous nuclear ribonucleoprotein H2, N-terminally processed]	HNRNPH2
2029,09	2028,075	2030,104	2028,953	0,136	R.ATENDIYNFFSPLNPMR.V	P55795	HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2 (hnRNP H2) (FTP-3) (Heterogeneous nuclear ribonucleoprotein H') (hnRNP H') [Cleaved into: Heterogeneous nuclear ribonucleoprotein H2, N-terminally processed]	HNRNPH2
			2028,115	0,975	R.ALKEASMVITESPAALQLR.Y	P27105	STOM_HUMAN	Erythrocyte band 7 integral membrane protein (Protein 7.2b) (Stomatin)	STOM
2030,02	2029,000	2031,030	2031,000	0,985	R.NLHQSGFSLSGTVDEGVR.S	Q14195	DPYL3_HUMAN	Dihydropyrimidinase-related protein 3 (DRP-3) (Collapsin response mediator protein 4) (CRMP-4) (Unc-33-like phosphoprotein 1) (ULIP-1)	DPYSL3
			2031,013	0,997	R.LSASSLTMESFAFLWAGGR.A	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
2031,01	2029,999	2032,030	2031,013	0,002	R.LSASSLTMESFAFLWAGGR.A	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
			2031,000	0,015	R.NLHQSGFSLSGTVDEGVR.S	Q14195	DPYL3_HUMAN	Dihydropyrimidinase-related protein 3 (DRP-3) (Collapsin response mediator protein 4) (CRMP-4) (Unc-33-like phosphoprotein 1) (ULIP-1)	DPYSL3
			2032,021	1,007	R.VDFNVPMKNNQITNNQR.I	P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1
2032,01	2030,992	2033,024	2032,021	0,014	R.VDFNVPMKNNQITNNQR.I	P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1
			2031,013	0,995	R.LSASSLTMESFAFLWAGGR.A	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU
			2031,000	1,008	R.NLHQSGFSLSGTVDEGVR.S	Q14195	DPYL3_HUMAN	Dihydropyrimidinase-related protein 3 (DRP-3) (Collapsin response mediator protein 4) (CRMP-4) (Unc-33-like phosphoprotein 1) (ULIP-1)	DPYSL3
2033,01	2031,995	2034,028	2032,021	0,990	R.VDFNVPMKNNQITNNQR.I	P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1
2034,01	2032,995	2035,029	2034,870	0,858	R.GPPPSYGSSRYDDYSSSR.D	P38159	RBMX_HUMAN	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX
			2034,954	0,942	R.GNFGGSFAGSFGGAGGHAPGVAR.K	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			2034,961	0,949	K.QQLSAEELDAQLDAYNAR.M	Q86V81	THOC4_HUMAN	THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Aly/REF export factor) (Transcriptional coactivator Aly/REF) (bZIP-enhancing factor BEF)	ALYREF
2035,00	2033,979	2036,014	2034,961	0,035	K.QQLSAEELDAQLDAYNAR.M	Q86V81	THOC4_HUMAN	THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Aly/REF export factor) (Transcriptional coactivator Aly/REF) (bZIP-enhancing factor BEF)	ALYREF
			2034,954	0,042	R.GNFGGSFAGSFGGAGGHAPGVAR.K	P52272	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM
			2034,870	0,126	R.GPPPSYGSSRYDDYSSSR.D	P38159	RBMX_HUMAN	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX
			2035,970	0,974	K.NLDQEQLSQVLDAAMFER.I	P13861	KAP2_HUMAN	cAMP-dependent protein kinase type II-alpha regulatory subunit	PRKAR2A
2035,99	2034,976	2037,012	2035,970	0,024	K.NLDQEQLSQVLDAAMFER.I	P13861	KAP2_HUMAN	cAMP-dependent protein kinase type II-alpha regulatory subunit	PRKAR2A

2037,00	2035,978	2038,015	2037,026	0,030	K.AGSRYEDFSNLGTTLLR.L	P22695	QCR2_HUMAN	Cytochrome b-c1 complex subunit 2, mitochondrial (Complex III subunit 2) (Core protein II) (Ubiquinol-cytochrome-c reductase complex core protein 2)	UQCRC2
2038,02	2037,005	2039,043	2037,026	0,998	K.AGSRYEDFSNLGTTLLR.L	P22695	QCR2_HUMAN	Cytochrome b-c1 complex subunit 2, mitochondrial (Complex III subunit 2) (Core protein II) (Ubiquinol-cytochrome-c reductase complex core protein 2)	UQCRC2
2039,01 2039,01 2040,00	2037,992 2037,992 2038,981	2040,031 2040,031 2041,021	2040,158	0,157	R.LKPKPIDVQVITHHMQR.Y	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
2040,00	2038,981	2041,021	2040,158	0,157	R.LKPKPIDVQVITHHMQR.Y	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
2041,00	2039,981	2042,022	2041,113	0,111	K.LVINGNPITIFQERDPSK.I	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
			2040,158	0,844	R.LKPKPIDVQVITHHMQR.Y	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
2041,70	2040,679	2042,721	2042,110	0,409	K.HSHAGELEALGGVKPAVLTR.S	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
			2041,113	0,588	K.LVINGNPITIFQERDPSK.I	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
2042,02	2040,994	2043,036	2042,110	0,094	K.HSHAGELEALGGVKPAVLTR.S	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
			2041,113	0,903	K.LVINGNPITIFQERDPSK.I	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
			2042,997	0,982	K.AAWGKVGAAHAGEYGAEALER.M	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
2042,58	2041,563	2043,605	2042,997	0,413	K.AAWGKVGAAHAGEYGAEALER.M	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			2042,110	0,474	K.HSHAGELEALGGVKPAVLTR.S	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
2042,62	2041,600	2043,643	2042,997	0,375	K.AAWGKVGAAHAGEYGAEALER.M	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			2042,110	0,512	K.HSHAGELEALGGVKPAVLTR.S	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
2043,00	2041,978	2044,021	2042,997	0,002	K.AAWGKVGAAHAGEYGAEALER.M	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			2042,110	0,889	K.HSHAGELEALGGVKPAVLTR.S	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
			2044,021	1,021	K.KGFIGPGIDVPAPDMSTGER.E	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
2043,72	2042,702	2044,745	2044,021	0,297	K.KGFIGPGIDVPAPDMSTGER.E	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			2044,034	0,310	R.AALVAQNYINYQQGTPHR.V	Q9BS40	LXN_HUMAN	Latexin (Endogenous carboxypeptidase inhibitor) (EC1) (Protein MUM) (Tissue carboxypeptidase inhibitor) (TCI)	LXN
			2042,997	0,726	K.AAWGKVGAAHAGEYGAEALER.M	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
2044,56	2043,540	2045,585	2044,935	0,373	R.FFESFGDLSSPDVAVMGNPK.V	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
			2045,051	0,489	R.ELFSPHLALNFGIGDTRR.H	P68402	PA1B2_HUMAN	Platelet-activating factor acetylhydrolase IB subunit beta (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH subunit beta) (PAFAH subunit beta)	PAFAH1B2
			2045,074	0,511	R.AFQPFFELTMPYSVIR.G	P01023	A2MG_HUMAN	Alpha-2-macroglobulin (Alpha-2-M) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 5)	A2M
			2044,034	0,529	R.AALVAQNYINYQQGTPHR.V	Q9BS40	LXN_HUMAN	Latexin (Endogenous carboxypeptidase inhibitor) (EC1) (Protein MUM) (Tissue carboxypeptidase inhibitor) (TCI)	LXN
			2044,021	0,542	K.KGFIGPGIDVPAPDMSTGER.E	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
2045,00	2043,981	2046,026	2045,051	0,047	R.ELFSPHLALNFGIGDTRR.H	P68402	PA1B2_HUMAN	Platelet-activating factor acetylhydrolase IB subunit beta (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH subunit beta) (PAFAH subunit beta)	PAFAH1B2
			2044,935	0,069	R.FFESFGDLSSPDVAVMGNPK.V	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
			2045,074	0,070	R.AFQPFFELTMPYSVIR.G	P01023	A2MG_HUMAN	Alpha-2-macroglobulin (Alpha-2-M) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 5)	A2M
			2044,034	0,970	R.AALVAQNYINYQQGTPHR.V	Q9BS40	LXN_HUMAN	Latexin (Endogenous carboxypeptidase inhibitor) (EC1) (Protein MUM) (Tissue carboxypeptidase inhibitor) (TCI)	LXN
			2044,021	0,983	K.KGFIGPGIDVPAPDMSTGER.E	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
2045,51	2044,485	2046,530	2045,074	0,434	R.AFQPFFELTMPYSVIR.G	P01023	A2MG_HUMAN	Alpha-2-macroglobulin (Alpha-2-M) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 5)	A2M
			2045,051	0,457	R.ELFSPHLALNFGIGDTRR.H	P68402	PA1B2_HUMAN	Platelet-activating factor acetylhydrolase IB subunit beta (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH subunit beta) (PAFAH subunit beta)	PAFAH1B2
			2044,935	0,573	R.FFESFGDLSSPDVAVMGNPK.V	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD

2046,00	2044,980	2047,026	2045,074	0,929	R.AFPQPFVFLTMPYSVIR.G	P01023	A2MG_HUMAN	Alpha-2-macroglobulin (Alpha-2-M) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 5)	A2M
			2045,051	0,952	R.ELFSPLHALNFGVIGGDTTR.H	P68402	PA1B2_HUMAN	Platelet-activating factor acetylhydrolase IB subunit beta [EC 3.1.1.47] (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH subunit beta) (PAFAH subunit beta)	PAFAH1B2
2047,00 2048,03	2045,979 2047,009	2048,026 2049,057	2048,975	0,942	K.SMEAEMIQLQEELAAER.A	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIa)	MYH9
			2049,051	1,018	R.LGPSDYFGEIALLMNRPR.A	P10644	KAP0_HUMAN	cAMP-dependent protein kinase type I-alpha regulatory subunit (Tissue-specific extinguisher 1) (TSE1)	PRKAR1A
2049,09	2048,065	2050,114	2049,078	0,011	R.VILQDFTGVPVAVDFAAMR.D	P21399	ACOC_HUMAN	Cytoplasmic aconitate hydratase (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase) (Ferritin repressor protein) (Iron regulatory protein 1) (IRP1) (Iron-responsive element-binding protein 1) (IRE-BP 1)	ACO1
			2049,051	0,038	R.LGPSDYFGEIALLMNRPR.A	P10644	KAP0_HUMAN	cAMP-dependent protein kinase type I-alpha regulatory subunit (Tissue-specific extinguisher 1) (TSE1)	PRKAR1A
			2048,975	0,114	K.SMEAEMIQLQEELAAER.A	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIa)	MYH9
			2049,781	0,692	R.GGHMDDGGYSMNFMN5SSR.G	P38159	RBMX_HUMAN	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX
2050,02	2048,994	2051,044	2049,781	0,238	R.GGHMDDGGYSMNFMN5SSR.G	P38159	RBMX_HUMAN	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX
			2049,078	0,941	R.VILQDFTGVPVAVDFAAMR.D	P21399	ACOC_HUMAN	Cytoplasmic aconitate hydratase (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase) (Ferritin repressor protein) (Iron regulatory protein 1) (IRP1) (Iron-responsive element-binding protein 1) (IRE-BP 1)	ACO1
			2049,051	0,968	R.LGPSDYFGEIALLMNRPR.A	P10644	KAP0_HUMAN	cAMP-dependent protein kinase type I-alpha regulatory subunit (Tissue-specific extinguisher 1) (TSE1)	PRKAR1A
2050,97 2051,10 2052,00	2049,943 2050,071 2050,978	2051,994 2052,122 2053,030	2052,929	0,925	K.TYGADLASVDFQHASEDAR.K	P30740	ILEU_HUMAN	Leukocyte elastase inhibitor (LEI) (Monocyte/neutrophil elastase inhibitor) (EI) (M/NEI) (Peptidase inhibitor 2) (Pi-2) (Serpin B1)	SERPINB1
2053,02	2051,998	2054,051	2052,929	0,095	K.TYGADLASVDFQHASEDAR.K	P30740	ILEU_HUMAN	Leukocyte elastase inhibitor (LEI) (Monocyte/neutrophil elastase inhibitor) (EI) (M/NEI) (Peptidase inhibitor 2) (Pi-2) (Serpin B1)	SERPINB1
			2053,972	0,947	R.QVMEQHQQQRQESLER.R	Q9UI08	EVL_HUMAN	Ena/VASP-like protein (Ena/vasodilator-stimulated phosphoprotein-like)	EVL
2054,03	2053,005	2055,059	2053,972	0,060	R.QVMEQHQQQRQESLER.R	Q9UI08	EVL_HUMAN	Ena/VASP-like protein (Ena/vasodilator-stimulated phosphoprotein-like)	EVL
			2055,025	0,993	R.ISSFETFGSSQLPDKGAQR.L	Q14005	IL16_HUMAN	Pro-interleukin-16 [Cleaved into: Interleukin-16 (IL-16) (Lymphocyte chemoattractant factor) (LCF)]	IL16
2054,98	2053,953	2056,008	2055,025	0,044	R.ISSFETFGSSQLPDKGAQR.L	Q14005	IL16_HUMAN	Pro-interleukin-16 [Cleaved into: Interleukin-16 (IL-16) (Lymphocyte chemoattractant factor) (LCF)]	IL16
			2055,093	0,112	K.LEGVLA EVAQHYQDTLIR.A	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
			2053,972	1,009	R.QVMEQHQQQRQESLER.R	Q9UI08	EVL_HUMAN	Ena/VASP-like protein (Ena/vasodilator-stimulated phosphoprotein-like)	EVL
2055,03	2054,003	2056,058	2055,025	0,005	R.ISSFETFGSSQLPDKGAQR.L	Q14005	IL16_HUMAN	Pro-interleukin-16 [Cleaved into: Interleukin-16 (IL-16) (Lymphocyte chemoattractant factor) (LCF)]	IL16
			2055,093	0,063	K.LEGVLA EVAQHYQDTLIR.A	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
2056,08	2055,056	2057,112	2055,093	0,991	K.LEGVLA EVAQHYQDTLIR.A	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195)	IQGAP1
2056,68 2057,00 2057,43 2057,63 2057,98	2055,649 2055,969 2056,399 2056,604 2056,952	2057,705 2058,026 2058,457 2058,662 2059,010	2058,949	0,968	R.FFESFGDLSTPDVAMGNPK.V	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2058,97	2057,945	2060,004	2058,949	0,026	R.FFESFGDLSTPDVAMGNPK.V	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2060,02 2060,99 2061,97	2058,989 2059,955 2060,944	2061,049 2062,016 2063,006							

2063,00	2061,972	2064,035	2063,933	0,929	R.EANFTVSSMHGDMPPQKER.E	P38919	IF4A3_HUMAN	Eukaryotic initiation factor 4A-III (eIF-4A-III) (eIF4A-III) (EC 3.6.4.13) (ATP-dependent RNA helicase DDX48) (ATP-dependent RNA helicase eIF4A-3) (DEAD box protein 48) (Eukaryotic initiation factor 4A-like NUK-34) (Eukaryotic translation initiation factor 4A isoform 3) (Nuclear matrix protein 265) (NMP 265) (hNMP 265) [Cleaved into: Eukaryotic initiation factor 4A-III, N-terminally processed]	EIF4A3
2063,62	2062,587	2064,651	2063,933	0,314	R.EANFTVSSMHGDMPPQKER.E	P38919	IF4A3_HUMAN	Eukaryotic initiation factor 4A-III (eIF-4A-III) (eIF4A-III) (EC 3.6.4.13) (ATP-dependent RNA helicase DDX48) (ATP-dependent RNA helicase eIF4A-3) (DEAD box protein 48) (Eukaryotic initiation factor 4A-like NUK-34) (Eukaryotic translation initiation factor 4A isoform 3) (Nuclear matrix protein 265) (NMP 265) (hNMP 265) [Cleaved into: Eukaryotic initiation factor 4A-III, N-terminally processed]	EIF4A3
			2064,091	0,472	K.HSQFIGYPITLFVEKER.D	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
2064,59	2063,562	2065,627	2064,928	0,333	R.QQHEGAQGALDSGEPPQCR.S	P33241	LSP1_HUMAN	Lymphocyte-specific protein 1 (47 kDa actin-binding protein) (52 kDa phosphoprotein) (pp52) (Lymphocyte-specific antigen WP34)	LSP1
			2064,938	0,343	R.QLNKHVDGYSYTFGER.Y	P01023	A2MG_HUMAN	Alpha-2-macroglobulin (Alpha-2-M) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 5)	A2M
			2064,091	0,503	K.HSQFIGYPITLFVEKER.D	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1
			2063,933	0,661	R.EANFTVSSMHGDMPPQKER.E	P38919	IF4A3_HUMAN	Eukaryotic initiation factor 4A-III (eIF-4A-III) (eIF4A-III) (EC 3.6.4.13) (ATP-dependent RNA helicase DDX48) (ATP-dependent RNA helicase eIF4A-3) (DEAD box protein 48) (Eukaryotic initiation factor 4A-like NUK-34) (Eukaryotic translation initiation factor 4A isoform 3) (Nuclear matrix protein 265) (NMP 265) (hNMP 265) [Cleaved into: Eukaryotic initiation factor 4A-III, N-terminally processed]	EIF4A3
2065,65	2064,614	2066,680	2064,938	0,709	R.QLNKHVDGYSYTFGER.Y	P01023	A2MG_HUMAN	Alpha-2-macroglobulin (Alpha-2-M) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 5)	A2M
			2064,928	0,719	R.QQHEGAQGALDSGEPPQCR.S	P33241	LSP1_HUMAN	Lymphocyte-specific protein 1 (47 kDa actin-binding protein) (52 kDa phosphoprotein) (pp52) (Lymphocyte-specific antigen WP34)	LSP1
2065,97 2066,55 2067,02	2064,938 2065,515 2065,986	2067,004 2067,582 2068,053	2067,896	0,876	K.GDRSEDFGVNEDLADSDAR.A	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
2068,04	2067,005	2069,073	2067,896	0,143	K.GDRSEDFGVNEDLADSDAR.A	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
2068,91	2067,876	2069,945	2067,896	1,015	K.GDRSEDFGVNEDLADSDAR.A	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
2069,05 2069,97 2070,06 2070,99 2072,08	2068,020 2068,935 2069,029 2069,954 2071,046	2070,089 2071,005 2071,099 2072,025 2073,118	2072,170	0,088	K.VINDPIHGHIPLPLVR.I	Q9Y3Z3	SAMH1_HUMAN	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 (dNTPase) (EC 3.1.5.-) (Dendritic cell-derived IFNG-induced protein) (DCIP) (Monocyte protein 5) (MOP-5) (SAM domain and HD domain-containing protein 1) (hSAMHD1)	SAMHD1
2073,08	2072,043	2074,117	2072,170	0,910	K.VINDPIHGHIPLPLVR.I	Q9Y3Z3	SAMH1_HUMAN	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 (dNTPase) (EC 3.1.5.-) (Dendritic cell-derived IFNG-induced protein) (DCIP) (Monocyte protein 5) (MOP-5) (SAM domain and HD domain-containing protein 1) (hSAMHD1)	SAMHD1
2074,07	2073,035	2075,109	2074,947	0,875	R.FFESFGDLSTPDVAMGNPK.V	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2075,04	2074,004	2076,079	2074,947	0,094	R.FFESFGDLSTPDVAMGNPK.V	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2075,94	2074,903	2076,979	2076,086	0,145	K.QLQGPEKPPKPEQVESR.A	O60664	PLIN3_HUMAN	Perilipin-3 (47 kDa mannose 6-phosphate receptor-binding protein) (47 kDa MPR-binding protein) (Cargo selection protein TIP47) (Mannose-6-phosphate receptor-binding protein 1) (Placental protein 17) (PP17)	PLIN3
			2076,194	0,253	K.AIPDLTAPVAAVQAAVSNLVR.V	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL
			2074,947	0,994	R.FFESFGDLSTPDVAMGNPK.V	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2076,07	2075,030	2077,106	2076,086	0,019	K.QLQGPEKPPKPEQVESR.A	O60664	PLIN3_HUMAN	Perilipin-3 (47 kDa mannose 6-phosphate receptor-binding protein) (47 kDa MPR-binding protein) (Cargo selection protein TIP47) (Mannose-6-phosphate receptor-binding protein 1) (Placental protein 17) (PP17)	PLIN3
			2076,194	0,126	K.AIPDLTAPVAAVQAAVSNLVR.V	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL
2077,05	2076,013	2078,090	2076,194	0,857	K.AIPDLTAPVAAVQAAVSNLVR.V	P18206	VINC_HUMAN	Vinculin (Metavinculin) (MV)	VCL

			2076,086	0,965	K.LLQGEPEKPPKEQVESR.A	O60664	PLIN3_HUMAN	Perilipin-3 (47 kDa mannose 6-phosphate receptor-binding protein) (47 kDa MPR-binding protein) (Cargo selection protein TIP47) (Mannose-6-phosphate receptor-binding protein 1) (Placental protein 17) (PP17)	PLIN3
2078,05 2079,04	2077,013 2077,996	2079,091 2080,075	2080,071	1,036	R.VFEVSLADLQNDEVAFRK.F	P61247	RS3A_HUMAN	40S ribosomal protein S3a (Small ribosomal subunit protein eS1) (v-fos transformation effector protein) (Fte-1)	RP53A
2079,69	2078,648	2080,727	2080,071	0,383	R.VFEVSLADLQNDEVAFRK.F	P61247	RS3A_HUMAN	40S ribosomal protein S3a (Small ribosomal subunit protein eS1) (v-fos transformation effector protein) (Fte-1)	RP53A
2080,01	2078,971	2081,051	2080,071	0,060	R.VFEVSLADLQNDEVAFRK.F	P61247	RS3A_HUMAN	40S ribosomal protein S3a (Small ribosomal subunit protein eS1) (v-fos transformation effector protein) (Fte-1)	RP53A
			2081,037	1,026	R.HTFMGVVSLGSPSGEVSHPR.K	P02765	FETUA_HUMAN	Alpha-2-HS-glycoprotein (Alpha-2-Z-globulin) (Ba-alpha-2-glycoprotein) (Fetuin-A) [Cleaved into: Alpha-2-HS-glycoprotein chain A; Alpha-2-HS-glycoprotein chain B]	AHSG
2080,66	2079,617	2081,697	2081,037	0,380	R.HTFMGVVSLGSPSGEVSHPR.K	P02765	FETUA_HUMAN	Alpha-2-HS-glycoprotein (Alpha-2-Z-globulin) (Ba-alpha-2-glycoprotein) (Fetuin-A) [Cleaved into: Alpha-2-HS-glycoprotein chain A; Alpha-2-HS-glycoprotein chain B]	AHSG
			2080,071	0,586	R.VFEVSLADLQNDEVAFRK.F	P61247	RS3A_HUMAN	40S ribosomal protein S3a (Small ribosomal subunit protein eS1) (v-fos transformation effector protein) (Fte-1)	RP53A
2081,01	2079,973	2082,054	2081,037	0,024	R.HTFMGVVSLGSPSGEVSHPR.K	P02765	FETUA_HUMAN	Alpha-2-HS-glycoprotein (Alpha-2-Z-globulin) (Ba-alpha-2-glycoprotein) (Fetuin-A) [Cleaved into: Alpha-2-HS-glycoprotein chain A; Alpha-2-HS-glycoprotein chain B]	AHSG
			2080,071	0,942	R.VFEVSLADLQNDEVAFRK.F	P61247	RS3A_HUMAN	40S ribosomal protein S3a (Small ribosomal subunit protein eS1) (v-fos transformation effector protein) (Fte-1)	RP53A
			2081,998	0,984	K.FYPEDVSEELIQDITQR.L	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
2082,02	2080,982	2083,064	2081,998	0,025	K.FYPEDVSEELIQDITQR.L	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			2081,037	0,986	R.HTFMGVVSLGSPSGEVSHPR.K	P02765	FETUA_HUMAN	Alpha-2-HS-glycoprotein (Alpha-2-Z-globulin) (Ba-alpha-2-glycoprotein) (Fetuin-A) [Cleaved into: Alpha-2-HS-glycoprotein chain A; Alpha-2-HS-glycoprotein chain B]	AHSG
2083,03	2081,984	2084,067	2083,918	0,892	K.IIHEDGYSEECRQYR.A	P04899	GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2 (Adenylate cyclase-inhibiting G alpha protein)	GNAI2
			2081,998	1,028	K.FYPEDVSEELIQDITQR.L	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
2084,01	2082,971	2085,055	2083,918	0,095	K.IIHEDGYSEECRQYR.A	P04899	GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2 (Adenylate cyclase-inhibiting G alpha protein)	GNAI2
			2084,947	0,934	R.AQAVSEDAGGNEGRAAEAEPR.A	P55884	EIF3B_HUMAN	Eukaryotic translation initiation factor 3 subunit B (eIF3b) (Eukaryotic translation initiation factor 3 subunit 9) (Prt1 homolog) (hPrt1) (eIF-3-eta) (eIF3 p110) (eIF3 p116)	EIF3B
2084,99	2083,950	2086,035	2084,947	0,045	R.AQAVSEDAGGNEGRAAEAEPR.A	P55884	EIF3B_HUMAN	Eukaryotic translation initiation factor 3 subunit B (eIF3b) (Eukaryotic translation initiation factor 3 subunit 9) (Prt1 homolog) (hPrt1) (eIF-3-eta) (eIF3 p110) (eIF3 p116)	EIF3B
2086,00 2086,63	2084,958 2085,586	2087,044 2087,673	2087,088 2087,088	0,458 0,458	K.GHYTEGAELVDSVLDVVRK.E K.GHYTEGAELVDSVLDVVRK.E	P07437 P68371	TB85_HUMAN TB84B_HUMAN	Tubulin beta chain (Tubulin beta-5 chain) Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB TUBB4B
2086,94	2085,900	2087,987	2087,088 2087,088	0,145 0,145	K.GHYTEGAELVDSVLDVVRK.E K.GHYTEGAELVDSVLDVVRK.E	P07437 P68371	TB85_HUMAN TB84B_HUMAN	Tubulin beta chain (Tubulin beta-5 chain) Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB TUBB4B
2087,10	2086,055	2088,142	2087,088 2087,088	0,010 0,010	K.GHYTEGAELVDSVLDVVRK.E K.GHYTEGAELVDSVLDVVRK.E	P07437 P68371	TB85_HUMAN TB84B_HUMAN	Tubulin beta chain (Tubulin beta-5 chain) Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB TUBB4B
			2088,061 2088,074	0,963 0,976	K.VGNIEKIDLMVGDEASELR.S R.IDSGLYLGSGYFTAIQNLK.K	P61160 P02788	ARP2_HUMAN TRFL_HUMAN	Actin-related protein 2 (Actin-like protein 2) Lactotransferrin (Lactoferrin) (EC 3.4.21.-) (Growth-inhibiting protein 12) (Tala lactoferrin) [Cleaved into: Lactoferrin-H (Lfcin-H); Kallidin-1; Lactoferrin-A; Lactoferrin-B; Lactoferrin-C]	ACTR2 LTF
			2088,075	0,977	R.EAEAAIYHLQFEELRR.L	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
2088,05	2087,002	2089,090	2088,061 2088,074	0,015 0,028	K.VGNIEKIDLMVGDEASELR.S R.IDSGLYLGSGYFTAIQNLK.K	P61160 P02788	ARP2_HUMAN TRFL_HUMAN	Actin-related protein 2 (Actin-like protein 2) Lactotransferrin (Lactoferrin) (EC 3.4.21.-) (Growth-inhibiting protein 12) (Tala lactoferrin) [Cleaved into: Lactoferrin-H (Lfcin-H); Kallidin-1; Lactoferrin-A; Lactoferrin-B; Lactoferrin-C]	ACTR2 LTF
			2088,075	0,029	R.EAEAAIYHLQFEELRR.L	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
			2087,088 2087,088	0,957 0,957	K.GHYTEGAELVDSVLDVVRK.E K.GHYTEGAELVDSVLDVVRK.E	P07437 P68371	TB85_HUMAN TB84B_HUMAN	Tubulin beta chain (Tubulin beta-5 chain) Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB TUBB4B
			2089,033	0,987	K.FITHAPPGGEFNEVFNDVR.L	P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (CapZ alpha-1)	CAPZA1

2088,39	2087,344	2089,432	2088,075	0,313	R.EAEAAIYHLQFEEELRR.L	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
			2088,074	0,314	R.IDSGLYLGSGYFTAIQNLR.K	P02788	TRFL_HUMAN	Lactotransferrin (Lactoferrin) (EC 3.4.21.-) (Growth-inhibiting protein 12) (Tala lactoferrin) [Cleaved into: Lactoferricin-H (Lfcin-H); Kallistatin-1; Lactoferronin-A; Lactoferronin-B; Lactoferronin-C]	LTF
			2088,061	0,327	K.VGNIEKDLVMVGDEASELR.S	P61160	ARP2_HUMAN	Actin-related protein 2 (Actin-like protein 2)	ACTR2
			2089,033	0,645	K.FITHAPPGFNEVFNDVRL	P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (CapZ alpha-1)	CAPZA1
2089,05	2088,008	2090,097	2089,033	0,019	K.FITHAPPGFNEVFNDVRL	P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (CapZ alpha-1)	CAPZA1
			2089,998	0,946	R.ESGGAQVQVAGDMLPNSTER.A	Q15365	PCBP1_HUMAN	Poly(rC)-binding protein 1 (Alpha-CP1) (Heterogeneous nuclear ribonucleoprotein E1) (hnRNP E1) (Nucleic acid-binding protein SUB2.3)	PCBP1
			2088,075	0,977	R.EAEAAIYHLQFEEELRR.L	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
			2088,074	0,978	R.IDSGLYLGSGYFTAIQNLR.K	P02788	TRFL_HUMAN	Lactotransferrin (Lactoferrin) (EC 3.4.21.-) (Growth-inhibiting protein 12) (Tala lactoferrin) [Cleaved into: Lactoferricin-H (Lfcin-H); Kallistatin-1; Lactoferronin-A; Lactoferronin-B; Lactoferronin-C]	LTF
			2088,061	0,991	K.VGNIEKDLVMVGDEASELR.S	P61160	ARP2_HUMAN	Actin-related protein 2 (Actin-like protein 2)	ACTR2
2090,03	2088,985	2091,075	2089,998	0,032	R.ESGGAQVQVAGDMLPNSTER.A	Q15365	PCBP1_HUMAN	Poly(rC)-binding protein 1 (Alpha-CP1) (Heterogeneous nuclear ribonucleoprotein E1) (hnRNP E1) (Nucleic acid-binding protein SUB2.3)	PCBP1
			2089,033	0,997	K.FITHAPPGFNEVFNDVRL	P52907	CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 (CapZ alpha-1)	CAPZA1
2091,00	2089,957	2092,048	2091,993	0,990	R.QVQCNGPPEQVFELYQR.W	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2089,998	1,005	R.ESGGAQVQVAGDMLPNSTER.A	Q15365	PCBP1_HUMAN	Poly(rC)-binding protein 1 (Alpha-CP1) (Heterogeneous nuclear ribonucleoprotein E1) (hnRNP E1) (Nucleic acid-binding protein SUB2.3)	PCBP1
2091,01	2089,962	2092,053	2091,993	0,986	R.QVQCNGPPEQVFELYQR.W	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2089,998	1,009	R.ESGGAQVQVAGDMLPNSTER.A	Q15365	PCBP1_HUMAN	Poly(rC)-binding protein 1 (Alpha-CP1) (Heterogeneous nuclear ribonucleoprotein E1) (hnRNP E1) (Nucleic acid-binding protein SUB2.3)	PCBP1
2092,00	2090,953	2093,045	2091,993	0,007	R.QVQCNGPPEQVFELYQR.W	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2092,084	0,085	R.RPLRPQVVTDDGGAPEAK.D	Q9HDC9	APMAP_HUMAN	Adipocyte plasma membrane-associated protein (Protein BSCv)	APMAP
2092,99	2091,946	2094,039	2093,067	0,075	R.LAKVDATEESDLAQYGVGR.G	P07237	PDIA1_HUMAN	Protein disulfide-isomerase (PDI) (EC 5.3.4.1) (Cellular thyroid hormone-binding protein) (Prolyl 4-hydroxylase subunit beta) (p55)	P4HB
			2093,072	0,080	K.YMNSGPVVMVWEGLVVVK.T	P22392	NDKB_HUMAN	Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (EC 2.7.4.6) (C-myc purine-binding transcription factor PUF) (Histidine protein kinase NDKB) (EC 2.7.13.3) (nm23-H2)	NME2
			2093,146	0,154	R.VSLAADRGGADVASIHLTLAR.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2092,084	0,908	R.RPLRPQVVTDDGGAPEAK.D	Q9HDC9	APMAP_HUMAN	Adipocyte plasma membrane-associated protein (Protein BSCv)	APMAP
			2091,993	0,999	R.QVQCNGPPEQVFELYQR.W	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2094,02	2092,975	2095,070	2094,060	0,038	K.SYELPDGQVITIGNERFR.C	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			2094,060	0,038	K.SYELPDGQVITIGNERFR.C	Q6S8J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			2094,060	0,038	K.SYELPDGQVITIGNERFR.C	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2094,060	0,038	R.SYELPDGQVITIGNERFR.C	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
			2094,101	0,079	K.HSQFQGYPTLYLEKER.E	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			2093,146	0,876	R.VSLAADRGGADVASIHLTLAR.A	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2093,072	0,951	K.YMNSGPVVMVWEGLVVVK.T	P22392	NDKB_HUMAN	Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (EC 2.7.4.6) (C-myc purine-binding transcription factor PUF) (Histidine protein kinase NDKB) (EC 2.7.13.3) (nm23-H2)	NME2
			2093,067	0,955	R.LAKVDATEESDLAQYGVGR.G	P07237	PDIA1_HUMAN	Protein disulfide-isomerase (PDI) (EC 5.3.4.1) (Cellular thyroid hormone-binding protein) (Prolyl 4-hydroxylase subunit beta) (p55)	P4HB
2095,03	2093,983	2096,078	2094,101	0,929	K.HSQFQGYPTLYLEKER.E	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			2095,969	0,938	K.AAGIDQENWHEGKENIR.A	P28838	AMPL_HUMAN	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase 3) (LAP-3) (Leucyl aminopeptidase) (Peptidase 5) (Proline aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase)	LAP3
			2095,992	0,961	R.INNVPAEGENEVNNELANR.M	Q9NUQ9	FA49B_HUMAN	Protein FAM49B (L1)	FAM49B
			2094,060	0,970	K.SYELPDGQVITIGNERFR.C	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			2094,060	0,970	K.SYELPDGQVITIGNERFR.C	Q6S8J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE
			2094,060	0,970	K.SYELPDGQVITIGNERFR.C	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2094,060	0,970	R.SYELPDGQVITIGNERFR.C	Q562R1	ACTBL_HUMAN	Beta-actin-like protein 2 (Kappa-actin)	ACTBL2
2096,02	2094,969	2097,065	2095,992	0,026	R.INNVPAEGENEVNNELANR.M	Q9NUQ9	FA49B_HUMAN	Protein FAM49B (L1)	FAM49B

2096,91	2095,861	2097,957	2095,969	0,049	K.AAGIDQEQNWHEGKENIR.A	P28838	AMPL_HUMAN	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase 3) (LAP-3) (Leucyl aminopeptidase) (Peptidase S) (Proline aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase)	LAP3
			2096,991	0,974	R.GTVTDFPGFDERADAETLR.K	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
			2097,043	1,026	R.VAPAEQPEAPDSTAAGGSASKR.M	Q3LXA3	TKFC_HUMAN	Triokinase/FMN cyclase (Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)) [Includes: ATP-dependent dihydroxyacetone kinase (DHA kinase) (EC 2.7.1.28) (EC 2.7.1.29) (Glycerone kinase) (Triokinase) (Triose kinase); FAD-AMP lyase (cyclizing) (EC 4.6.1.15) (FAD-AMP lyase (cyclic FMN forming)) (FMN cyclase)]	TKFC
			2096,991	0,082	R.GTVTDFPGFDERADAETLR.K	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
			2097,043	0,134	R.VAPAEQPEAPDSTAAGGSASKR.M	Q3LXA3	TKFC_HUMAN	Triokinase/FMN cyclase (Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)) [Includes: ATP-dependent dihydroxyacetone kinase (DHA kinase) (EC 2.7.1.28) (EC 2.7.1.29) (Glycerone kinase) (Triokinase) (Triose kinase); FAD-AMP lyase (cyclizing) (EC 4.6.1.15) (FAD-AMP lyase (cyclic FMN forming)) (FMN cyclase)]	TKFC
			2095,992	0,918	R.INNVPAEGENEVNNELANR.M	Q9NUQ9	FA49B_HUMAN	Protein FAM49B (L1)	FAM49B
			2095,969	0,941	K.AAGIDQEQNWHEGKENIR.A	P28838	AMPL_HUMAN	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase 3) (LAP-3) (Leucyl aminopeptidase) (Peptidase S) (Proline aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase)	LAP3
			2097,043	0,024	R.VAPAEQPEAPDSTAAGGSASKR.M	Q3LXA3	TKFC_HUMAN	Triokinase/FMN cyclase (Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)) [Includes: ATP-dependent dihydroxyacetone kinase (DHA kinase) (EC 2.7.1.28) (EC 2.7.1.29) (Glycerone kinase) (Triokinase) (Triose kinase); FAD-AMP lyase (cyclizing) (EC 4.6.1.15) (FAD-AMP lyase (cyclic FMN forming)) (FMN cyclase)]	TKFC
			2096,991	0,076	R.GTVTDFPGFDERADAETLR.K	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
			2097,043	0,977	R.VAPAEQPEAPDSTAAGGSASKR.M	Q3LXA3	TKFC_HUMAN	Triokinase/FMN cyclase (Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)) [Includes: ATP-dependent dihydroxyacetone kinase (DHA kinase) (EC 2.7.1.28) (EC 2.7.1.29) (Glycerone kinase) (Triokinase) (Triose kinase); FAD-AMP lyase (cyclizing) (EC 4.6.1.15) (FAD-AMP lyase (cyclic FMN forming)) (FMN cyclase)]	TKFC
2098,02	2096,971	2099,069	2096,991	1,029	R.GTVTDFPGFDERADAETLR.K	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
			2101,057	0,991	K.FIIHAPPGEFNEVFNDVR.L	P47755	CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 (CapZ alpha-2)	CAPZA2
2098,93 2099,08 2099,92 2100,07	2097,880 2098,035 2098,868 2099,016	2099,979 2100,134 2100,968 2101,116	2101,057	0,991	K.FIIHAPPGEFNEVFNDVR.L	P47755	CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 (CapZ alpha-2)	CAPZA2
			2102,018	1,042	R.TSAEAPSHHLQQQQQQQR.L	Q92609	TBCD5_HUMAN	TBC1 domain family member 5	TBC1D5
2101,98	2100,925	2103,027	2102,018	0,041	R.TSAEAPSHHLQQQQQQQR.L	Q92609	TBCD5_HUMAN	TBC1 domain family member 5	TBC1D5
			2101,057	0,919	K.FIIHAPPGEFNEVFNDVR.L	P47755	CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 (CapZ alpha-2)	CAPZA2
2102,97	2101,915	2104,018	2102,018	0,949	R.TSAEAPSHHLQQQQQQQR.L	Q92609	TBCD5_HUMAN	TBC1 domain family member 5	TBC1D5
2104,07	2103,013	2105,118	2104,084	0,018	R.AAMKGLTGDEDTIEILASR.T	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
			2104,127	0,062	R.ILEAHQNVAQLSLAEQQLR.F	Q86UX7	URP2_HUMAN	Fermitin family homolog 3 (Kindlin-3) (MIG2-like protein) (Unc-112-related protein 2)	FERMT3
			2105,099	1,033	K.VFLENVIRDAVITYTEHAK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4

2105,04	2103,989	2106,094	2105,099	0,057	K.VFLENVIRDAVITYTEHAK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
			2105,903	0,861	K.RNTSSDNSDEVMPAQSPR.E	Q9HCK8	CHD8_HUMAN	Chromodomain-helicase-DNA-binding protein 8 (CHD-8) (EC 3.6.4.12) (ATP-dependent helicase CHD8) (Helicase with SNF2 domain 1)	CHD8
			2104,127	0,914	R.ILEAHQNVAQLSLAEALQR.F	Q86UX7	URP2_HUMAN	Fermitin family homolog 3 (Kindlin-3) (MIG2-like protein) (Unc-112-related protein 2)	FERMT3
			2104,084	0,957	R.AAMKGLGTDEDTJELASR.T	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
2106,01	2104,953	2107,059	2105,903	0,103	K.RNTSSDNSDEVMPAQSPR.E	Q9HCK8	CHD8_HUMAN	Chromodomain-helicase-DNA-binding protein 8 (CHD-8) (EC 3.6.4.12) (ATP-dependent helicase CHD8) (Helicase with SNF2 domain 1)	CHD8
			2105,099	0,907	K.VFLENVIRDAVITYTEHAK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
2106,04	2104,982	2107,088	2105,903	0,133	K.RNTSSDNSDEVMPAQSPR.E	Q9HCK8	CHD8_HUMAN	Chromodomain-helicase-DNA-binding protein 8 (CHD-8) (EC 3.6.4.12) (ATP-dependent helicase CHD8) (Helicase with SNF2 domain 1)	CHD8
			2105,099	0,937	K.VFLENVIRDAVITYTEHAK.R	P62805	H4_HUMAN	Histone H4	HIST1H4A; HIST1H4B; HIST1H4C; HIST1H4D; HIST1H4E; HIST1H4F; HIST1H4H; HIST1H4I; HIST1H4J; HIST1H4K; HIST1H4L; HIST2H4A; HIST2H4B; HIST4H4
2106,98	2105,925	2108,032	2107,098	0,119	K.IGEHTPSALAIMENANVLAR.Y	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
			2107,112	0,133	K.REEAPSLRPAPPPISGGGYR.A	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
2107,02	2105,964	2108,071	2107,098	0,080	K.IGEHTPSALAIMENANVLAR.Y	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
			2107,112	0,094	K.REEAPSLRPAPPPISGGGYR.A	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
2108,01	2106,959	2109,067	2107,112	0,901	K.REEAPSLRPAPPPISGGGYR.A	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
			2107,098	0,915	K.IGEHTPSALAIMENANVLAR.Y	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA
2109,06 2110,03 2111,05 2112,03 2113,03	2108,004 2108,979 2109,992 2110,972 2111,972	2110,113 2111,089 2112,103 2113,084 2114,085	2113,141	0,113	R.ALMLQGVLLADAVAVTMGPK.G	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
2114,03	2112,973	2115,087	2113,141	0,888	R.ALMLQGVLLADAVAVTMGPK.G	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
2115,10	2114,043	2116,158	2116,002	0,902	K.TTHFVEGGDAGNREDQINR.L	P18124	RL7_HUMAN	60S ribosomal protein L7 (Large ribosomal subunit protein uL30)	RPL7
2116,10	2115,044	2117,160	2116,002	0,099	K.TTHFVEGGDAGNREDQINR.L	P18124	RL7_HUMAN	60S ribosomal protein L7 (Large ribosomal subunit protein uL30)	RPL7
2117,10	2116,043	2118,160	2117,924	0,823	K.LSEGSQPAEEEDQETPSR.N	Q9UKV3	ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus (Acinus)	ACIN1
2118,09	2117,029	2119,147	2117,924	0,164	K.LSEGSQPAEEEDQETPSR.N	Q9UKV3	ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus (Acinus)	ACIN1
2118,09	2117,029	2119,147	2117,924	0,164	K.LSEGSQPAEEEDQETPSR.N	Q9UKV3	ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus (Acinus)	ACIN1
2119,08	2118,025	2120,144	2120,051	0,966	R.GLGGEVPSHQGPDPYRQLR.E	Q6UW68	TM205_HUMAN	Transmembrane protein 205	TMEM205
2120,07	2119,011	2121,131	2120,051	0,020	R.GLGGEVPSHQGPDPYRQLR.E	Q6UW68	TM205_HUMAN	Transmembrane protein 205	TMEM205

			2121,038	0,967	K.ALRTDYNASVSPDSSGPER.I	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
2121,01	2119,946	2122,067	2121,038	0,031	K.ALRTDYNASVSPDSSGPER.I	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
			2120,051	0,956	R.GLGGEVPGSHQGPDPYRQLR.E	Q6UW68	TM205_HUMAN	Transmembrane protein 205	TMEM205
2121,99	2120,925	2123,047	2122,186	0,200	K.LLAALLEDEGGSGRPLLQAAK.G	Q9Y490	TLN1_HUMAN	Talin-1	TLN1
			2121,038	0,949	K.ALRTDYNASVSPDSSGPER.I	P61978	HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK
2122,98	2121,919	2124,042	2122,186	0,795	K.LLAALLEDEGGSGRPLLQAAK.G	Q9Y490	TLN1_HUMAN	Talin-1	TLN1
2123,98	2122,920	2125,044							
2125,02	2123,962	2126,087	2125,151	0,127	K.AQFAQPEILIGTIPGAGGTQRL	P30084	ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial (EC 4.2.1.17) (Enoyl-CoA hydratase 1) (Short-chain enoyl-CoA hydratase) (SCEH)	ECHS1
2126,05	2124,984	2127,110	2125,151	0,895	K.AQFAQPEILIGTIPGAGGTQRL	P30084	ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial (EC 4.2.1.17) (Enoyl-CoA hydratase 1) (Short-chain enoyl-CoA hydratase) (SCEH)	ECHS1
2127,06	2125,993	2128,120	2127,153	0,096	K.QVDQFLGVPIAAPLAERR.F	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2128,101	1,044	R.GGHFAAFEEPELLAQDIRK.F	P07099	HYEP_HUMAN	Epoxide hydrolase 1 (EC 3.3.2.9) (Epoxide hydratase) (Microsomal epoxide hydrolase) (mEH)	EPHX1
2128,05	2126,987	2129,115	2128,101	0,050	R.GGHFAAFEEPELLAQDIRK.F	P07099	HYEP_HUMAN	Epoxide hydrolase 1 (EC 3.3.2.9) (Epoxide hydratase) (Microsomal epoxide hydrolase) (mEH)	EPHX1
			2127,153	0,898	K.QVDQFLGVPIAAPLAERR.F	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2129,02	2127,959	2130,088	2129,135	0,112	R.ALMLQGVLDLADAVAVTMGPK.G	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
			2129,180	0,157	R.DLEKPFLLPVEAVSVPGR.G	P49411	EFTU_HUMAN	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	TUFM
			2128,101	0,923	R.GGHFAAFEEPELLAQDIRK.F	P07099	HYEP_HUMAN	Epoxide hydrolase 1 (EC 3.3.2.9) (Epoxide hydratase) (Microsomal epoxide hydrolase) (mEH)	EPHX1
2130,05	2128,984	2131,114	2130,110	0,061	R.TLSDYNIQKESTLHLVLR.L	P62987	RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 (CEP52) (Ubiquitin A-52 residue ribosomal protein fusion product 1) [Cleaved into: Ubiquitin; 60S ribosomal protein L40 (Large ribosomal subunit protein eL40)]	UBA52
			2130,227	0,178	R.QIIQNPSLLPALLQIQIGR.E	P54727	RD23B_HUMAN	UV excision repair protein RAD23 homolog B (HR23B) (hHR23B) (XP-C repair-complementing complex 58 kDa protein) (p58)	RAD23B
			2129,180	0,869	R.DLEKPFLLPVEAVSVPGR.G	P49411	EFTU_HUMAN	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	TUFM
			2129,135	0,914	R.ALMLQGVLDLADAVAVTMGPK.G	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
			2130,969	0,920	R.YTTPEDATPEPGEDPRVTR.A	P63092	GNA52_HUMAN	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short (Adenylate cyclase-stimulating G alpha protein)	GNA5
2131,06	2129,995	2132,126	2130,969	0,091	R.YTTPEDATPEPGEDPRVTR.A	P63092	GNA52_HUMAN	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short (Adenylate cyclase-stimulating G alpha protein)	GNA5
			2130,227	0,834	R.QIIQNPSLLPALLQIQIGR.E	P54727	RD23B_HUMAN	UV excision repair protein RAD23 homolog B (HR23B) (hHR23B) (XP-C repair-complementing complex 58 kDa protein) (p58)	RAD23B
			2130,110	0,950	R.TLSDYNIQKESTLHLVLR.L	P62987	RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 (CEP52) (Ubiquitin A-52 residue ribosomal protein fusion product 1) [Cleaved into: Ubiquitin; 60S ribosomal protein L40 (Large ribosomal subunit protein eL40)]	UBA52
2132,07	2131,007	2133,139							
2133,07	2132,004	2134,137							
2134,05	2132,987	2135,121							
2135,04	2133,974	2136,109							
2137,08	2136,013	2138,150							
2138,08	2137,015	2139,153							
2139,07	2137,999	2140,138	2140,094	1,025	R.RGHLFLQTDQPIYNPGQQR.V	P0C0L5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
2140,07	2138,997	2141,138	2140,094	0,026	R.RGHLFLQTDQPIYNPGQQR.V	P0C0L5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
			2141,104	1,036	K.SPYLYPLYGLGELPQGFAR.L	P31150	GDIA_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			2141,104	1,036	K.SPYLYPLYGLGELPQGFAR.L	P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
2141,06	2139,994	2142,135	2141,104	0,039	K.SPYLYPLYGLGELPQGFAR.L	P31150	GDIA_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			2141,104	0,039	K.SPYLYPLYGLGELPQGFAR.L	P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2

			2140,094	0,971	R.RGHLFLQTDQPIYNPGQR.V	P0COL5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleared into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
2142,05	2140,983	2143,125	2141,104	0,951	K.SPLYLYPLYLGLGELPQGFAR.L	P31150	GDIA_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			2141,104	0,951	K.SPLYLYPLYLGLGELPQGFAR.L	P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
2143,02	2141,950	2144,093	2144,001	0,979	R.EGQEQQLTKDYGN SPLHR.F	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
2144,03	2142,958	2145,102	2144,001	0,030	R.EGQEQQLTKDYGN SPLHR.F	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
2145,03	2143,960	2146,105	2144,001	1,031	R.EGQEQQLTKDYGN SPLHR.F	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
2146,05	2144,975	2147,121	2146,171	0,123	R.AHVIVMAATNRPNSDPALR.R	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (155 Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
2147,05	2145,980	2148,128	2146,171	0,883	R.AHVIVMAATNRPNSDPALR.R	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (155 Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
2148,05	2146,980	2149,128	2148,198	0,144	K.TLLGDGPVVTDPKAPNVVVTR.L	P52566	GDIR2_HUMAN	Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Ly-GDI) (Rho-GDI beta)	ARHGDIB
2149,05	2147,975	2150,124	2148,198	0,852	K.TLLGDGPVVTDPKAPNVVVTR.L	P52566	GDIR2_HUMAN	Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Ly-GDI) (Rho-GDI beta)	ARHGDIB
			2150,085	1,036	R.THNLEPYFESFINNLR.R	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
2150,04	2148,967	2151,117	2150,085	0,043	R.THNLEPYFESFINNLR.R	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
			2151,093	1,052	K.FDLGQDVIDFTGHALALYR.T	P31150	GDIA_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			2151,093	1,052	K.FDLGQDVIDFTGHALALYR.T	P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
2151,04	2149,969	2152,120	2151,093	0,049	K.FDLGQDVIDFTGHALALYR.T	P31150	GDIA_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			2151,093	0,049	K.FDLGQDVIDFTGHALALYR.T	P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
			2150,085	0,959	R.THNLEPYFESFINNLR.R	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
2152,05	2150,971	2153,123	2151,093	0,953	K.FDLGQDVIDFTGHALALYR.T	P31150	GDIA_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			2151,093	0,953	K.FDLGQDVIDFTGHALALYR.T	P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
			2153,009	0,962	K.MVEAAKGAAAHPDSEEQQR.L	Q9Y490	TLN1_HUMAN	Talin-1	TLN1
2153,06	2151,986	2154,139	2153,009	0,053	K.MVEAAKGAAAHPDSEEQQR.L	Q9Y490	TLN1_HUMAN	Talin-1	TLN1
			2154,070	1,008	R.EIFDSRGNPTVEVDLFTSK.G	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
2154,06	2152,985	2155,139	2154,070	0,008	R.EIFDSRGNPTVEVDLFTSK.G	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			2153,009	1,053	K.MVEAAKGAAAHPDSEEQQR.L	Q9Y490	TLN1_HUMAN	Talin-1	TLN1
2155,06	2153,986	2156,141	2154,070	0,994	R.EIFDSRGNPTVEVDLFTSK.G	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
2156,01	2154,934	2157,090							
2157,02	2155,937	2158,094	2157,105	0,089	R.VELKGTVRPANDFNPDADAK.A	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6
2158,05	2156,968	2159,126	2157,105	0,943	R.VELKGTVRPANDFNPDADAK.A	P08133	ANXA6_HUMAN	Annexin A6 (67 kDa calelectrin) (Annexin VI) (Annexin-6) (Calphobindin-II) (CPB-II) (Chromobindin-20) (Lipocortin VI) (Protein III) (p68) (p70)	ANXA6

2159,05	2157,973	2160,132	2160,120	1,067	R.QLVEQVEQIQKEQNYQR.W	Q98VK6	TMED9_HUMAN	Transmembrane emp24 domain-containing protein 9 (GMP25) (Glycoprotein 25L2) (p24 family protein alpha-2) (p24alpha2) (p25)	TMED9
2160,06	2158,978	2161,138	2160,120	0,061	R.QLVEQVEQIQKEQNYQR.W	Q98VK6	TMED9_HUMAN	Transmembrane emp24 domain-containing protein 9 (GMP25) (Glycoprotein 25L2) (p24 family protein alpha-2) (p24alpha2) (p25)	TMED9
			2160,960	0,901	K.AQPAQPADEPAEKADEPMEH.-	P25786	PSA1_HUMAN	Proteasome subunit alpha type-1 (EC 3.4.25.1) (30 kDa prosomal protein) (PROS-30) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome component C2) (Proteasome nu chain)	PSMA1
			2161,102	1,044	R.QLLDQVEQIQKEQDYQR.Y	Q7Z7H5	TMED4_HUMAN	Transmembrane emp24 domain-containing protein 4 (Endoplasmic reticulum stress-response protein 25) (ERS25) (GMP25iso) (Putative NF-kappa-B-activating protein 156) (p24 family protein alpha-3) (p24alpha3)	TMED4
2161,06	2159,981	2162,142	2161,102	0,040	R.QLLDQVEQIQKEQDYQR.Y	Q7Z7H5	TMED4_HUMAN	Transmembrane emp24 domain-containing protein 4 (Endoplasmic reticulum stress-response protein 25) (ERS25) (GMP25iso) (Putative NF-kappa-B-activating protein 156) (p24 family protein alpha-3) (p24alpha3)	TMED4
			2160,960	0,102	K.AQPAQPADEPAEKADEPMEH.-	P25786	PSA1_HUMAN	Proteasome subunit alpha type-1 (EC 3.4.25.1) (30 kDa prosomal protein) (PROS-30) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome component C2) (Proteasome nu chain)	PSMA1
			2160,120	0,942	R.QLVEQVEQIQKEQNYQR.W	Q98VK6	TMED9_HUMAN	Transmembrane emp24 domain-containing protein 9 (GMP25) (Glycoprotein 25L2) (p24 family protein alpha-2) (p24alpha2) (p25)	TMED9
2162,06	2160,982	2163,144	2161,102	0,961	R.QLLDQVEQIQKEQDYQR.Y	Q7Z7H5	TMED4_HUMAN	Transmembrane emp24 domain-containing protein 4 (Endoplasmic reticulum stress-response protein 25) (ERS25) (GMP25iso) (Putative NF-kappa-B-activating protein 156) (p24 family protein alpha-3) (p24alpha3)	TMED4
			2163,066	1,003	R.FGQAATMEGIGAIGTTPAFNR.A	Q15233	NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrb)) (p54nrb)	NONO
2163,99	2162,907	2165,071	2164,080	0,091	R.ISGASEKDIVHSGLAYTMER.S	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			2163,066	0,923	R.FGQAATMEGIGAIGTTPAFNR.A	Q15233	NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrb)) (p54nrb)	NONO
			2164,987	0,997	R.IEIESFYEGEDFSETLTR.A	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
2164,98	2163,898	2166,063	2164,987	0,007	R.IEIESFYEGEDFSETLTR.A	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			2164,080	0,900	R.ISGASEKDIVHSGLAYTMER.S	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
2166,00	2164,913	2167,079	2164,987	1,009	R.IEIESFYEGEDFSETLTR.A	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BiP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
2167,02	2165,935	2168,102	2168,119	0,127	R.GENLVSMTEVGPPPKDTGIAR.V	P14678	RSMB_HUMAN	Small nuclear ribonucleoprotein-associated proteins B and B' (snRNP-B) (5m protein B/B') (5m-B/B') (5mB/B')	SNRPB
2167,99	2166,908	2169,076	2168,198	0,206	R.QLTLGGPTNTGAALFVLR.N	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			2169,065	1,072	R.NLHQSGFSLGAQIDDNIPR.R	Q16555	DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) (Unc-33-like phosphoprotein 2) (ULIP-2)	DPYSL2
2168,98	2167,892	2170,061	2169,065	0,088	R.NLHQSGFSLGAQIDDNIPR.R	Q16555	DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) (Unc-33-like phosphoprotein 2) (ULIP-2)	DPYSL2
			2168,198	0,779	R.QLTLGGPTNTGAALFVLR.N	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			2168,119	0,858	R.GENLVSMTEVGPPPKDTGIAR.V	P14678	RSMB_HUMAN	Small nuclear ribonucleoprotein-associated proteins B and B' (snRNP-B) (5m protein B/B') (5m-B/B') (5mB/B')	SNRPB
2169,99	2168,910	2171,080	2169,065	0,930	R.NLHQSGFSLGAQIDDNIPR.R	Q16555	DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) (Unc-33-like phosphoprotein 2) (ULIP-2)	DPYSL2
2171,02	2169,932	2172,103	2172,244	0,227	K.LSDLAPISEQIKEVITFR.E	Q01518	CAP1_HUMAN	Adenylyl cyclase-associated protein 1 (CAP 1)	CAP1
2172,02	2170,932	2173,104	2172,244	0,767	K.LSDLAPISEQIKEVITFR.E	Q01518	CAP1_HUMAN	Adenylyl cyclase-associated protein 1 (CAP 1)	CAP1
2173,01	2171,925	2174,098	2172,244	0,211	R.AEVQKLQMEAPHIVGTGR.V	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-1 (eIF-4A-1) (eIF4A-1) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
2173,98	2172,891	2175,065	2174,189	0,211	R.AEVQKLQMEAPHIVGTGR.V	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-1 (eIF-4A-1) (eIF4A-1) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1

			2174,255	0,277	R.HEIVQTLSLKDGUPLDIR.F	Q13228	SBP1_HUMAN	Methanethiol oxidase (MTO) (EC 1.8.3.4) (56 kDa selenium-binding protein) (SBP56) (SP56) (Selenium-binding protein 1)	SELENBP1
2175,03	2173,946	2176,121	2175,161 2174,255	0,128 0,778	K.SRLEDIPVASLPDLHDIER.A R.HEIVQTLSLKDGUPLDIR.F	P01266 Q13228	THYG_HUMAN SBP1_HUMAN	Thyroglobulin (Tg) Methanethiol oxidase (MTO) (EC 1.8.3.4) (56 kDa selenium-binding protein) (SBP56) (SP56) (Selenium-binding protein 1)	TG SELENBP1
			2174,189	0,845	R.AEVQLKQMEAPHIVGTPGR.V	P60842	IF4A1_HUMAN	Eukaryotic initiation factor 4A-1 (eIF-4A-1) (eIF4A-1) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1
			2176,074	1,040	K.AGYTDKVGMDVAASEFFR.S	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
2176,04	2174,956	2177,132	2176,074	0,030	K.AGYTDKVGMDVAASEFFR.S	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
			2175,161 2176,952	0,883 0,908	K.SRLEDIPVASLPDLHDIER.A R.YHTSQSGDEMTSLSEYVSR.M	P01266 P08238	THYG_HUMAN HS90B_HUMAN	Thyroglobulin (Tg) Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	TG HSP90AB1
2177,06	2175,971	2178,148	2176,952	0,107	R.YHTSQSGDEMTSLSEYVSR.M	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			2176,074	0,986	K.AGYTDKVGMDVAASEFFR.S	P06733	ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1
2178,06	2176,973	2179,151	2179,123	1,061	K.IHVFYIDYGNREVLPSR.L	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
2179,07	2177,976	2180,155	2179,123	0,058	K.IHVFYIDYGNREVLPSR.L	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
2180,04	2178,948	2181,128	2179,123	0,915	K.IHVFYIDYGNREVLPSR.L	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
2181,03 2182,04 2183,05	2179,941 2180,948 2181,962	2182,122 2183,130 2184,145	2184,107	1,053	K.DTDAAVGDNIGYITFVLFPR.H	O15144	ARPC2_HUMAN	Actin-related protein 2/3 complex subunit 2 (Arp2/3 complex 34 kDa subunit) (p34-ARC)	ARPC2
2184,03	2182,934	2185,118	2184,107 2185,043	0,081 1,017	K.DTDAAVGDNIGYITFVLFPR.H K.SLAGSSGPGASSGTSGDHGELVVR.I	O15144 P29692	ARPC2_HUMAN EF1D_HUMAN	Actin-related protein 2/3 complex subunit 2 (Arp2/3 complex 34 kDa subunit) (p34-ARC) Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO-4)	ARPC2 EEF1D
2185,04	2183,944	2186,129	2185,043 2184,107	0,007 0,930	K.SLAGSSGPGASSGTSGDHGELVVR.I K.DTDAAVGDNIGYITFVLFPR.H	P29692 O15144	EF1D_HUMAN ARPC2_HUMAN	Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO-4) Actin-related protein 2/3 complex subunit 2 (Arp2/3 complex 34 kDa subunit) (p34-ARC)	EEF1D ARPC2
2186,01	2184,914	2187,100	2186,969 2185,043	0,961 0,964	R.EMEENFAVEAANYQDTIGR.L K.SLAGSSGPGASSGTSGDHGELVVR.I	P08670 P29692	VIME_HUMAN EF1D_HUMAN	Vimentin Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO-4)	VIM EEF1D
2186,98	2185,886	2188,073	2186,969	0,011	R.EMEENFAVEAANYQDTIGR.L	P08670	VIME_HUMAN	Vimentin	VIM
2187,97	2186,878	2189,066	2186,969	1,004	R.EMEENFAVEAANYQDTIGR.L	P08670	VIME_HUMAN	Vimentin	VIM
2188,99	2187,895	2190,084	2189,922 2190,015	0,932 1,025	R.NMGPGYGGNGYPGSGSGSGGYGGR.S R.NEHVDYVDVGGAYVGTQNR.I	P22626 P21397	ROA2_HUMAN AOFA_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1) Amine oxidase [flavin-containing] A (EC 1.4.3.4) (Monoamine oxidase type A) (MAO-A)	HNRNPA2B1 MAOA
2189,97	2188,874	2191,064	2190,015 2189,922 2190,096	0,046 0,047 0,128	R.NEHVDYVDVGGAYVGTQNR.I R.NMGPGYGGNGYPGSGSGSGGYGGR.S R.DGHFTLFAPTNEAFELPR.G	P21397 P22626 Q15063	AOFA_HUMAN ROA2_HUMAN POSTN_HUMAN	Amine oxidase [flavin-containing] A (EC 1.4.3.4) (Monoamine oxidase type A) (MAO-A) Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1) Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	MAOA HNRNPA2B1 POSTN
2191,00	2189,902	2192,093	2191,086 2190,096 2190,015 2189,922 2192,076	0,089 0,901 0,983 1,075 1,078	R.GEGAGQPSTSAQGGQPAAPAPQKR.G R.DGHFTLFAPTNEAFELPR.G R.NEHVDYVDVGGAYVGTQNR.I R.NMGPGYGGNGYPGSGSGSGGYGGR.S K.VPADTEVVCAPPTAYIDFAR.Q	P52926 Q15063 P21397 P22626 P60174	HMGA2_HUMAN POSTN_HUMAN AOFA_HUMAN ROA2_HUMAN TPIS_HUMAN	High mobility group protein HMGI-C (High mobility group AT-hook protein 2) Periostin (PN) (Osteoblast-specific factor 2) (OSF-2) Amine oxidase [flavin-containing] A (EC 1.4.3.4) (Monoamine oxidase type A) (MAO-A) Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1) Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase)	HMGA2 POSTN MAOA HNRNPA2B1 TPI1
2191,99	2190,893	2193,085	2192,076 2191,086	0,086 0,904	K.VPADTEVVCAPPTAYIDFAR.Q R.GEGAGQPSTSAQGGQPAAPAPQKR.G	P60174 P52926	TPIS_HUMAN HMGA2_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase) High mobility group protein HMGI-C (High mobility group AT-hook protein 2)	TPI1 HMGA2
2192,99	2191,889	2194,082	2192,076 2194,025	0,910 1,040	K.VPADTEVVCAPPTAYIDFAR.Q R.YGGLHFSQDEVFSPGSDR.A	P60174 P12110	TPIS_HUMAN CO6A2_HUMAN	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Methylglyoxal synthase) (EC 4.2.3.3) (Triose-phosphate isomerase) Collagen alpha-2(VI) chain	TPI1 COL6A2
2193,98	2192,879	2195,073	2194,025	0,049	R.YGGLHFSQDEVFSPGSDR.A	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2

2194,99	2193,893	2196,088	2195,081	0,090	R.GTVRDYPDFSPSVDAEAIQK.A	P12429	ANXA3_HUMAN	Annexin A3 (35-alpha calcimedlin) (Annexin III) (Annexin-3) (Inositol 1,2-cyclic phosphate 2-phosphohydrolase) (Lipocortin III) (Placental anticoagulant protein III) (PAP-III)	ANXA3
			2194,025	0,966	R.YGGLHFSQVEVFPSPGSDR.A	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
2196,01	2194,910	2197,106	2195,081	0,927	R.GTVRDYPDFSPSVDAEAIQK.A	P12429	ANXA3_HUMAN	Annexin A3 (35-alpha calcimedlin) (Annexin III) (Annexin-3) (Inositol 1,2-cyclic phosphate 2-phosphohydrolase) (Lipocortin III) (Placental anticoagulant protein III) (PAP-III)	ANXA3
2197,08	2195,980	2198,177	2197,165	0,087	K.TAVNALWGKVVNDVAVGGEALGR.L	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
2198,08	2196,982	2199,180	2197,165	0,916	K.TAVNALWGKVVNDVAVGGEALGR.L	P02042	HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	HBD
			2199,145	1,064	R.LLSTQAEESQGPVLKMPQSQR.A	Q14005	IL16_HUMAN	Pro-interleukin-16 [Cleared into: Interleukin-16 (IL-16) (Lymphocyte chemoattractant factor) (LCF)]	IL16
2198,97	2197,873	2200,071	2199,145	0,173	R.LLSTQAEESQGPVLKMPQSQR.A	Q14005	IL16_HUMAN	Pro-interleukin-16 [Cleared into: Interleukin-16 (IL-16) (Lymphocyte chemoattractant factor) (LCF)]	IL16
			2200,030	1,058	K.GLSEDTTEETLKESFDGSVR.A	P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL
2199,96	2198,859	2201,059	2200,030	0,071	K.GLSEDTTEETLKESFDGSVR.A	P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL
			2199,145	0,814	R.LLSTQAEESQGPVLKMPQSQR.A	Q14005	IL16_HUMAN	Pro-interleukin-16 [Cleared into: Interleukin-16 (IL-16) (Lymphocyte chemoattractant factor) (LCF)]	IL16
2200,92	2199,821	2202,022	2201,148	0,226	R.YNEDLEDAIHTAILTK.E	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
			2200,030	0,892	K.GLSEDTTEETLKESFDGSVR.A	P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL
2200,98	2199,876	2202,077	2201,148	0,171	R.YNEDLEDAIHTAILTK.E	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
			2200,030	0,947	K.GLSEDTTEETLKESFDGSVR.A	P19338	NUCL_HUMAN	Nucleolin (Protein C23)	NCL
2201,96	2200,863	2203,065	2201,148	0,816	R.YNEDLEDAIHTAILTK.E	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
2203,03	2201,926	2204,129	2203,143	0,116	R.IGQPTLLLYVDAGPETMTQR.L	P00568	KAD1_HUMAN	Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	AK1
2203,97	2202,866	2205,070	2204,143	0,175	R.FIFEDQIRPQDREELLR.A	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
			2203,143	0,825	R.IGQPTLLLYVDAGPETMTQR.L	P00568	KAD1_HUMAN	Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	AK1
2205,01	2203,912	2206,117	2204,143	0,872	R.FIFEDQIRPQDREELLR.A	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
			2205,900	0,885	R.NMGPGYGGNGYGGSGGSGGYGGR.S	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
2206,99	2205,890	2208,097	2206,147	0,847	K.ILRGDQHCIGIEVVAGIPR.T	P07858	CATB_HUMAN	Cathepsin B [EC 3.4.22.1] (APP secretase) (APPS) (Cathepsin B1) [Cleared into: Cathepsin B light chain; Cathepsin B heavy chain]	CTSB
			2205,900	1,093	R.NMGPGYGGNGYGGSGGSGGYGGR.S	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
2207,99	2206,882	2209,090	2209,021	1,035	R.THYSNIEANESEVRQFR.R	P04632	CPNS1_HUMAN	Calpain small subunit 1 (CSS1) (Calcium-activated neutral proteinase small subunit) (CANP small subunit) (Calcium-dependent protease small subunit) (CDPS) (Calcium-dependent protease small subunit 1) (Calpain regulatory subunit)	CAPNS1
2209,00	2207,893	2210,102	2209,021	0,023	R.THYSNIEANESEVRQFR.R	P04632	CPNS1_HUMAN	Calpain small subunit 1 (CSS1) (Calcium-activated neutral proteinase small subunit) (CANP small subunit) (Calcium-dependent protease small subunit) (CDPS) (Calcium-dependent protease small subunit 1) (Calpain regulatory subunit)	CAPNS1
2209,99	2208,888	2211,098	2209,021	0,973	R.THYSNIEANESEVRQFR.R	P04632	CPNS1_HUMAN	Calpain small subunit 1 (CSS1) (Calcium-activated neutral proteinase small subunit) (CANP small subunit) (Calcium-dependent protease small subunit) (CDPS) (Calcium-dependent protease small subunit 1) (Calpain regulatory subunit)	CAPNS1
2215,04	2213,929	2216,144	2215,078	0,042	K.DLYANTVLSGGTTMYPGIADR.M	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleared into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			2215,095	0,058	R.SFFHQHYLGGQEPTPSNIR.M	P46379	BAG6_HUMAN	Large proline-rich protein BAG6 (BAG family molecular chaperone regulator 6) (BCL2-associated athanogene 6) (BAG-6) (HLA-B-associated transcript 3) (Protein G3) (Protein Scythe)	BAG6
2216,04	2214,930	2217,146	2215,095	0,944	R.SFFHQHYLGGQEPTPSNIR.M	P46379	BAG6_HUMAN	Large proline-rich protein BAG6 (BAG family molecular chaperone regulator 6) (BCL2-associated athanogene 6) (BAG-6) (HLA-B-associated transcript 3) (Protein G3) (Protein Scythe)	BAG6

			2215,078	0,960	K.DLYANTVLSGGTTMYPGIADR.M	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
2217,03	2215,918	2218,135							
2218,03	2216,920	2219,138							
2219,02	2217,915	2220,134							
2220,01	2218,899	2221,119	2220,148	0,138	R.ALLELQLEPEELYQTFQR.I	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
2221,02	2219,907	2222,128	2220,148	0,869	R.ALLELQLEPEELYQTFQR.I	P13639	EF2_HUMAN	Elongation factor 2 (EF-2)	EEF2
2222,02	2220,909	2223,131	2222,924	0,904	R.MREDYDSVEQDGPQPQR.S	Q9Y559	RBM8A_HUMAN	RNA-binding protein 8A (Binder of OVCA1-1) (BOV-1) (RNA-binding motif protein 8A) (RNA-binding protein Y14) (Ribonucleoprotein RBM8A)	RBM8A
2223,02	2221,908	2224,131	2222,924	0,096	R.MREDYDSVEQDGPQPQR.S	Q9Y559	RBM8A_HUMAN	RNA-binding protein 8A (Binder of OVCA1-1) (BOV-1) (RNA-binding motif protein 8A) (RNA-binding protein Y14) (Ribonucleoprotein RBM8A)	RBM8A
2224,05	2222,939	2225,163	2225,132 2225,160	1,081 1,109	R.LGQSDPAPLQHQMIDIYQKR.C R.IYLTADNLVLNLQDESFT.R.G	P29401 Q99623	TKT_HUMAN PHB2_HUMAN	Transketolase (TK) (EC 2.2.1.1) Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	TKT PHB2
2225,05	2223,941	2226,166	2225,132 2225,160	0,078 0,107	R.LGQSDPAPLQHQMIDIYQKR.C R.IYLTADNLVLNLQDESFT.R.G	P29401 Q99623	TKT_HUMAN PHB2_HUMAN	Transketolase (TK) (EC 2.2.1.1) Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	TKT PHB2
2226,05	2224,939	2227,165	2225,160	0,892	R.IYLTADNLVLNLQDESFT.R.G	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
			2225,132	0,920	R.LGQSDPAPLQHQMIDIYQKR.C	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
2227,09	2225,976	2228,203	2227,217	0,128	K.MSVQPTVSLGGFEITPPVLR.L	P06748	NPM_HUMAN	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	NPM1
			2228,085	0,995	K.DLYANNVLSGGTTMYPGIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2228,085	0,995	R.TEELNREVAGHTEQLQMSR.S	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cyokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			2228,088	0,998	R.SVMTEEYKVPDGMVGFIIGR.G	Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1) (DNA helicase V) (hDH V)	FUBP1
			2228,105	1,016	R.IMDPNIVGSEHYDVARGVQK.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			2228,154	1,064	K.SAVTALWGVKNVDEVGGEALGR.L	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2228,06	2226,946	2229,175	2228,085	0,024	K.DLYANNVLSGGTTMYPGIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2228,085	0,024	R.TEELNREVAGHTEQLQMSR.S	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cyokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
			2228,088	0,027	R.SVMTEEYKVPDGMVGFIIGR.G	Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1) (DNA helicase V) (hDH V)	FUBP1
			2228,105	0,045	R.IMDPNIVGSEHYDVARGVQK.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			2228,154	0,093	K.SAVTALWGVKNVDEVGGEALGR.L	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			2227,217	0,843	K.MSVQPTVSLGGFEITPPVLR.L	P06748	NPM_HUMAN	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	NPM1
2229,06	2227,942	2230,171	2228,154	0,903	K.SAVTALWGVKNVDEVGGEALGR.L	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			2228,105	0,952	R.IMDPNIVGSEHYDVARGVQK.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			2228,088	0,969	R.SVMTEEYKVPDGMVGFIIGR.G	Q96AE4	FUBP1_HUMAN	Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1) (DNA helicase V) (hDH V)	FUBP1
			2228,085	0,972	K.DLYANNVLSGGTTMYPGIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2228,085	0,972	R.TEELNREVAGHTEQLQMSR.S	P08727	K1C19_HUMAN	Keratin, type I cytoskeletal 19 (Cyokeratin-19) (CK-19) (Keratin-19) (K19)	KRT19
2230,04	2228,928	2231,158	2231,077	1,034	K.DLYANTVLSGGTTMYPGIADR.M	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
2231,08	2229,965	2232,196	2231,077	0,003	K.DLYANTVLSGGTTMYPGIADR.M	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
2232,05	2230,935	2233,167	2231,077	0,975	K.DLYANTVLSGGTTMYPGIADR.M	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
2233,06	2231,948	2234,181							
2234,07	2232,949	2235,183	2235,073	1,007	R.QQLAQYQQQSQASAPSTR.T	Q15007	FL2D_HUMAN	Pre-mRNA-splicing regulator WTAP (Female-lethal(2)D homolog) (hFL(2)D) (WT1-associated protein) (Wilms tumor 1-associating protein)	WTAP
			2235,158	1,092	R.ITPSYVAFTPEGERLUGDAAK.N	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BIP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPAS

2235,01	2233,892	2236,127	2235,073	0,064	R.QQLAQYQQQSQASAPSTR.T	Q15007	FL2D_HUMAN	Pre-mRNA-splicing regulator WTAP (Female-lethal(2)D homolog) (hFL(2)D) (WT1-associated protein) (Wilms tumor 1-associating protein)	WTAP
			2235,158	0,149	R.ITPSYVAFTPEGERLIGDAAK.N	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BIP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			2235,218	0,208	R.EALAQTVLAEVPTQLVSYFR.A	Q99829	CPNE1_HUMAN	Copine-1 (Chromobindin 17) (Copine I)	CPNE1
2236,04	2234,926	2237,163	2235,218	0,827	R.EALAQTVLAEVPTQLVSYFR.A	Q99829	CPNE1_HUMAN	Copine-1 (Chromobindin 17) (Copine I)	CPNE1
			2235,158	0,886	R.ITPSYVAFTPEGERLIGDAAK.N	P11021	BIP_HUMAN	Endoplasmic reticulum chaperone BIP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	HSPA5
			2235,073	0,971	R.QQLAQYQQQSQASAPSTR.T	Q15007	FL2D_HUMAN	Pre-mRNA-splicing regulator WTAP (Female-lethal(2)D homolog) (hFL(2)D) (WT1-associated protein) (Wilms tumor 1-associating protein)	WTAP
2237,06	2235,943	2238,180							
2238,06	2236,937	2239,175							
2239,06	2237,940	2240,179							
2240,09	2238,973	2241,213	2240,179	0,086	R.IAPAAFSGQPQAVIMTSGPLKR.E	Q9HAP2	MLXIP_HUMAN	MLX-interacting protein (Class E basic helix-loop-helix protein 36) (bHLHe36) (Transcriptional activator MondoA)	MLXIP
			2240,200	0,107	R.AKDFSILDDVAITELSFSR.E	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
			2241,133	1,040	K.SIATTLIDDTSEVLDELYR.V	O95379	TFIP8_HUMAN	Tumor necrosis factor alpha-induced protein 8 (TNF alpha-induced protein 8) (Head and neck tumor and metastasis-related protein) (MDC-3.13) (NF-kappa-B-inducible DED-containing protein) (NDED) (SCC-S2) (TNF-induced protein GG2-1)	TNFAIP8
2241,05	2239,925	2242,166	2241,133	0,087	K.SIATTLIDDTSEVLDELYR.V	O95379	TFIP8_HUMAN	Tumor necrosis factor alpha-induced protein 8 (TNF alpha-induced protein 8) (Head and neck tumor and metastasis-related protein) (MDC-3.13) (NF-kappa-B-inducible DED-containing protein) (NDED) (SCC-S2) (TNF-induced protein GG2-1)	TNFAIP8
			2240,200	0,846	R.AKDFSILDDVAITELSFSR.E	Q99623	PHB2_HUMAN	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2
			2240,179	0,866	R.IAPAAFSGQPQAVIMTSGPLKR.E	Q9HAP2	MLXIP_HUMAN	MLX-interacting protein (Class E basic helix-loop-helix protein 36) (bHLHe36) (Transcriptional activator MondoA)	MLXIP
2242,06	2240,944	2243,186	2242,177	0,112	K.IIAEGANGPTTPEADKIFLER.N	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			2241,133	0,932	K.SIATTLIDDTSEVLDELYR.V	O95379	TFIP8_HUMAN	Tumor necrosis factor alpha-induced protein 8 (TNF alpha-induced protein 8) (Head and neck tumor and metastasis-related protein) (MDC-3.13) (NF-kappa-B-inducible DED-containing protein) (NDED) (SCC-S2) (TNF-induced protein GG2-1)	TNFAIP8
2242,18	2241,057	2243,299	2242,177	0,000	K.IIAEGANGPTTPEADKIFLER.N	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			2241,133	1,045	K.SIATTLIDDTSEVLDELYR.V	O95379	TFIP8_HUMAN	Tumor necrosis factor alpha-induced protein 8 (TNF alpha-induced protein 8) (Head and neck tumor and metastasis-related protein) (MDC-3.13) (NF-kappa-B-inducible DED-containing protein) (NDED) (SCC-S2) (TNF-induced protein GG2-1)	TNFAIP8
2242,99	2241,869	2244,112	2242,177	0,813	K.IIAEGANGPTTPEADKIFLER.N	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
			2244,099	1,108	K.VMPYVDILFGNETEATFAR.E	P55263	ADK_HUMAN	Adenosine kinase (AK) (EC 2.7.1.20) (Adenosine 5'-phosphotransferase)	ADK
2243,17	2242,053	2244,296	2244,099	0,924	K.VMPYVDILFGNETEATFAR.E	P55263	ADK_HUMAN	Adenosine kinase (AK) (EC 2.7.1.20) (Adenosine 5'-phosphotransferase)	ADK
			2242,177	0,998	K.IIAEGANGPTTPEADKIFLER.N	P00367	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	GLUD1
2244,12	2242,996	2245,240	2244,099	0,019	K.VMPYVDILFGNETEATFAR.E	P55263	ADK_HUMAN	Adenosine kinase (AK) (EC 2.7.1.20) (Adenosine 5'-phosphotransferase)	ADK
2245,01	2243,889	2246,134	2244,099	0,913	K.VMPYVDILFGNETEATFAR.E	P55263	ADK_HUMAN	Adenosine kinase (AK) (EC 2.7.1.20) (Adenosine 5'-phosphotransferase)	ADK
2245,17	2244,048	2246,293	2244,099	1,071	K.VMPYVDILFGNETEATFAR.E	P55263	ADK_HUMAN	Adenosine kinase (AK) (EC 2.7.1.20) (Adenosine 5'-phosphotransferase)	ADK
2246,12	2244,994	2247,240							
2247,12	2245,999	2248,246							
2248,13	2247,004	2249,252							
2249,11	2247,988	2250,237	2250,202	1,090	R.VLAGQTLDINMAGEPKPDRPK.G	Q9UKM9	RALY_HUMAN	RNA-binding protein Raly (Autoantigen p542) (Heterogeneous nuclear ribonucleoprotein C-like 2) (hnRNP core protein C-like 2) (hnRNP associated with lethal yellow protein homolog)	RALY
2250,11	2248,981	2251,231	2250,202	0,096	R.VLAGQTLDINMAGEPKPDRPK.G	Q9UKM9	RALY_HUMAN	RNA-binding protein Raly (Autoantigen p542) (Heterogeneous nuclear ribonucleoprotein C-like 2) (hnRNP core protein C-like 2) (hnRNP associated with lethal yellow protein homolog)	RALY
2251,09	2249,967	2252,218	2250,202	0,890	R.VLAGQTLDINMAGEPKPDRPK.G	Q9UKM9	RALY_HUMAN	RNA-binding protein Raly (Autoantigen p542) (Heterogeneous nuclear ribonucleoprotein C-like 2) (hnRNP core protein C-like 2) (hnRNP associated with lethal yellow protein homolog)	RALY

2252,09	2250,967	2253,220	2252,974	0,881	K.APKPDGPGGGPGGSHMGGNYGDDR.R	P35637	FUS_HUMAN	RNA-binding protein FUS (75 kDa DNA-pairing protein) (Oncogene FUS) (Oncogene TLS) (POMp75) (Translocated in liposarcoma protein)	FUS
			2253,124	1,030	R.LNFSHGTHEYHAETIKNVR.T	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
2253,10	2251,975	2254,228	2253,124	0,023	R.LNFSHGTHEYHAETIKNVR.T	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
			2252,974	0,127	K.APKPDGPGGGPGGSHMGGNYGDDR.R	P35637	FUS_HUMAN	RNA-binding protein FUS (75 kDa DNA-pairing protein) (Oncogene FUS) (Oncogene TLS) (POMp75) (Translocated in liposarcoma protein)	FUS
2254,06	2252,936	2255,190	2254,289	0,225	R.QVRPVTEKLPANHLTLGQR.V	P38606	VATA_HUMAN	V-type proton ATPase catalytic subunit A (V-ATPase subunit A) (EC 7.1.2.2) (V-ATPase 69 kDa subunit) (Vacuolar ATPase isoform VA68) (Vacuolar proton pump subunit alpha)	ATP6V1A
			2253,124	0,940	R.LNFSHGTHEYHAETIKNVR.T	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM
			2255,127	1,063	R.HPGSFDVVHVKDANGNSFATR.L	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein e54)	RPS4X
			2252,974	1,089	K.APKPDGPGGGPGGSHMGGNYGDDR.R	P35637	FUS_HUMAN	RNA-binding protein FUS (75 kDa DNA-pairing protein) (Oncogene FUS) (Oncogene TLS) (POMp75) (Translocated in liposarcoma protein)	FUS
2255,06	2253,935	2256,190	2255,127	0,064	R.HPGSFDVVHVKDANGNSFATR.L	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein e54)	RPS4X
			2254,289	0,774	R.QVRPVTEKLPANHLTLGQR.V	P38606	VATA_HUMAN	V-type proton ATPase catalytic subunit A (V-ATPase subunit A) (EC 7.1.2.2) (V-ATPase 69 kDa subunit) (Vacuolar ATPase isoform VA68) (Vacuolar proton pump subunit alpha)	ATP6V1A
			2256,047	0,984	K.EIINVGHSHFVNFDNDNR.S	P00915	CAH1_HUMAN	Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase I) (Carbonic anhydrase B) (CAB) (Carbonic anhydrase I) (CA-I)	CA1
			2256,145	1,082	R.AVANETGAFFFLINGPEIMSK.L	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (155 Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
2256,08	2254,952	2257,208	2256,047	0,033	K.EIINVGHSHFVNFDNDNR.S	P00915	CAH1_HUMAN	Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase I) (Carbonic anhydrase B) (CAB) (Carbonic anhydrase I) (CA-I)	CA1
			2256,145	0,065	R.AVANETGAFFFLINGPEIMSK.L	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (155 Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			2255,127	0,953	R.HPGSFDVVHVKDANGNSFATR.L	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein e54)	RPS4X
			2257,152	1,072	R.ISAIAHRGGSHDAPENTLAAIR.Q	Q9NZC3	GDE1_HUMAN	Glycerophosphodiester phosphodiesterase 1 (EC 3.1.4.-) (EC 3.1.4.44) (Membrane-interacting protein of RGS16) (RGS16-interacting membrane protein)	GDE1
2257,11	2255,977	2258,234	2257,152	0,046	R.ISAIAHRGGSHDAPENTLAAIR.Q	Q9NZC3	GDE1_HUMAN	Glycerophosphodiester phosphodiesterase 1 (EC 3.1.4.-) (EC 3.1.4.44) (Membrane-interacting protein of RGS16) (RGS16-interacting membrane protein)	GDE1
			2257,211	0,106	R.ALDDKPPPPPPVGNRPSIHR.E	O43516	WIPF1_HUMAN	WAS/WASL-interacting protein family member 1 (Protein PRPL-2) (Wiskott-Aldrich syndrome protein-interacting protein) (WASP-interacting protein)	WIPF1
			2256,145	0,960	R.AVANETGAFFFLINGPEIMSK.L	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (155 Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP
			2256,047	1,058	K.EIINVGHSHFVNFDNDNR.S	P00915	CAH1_HUMAN	Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase I) (Carbonic anhydrase B) (CAB) (Carbonic anhydrase I) (CA-I)	CA1
2258,13	2257,002	2259,260	2257,211	0,920	R.ALDDKPPPPPPVGNRPSIHR.E	O43516	WIPF1_HUMAN	WAS/WASL-interacting protein family member 1 (Protein PRPL-2) (Wiskott-Aldrich syndrome protein-interacting protein) (WASP-interacting protein)	WIPF1
			2257,152	0,979	R.ISAIAHRGGSHDAPENTLAAIR.Q	Q9NZC3	GDE1_HUMAN	Glycerophosphodiester phosphodiesterase 1 (EC 3.1.4.-) (EC 3.1.4.44) (Membrane-interacting protein of RGS16) (RGS16-interacting membrane protein)	GDE1
2259,15	2258,020	2260,279	2260,050	0,901	R.FQSSHHPTDITSLDQYVER.M	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
2260,09	2258,961	2261,221	2260,050	0,041	R.FQSSHHPTDITSLDQYVER.M	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
2261,10	2259,971	2262,232	2260,050	1,051	R.FQSSHHPTDITSLDQYVER.M	P14625	ENPL_HUMAN	Endoplasmic (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1
2262,12	2260,987	2263,249							
2263,12	2261,993	2264,256							

2264,14	2263,009	2265,273	2265,060	0,919	K.TFPGFFSPMLGEFVSETESR.G	P02671	FIBA_HUMAN	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	FGA
			2265,062	0,921	K.ADRDESSPYAAMLAAQDVAQR.C	P62263	RS14_HUMAN	40S ribosomal protein S14 (Small ribosomal subunit protein uS11)	RPS14
2265,15	2264,022	2266,287	2265,062	0,092	K.ADRDESSPYAAMLAAQDVAQR.C	P62263	RS14_HUMAN	40S ribosomal protein S14 (Small ribosomal subunit protein uS11)	RPS14
			2265,060	0,095	K.TFPGFFSPMLGEFVSETESR.G	P02671	FIBA_HUMAN	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	FGA
			2266,087	0,933	R.IPSAVGYQPTLATDMGTMQER.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
2266,10	2264,966	2267,232	2266,087	0,011	R.IPSAVGYQPTLATDMGTMQER.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			2265,062	1,036	K.ADRDESSPYAAMLAAQDVAQR.C	P62263	RS14_HUMAN	40S ribosomal protein S14 (Small ribosomal subunit protein uS11)	RPS14
			2265,060	1,039	K.TFPGFFSPMLGEFVSETESR.G	P02671	FIBA_HUMAN	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	FGA
2267,10	2265,969	2268,236	2266,087	1,015	R.IPSAVGYQPTLATDMGTMQER.I	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial (EC 7.1.2.2) (ATP synthase F1 subunit beta)	ATP5F1B
			2268,131	1,028	K.IQALQQQADEAEADRAQGLQR.E	P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	TPM4
2268,11	2266,979	2269,247	2268,131	0,018	K.IQALQQQADEAEADRAQGLQR.E	P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	TPM4
			2269,10	0,970	K.IQALQQQADEAEADRAQGLQR.E	P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	TPM4
2270,10	2268,963	2271,233	2270,086	0,985	R.NIELICQENEGENDPVLQR.I	Q15691	MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1) (End-binding protein 1) (EB1)	MAPRE1
			2270,086	0,012	R.NIELICQENEGENDPVLQR.I	Q15691	MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1) (End-binding protein 1) (EB1)	MAPRE1
			2270,995	0,897	R.GGGGNFGPGGSNFRGSDGYGSGR.G	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
2270,10	2268,963	2271,233	2271,119	1,021	R.FTYRSDSFENPVLQHQHFR.N	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	XRCC6
			2270,086	0,012	R.NIELICQENEGENDPVLQR.I	Q15691	MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1) (End-binding protein 1) (EB1)	MAPRE1
			2270,995	0,897	R.GGGGNFGPGGSNFRGSDGYGSGR.G	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
2271,10	2269,960	2272,231	2271,119	1,021	R.FTYRSDSFENPVLQHQHFR.N	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	XRCC6
			2270,086	1,009	R.NIELICQENEGENDPVLQR.I	Q15691	MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1) (End-binding protein 1) (EB1)	MAPRE1
			2272,176	1,080	R.TQTSDPAMLPTMIGLLAEAGVR.L	O43175	SERA_HUMAN	D-3-phosphoglycerate dehydrogenase (3-PGDH) (EC 1.1.1.95) (2-oxoglutarate reductase) (EC 1.1.1.399) (Malate dehydrogenase) (EC 1.1.1.37)	PHGDH
2272,11	2270,974	2273,246	2272,176	0,065	R.TQTSDPAMLPTMIGLLAEAGVR.L	O43175	SERA_HUMAN	D-3-phosphoglycerate dehydrogenase (3-PGDH) (EC 1.1.1.95) (2-oxoglutarate reductase) (EC 1.1.1.399) (Malate dehydrogenase) (EC 1.1.1.37)	PHGDH
			2271,119	0,991	R.FTYRSDSFENPVLQHQHFR.N	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	XRCC6
			2270,995	1,115	R.GGGGNFGPGGSNFRGSDGYGSGR.G	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1

2273,13	2271,991	2274,265	2272,176	0,952	R.TQTSDPAMLPMTMIGLLAEAGVR.L	O43175	SERA_HUMAN	D-3-phosphoglycerate dehydrogenase (3-PGDH) (EC 1.1.1.95) (2-oxoglutarate reductase) (EC 1.1.1.399) (Malate dehydrogenase) (EC 1.1.1.37)	PHGDH
2274,15	2273,010	2275,284	2275,280	1,133	R.IAIPGLAGAGNSVLLVSNLNP.R.V	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
2275,16	2274,018	2276,293	2275,280	0,124	R.IAIPGLAGAGNSVLLVSNLNP.R.V	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
2276,15	2275,016	2277,292	2275,280	0,875	R.IAIPGLAGAGNSVLLVSNLNP.R.V	P26599	PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	PTBP1
2277,07	2275,928	2278,205	2277,159	1,005	R.GFGFVTFDDHDPVDKIVLQK.Y	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			2277,159	0,092	R.GFGFVTFDDHDPVDKIVLQK.Y	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
2278,10	2276,958	2279,236	2277,159	0,938	R.GFGFVTFDDHDPVDKIVLQK.Y	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			2279,178	1,081	R.KFDLGQDVIDFTGHALALYR.T	P31150	GDIA_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			2279,178	1,081	K.KFDLGQDVIDFTGHALALYR.T	P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
2279,12	2277,977	2280,256	2279,178	0,061	R.KFDLGQDVIDFTGHALALYR.T	P31150	GDIA_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			2279,178	0,061	K.KFDLGQDVIDFTGHALALYR.T	P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
			2280,113	0,996	R.AEEYEFLTPVEEAPKGM.LAR.G	P52565	GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)	ARHGDI1A
			2280,180	1,063	R.AVFVDLEPTVIDEVRTGT.YR.Q	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
2280,12	2278,982	2281,262	2280,113	0,009	R.AEEYEFLTPVEEAPKGM.LAR.G	P52565	GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)	ARHGDI1A
			2280,180	0,058	R.AVFVDLEPTVIDEVRTGT.YR.Q	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2279,178	0,944	R.KFDLGQDVIDFTGHALALYR.T	P31150	GDIA_HUMAN	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine diphosphate dissociation inhibitor 1) (GDI-1) (Oligophrenin-2) (Protein XAP-4)	GDI1
			2279,178	0,944	K.KFDLGQDVIDFTGHALALYR.T	P50395	GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2
			2281,134	1,012	R.AKFYPEDVSEELIQDITQR.L	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
2281,12	2279,979	2282,260	2281,134	0,014	R.AKFYPEDVSEELIQDITQR.L	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
			2280,180	0,940	R.AVFVDLEPTVIDEVRTGT.YR.Q	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2280,113	1,007	R.AEEYEFLTPVEEAPKGM.LAR.G	P52565	GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)	ARHGDI1A
			2282,248	1,128	K.VVPLADIITPNQFEALLSGR.K	O00764	PDXK_HUMAN	Pyridoxal kinase (EC 2.7.1.35) (Pyridoxine kinase)	PDXK
2282,12	2280,983	2283,266	2282,248	0,123	K.VVPLADIITPNQFEALLSGR.K	O00764	PDXK_HUMAN	Pyridoxal kinase (EC 2.7.1.35) (Pyridoxine kinase)	PDXK
			2281,134	0,991	R.AKFYPEDVSEELIQDITQR.L	P26038	MOES_HUMAN	Moesin (Membrane-organizing extension spike protein)	MSN
2283,10	2281,960	2284,244	2282,248	0,854	K.VVPLADIITPNQFEALLSGR.K	O00764	PDXK_HUMAN	Pyridoxal kinase (EC 2.7.1.35) (Pyridoxine kinase)	PDXK
2284,11 2285,09	2282,967 2283,951	2285,251 2286,237	2286,103	1,009	R.FFESGDLSTPDVAVMG.NPKVK.A	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			2286,218	1,123	R.FLFVLLGPEAPHIDYQLGR.A	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
2286,09	2284,945	2287,231	2286,103	0,015	R.FFESGDLSTPDVAVMG.NPKVK.A	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			2286,218	0,129	R.FLFVLLGPEAPHIDYQLGR.A	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
2286,09	2284,945	2287,231	2286,103	0,015	R.FFESGDLSTPDVAVMG.NPKVK.A	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			2286,218	0,129	R.FLFVLLGPEAPHIDYQLGR.A	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
2287,15	2286,005	2288,292	2287,244	0,096	R.YFILPDSLPLDTLLVDVEPK.V	P62314	SMD1_HUMAN	Small nuclear ribonucleoprotein Sm D1 (Sm-D1) (Sm-D autoantigen) (snRNP core protein D1)	SNRPD1

2288,15	2287,010	2289,299	2286,218	0,931	R.FLVLGPEAPHIDYQLGR.A	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
			2288,153	1,004	R.VQDDEVGDGTTSVTVLAAELLR.E	P78371	TCPB_HUMAN	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	CCT2
			2288,192	1,044	K.TLTGKTITLEVEPSDTIENVK.A	P62987	RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 (CEP52) (Ubiquitin A-52 residue ribosomal protein fusion product 1) [Cleaved into: Ubiquitin; 60S ribosomal protein L40 (Large ribosomal subunit protein eL40)]	UBA52
			2286,103	1,046	R.FFESFGDLSTPDVAMGNPKVK.A	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			2288,153	0,002	R.VQDDEVGDGTTSVTVLAAELLR.E	P78371	TCPB_HUMAN	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	CCT2
2289,11	2287,963	2290,252	2288,192	0,038	K.TLTGKTITLEVEPSDTIENVK.A	P62987	RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 (CEP52) (Ubiquitin A-52 residue ribosomal protein fusion product 1) [Cleaved into: Ubiquitin; 60S ribosomal protein L40 (Large ribosomal subunit protein eL40)]	UBA52
			2287,244	0,910	R.YFILPDSLPLDTLLVDVEPK.V	P62314	SMD1_HUMAN	Small nuclear ribonucleoprotein Sm D1 (Sm-D1) (Sm-D autoantigen) (snRNP core protein D1)	SNRPD1
			2288,192	0,915	K.TLTGKTITLEVEPSDTIENVK.A	P62987	RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 (CEP52) (Ubiquitin A-52 residue ribosomal protein fusion product 1) [Cleaved into: Ubiquitin; 60S ribosomal protein L40 (Large ribosomal subunit protein eL40)]	UBA52
			2290,031	0,923	R.AAPEASGTPSSDAVSLEEEMR.K	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
			2290,055	0,947	R.GIYNQEENVRFDSDVGEYR.A	Q9TQE0	2B19_HUMAN	HLA class II histocompatibility antigen, DRB1-9 beta chain (MHC class II antigen DRB1*9) (DR-9) (DR9)	HLA-DRB1
2290,11	2288,969	2291,260	2288,153	0,955	R.VQDDEVGDGTTSVTVLAAELLR.E	P78371	TCPB_HUMAN	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	CCT2
			2290,055	0,060	R.GIYNQEENVRFDSDVGEYR.A	Q9TQE0	2B19_HUMAN	HLA class II histocompatibility antigen, DRB1-9 beta chain (MHC class II antigen DRB1*9) (DR-9) (DR9)	HLA-DRB1
			2290,031	0,084	R.AAPEASGTPSSDAVSLEEEMR.K	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
			2291,140	1,026	R.THMQNIKIDITSSIHFEAYR.V	Q9UHD8	SEPT9_HUMAN	Septin-9 (MLL septin-like fusion protein MSF-A) (MLL septin-like fusion protein) (Ovarian/Breast septin) (Ov/Br septin) (Septin D1)	SEPT9
			2291,190	1,075	K.VAGHPNIVINNAAGNFISPTER.L	Q16698	DECR_HUMAN	2,4-dienoyl-CoA reductase, mitochondrial (EC 1.3.1.34) (2,4-dienoyl-CoA reductase [NADPH]) (4-enoyl-CoA reductase [NADPH]) (Short chain dehydrogenase/reductase family 18C member 1)	DECR1
2291,11	2289,960	2292,251	2291,140	0,035	R.THMQNIKIDITSSIHFEAYR.V	Q9UHD8	SEPT9_HUMAN	Septin-9 (MLL septin-like fusion protein MSF-A) (MLL septin-like fusion protein) (Ovarian/Breast septin) (Ov/Br septin) (Septin D1)	SEPT9
			2291,190	0,084	K.VAGHPNIVINNAAGNFISPTER.L	Q16698	DECR_HUMAN	2,4-dienoyl-CoA reductase, mitochondrial (EC 1.3.1.34) (2,4-dienoyl-CoA reductase [NADPH]) (4-enoyl-CoA reductase [NADPH]) (Short chain dehydrogenase/reductase family 18C member 1)	DECR1
			2290,055	1,051	R.GIYNQEENVRFDSDVGEYR.A	Q9TQE0	2B19_HUMAN	HLA class II histocompatibility antigen, DRB1-9 beta chain (MHC class II antigen DRB1*9) (DR-9) (DR9)	HLA-DRB1
			2290,031	1,075	R.AAPEASGTPSSDAVSLEEEMR.K	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
			2293,021	0,911	R.FNKNNEGTYYSYPNYPQSR.S	P00450	CERU_HUMAN	Ceruloplasmin (EC 1.16.3.1) (Ferroxidase)	CP
2292,11	2290,964	2293,256	2291,190	0,920	K.VAGHPNIVINNAAGNFISPTER.L	Q16698	DECR_HUMAN	2,4-dienoyl-CoA reductase, mitochondrial (EC 1.3.1.34) (2,4-dienoyl-CoA reductase [NADPH]) (4-enoyl-CoA reductase [NADPH]) (Short chain dehydrogenase/reductase family 18C member 1)	DECR1
			2291,140	0,970	R.THMQNIKIDITSSIHFEAYR.V	Q9UHD8	SEPT9_HUMAN	Septin-9 (MLL septin-like fusion protein MSF-A) (MLL septin-like fusion protein) (Ovarian/Breast septin) (Ov/Br septin) (Septin D1)	SEPT9
			2293,021	0,077	R.FNKNNEGTYYSYPNYPQSR.S	P00450	CERU_HUMAN	Ceruloplasmin (EC 1.16.3.1) (Ferroxidase)	CP
			2293,021	1,069	R.FNKNNEGTYYSYPNYPQSR.S	P00450	CERU_HUMAN	Ceruloplasmin (EC 1.16.3.1) (Ferroxidase)	CP
			2295,266	0,162	R.VAPEEHPVLLTEAPLNPKANR.E	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
2296,08	2294,933	2297,229	2296,144	1,040	R.GAGSYTIMVLFADQATPTSPIR.V	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			2296,144	0,064	R.GAGSYTIMVLFADQATPTSPIR.V	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			2295,266	0,815	R.VAPEEHPVLLTEAPLNPKANR.E	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			2296,144	0,932	R.GAGSYTIMVLFADQATPTSPIR.V	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			2298,147	1,071	K.AEPPKAPEQEQAAPGAAGGEAPK.A	P80723	BASP1_HUMAN	Brain acid soluble protein 1 (22 kDa neuronal tissue-enriched acidic protein) (Neuronal axonal membrane protein NAP-22)	BASP1

2298,10	2296,947	2299,245	2298,147	0,051	K.AEPPKAPEQEQAAPGAAGGEAPK.A	P80723	BASP1_HUMAN	Brain acid soluble protein 1 (22 kDa neuronal tissue-enriched acidic protein) (Neuronal axonal membrane protein NAP-22)	BASP1			
			2299,229	1,132	R.SGRLPPPPSERPPPPVRDPPGR.S	O43516	WIPF1_HUMAN	WAS/WASL-interacting protein family member 1 (Protein PRPL-2) (Wiskott-Aldrich syndrome protein-interacting protein) (WASP-interacting protein)	WIPF1			
2299,09	2297,944	2300,243	2299,229	0,135	R.SGRLPPPPSERPPPPVRDPPGR.S	O43516	WIPF1_HUMAN	WAS/WASL-interacting protein family member 1 (Protein PRPL-2) (Wiskott-Aldrich syndrome protein-interacting protein) (WASP-interacting protein)	WIPF1			
			2300,025	0,932	R.VNIAFNNDMPEDSDTYLHR.V	Q13838	DX398_HUMAN	Spliceosome RNA helicase DDX398 (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	DDX398			
			2298,147	0,946	K.AEPPKAPEQEQAAPGAAGGEAPK.A	P80723	BASP1_HUMAN	Brain acid soluble protein 1 (22 kDa neuronal tissue-enriched acidic protein) (Neuronal axonal membrane protein NAP-22)	BASP1			
			2300,119 2300,159	1,026 1,065	K.NYAEAKDVLGMFLYEYAR.R R.AGELTEDEVERVITIMQNPR.Q	P02768 P62269	ALBU_HUMAN RS18_HUMAN	Serum albumin 40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	ALB RPS18			
2300,09	2298,939	2301,239	2300,119 2300,025	0,030 0,064	K.NYAEAKDVLGMFLYEYAR.R R.VNIAFNNDMPEDSDTYLHR.V	P02768 Q13838	ALBU_HUMAN DX398_HUMAN	Serum albumin Spliceosome RNA helicase DDX398 (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	ALB DDX398			
			2300,159	0,069	R.AGELTEDEVERVITIMQNPR.Q	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18			
			2299,229	0,861	R.SGRLPPPPSERPPPPVRDPPGR.S	O43516	WIPF1_HUMAN	WAS/WASL-interacting protein family member 1 (Protein PRPL-2) (Wiskott-Aldrich syndrome protein-interacting protein) (WASP-interacting protein)	WIPF1			
			2301,10	2299,947	2302,248	2300,159	0,939	R.AGELTEDEVERVITIMQNPR.Q	P62269	RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) (Small ribosomal subunit protein uS13)	RPS18
						2300,119 2300,025	0,979 1,073	K.NYAEAKDVLGMFLYEYAR.R R.VNIAFNNDMPEDSDTYLHR.V	P02768 Q13838	ALBU_HUMAN DX398_HUMAN	Serum albumin Spliceosome RNA helicase DDX398 (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	ALB DDX398
2302,08	2300,925	2303,227	2302,205	1,107	R.AHVIVMAATNRPNISIDPALRR.F	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP			
			2302,205	0,129	R.AHVIVMAATNRPNISIDPALRR.F	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP			
2303,13	2301,975	2304,278	2303,058	0,983	R.EQPPRFAQPGSFYEYAMR.W	Q15233	NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrb)) (p54nrb)	NONO			
			2302,205	0,068	R.EQPPRFAQPGSFYEYAMR.W	Q15233	NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrb)) (p54nrb)	NONO			
2304,12	2302,971	2305,276	2303,058	0,921	R.AHVIVMAATNRPNISIDPALRR.F	P55072	TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP			
			2303,058	1,065	R.EQPPRFAQPGSFYEYAMR.W	Q15233	NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrb)) (p54nrb)	NONO			
2305,11 2306,11	2303,955 2304,960	2306,260 2307,266	2307,144	1,031	R.IQYQLVDISQDNALRDEM.R.A	Q9H299	SH3L3_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 3 (SH3 domain-binding protein 1) (SH3BP-1)	SH3BGLR3			
			2307,13	2305,975	2308,282	2307,144	0,015	R.IQYQLVDISQDNALRDEM.R.A	Q9H299	SH3L3_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 3 (SH3 domain-binding protein 1) (SH3BP-1)	SH3BGLR3
2308,14	2306,982	2309,290				2307,144	0,992	R.IQYQLVDISQDNALRDEM.R.A	Q9H299	SH3L3_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 3 (SH3 domain-binding protein 1) (SH3BP-1)	SH3BGLR3
			2309,254	1,118	R.VAPEEHPIILLTEAPLNPKANR.E	Q6S8J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE			
2309,11	2307,960	2310,269	2309,254	0,139	R.VAPEEHPIILLTEAPLNPKANR.E	Q6S8J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE			
			2310,108	0,994	K.IGGDAATTNNSTPDFGFGGQKR.Q	Q92945	FUBP2_HUMAN	Far upstream element-binding protein 2 (FUSE-binding protein 2) (KH type-splicing regulatory protein) (KSRP) (p75)	KHSRP			
2310,13	2308,973	2311,283	2310,108	0,019	K.IGGDAATTNNSTPDFGFGGQKR.Q	Q92945	FUBP2_HUMAN	Far upstream element-binding protein 2 (FUSE-binding protein 2) (KH type-splicing regulatory protein) (KSRP) (p75)	KHSRP			
			2309,254	0,874	R.VAPEEHPIILLTEAPLNPKANR.E	Q6S8J3	POTEE_HUMAN	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	POTEE			
2311,20	2310,044	2312,355	2310,108	1,091	K.IGGDAATTNNSTPDFGFGGQKR.Q	Q92945	FUBP2_HUMAN	Far upstream element-binding protein 2 (FUSE-binding protein 2) (KH type-splicing regulatory protein) (KSRP) (p75)	KHSRP			

2312,19	2311,031	2313,344	2313,096	0,908	R.AAVFHEKDYDSLAQPGFFDR.F	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
2313,12	2311,959	2314,272	2313,096	0,020	R.AAVFHEKDYDSLAQPGFFDR.F	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
2314,12	2312,962	2315,276	2313,096	1,023	R.AAVFHEKDYDSLAQPGFFDR.F	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain	COL6A2
2315,14 2316,12	2313,983 2314,965	2316,298 2317,281	2317,177	1,054	R.AKPDFKELTVSNNDINEAGVR.V	P13489	RINI_HUMAN	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor) (Ribonuclease/angiogenin inhibitor 1) (RAI)	RNH1
2317,12	2315,957	2318,274	2317,177	0,061	R.AKPDFKELTVSNNDINEAGVR.V	P13489	RINI_HUMAN	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor) (Ribonuclease/angiogenin inhibitor 1) (RAI)	RNH1
2317,12	2315,957	2318,274	2317,177	0,061	R.AKPDFKELTVSNNDINEAGVR.V	P13489	RINI_HUMAN	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor) (Ribonuclease/angiogenin inhibitor 1) (RAI)	RNH1
2318,10	2316,937	2319,255	2317,177	0,919	R.AKPDFKELTVSNNDINEAGVR.V	P13489	RINI_HUMAN	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor) (Ribonuclease/angiogenin inhibitor 1) (RAI)	RNH1
2319,13	2317,967	2320,286	2320,088	0,962	R.SREYQLNDSAAYYLNDLER.I	P04899	GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2 (Adenylate cyclase-inhibiting G alpha protein)	GNAI2
			2320,098	0,971	R.NPPGFAFVEFEDPRDAADAVR.E	P84103	SRSF3_HUMAN	Serine/arginine-rich splicing factor 3 (Pre-mRNA-splicing factor SRP20) (Splicing factor, arginine/serine-rich 3)	SRSF3
2320,14	2318,983	2321,304	2320,098	0,046	R.NPPGFAFVEFEDPRDAADAVR.E	P84103	SRSF3_HUMAN	Serine/arginine-rich splicing factor 3 (Pre-mRNA-splicing factor SRP20) (Splicing factor, arginine/serine-rich 3)	SRSF3
			2320,088	0,055	R.SREYQLNDSAAYYLNDLER.I	P04899	GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2 (Adenylate cyclase-inhibiting G alpha protein)	GNAI2
2321,13	2319,971	2322,292	2320,098	1,034	R.NPPGFAFVEFEDPRDAADAVR.E	P84103	SRSF3_HUMAN	Serine/arginine-rich splicing factor 3 (Pre-mRNA-splicing factor SRP20) (Splicing factor, arginine/serine-rich 3)	SRSF3
			2320,088	1,043	R.SREYQLNDSAAYYLNDLER.I	P04899	GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2 (Adenylate cyclase-inhibiting G alpha protein)	GNAI2
2322,12 2323,13 2324,09	2320,956 2321,968 2322,930	2323,278 2324,291 2325,255	2325,199	1,106	K.ISFPAIQAAAPSFNSFPQIFR.D	P23381	SYWC_HUMAN	Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleaved into: T1-TrpRS; T2-TrpRS]	WARS
2325,10	2323,939	2326,265	2325,199	0,097	K.ISFPAIQAAAPSFNSFPQIFR.D	P23381	SYWC_HUMAN	Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleaved into: T1-TrpRS; T2-TrpRS]	WARS
2326,11	2324,951	2327,277	2326,268	0,154	K.GTVLLDLQETSLAGVANQLLDR.F	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
			2325,199	0,916	K.ISFPAIQAAAPSFNSFPQIFR.D	P23381	SYWC_HUMAN	Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleaved into: T1-TrpRS; T2-TrpRS]	WARS
2327,11	2325,949	2328,276	2326,268	0,844	K.GTVLLDLQETSLAGVANQLLDR.F	P02730	B3AT_HUMAN	Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (Anion exchanger 1) (Solute carrier family 4 member 1) (CD antigen CD233)	SLC4A1
			2328,143	1,031	R.VAMQDATAQMAMLQFISSGLSK.V	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
2328,11	2326,943	2329,271	2328,143	0,035	R.VAMQDATAQMAMLQFISSGLSK.V	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
2329,12	2327,957	2330,286	2330,023	0,901	R.AFVHWYVGEEMEEGEFSEAR.E	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2328,143	0,979	R.VAMQDATAQMAMLQFISSGLSK.V	Q99798	ACON_HUMAN	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	ACO2
2330,13	2328,965	2331,295	2330,023	0,107	R.AFVHWYVGEEMEEGEFSEAR.E	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
2331,14	2329,970	2332,301	2330,023	1,113	R.AFVHWYVGEEMEEGEFSEAR.E	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
2332,12 2333,11 2334,11	2330,953 2331,945 2332,944	2333,285 2334,278 2335,278	2335,148	1,037	R.QVQFSEHVVHESGRPVQR.A	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
2335,11	2333,946	2336,281	2335,148	0,035	R.QVQFSEHVVHESGRPVQR.A	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
2336,11	2334,945	2337,281	2335,148	0,964	R.QVQFSEHVVHESGRPVQR.A	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
2337,13	2335,960	2338,297	2338,180	1,052	R.EVAFAAQFGSDLAATQQLLSR.G	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATPSF1A

2338,09	2336,923	2339,262	2338,180	0,088	R.EVAFAAQFGSDLAATQQLSR.G	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
2339,03	2337,864	2340,203	2338,180	0,853	R.EVAFAAQFGSDLAATQQLSR.G	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial (ATP synthase F1 subunit alpha)	ATP5F1A
2340,05 2341,07 2342,10	2338,875 2339,903 2342,244 2343,268	2341,215 2342,244 2343,268	2343,176	1,080	R.KDLYANTVLSGGTTMYPGIADR.M	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleared into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
2343,14	2341,968	2344,311	2343,176	0,037	R.KDLYANTVLSGGTTMYPGIADR.M	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleared into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
2344,15	2342,979	2345,323	2343,176	0,974	R.KDLYANTVLSGGTTMYPGIADR.M	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleared into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
2345,16	2343,983	2346,328	2346,011	0,855	R.AFVHWYVVGEGMEEGEFSEAR.E	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleared into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
2346,16	2344,987	2347,333	2346,011	0,150	R.AFVHWYVVGEGMEEGEFSEAR.E	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleared into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
2347,16	2345,983	2348,330	2348,160	1,003	R.QARPGQSPGSPLEERQTQR.S	A8MVU1	NCF1C_HUMAN	Putative neutrophil cytosol factor 1C (NCF-1C) (Putative SH3 and PX domain-containing protein 1C)	NCF1C
			2346,011	1,146	R.AFVHWYVVGEGMEEGEFSEAR.E	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleared into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
2348,15	2346,974	2349,322	2348,160	0,012	R.QARPGQSPGSPLEERQTQR.S	A8MVU1	NCF1C_HUMAN	Putative neutrophil cytosol factor 1C (NCF-1C) (Putative SH3 and PX domain-containing protein 1C)	NCF1C
2349,13	2347,960	2350,309	2348,160	0,975	R.QARPGQSPGSPLEERQTQR.S	A8MVU1	NCF1C_HUMAN	Putative neutrophil cytosol factor 1C (NCF-1C) (Putative SH3 and PX domain-containing protein 1C)	NCF1C
2350,16	2348,983	2351,334	2351,081	0,923	R.HQGVMMVGMGQKDSYVGDEAQSK.R	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleared into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2351,081	0,923	R.HQGVMMVGMGQKDSYVGDEAQSK.R	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleared into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
			2351,130	0,971	K.LQEEMLQREEAENTLQSF.R.Q	P08670	VIME_HUMAN	Vimentin	VIM
			2351,238	1,080	K.AGAAPYVQAFDSLQAGPVAEYLK.I	Q01518	CAP1_HUMAN	Adenylyl cyclase-associated protein 1 (CAP 1)	CAP1
			2351,272	1,113	R.TVATPLNQVANPNNSAIFGGARPR.E	Q15056	IF4H_HUMAN	Eukaryotic translation initiation factor 4H (eIF-4H) (Williams-Beuren syndrome chromosomal region 1 protein)	EIF4H
2351,19	2350,010	2352,361	2351,238	0,053	K.AGAAPYVQAFDSLQAGPVAEYLK.I	Q01518	CAP1_HUMAN	Adenylyl cyclase-associated protein 1 (CAP 1)	CAP1
			2351,130	0,056	K.LQEEMLQREEAENTLQSF.R.Q	P08670	VIME_HUMAN	Vimentin	VIM
			2351,272	0,086	R.TVATPLNQVANPNNSAIFGGARPR.E	Q15056	IF4H_HUMAN	Eukaryotic translation initiation factor 4H (eIF-4H) (Williams-Beuren syndrome chromosomal region 1 protein)	EIF4H
			2351,081	0,104	R.HQGVMMVGMGQKDSYVGDEAQSK.R	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleared into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2351,081	0,104	R.HQGVMMVGMGQKDSYVGDEAQSK.R	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleared into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
2352,17	2350,996	2353,348	2351,272	0,900	R.TVATPLNQVANPNNSAIFGGARPR.E	Q15056	IF4H_HUMAN	Eukaryotic translation initiation factor 4H (eIF-4H) (Williams-Beuren syndrome chromosomal region 1 protein)	EIF4H
			2351,238	0,934	K.AGAAPYVQAFDSLQAGPVAEYLK.I	Q01518	CAP1_HUMAN	Adenylyl cyclase-associated protein 1 (CAP 1)	CAP1
			2351,130	1,042	K.LQEEMLQREEAENTLQSF.R.Q	P08670	VIME_HUMAN	Vimentin	VIM
			2351,081	1,091	R.HQGVMMVGMGQKDSYVGDEAQSK.R	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleared into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2351,081	1,091	R.HQGVMMVGMGQKDSYVGDEAQSK.R	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) [Cleared into: Actin, cytoplasmic 2, N-terminally processed]	ACTG1
2353,15	2351,978	2354,331	2354,099	0,944	R.NQANACQQQQAAPVEGVGEQR.V	P02549	SPTA1_HUMAN	Spectrin alpha chain, erythrocytic 1 (Erythroid alpha-spectrin)	SPTA1
2354,15	2352,970	2355,324	2354,099	0,048	R.NQANACQQQQAAPVEGVGEQR.V	P02549	SPTA1_HUMAN	Spectrin alpha chain, erythrocytic 1 (Erythroid alpha-spectrin)	SPTA1
2355,13	2353,955	2356,310	2356,160	1,027	R.KDLYANNVLSGGTTMYPGIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleared into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2356,163	1,030	K.GGPGSAVSPYPTFNPSSDVAALHK.A	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
			2354,099	1,034	R.NQANACQQQQAAPVEGVGEQR.V	P02549	SPTA1_HUMAN	Spectrin alpha chain, erythrocytic 1 (Erythroid alpha-spectrin)	SPTA1
2356,10	2354,919	2357,275	2356,160	0,063	R.KDLYANNVLSGGTTMYPGIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleared into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1
			2356,163	0,066	K.GGPGSAVSPYPTFNPSSDVAALHK.A	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
2357,15	2355,970	2358,327	2356,163	0,986	K.GGPGSAVSPYPTFNPSSDVAALHK.A	P04083	ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	ANXA1
			2356,160	0,988	R.KDLYANNVLSGGTTMYPGIADR.M	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleared into: Actin, alpha cardiac muscle 1, intermediate form]	ACTC1

2358,18	2356,999	2359,357	2359,182	1,004	R.ADPKPTHVTHHPISDHEATLR.C	P30492	1B54_HUMAN	HLA class I histocompatibility antigen, B-54 alpha chain (Bw-22) (Bw-54) (MHC class I antigen B*54)	HLA-B
			2359,182	1,004	R.ADPKPTHVTHHPISDHEATLR.C	P30460	1B08_HUMAN	HLA class I histocompatibility antigen, B-8 alpha chain (MHC class I antigen B*8)	HLA-B
2359,16	2357,975	2360,335	2359,182	0,027	R.ADPKPTHVTHHPISDHEATLR.C	P30492	1B54_HUMAN	HLA class I histocompatibility antigen, B-54 alpha chain (Bw-22) (Bw-54) (MHC class I antigen B*54)	HLA-B
			2359,182	0,027	R.ADPKPTHVTHHPISDHEATLR.C	P30460	1B08_HUMAN	HLA class I histocompatibility antigen, B-8 alpha chain (MHC class I antigen B*8)	HLA-B
2360,12	2358,941	2361,301	2359,182	0,939	R.ADPKPTHVTHHPISDHEATLR.C	P30492	1B54_HUMAN	HLA class I histocompatibility antigen, B-54 alpha chain (Bw-22) (Bw-54) (MHC class I antigen B*54)	HLA-B
			2359,182	0,939	R.ADPKPTHVTHHPISDHEATLR.C	P30460	1B08_HUMAN	HLA class I histocompatibility antigen, B-8 alpha chain (MHC class I antigen B*8)	HLA-B
2361,13	2359,950	2362,311	2362,248	1,117	K.QLTQPETHFGREPAASIRP.RA	Q9UJU6	DBNL_HUMAN	Drebrin-like protein (Cervical SH3P7) (Cervical mucin-associated protein) (Drebrin-F) (HPK1-interacting protein of 55 kDa) (HIP-55) (SH3 domain-containing protein 7)	DBNL
2362,14	2360,959	2363,321	2362,248	0,108	K.QLTQPETHFGREPAASIRP.RA	Q9UJU6	DBNL_HUMAN	Drebrin-like protein (Cervical SH3P7) (Cervical mucin-associated protein) (Drebrin-F) (HPK1-interacting protein of 55 kDa) (HIP-55) (SH3 domain-containing protein 7)	DBNL
2363,19	2362,005	2364,368	2362,248	0,939	K.QLTQPETHFGREPAASIRP.RA	Q9UJU6	DBNL_HUMAN	Drebrin-like protein (Cervical SH3P7) (Cervical mucin-associated protein) (Drebrin-F) (HPK1-interacting protein of 55 kDa) (HIP-55) (SH3 domain-containing protein 7)	DBNL
2364,20	2363,022	2365,386	2367,231	1,039	R.VNHLYSLSDALVIFQLYEK.I	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
2365,20	2364,022	2366,387				P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
2366,19	2365,008	2367,374				P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
2367,20	2366,017	2368,384	2367,231	0,030	R.VNHLYSLSDALVIFQLYEK.I	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			2368,164	0,963	K.AHYGGFTVQNEANKYQISV.NK.Y	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
			2368,219	1,019	R.VHGPQISGSGTTNKNPKFTVETR.G	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
2368,21	2367,021	2369,389	2368,219	0,014	R.VHGPQISGSGTTNKNPKFTVETR.G	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			2368,164	0,042	K.AHYGGFTVQNEANKYQISV.NK.Y	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
			2367,231	0,975	R.VNHLYSLSDALVIFQLYEK.I	P13796	PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	LCP1
2369,20	2368,020	2370,389	2368,219	0,985	R.VHGPQISGSGTTNKNPKFTVETR.G	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			2370,232	1,028	K.MPGGPKPGGGPGLSTPGGHKPPHR.G	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
			2368,164	1,041	K.AHYGGFTVQNEANKYQISV.NK.Y	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
2370,19	2369,004	2371,374	2370,232	0,043	K.MPGGPKPGGGPGLSTPGGHKPPHR.G	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
			2371,269	1,080	R.DLSAAGIGLLAAATQSLMPASLGR.M	P43243	MATR3_HUMAN	Matrin-3	MATR3
			2371,269	0,085	R.DLSAAGIGLLAAATQSLMPASLGR.M	P43243	MATR3_HUMAN	Matrin-3	MATR3
2371,18	2369,999	2372,370	2372,042	0,858	R.GGNFGFGDSRGGGNGFGPGSGSNFR.G	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			2370,232	0,952	K.MPGGPKPGGGPGLSTPGGHKPPHR.G	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
2372,19	2371,003	2373,375	2372,042	0,147	R.GGNFGFGDSRGGGNGFGPGSGSNFR.G	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
			2371,269	0,920	R.DLSAAGIGLLAAATQSLMPASLGR.M	P43243	MATR3_HUMAN	Matrin-3	MATR3
2373,19	2372,006	2374,379	2374,165	0,972	R.VFIMDSCELIPEYLN.FIR.G	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
			2372,042	1,150	R.GGNFGFGDSRGGGNGFGPGSGSNFR.G	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
2374,20	2373,012	2375,386	2374,165	0,034	R.VFIMDSCELIPEYLN.FIR.G	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
2375,20	2374,016	2376,391	2374,165	1,039	R.VFIMDSCELIPEYLN.FIR.G	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1
2376,19	2375,001	2377,378	2377,090	0,901	R.THMQDLKDVTTNNVHYENYR.S	Q16181	SEPT7_HUMAN	Septin-7 (CDC10 protein homolog)	SEPT7
			2377,170	0,980	R.QVQSLTCEVDALKGTTNESLR.Q	P08670	VIME_HUMAN	Vimentin	VIM
2377,19	2376,001	2378,378	2377,170	0,020	R.QVQSLTCEVDALKGTTNESLR.Q	P08670	VIME_HUMAN	Vimentin	VIM
			2377,090	0,099	R.THMQDLKDVTTNNVHYENYR.S	Q16181	SEPT7_HUMAN	Septin-7 (CDC10 protein homolog)	SEPT7
2378,17	2376,981	2379,359	2377,170	1,000	R.QVQSLTCEVDALKGTTNESLR.Q	P08670	VIME_HUMAN	Vimentin	VIM
			2377,090	1,079	R.THMQDLKDVTTNNVHYENYR.S	Q16181	SEPT7_HUMAN	Septin-7 (CDC10 protein homolog)	SEPT7
2379,17	2377,985	2380,364							

2380,19	2378,997	2381,377	2381,160	0,973	R.SLDMDSIIAEVKAQYEDIANR.S	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
2381,21	2380,021	2382,402	2381,160	0,052	R.SLDMDSIIAEVKAQYEDIANR.S	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
2382,22	2381,026	2383,408	2381,160	1,057	R.SLDMDSIIAEVKAQYEDIANR.S	P05787	K2C8_HUMAN	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Type-II keratin Kb8)	KRT8
2383,21	2382,018	2384,401	2383,974	0,765	R.GGGGGGSGSGSSYSGSGGSGSGGGGGGGR.G	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
2384,21	2383,017	2385,401	2383,974	0,235	R.GGGGGGSGSGSSYSGSGGSGSGGGGGGGR.G	P04264	K2C1_HUMAN	Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1
			2385,179	0,969	R.KGGTSEMYLIQPDSSVKPYR.V	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
			2385,278	1,069	R.VQLREQHLYYQDQLLPVSR.I	Q98ZJ3	TRYD_HUMAN	Tryptase delta (EC 3.4.21.59) (Delta-tryptase) (HmMCP-3-like tryptase III) (Mast cell mMCP-7-like) (Tryptase-3)	TPSD1
2385,20	2384,003	2386,388	2385,179	0,017	R.KGGTSEMYLIQPDSSVKPYR.V	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
			2385,278	0,082	R.VQLREQHLYYQDQLLPVSR.I	Q98ZJ3	TRYD_HUMAN	Tryptase delta (EC 3.4.21.59) (Delta-tryptase) (HmMCP-3-like tryptase III) (Mast cell mMCP-7-like) (Tryptase-3)	TPSD1
2386,19	2384,994	2387,380	2385,278	0,910	R.VQLREQHLYYQDQLLPVSR.I	Q98ZJ3	TRYD_HUMAN	Tryptase delta (EC 3.4.21.59) (Delta-tryptase) (HmMCP-3-like tryptase III) (Mast cell mMCP-7-like) (Tryptase-3)	TPSD1
			2385,179	1,009	R.KGGTSEMYLIQPDSSVKPYR.V	P02675	FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB
2387,16	2385,967	2388,354	2389,177	1,019	R.FLHNPDAAQGFVGCALSTIQR.F	Q13228	SBP1_HUMAN	Methanethiol oxidase (MTO) (EC 1.8.3.4) (S6 kDa selenium-binding protein) (SBP56) (SP56) (Selenium-binding protein 1)	SELENBP1
2388,16	2386,964	2389,352							
2389,18	2387,985	2390,374	2389,177	0,003	R.FLHNPDAAQGFVGCALSTIQR.F	Q13228	SBP1_HUMAN	Methanethiol oxidase (MTO) (EC 1.8.3.4) (S6 kDa selenium-binding protein) (SBP56) (SP56) (Selenium-binding protein 1)	SELENBP1
			2390,300	1,120	K.HHGPQTLYLPVTLSSIPVFQR.G	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
2390,20	2389,008	2391,398	2390,300	0,097	K.HHGPQTLYLPVTLSSIPVFQR.G	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
			2389,177	1,027	R.FLHNPDAAQGFVGCALSTIQR.F	Q13228	SBP1_HUMAN	Methanethiol oxidase (MTO) (EC 1.8.3.4) (S6 kDa selenium-binding protein) (SBP56) (SP56) (Selenium-binding protein 1)	SELENBP1
2391,21	2390,015	2392,406	2390,300	0,910	K.HHGPQTLYLPVTLSSIPVFQR.G	Q14697	GANAB_HUMAN	Neutral alpha-glucosidase AB (EC 3.2.1.207) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	GANAB
2392,20	2391,004	2393,396	2395,302	1,120	R.KPGISLLSYEASVPSPVSTHGR.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2393,19	2391,996	2394,389							
2394,18	2392,985	2395,380							
2395,32	2394,123	2396,518	2395,302	0,018	R.KPGISLLSYEASVPSPVSTHGR.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
			2396,076	0,756	R.RPGGEPSPGTTGQSYNQYSQR.Y	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
2396,34	2395,138	2397,534	2396,076	0,260	R.RPGGEPSPGTTGQSYNQYSQR.Y	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
			2397,146	0,810	R.YFEITSEAPFLHYLSMFSSK.E	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
			2395,302	1,034	R.KPGISLLSYEASVPSPVSTHGR.L	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2397,25	2396,055	2398,452	2397,146	0,108	R.YFEITSEAPFLHYLSMFSSK.E	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
			2396,076	1,177	R.RPGGEPSPGTTGQSYNQYSQR.Y	P02751	FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1
2398,23	2397,028	2399,426	2397,146	1,081	R.YFEITSEAPFLHYLSMFSSK.E	P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein A) (Clipin-A) (Coronin-like protein p57) (Tryptophan aspartate-containing coat protein) (TACO)	CORO1A
2399,19	2397,990	2400,390	2403,143	0,960	R.QHHPPYHQHHQPPPGPGGGR.S	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
2400,19	2398,995	2401,395							
2401,17	2399,971	2402,372							
2402,18	2400,982	2403,384							
2403,18	2401,979	2404,382	2403,143	0,038	R.QHHPPYHQHHQPPPGPGGGR.S	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
2404,17	2402,969	2405,373	2403,143	1,028	R.QHHPPYHQHHQPPPGPGGGR.S	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ

2405,17	2403,971	2406,376	2406,188	1,015	K.AMQDAEVSQSDIGEVILVGGMTR.M	P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9
2406,17	2404,968	2407,374	2406,188	0,018	K.AMQDAEVSQSDIGEVILVGGMTR.M	P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9
2407,19	2405,985	2408,392	2406,188	1,000	K.AMQDAEVSQSDIGEVILVGGMTR.M	P38646	GRP75_HUMAN	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9
2408,20	2406,998	2409,406	2409,208	1,006	R.FDGAENVLDTEFQTNLVPYPR.I	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
2409,17	2407,968	2410,377	2409,208	0,035	R.FDGAENVLDTEFQTNLVPYPR.I	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
2410,17	2408,965	2411,376	2409,208	0,962	R.FDGAENVLDTEFQTNLVPYPR.I	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2411,278	1,108	R.SSAVDPEPQVKLEDVPLAFTR.L	Q5SSJ5	HP1B3_HUMAN	Heterochromatin protein 1-binding protein 3 (Protein HP1-BP74)	HP1BP3
2411,17	2409,968	2412,379	2411,278	0,105	R.SSAVDPEPQVKLEDVPLAFTR.L	Q5SSJ5	HP1B3_HUMAN	Heterochromatin protein 1-binding protein 3 (Protein HP1-BP74)	HP1BP3
2412,18	2410,976	2413,388	2411,278	0,903	R.SSAVDPEPQVKLEDVPLAFTR.L	Q5SSJ5	HP1B3_HUMAN	Heterochromatin protein 1-binding protein 3 (Protein HP1-BP74)	HP1BP3
2413,19	2411,980	2414,393							
2414,20	2412,990	2415,404	2415,208	1,010	R.QLFHPEQLITGKEDAANNYAR.G	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
2415,19	2413,984	2416,399	2415,208	0,016	R.QLFHPEQLITGKEDAANNYAR.G	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
2416,20	2414,994	2417,410	2415,208	0,995	R.QLFHPEQLITGKEDAANNYAR.G	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
2417,22	2416,009	2418,426							
2418,21	2417,000	2419,418							
2419,20	2417,989	2420,408							
2420,19	2418,976	2421,396							
2421,19	2419,976	2422,397							
2422,19	2420,982	2423,405	2423,084	0,890	K.TVETRDGQVINETSQHDDLE.-	P08670	VIME_HUMAN	Vimentin	VIM
			2423,286	1,092	R.NLEALALDLMEPEQAVDLTLPK.V	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	XRCC6
2423,18	2421,968	2424,391	2423,084	0,096	K.TVETRDGQVINETSQHDDLE.-	P08670	VIME_HUMAN	Vimentin	VIM
			2423,286	0,106	R.NLEALALDLMEPEQAVDLTLPK.V	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	XRCC6
			2424,303	1,123	K.RSPEAPQPVIAEPAVPAPLPK.K	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
2424,18	2422,965	2425,389	2424,303	0,125	K.RSPEAPQPVIAEPAVPAPLPK.K	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
			2423,286	0,892	R.NLEALALDLMEPEQAVDLTLPK.V	P12956	XRCC6_HUMAN	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	XRCC6
			2425,158	0,981	R.YADLTEDQLPSCESLKDTIAR.A	P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG-dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	PGAM1
			2423,084	1,094	K.TVETRDGQVINETSQHDDLE.-	P08670	VIME_HUMAN	Vimentin	VIM

2425,18	2423,966	2426,391	2425,158	0,020	R.YADLTEDQLPSCESLKDTIAR.A	P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG-dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	PGAM1
			2424,303	0,876	K.RSPEAPQPVIAMEEPAVPAPLPK.K	P14317	HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75)	HCLS1
2426,19	2424,973	2427,400	2425,158	1,028	R.YADLTEDQLPSCESLKDTIAR.A	P18669	PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.11) (EC 5.4.2.4) (BPG-dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	PGAM1
2427,17	2425,958	2428,385	2428,173	1,002	K.AMGIMNSFVNDIFERIAGEASR.L	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
			2428,173	1,002	K.AMGIMNSFVNDIFERIAGEASR.L	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
2428,17	2426,957	2429,386	2428,173	0,001	K.AMGIMNSFVNDIFERIAGEASR.L	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
			2428,173	0,001	K.AMGIMNSFVNDIFERIAGEASR.L	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
2429,18	2427,961	2430,390	2428,173	1,003	K.AMGIMNSFVNDIFERIAGEASR.L	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
			2428,173	1,003	K.AMGIMNSFVNDIFERIAGEASR.L	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
2430,19	2428,977	2431,408							
2431,20	2429,983	2432,414							
2432,20	2430,987	2433,420							
2433,20	2431,983	2434,416							
2434,20	2432,986	2435,420							
2435,19	2433,975	2436,410							
2436,18	2434,966	2437,402	2437,215	1,030	K.SVTEQGAELSNEERNLLSVAYK.N	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
			2437,227	1,042	R.GQPLSPEKYVTSAPMPEPQAPGR.Y	P01871	IGHM_HUMAN	Immunoglobulin heavy constant mu (Ig mu chain C region) (Ig mu chain C region BOT) (Ig mu chain C region GAL) (Ig mu chain C region OU)	IGHM
2437,18	2435,963	2438,400	2437,215	0,033	K.SVTEQGAELSNEERNLLSVAYK.N	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
			2437,227	0,045	R.GQPLSPEKYVTSAPMPEPQAPGR.Y	P01871	IGHM_HUMAN	Immunoglobulin heavy constant mu (Ig mu chain C region) (Ig mu chain C region BOT) (Ig mu chain C region GAL) (Ig mu chain C region OU)	IGHM
			2438,181	0,999	R.HYFQNTQGLIFVVDNDNRER.V	P61204	ARF3_HUMAN	ADP-ribosylation factor 3	ARF3
2438,20	2436,976	2439,415	2438,181	0,015	R.HYFQNTQGLIFVVDNDNRER.V	P61204	ARF3_HUMAN	ADP-ribosylation factor 3	ARF3
			2437,227	0,969	R.GQPLSPEKYVTSAPMPEPQAPGR.Y	P01871	IGHM_HUMAN	Immunoglobulin heavy constant mu (Ig mu chain C region) (Ig mu chain C region BOT) (Ig mu chain C region GAL) (Ig mu chain C region OU)	IGHM
			2437,215	0,981	K.SVTEQGAELSNEERNLLSVAYK.N	P63104	1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ
2439,20	2437,977	2440,417	2440,198	1,001	R.VSGQGLHEGHTFEPAEFIIDTR.D	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
			2438,181	1,016	R.HYFQNTQGLIFVVDNDNRER.V	P61204	ARF3_HUMAN	ADP-ribosylation factor 3	ARF3
2440,25	2439,026	2441,466	2440,198	0,048	R.VSGQGLHEGHTFEPAEFIIDTR.D	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
2441,25	2440,034	2442,476	2440,198	1,057	R.VSGQGLHEGHTFEPAEFIIDTR.D	P21333	FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	FLNA
2442,20	2440,977	2443,419							
2443,20	2441,975	2444,418	2444,166	0,970	K.AMGIMNSFVNDIFERIAGEASR.L	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
			2444,166	0,970	K.AMGIMNSFVNDIFERIAGEASR.L	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
			2444,320	1,123	R.EPGQDLVLPLSITTFIPISFR.L	P01024	CO3_HUMAN	Complement C3 (C3 and P2P-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
2444,19	2442,968	2445,412	2444,166	0,024	K.AMGIMNSFVNDIFERIAGEASR.L	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
			2444,166	0,024	K.AMGIMNSFVNDIFERIAGEASR.L	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
			2444,320	0,129	R.EPGQDLVLPLSITTFIPISFR.L	P01024	CO3_HUMAN	Complement C3 (C3 and P2P-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
2445,19	2443,968	2446,413	2444,320	0,871	R.EPGQDLVLPLSITTFIPISFR.L	P01024	CO3_HUMAN	Complement C3 (C3 and P2P-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3

			2444,166	1,024	K.AMGIIMNSFVNDIFERIAGEASR.L	Q99877	H2B1N_HUMAN	Histone H2B type 1-N (Histone H2B.d) (H2B/d)	HIST1H2BN
			2444,166	1,024	K.AMGIIMNSFVNDIFERIAGEASR.L	P33778	H2B1B_HUMAN	Histone H2B type 1-B (Histone H2B.1) (Histone H2B.f) (H2B/f)	HIST1H2BB
			2446,221	1,030	R.LVEEGIVSPDLDLVMSEGLGMR.Y	Q9Y252	CRYL1_HUMAN	Lambda-crystallin homolog (EC 1.1.1.45) (L-gulonate 3-dehydrogenase) (Gul3DH)	CRYL1
2446,20	2444,980	2447,426	2446,221	0,017	R.LVEEGIVSPDLDLVMSEGLGMR.Y	Q9Y252	CRYL1_HUMAN	Lambda-crystallin homolog (EC 1.1.1.45) (L-gulonate 3-dehydrogenase) (Gul3DH)	CRYL1
			2447,291	1,088	R.ILGGVISAIEAAQYNPEPPPR.T	P04632	CPNS1_HUMAN	Calpain small subunit 1 (CSS1) (Calcium-activated neutral proteinase small subunit) (CANP small subunit) (Calcium-dependent protease small subunit) (CDPS) (Calcium-dependent protease small subunit 1) (Calpain regulatory subunit)	CAPNS1
2447,20	2445,974	2448,421	2447,291	0,093	R.ILGGVISAIEAAQYNPEPPPR.T	P04632	CPNS1_HUMAN	Calpain small subunit 1 (CSS1) (Calcium-activated neutral proteinase small subunit) (CANP small subunit) (Calcium-dependent protease small subunit) (CDPS) (Calcium-dependent protease small subunit 1) (Calpain regulatory subunit)	CAPNS1
			2446,221	0,977	R.LVEEGIVSPDLDLVMSEGLGMR.Y	Q9Y252	CRYL1_HUMAN	Lambda-crystallin homolog (EC 1.1.1.45) (L-gulonate 3-dehydrogenase) (Gul3DH)	CRYL1
2448,21	2446,982	2449,430	2447,291	0,915	R.ILGGVISAIEAAQYNPEPPPR.T	P04632	CPNS1_HUMAN	Calpain small subunit 1 (CSS1) (Calcium-activated neutral proteinase small subunit) (CANP small subunit) (Calcium-dependent protease small subunit) (CDPS) (Calcium-dependent protease small subunit 1) (Calpain regulatory subunit)	CAPNS1
			2449,348	1,142	R.EVTINQSLAPLRLDADPSLQR.V	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7)	KRT7
2449,20	2447,976	2450,425	2449,348	0,148	R.EVTINQSLAPLRLDADPSLQR.V	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7)	KRT7
2450,20	2448,976	2451,426	2449,348	0,853	R.EVTINQSLAPLRLDADPSLQR.V	P08729	K2C7_HUMAN	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (CK-7) (Keratin-7) (K7) (Sarcolectin) (Type-II keratin Kb7)	KRT7
2451,20	2449,979	2452,430	2452,264	1,060	R.HLUSTHFAPGDFQGFAVNPQR.N	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
2452,22	2450,991	2453,443	2452,264	0,047	R.HLUSTHFAPGDFQGFAVNPQR.N	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
2453,21	2451,984	2454,437	2452,264	0,947	R.HLUSTHFAPGDFQGFAVNPQR.N	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2
2454,24	2453,010	2455,464	2463,211	0,998	R.NFSDNQLQEGKNVIGLQMGTNR.G	P37802	TAGL2_HUMAN	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	TAGLN2
2455,24	2454,015	2456,470							
2456,28	2455,052	2457,508							
2457,23	2455,998	2458,456							
2458,23	2456,997	2459,455							
2459,21	2457,982	2460,441							
2460,21	2458,983	2461,443							
2460,21	2458,983	2461,443							
2461,21	2459,984	2462,445							
2462,21	2460,983	2463,445							
2463,23	2461,996	2464,459	2463,211	0,017	R.NFSDNQLQEGKNVIGLQMGTNR.G	P37802	TAGL2_HUMAN	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	TAGLN2
2464,15	2462,923	2465,387	2463,211	0,943	R.NFSDNQLQEGKNVIGLQMGTNR.G	P37802	TAGL2_HUMAN	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	TAGLN2
2464,21	2462,979	2465,443	2463,211	1,000	R.NFSDNQLQEGKNVIGLQMGTNR.G	P37802	TAGL2_HUMAN	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	TAGLN2
2465,24	2464,008	2466,473	2466,176	0,935	R.LYFGTSGYFSQHDLFSSPEKR.W	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2466,24	2465,008	2467,475	2466,176	0,066	R.LYFGTSGYFSQHDLFSSPEKR.W	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2467,27	2466,034	2468,501	2468,175	0,908	K.FVDGLMIHSGDPVNYYVDTAVR.H	P23396	RS3_HUMAN	40S ribosomal protein S3 (EC 4.2.99.18) (Small ribosomal subunit protein uS3)	RPS3
			2466,176	1,092	R.LYFGTSGYFSQHDLFSSPEKR.W	P01266	THYG_HUMAN	Thyroglobulin (Tg)	TG
2468,28	2467,042	2469,511	2468,175	0,102	K.FVDGLMIHSGDPVNYYVDTAVR.H	P23396	RS3_HUMAN	40S ribosomal protein S3 (EC 4.2.99.18) (Small ribosomal subunit protein uS3)	RPS3
2469,24	2468,008	2470,477	2468,175	1,068	K.FVDGLMIHSGDPVNYYVDTAVR.H	P23396	RS3_HUMAN	40S ribosomal protein S3 (EC 4.2.99.18) (Small ribosomal subunit protein uS3)	RPS3
2470,25	2469,010	2471,480	2472,174	0,929	R.IAQLEEEEEEQGNTEIHDR.L	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
2471,24	2470,009	2472,481							
2471,24	2470,009	2472,481	2472,174	0,929	R.IAQLEEEEEEQGNTEIHDR.L	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
2472,24	2471,004	2473,476	2472,174	0,066	R.IAQLEEEEEEQGNTEIHDR.L	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
2473,23	2471,997	2474,470	2474,219	0,986	R.GPLLVDQVVFTDEMAHFDREI.I	P04040	CATA_HUMAN	Catalase (EC 1.11.1.6)	CAT

			2472,174	1,059	R.IAQLEEEEEEQGNTEIUNDR.L	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9
2474,23	2472,992	2475,467	2474,219	0,011	R.GPLLQDVVFTDEMAHFDRER.I	P04040	CATA_HUMAN	Catalase (EC 1.11.1.6)	CAT
2475,23	2473,996	2476,471	2474,219	1,014	R.GPLLQDVVFTDEMAHFDRER.I	P04040	CATA_HUMAN	Catalase (EC 1.11.1.6)	CAT
2476,25	2475,007	2477,484							
2477,22	2475,986	2478,463							
2478,22	2476,977	2479,455							
2478,22	2476,977	2479,455							
2479,21	2477,974	2480,453							
2480,23	2478,987	2481,467							
2481,23	2479,986	2482,467	2482,202	0,975	R.AEPEDHYFLLEPTPLNTPENR.E	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
2482,23	2480,993	2483,475	2482,202	0,032	R.AEPEDHYFLLEPTPLNTPENR.E	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
			2483,297	1,063	R.VTASDPLDTLGSEGALSPGGVASLLR.L	P0C0L5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
2483,24	2481,999	2484,482	2483,297	0,056	R.VTASDPLDTLGSEGALSPGGVASLLR.L	P0C0L5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
			2484,192	0,952	K.LMENMRNDIASHPPEGSYAPR.R	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
			2482,202	1,039	R.AEPEDHYFLLEPTPLNTPENR.E	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
2484,24	2483,001	2485,486	2484,192	0,051	K.LMENMRNDIASHPPEGSYAPR.R	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
			2483,297	0,947	R.VTASDPLDTLGSEGALSPGGVASLLR.L	P0C0L5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
2485,26	2484,015	2486,500	2484,192	1,065	K.LMENMRNDIASHPPEGSYAPR.R	Q7KZF4	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (EC 3.1.31.1) (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1
2486,26	2485,017	2487,504							
2487,26	2486,012	2488,499	2488,229	0,973	R.EFTESQLQEGKHVIGLQMGSNR.G	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein W53-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
2488,26	2487,015	2489,503	2488,229	0,030	R.EFTESQLQEGKHVIGLQMGSNR.G	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein W53-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
2489,25	2488,005	2490,494	2488,229	1,021	R.EFTESQLQEGKHVIGLQMGSNR.G	Q01995	TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein W53-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	TAGLN
2490,25	2489,002	2491,492	2491,168	0,921	R.AGFALDEGIANPTDAFTVFYSER.S	Q03154	ACY1_HUMAN	Aminoacylase-1 (ACY-1) (EC 3.5.1.14) (N-acyl-L-amino-acid amidohydrolase)	ACY1
2491,24	2489,999	2492,490	2491,168	0,076	R.AGFALDEGIANPTDAFTVFYSER.S	Q03154	ACY1_HUMAN	Aminoacylase-1 (ACY-1) (EC 3.5.1.14) (N-acyl-L-amino-acid amidohydrolase)	ACY1
			2492,255	1,011	R.FPNGVQLSPAEDFVLVAETTMAR.I	Q9HDC9	APMAP_HUMAN	Adipocyte plasma membrane-associated protein (Protein BSCv)	APMAP
2492,25	2491,004	2493,496	2492,255	0,006	R.FPNGVQLSPAEDFVLVAETTMAR.I	Q9HDC9	APMAP_HUMAN	Adipocyte plasma membrane-associated protein (Protein BSCv)	APMAP
			2491,168	1,082	R.AGFALDEGIANPTDAFTVFYSER.S	Q03154	ACY1_HUMAN	Aminoacylase-1 (ACY-1) (EC 3.5.1.14) (N-acyl-L-amino-acid amidohydrolase)	ACY1
2493,23	2491,988	2494,481	2492,255	0,979	R.FPNGVQLSPAEDFVLVAETTMAR.I	Q9HDC9	APMAP_HUMAN	Adipocyte plasma membrane-associated protein (Protein BSCv)	APMAP
2494,23	2492,987	2495,481	2495,039	0,805	R.GFGDGYNGYGGPGGGNFGGSPGYGGGR.G	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
2495,23	2493,981	2496,476	2495,039	0,189	R.GFGDGYNGYGGPGGGNFGGSPGYGGGR.G	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
2496,25	2495,004	2497,500	2497,175	0,923	K.TIGGGDDSFNTFFSETGAGKHVPR.A	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B
			2497,197	0,945	R.VVTNYSAHDQNSNLLIEYFR.N	P21980	TGM2_HUMAN	Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (Transglutaminase C) (TG(C)) (TGC) (TGase C) (Transglutaminase H) (TGase H) (Transglutaminase-2) (TGase-2)	TGM2
			2497,259	1,008	R.LLQDSVDFSLADAINTEFKNTR.T	P08670	VIME_HUMAN	Vimentin	VIM
			2495,039	1,213	R.GFGDGYNGYGGPGGGNFGGSPGYGGGR.G	P22626	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1
2497,24	2495,989	2498,486	2497,259	0,022	R.LLQDSVDFSLADAINTEFKNTR.T	P08670	VIME_HUMAN	Vimentin	VIM
			2497,197	0,041	R.VVTNYSAHDQNSNLLIEYFR.N	P21980	TGM2_HUMAN	Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (Transglutaminase C) (TG(C)) (TGC) (TGase C) (Transglutaminase H) (TGase H) (Transglutaminase-2) (TGase-2)	TGM2
			2497,175	0,063	K.TIGGGDDSFNTFFSETGAGKHVPR.A	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-1B chain]	TUBA1B

2498,24	2496,986	2499,485	2497,259 2497,197	0,976 1,039	R.LLQDSVDFSLADAIINTEFNTR.T R.VVTNVNSAHDQNSNLLIEYFR.N	P08670 P21980	VIME_HUMAN TGM2_HUMAN	Vimentin Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (Transglutaminase C) (TG(C)) (TGase C) (Transglutaminase H) (TGase H) (Transglutaminase-2) (TGase-2)	VIM TGM2
			2497,175	1,060	K.TIGGGDDSFNTFSETGAGKHVPR.A	P68363	TBA18_HUMAN	Tubulin alpha-18 chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha- ubiquitous chain) [Cleaved into: Detyrosinated tubulin alpha-18 chain]	TUBA18
2499,25 2500,24 2501,24 2504,25 2505,24 2506,24 2507,24	2497,998 2498,994 2499,990 2502,995 2503,984 2504,989 2505,984	2500,497 2501,494 2502,491 2505,499 2506,489 2507,495 2508,492	2508,220	0,982	R.TSRPENAIYYNNNDFQVGQAK.V	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
2508,23	2506,979	2509,488	2508,220	0,014	R.TSRPENAIYYNNNDFQVGQAK.V	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
2509,22	2507,967	2510,476	2510,186	0,964	R.GFGFVTYATVEEVDAAMNARPHK.V	P09651	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single- strand RNA-binding protein) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	HNRNPA1
			2508,220	1,002	R.TSRPENAIYYNNNDFQVGQAK.V	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	TKT
2510,22	2508,966	2511,476	2510,186	0,036	R.GFGFVTYATVEEVDAAMNARPHK.V	P09651	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single- strand RNA-binding protein) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	HNRNPA1
2511,24	2509,983	2512,494	2510,186	1,053	R.GFGFVTYATVEEVDAAMNARPHK.V	P09651	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single- strand RNA-binding protein) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	HNRNPA1
2512,24 2513,23 2514,23	2510,986 2511,977 2512,977	2513,498 2514,491 2515,491	2515,341	1,107	R.VEVGVLKPGMVVTFAPVNVTEVK.S	P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1
2515,25	2513,990	2516,506	2515,341	0,093	R.VEVGVLKPGMVVTFAPVNVTEVK.S	P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1
2516,26	2514,998	2517,514	2515,341	0,915	R.VEVGVLKPGMVVTFAPVNVTEVK.S	P68104	EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1
2517,26 2519,25 2520,25	2516,005 2517,988 2518,987	2518,522 2520,508 2521,507	2521,338	1,091	K.LAQQYYLVYQEPIPTAQLVQR.V	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
2521,24	2519,978	2522,499	2521,338	0,100	K.LAQQYYLVYQEPIPTAQLVQR.V	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
2522,23	2520,973	2523,495	2521,338	0,896	K.LAQQYYLVYQEPIPTAQLVQR.V	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
			2523,372	1,137	R.ULTAVHDAILEDLVFPSEIVGKR.I	P62081	RS7_HUMAN	40S ribosomal protein S7 (Small ribosomal subunit protein eS7)	RPS7
2523,25	2521,984	2524,507	2523,372	0,126	R.ULTAVHDAILEDLVFPSEIVGKR.I	P62081	RS7_HUMAN	40S ribosomal protein S7 (Small ribosomal subunit protein eS7)	RPS7
2524,26	2522,994	2525,519	2523,372	0,885	R.ULTAVHDAILEDLVFPSEIVGKR.I	P62081	RS7_HUMAN	40S ribosomal protein S7 (Small ribosomal subunit protein eS7)	RPS7
2525,26 2526,28 2527,26 2528,25 2529,25 2530,28 2531,25 2532,25 2533,25 2534,26 2535,25 2536,26 2537,27 2538,30 2539,22 2540,20 2541,21 2542,25	2523,997 2525,012 2525,994 2526,986 2527,989 2529,012 2529,985 2530,988 2531,986 2532,991 2533,987 2534,990 2536,004 2537,035 2537,947 2538,932 2539,940 2540,976	2526,522 2527,538 2528,521 2529,515 2530,518 2531,542 2532,517 2533,520 2534,520 2535,525 2536,522 2537,526 2538,542 2539,573 2540,486 2541,472 2542,481 2543,519	2543,095	0,848	R.GMGGHGYGGAGDASSGFHGGHFVHMR.G	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNPH3
2543,26	2541,989	2544,532	2543,095	0,165	R.GMGGHGYGGAGDASSGFHGGHFVHMR.G	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNPH3
2544,27	2542,993	2545,538	2545,169	0,903	K.EFNAETFTFHADICTLSEKER.Q	P02768	ALBU_HUMAN	Serum albumin	ALB

			2543,095	1,171	R.GMGHGYGGAGDASSGFHGGHFVHMR.G	P31942	HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNPH3
2545,26	2543,990	2546,536	2545,169	0,094	K.EFNAETFTFHADICTLSEKER.Q	P02768	ALBU_HUMAN	Serum albumin	ALB
2546,27	2544,998	2547,545	2545,169	1,103	K.EFNAETFTFHADICTLSEKER.Q	P02768	ALBU_HUMAN	Serum albumin	ALB
2547,27	2545,996	2548,544							
2548,26	2546,991	2549,539							
2549,26	2547,989	2550,538							
2550,25	2548,974	2551,524							
2551,24	2549,965	2552,516							
2552,24	2550,967	2553,519	2553,390	1,147	K.TVASPGVTVEEAVEQIDIGGVTLLR.A	P31939	PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH [Cleaved into: Bifunctional purine biosynthesis protein PURH, N-terminally processed] [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (ATIC) (IMP synthase) (Inosinicasae)]	ATIC
2553,21	2551,929	2554,482	2553,390	0,185	K.TVASPGVTVEEAVEQIDIGGVTLLR.A	P31939	PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH [Cleaved into: Bifunctional purine biosynthesis protein PURH, N-terminally processed] [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (ATIC) (IMP synthase) (Inosinicasae)]	ATIC
2554,19	2552,914	2555,468	2553,390	0,801	K.TVASPGVTVEEAVEQIDIGGVTLLR.A	P31939	PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH [Cleaved into: Bifunctional purine biosynthesis protein PURH, N-terminally processed] [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (ATIC) (IMP synthase) (Inosinicasae)]	ATIC
			2555,302	1,111	R.GLPYKATENDIYNFFSPLNPVR.V	P52597	HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein F, N-terminally processed]	HNRNPF
2555,20	2553,919	2556,474	2555,302	0,105	R.GLPYKATENDIYNFFSPLNPVR.V	P52597	HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein F, N-terminally processed]	HNRNPF
2556,22	2554,939	2557,495	2555,302	0,915	R.GLPYKATENDIYNFFSPLNPVR.V	P52597	HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein F, N-terminally processed]	HNRNPF
2557,23	2555,955	2558,512							
2558,25	2556,968	2559,526							
2559,26	2557,982	2560,541	2560,259	0,997	K.LVQDVANNTNEEAGDGTTTATVLAR.S	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
2560,24	2558,963	2561,524	2560,259	0,015	K.LVQDVANNTNEEAGDGTTTATVLAR.S	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
2561,26	2559,981	2562,542	2560,259	1,003	K.LVQDVANNTNEEAGDGTTTATVLAR.S	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1
2562,23	2560,949	2563,511							
2563,26	2561,974	2564,537							
2565,26	2563,975	2566,540	2565,240	0,018	R.DMNQVLDAYENKKPFYLYTGR.G	P23381	SYWC_HUMAN	Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleaved into: T1-TrpRS; T2-TrpRS]	WARS
2566,25	2564,967	2567,534	2565,240	1,010	R.DMNQVLDAYENKKPFYLYTGR.G	P23381	SYWC_HUMAN	Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleaved into: T1-TrpRS; T2-TrpRS]	WARS
2567,24	2565,960	2568,527							
2568,28	2567,000	2569,569							
2569,25	2567,967	2570,537	2570,357	1,105	K.VNVDEVGGEALGRLLVVPWTQR.F	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2570,27	2568,986	2571,557	2570,357	0,086	K.VNVDEVGGEALGRLLVVPWTQR.F	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			2571,295	1,023	K.GNDISSGTVLSDYVGSGPPKGTGLHR.Y	P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPPP) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1

2571,27	2569,986	2572,557	2571,295	0,023	K.GNDISSGTVLSDYVVGSGPPKGTGLHR.Y	P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPPP) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) [RKIP] [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1
			2570,357	0,914	K.VNVDEVGEALGRLLVVPWTQR.F	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2572,27	2570,987	2573,559	2571,295	0,978	K.GNDISSGTVLSDYVVGSGPPKGTGLHR.Y	P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPPP) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) [RKIP] [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1
			2573,324	1,051	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	Q9Y490	TLN1_HUMAN	Talin-1	TLN1
2573,23	2571,946	2574,519	2573,324	0,091	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	Q9Y490	TLN1_HUMAN	Talin-1	TLN1
			2574,380	1,148	R.LTVAAPSGGPGFLSIERPDSRPPR.V	POC0L5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
2574,23	2572,945	2575,519	2574,380	0,148	R.LTVAAPSGGPGFLSIERPDSRPPR.V	POC0L5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
			2573,324	0,909	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	Q9Y490	TLN1_HUMAN	Talin-1	TLN1
			2575,306	1,074	K.TFSHELSDFGLESTAGEIPVVAIR.T	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	PDIA3
2575,24	2573,955	2576,530	2575,306	0,064	K.TFSHELSDFGLESTAGEIPVVAIR.T	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	PDIA3
			2574,380	0,862	R.LTVAAPSGGPGFLSIERPDSRPPR.V	POC0L5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2
2576,29	2575,001	2577,577	2575,306	0,983	K.TFSHELSDFGLESTAGEIPVVAIR.T	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	PDIA3
			2577,376	1,087	R.NIVEAAAVRDISEASVFDAYVLPK.L	P62854	RS26_HUMAN	40S ribosomal protein S26 (Small ribosomal subunit protein eS26)	RPS26
2577,32	2576,027	2578,604	2577,376	0,060	R.NIVEAAAVRDISEASVFDAYVLPK.L	P62854	RS26_HUMAN	40S ribosomal protein S26 (Small ribosomal subunit protein eS26)	RPS26
			2578,306	0,991	R.TMQALPYSTVGNSNNYLHLSVLR.T	P01024	CO3_HUMAN	Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
2578,31	2577,025	2579,604	2578,306	0,008	R.TMQALPYSTVGNSNNYLHLSVLR.T	P01024	CO3_HUMAN	Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
			2577,376	0,939	R.NIVEAAAVRDISEASVFDAYVLPK.L	P62854	RS26_HUMAN	40S ribosomal protein S26 (Small ribosomal subunit protein eS26)	RPS26
2579,31	2578,022	2580,602	2578,306	1,006	R.TMQALPYSTVGNSNNYLHLSVLR.T	P01024	CO3_HUMAN	Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3
2580,30	2579,005	2581,586	2581,332	1,037	K.VGAVDADKHSLGGQGVQGVQFPTIK.I	Q15084	PDIA6_HUMAN	Protein disulfide-isomerase A6 (EC 5.3.4.1) (Endoplasmic reticulum protein 5) (ER protein 5) (Erp5) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)	PDIA6

2581,28	2579,986	2582,568	2581,332	0,055	K.VGAVDADKHHSLGGQYGVQGFPPTK.I	Q15084	PDIA6_HUMAN	Protein disulfide-isomerase A6 (EC 5.3.4.1) (Endoplasmic reticulum protein 5) (ER protein 5) (Erp5) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)	PDIA6
			2582,273	0,996	K.VGAHAGEYGAEALERMFSLFPTTK.T	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
2582,24	2580,949	2583,531	2582,273	0,034	K.VGAHAGEYGAEALERMFSLFPTTK.T	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			2581,332	0,908	K.VGAVDADKHHSLGGQYGVQGFPPTK.I	Q15084	PDIA6_HUMAN	Protein disulfide-isomerase A6 (EC 5.3.4.1) (Endoplasmic reticulum protein 5) (ER protein 5) (Erp5) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)	PDIA6
2583,23	2581,939	2584,522	2582,273	0,957	K.VGAHAGEYGAEALERMFSLFPTTK.T	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			2584,283	1,053	R.VLTQIGTSIQDFIEADDLSFR.A	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
2584,37	2583,077	2585,661	2584,283	0,086	R.VLTQIGTSIQDFIEADDLSFR.A	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
2585,42	2584,129	2586,714	2586,243	0,822	K.GTFATLSELHCDKLHVDPENFR.L	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
			2584,283	1,138	R.VLTQIGTSIQDFIEADDLSFR.A	Q15063	POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN
2586,22	2584,923	2587,509	2586,243	0,027	K.GTFATLSELHCDKLHVDPENFR.L	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2586,43	2585,133	2587,719	2586,243	0,183	K.GTFATLSELHCDKLHVDPENFR.L	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2587,33	2586,034	2588,621	2586,243	1,085	K.GTFATLSELHCDKLHVDPENFR.L	P68871	HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB
2588,23 2589,25	2586,939 2587,959	2589,527 2590,548	2590,253	1,000	R.TDITYPAGFMDVISIDKTGENFR.L	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein e54)	RPS4X
2590,26	2588,962	2591,552	2590,253	0,004	R.TDITYPAGFMDVISIDKTGENFR.L	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein e54)	RPS4X
2591,26	2589,965	2592,556	2590,253	1,008	R.TDITYPAGFMDVISIDKTGENFR.L	P62701	RS4X_HUMAN	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein) (Small ribosomal subunit protein e54)	RPS4X
2592,27 2593,27 2594,28	2590,971 2591,972 2592,982	2593,564 2594,565 2595,576	2595,361	1,082	K.VIHDNFGIVEGLMTTVHAITATQK.T	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
2595,29	2593,992	2596,587	2595,361	0,071	K.VIHDNFGIVEGLMTTVHAITATQK.T	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
2596,30	2595,004	2597,601	2595,361	0,942	K.VIHDNFGIVEGLMTTVHAITATQK.T	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
2596,90	2595,600	2598,196	2597,271	0,968	K.LGHPEALSAGTGSQPPSFTYAQQR.E	Q15942	ZYX_HUMAN	Zyxin (Zyxin-2)	ZYX
			2597,271	0,372	K.LGHPEALSAGTGSQPPSFTYAQQR.E	Q15942	ZYX_HUMAN	Zyxin (Zyxin-2)	ZYX
2597,28	2595,981	2598,578	2597,271 2598,252	0,009 0,973	K.LGHPEALSAGTGSQPPSFTYAQQR.E K.VGAHAGEYGAEALERMFSLFPTTK.T	Q15942 P69905	ZYX_HUMAN HBA_HUMAN	Zyxin (Zyxin-2) Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	ZYX HBA1; HBA2
2597,91	2596,610	2599,208	2598,343	1,064	R.FGNPLLVQDVESYDPVLNPNLR.E	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
			2598,252	0,343	K.VGAHAGEYGAEALERMFSLFPTTK.T	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
2597,91	2596,610	2599,208	2598,343	0,434	R.FGNPLLVQDVESYDPVLNPNLR.E	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
			2597,271	0,638	K.LGHPEALSAGTGSQPPSFTYAQQR.E	Q15942	ZYX_HUMAN	Zyxin (Zyxin-2)	ZYX
2598,27	2596,973	2599,572	2598,252	0,020	K.VGAHAGEYGAEALERMFSLFPTTK.T	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
			2598,343	0,071	R.FGNPLLVQDVESYDPVLNPNLR.E	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
2598,91	2597,614	2600,213	2597,271 2599,294 2599,371	1,002 1,021 1,099	K.LGHPEALSAGTGSQPPSFTYAQQR.E K.QNCELFEQLGEYKFQNALLVR.Y R.NGKPVTTGVSETVFLPREDHLFR.K	Q15942 P02768 P01903	ZYX_HUMAN ALBU_HUMAN DRA_HUMAN	Zyxin (Zyxin-2) Serum albumin HLA class II histocompatibility antigen, DR alpha chain (MHC class II antigen DRA)	ZYX ALB HLA-DRA
			2598,294 2599,371	0,380 0,458	K.QNCELFEQLGEYKFQNALLVR.Y R.NGKPVTTGVSETVFLPREDHLFR.K	P02768 P01903	ALBU_HUMAN DRA_HUMAN	Serum albumin HLA class II histocompatibility antigen, DR alpha chain (MHC class II antigen DRA)	ALB HLA-DRA
2598,91	2597,614	2600,213	2598,343	0,570	R.FGNPLLVQDVESYDPVLNPNLR.E	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
			2598,252	0,661	K.VGAHAGEYGAEALERMFSLFPTTK.T	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
2599,28	2597,976	2600,575	2599,294 2599,371	0,018 0,096	K.QNCELFEQLGEYKFQNALLVR.Y R.NGKPVTTGVSETVFLPREDHLFR.K	P02768 P01903	ALBU_HUMAN DRA_HUMAN	Serum albumin HLA class II histocompatibility antigen, DR alpha chain (MHC class II antigen DRA)	ALB HLA-DRA
			2598,343	0,932	R.FGNPLLVQDVESYDPVLNPNLR.E	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	DYNC1H1
			2598,252	1,023	K.VGAHAGEYGAEALERMFSLFPTTK.T	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2

2600,26	2598,962	2601,563	2599,371	0,891	R.NGKPVTTGVSETVLPREDHLFR.K	P01903	DRA_HUMAN	HLA class II histocompatibility antigen, DR alpha chain (MHC class II antigen DRA)	HLA-DRA
			2599,294	0,969	K.QNCELFEQLGEYKFQNALLVR.Y	P02768	ALBU_HUMAN	Serum albumin	ALB
2601,30	2599,996	2602,597	2602,184	0,887	R.QMREMEENFAVEAANYQDTIGR.L	P08670	VIME_HUMAN	Vimentin	VIM
2602,30	2600,995	2603,598	2602,184	0,113	R.QMREMEENFAVEAANYQDTIGR.L	P08670	VIME_HUMAN	Vimentin	VIM
2603,29	2601,985	2604,588	2602,184	1,103	R.QMREMEENFAVEAANYQDTIGR.L	P08670	VIME_HUMAN	Vimentin	VIM
2606,31	2605,006	2607,612	2607,300	0,991	K.STUNSLFLTDLYSPEYPGPSHR.I	Q16181	SEPT7_HUMAN	Septin-7 (CDC10 protein homolog)	SEPT7
			2607,317	1,008	K.ALGISPFHEHAEVFTANDSGPRR.Y	P02766	TTHY_HUMAN	Transthyretin (ATTR) (Prealbumin) (TBPA)	TTR
2607,30	2605,998	2608,605	2607,300	0,002	K.STUNSLFLTDLYSPEYPGPSHR.I	Q16181	SEPT7_HUMAN	Septin-7 (CDC10 protein homolog)	SEPT7
			2607,317	0,016	K.ALGISPFHEHAEVFTANDSGPRR.Y	P02766	TTHY_HUMAN	Transthyretin (ATTR) (Prealbumin) (TBPA)	TTR
2608,30	2606,995	2609,603	2607,317	0,981	K.ALGISPFHEHAEVFTANDSGPRR.Y	P02766	TTHY_HUMAN	Transthyretin (ATTR) (Prealbumin) (TBPA)	TTR
			2607,300	0,999	K.STUNSLFLTDLYSPEYPGPSHR.I	Q16181	SEPT7_HUMAN	Septin-7 (CDC10 protein homolog)	SEPT7
2609,29	2607,981	2610,591							
2610,28	2608,975	2611,586							
2611,28	2609,977	2612,588	2612,267	0,984	R.NQINALTSFVDASMVYGSEELPAR.N	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
2612,28	2610,978	2613,590	2612,267	0,017	R.NQINALTSFVDASMVYGSEELPAR.N	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
2613,32	2612,010	2614,623	2612,267	1,050	R.NQINALTSFVDASMVYGSEELPAR.N	P05164	PERM_HUMAN	Myeloperoxidase (MPO) (EC 1.11.2.2) [Cleaved into: Myeloperoxidase; 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]	MPO
2614,30	2612,998	2615,612							
2617,32	2616,012	2618,629							
2618,32	2617,009	2619,627							
2619,33	2618,022	2620,642							
2623,34	2622,025	2624,648							
2625,32	2624,011	2626,636							
2626,32	2625,011	2627,638							
2628,31	2626,996	2629,624							
2629,32	2628,005	2630,635							
2636,34	2635,018	2637,655	2637,207	0,871	R.DGEDQTDTELVEPTRAGDGTQK.W	P13746	1A11_HUMAN	HLA class I histocompatibility antigen, A-11 alpha chain (MHC class I antigen A*11)	HLA-A
2637,32	2635,998	2638,636	2637,207	0,110	R.DGEDQTDTELVEPTRAGDGTQK.W	P13746	1A11_HUMAN	HLA class I histocompatibility antigen, A-11 alpha chain (MHC class I antigen A*11)	HLA-A
2638,33	2637,014	2639,653	2639,314	0,981	R.NLSPYVSNELLEAFSQFGPIER.A	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
			2637,207	1,126	R.DGEDQTDTELVEPTRAGDGTQK.W	P13746	1A11_HUMAN	HLA class I histocompatibility antigen, A-11 alpha chain (MHC class I antigen A*11)	HLA-A
2639,33	2638,006	2640,646	2639,314	0,012	R.NLSPYVSNELLEAFSQFGPIER.A	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
2640,33	2639,006	2641,646	2639,314	1,012	R.NLSPYVSNELLEAFSQFGPIER.A	P23246	SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMP100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ
2641,32	2639,997	2642,639							
2642,30	2640,983	2643,625							
2643,31	2641,986	2644,629							
2644,32	2642,996	2645,640							
2645,33	2644,012	2646,657							
2646,34	2645,015	2647,662							
2648,33	2647,007	2649,655	2649,450	1,119	R.KLAQQYYLVYQEPIPTAQLVQR.V	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
2649,32	2647,998	2650,647	2649,450	0,128	R.KLAQQYYLVYQEPIPTAQLVQR.V	P25787	PSA2_HUMAN	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	PSMA2
2651,34	2650,016	2652,667							
2655,31	2653,981	2656,636	2654,299	1,010	K.GADQAELEIAFDSSLVFPAEFR.A	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3
			2656,409	1,101	R.INALTAASEAACLVSVDETIKNPR.S	Q99832	TCPH_HUMAN	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein) [Cleaved into: T-complex protein 1 subunit eta, N-terminally processed]	CCT7
2656,31	2654,984	2657,641	2656,409	0,097	R.INALTAASEAACLVSVDETIKNPR.S	Q99832	TCPH_HUMAN	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein) [Cleaved into: T-complex protein 1 subunit eta, N-terminally processed]	CCT7
2658,30	2656,968	2659,627							
2659,29	2657,962	2660,621							
2660,30	2658,965	2661,626							
2660,39	2659,056	2661,717							
2661,44	2660,112	2662,773							
2662,68	2661,353	2664,015							
2664,30	2662,972	2665,636							

[illegible]

2712,80	2711,449	2714,161	2713,349	0,544	R.IAQLEEELEEEQGNTELINDRLK.K	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIa)	MYH9							
2713,91	2712,552	2715,266	2713,349	0,561	R.IAQLEEELEEEQGNTELINDRLK.K	P35579	MYH9_HUMAN	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIa)	MYH9							
2715,29	2713,935	2716,651	2724,347	1,032	R.MYSYVTEELPQLINAFVPDPQR.M	P10768	ESTD_HUMAN	S-formylglutathione hydrolase (FGH) (EC 3.1.2.12) (Esterase D) (Methylumbelliferyl-acetate deacetylase) (EC 3.1.1.56)	ESD							
2716,33	2714,971	2717,687			2724,356	1,041	K.EKYPFIPEEYTFIQNVPLEDR.V	Q00839	HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) [(Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)]	HNRNPU					
2717,34	2715,986	2718,703														
2719,30	2717,944	2720,663														
2720,30	2718,943	2721,663														
2721,29	2719,932	2722,653														
2722,31	2720,950	2723,673														
2723,31	2721,953	2724,677														
2727,31	2725,944	2728,671	2727,414	0,107			K.AVQGGGATPVVGAVQGPVPGMPPMTQAPR.I	P09012	SNRPA_HUMAN	U1 small nuclear ribonucleoprotein A (U1 snRNP A) (U1-A) (U1A)	SNRPA					
2728,34	2726,972	2729,700	2727,414	0,922	K.AVQGGGATPVVGAVQGPVPGMPPMTQAPR.I	P09012	SNRPA_HUMAN	U1 small nuclear ribonucleoprotein A (U1 snRNP A) (U1-A) (U1A)	SNRPA							
2729,35	2727,982	2730,712	2731,327	1,012	R.HHSDGVSLSGHLQPPPVTTEQHGAR.Y	O15533	TPSN_HUMAN	Tapasin (TPN) (TPSN) (NGS-17) (TAP-associated protein) (TAP-binding protein)	TAPBP							
2730,32	2728,950	2731,680														
2731,33	2729,967	2732,698	2731,327	0,005	R.HHSDGVSLSGHLQPPPVTTEQHGAR.Y	O15533	TPSN_HUMAN	Tapasin (TPN) (TPSN) (NGS-17) (TAP-associated protein) (TAP-binding protein)	TAPBP							
2743,30	2741,933	2744,676	2751,396	1,064	K.VSPETVDSVIMGNVLQSSSDAIYLR.H	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2							
2744,31	2742,934	2745,679														
2745,32	2743,944	2746,689														
2750,33	2748,957	2751,708														
2751,34	2749,965	2752,717	2751,396	0,055	K.VSPETVDSVIMGNVLQSSSDAIYLR.H	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2							
2762,41	2761,024	2763,787	2778,366	0,966	R.STQDVTIALDALSAYWIASHTTEER.G	P0C0L5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2							
2763,41	2762,033	2764,796														
2764,41	2763,029	2765,794														
2765,40	2764,016	2766,781														
2777,40	2776,011	2778,788														
2778,41	2777,016	2779,795	2778,366	0,040	R.STQDVTIALDALSAYWIASHTTEER.G	P0C0L5	CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B; C4B_2							
2798,40	2796,999	2799,797	2798,353	0,045	R.SGPFQGIFRPDNFVFGQSGAGNNWAK.G	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB							
			2798,353	0,045	R.SGPFQGIFRPDNFVFGQSGAGNNWAK.G	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B							
2799,41	2798,008	2800,808	2798,353	1,055	R.SGPFQGIFRPDNFVFGQSGAGNNWAK.G	P07437	TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain)	TUBB							
			2798,353	1,055	R.SGPFQGIFRPDNFVFGQSGAGNNWAK.G	P68371	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	TUBB4B							
2800,41	2799,009	2801,810	2846,381	0,073	R.AYYNGISLFNNPVPYWEVQPATFR.C	P21810	PGS1_HUMAN	Biglycan (Bone/cartilage proteoglycan I) (PG-S1)	BGN							
2801,41	2800,013	2802,815														
2803,48	2802,075	2804,879														
2832,42	2831,006	2833,838														
2833,41	2831,995	2834,828														
2833,41	2831,995	2834,828														
2834,41	2832,997	2835,831														
2835,42	2833,999	2836,835														
2836,43	2835,009	2837,846														
2837,43	2836,009	2838,846														
2846,45	2845,030	2847,877														
2847,45	2846,030	2848,877								2846,381	1,072	R.AYYNGISLFNNPVPYWEVQPATFR.C	P21810	PGS1_HUMAN	Biglycan (Bone/cartilage proteoglycan I) (PG-S1)	BGN
2848,47	2847,045	2849,893								2854,426	0,961	R.SLGSVQAPSYGARPVSSAASVYAGGSGSR.I	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18
2849,46	2848,036	2850,885														
2850,61	2849,187	2852,037														
2851,60	2850,178	2853,030														
2852,61	2851,186	2854,039														
2853,46	2852,037	2854,891														
2854,45	2853,024	2855,878														
2855,44	2854,010	2856,865	2854,426	1,012	R.SLGSVQAPSYGARPVSSAASVYAGGSGSR.I	P05783	K1C18_HUMAN	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	KRT18							

			2856,540	1,103	R.VVFGPELVSLGPEEQFTVLSSLAGRPK.R	Q14764	MVP_HUMAN	Major vault protein (MVP) (Lung resistance-related protein)	MVP
2856,44	2855,008	2857,864	2856,540	0,105	R.VVFGPELVSLGPEEQFTVLSSLAGRPK.R	Q14764	MVP_HUMAN	Major vault protein (MVP) (Lung resistance-related protein)	MVP
2857,43	2855,997	2858,854	2856,540	0,885	R.VVFGPELVSLGPEEQFTVLSSLAGRPK.R	Q14764	MVP_HUMAN	Major vault protein (MVP) (Lung resistance-related protein)	MVP
2858,45	2857,022	2859,880							
2865,49	2864,053	2866,919							
2866,49	2865,052	2867,918							
2867,49	2866,053	2868,920							
2868,49	2867,056	2869,925							
2869,50	2868,062	2870,931							
2870,48	2869,046	2871,916							
2871,50	2870,061	2872,933							
2872,47	2871,032	2873,905							
2873,47	2872,028	2874,902							
2874,46	2873,021	2875,896							
2875,45	2874,009	2876,884							
2876,44	2874,999	2877,875	2877,465	1,028	K.SALQAIGVEAHQAVMIGDDIVGDVGGAQR.C	Q9H008	LHPP_HUMAN	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase (hLHPP) (EC 3.1.3.-) (EC 3.6.1.1)	LHPP
2877,43	2875,996	2878,873	2877,465	0,030	K.SALQAIGVEAHQAVMIGDDIVGDVGGAQR.C	Q9H008	LHPP_HUMAN	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase (hLHPP) (EC 3.1.3.-) (EC 3.6.1.1)	LHPP
			2878,465	1,031	K.AGLSLKMDLVEVNEAFAPQYLAVR.S	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2
2878,44	2877,002	2879,881	2878,465	0,024	K.AGLSLKMDLVEVNEAFAPQYLAVR.S	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2
			2877,465	0,977	K.SALQAIGVEAHQAVMIGDDIVGDVGGAQR.C	Q9H008	LHPP_HUMAN	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase (hLHPP) (EC 3.1.3.-) (EC 3.6.1.1)	LHPP
2879,46	2878,025	2880,904	2880,233	0,768	R.SPEGPREEEAAGGEEESPDSPPHGEASR.G	Q96NY7	CLIC6_HUMAN	Chloride intracellular channel protein 6 (Parchorin)	CLIC6
			2878,465	0,999	K.AGLSLKMDLVEVNEAFAPQYLAVR.S	P42765	THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	ACAA2
2880,48	2879,036	2881,916	2880,233	0,243	R.SPEGPREEEAAGGEEESPDSPPHGEASR.G	Q96NY7	CLIC6_HUMAN	Chloride intracellular channel protein 6 (Parchorin)	CLIC6
2881,49	2880,046	2882,927	2880,233	1,254	R.SPEGPREEEAAGGEEESPDSPPHGEASR.G	Q96NY7	CLIC6_HUMAN	Chloride intracellular channel protein 6 (Parchorin)	CLIC6
2882,48	2881,042	2883,925							
2883,49	2882,047	2884,931							
2884,49	2883,050	2885,935							
2885,49	2884,047	2886,932							
2886,49	2885,047	2887,933							
2887,49	2886,046	2888,934	2888,233	0,743	K.QVYEEYGSSLEDDVVGDTSGYYQR.M	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
2888,49	2887,046	2889,934	2888,233	0,257	K.QVYEEYGSSLEDDVVGDTSGYYQR.M	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
2889,48	2888,035	2890,924	2888,233	1,246	K.QVYEEYGSSLEDDVVGDTSGYYQR.M	P08758	ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5
2891,47	2890,029	2892,920							
2892,47	2891,027	2893,919							
2893,48	2892,030	2894,924							
2894,51	2893,060	2895,954							
2895,49	2894,041	2896,937							
2896,47	2895,017	2897,914							
2897,45	2896,004	2898,901							
2908,47	2907,018	2909,926							
2909,47	2908,017	2910,926							
2915,59	2914,130	2917,046	2915,579	0,009	R.VGAGAPVYLAAVLEYLTAEILELAGNAAR.D	Q93077	H2A1C_HUMAN	Histone H2A type 1-C (Histone H2A/I)	HIST1H2AC
			2915,579	0,009	R.VGAGAPVYLAAVLEYLTAEILELAGNAAR.D	Q8IU66	H2A2B_HUMAN	Histone H2A type 2-B	HIST2H2AB
			2915,579	0,009	R.VGAGAPVYLAAVLEYLTAEILELAGNAAR.D	P16104	H2AX_HUMAN	Histone H2AX (H2a/x) (Histone H2A.X)	H2AFX
			2914,432	1,156	K.YLRAEPEDHYFLTPEPLNTPENR.E	P61158	ARP3_HUMAN	Actin-related protein 3 (Actin-like protein 3)	ACTR3
2916,63	2915,171	2918,087	2915,579	1,050	R.VGAGAPVYLAAVLEYLTAEILELAGNAAR.D	Q93077	H2A1C_HUMAN	Histone H2A type 1-C (Histone H2A/I)	HIST1H2AC
			2915,579	1,050	R.VGAGAPVYLAAVLEYLTAEILELAGNAAR.D	Q8IU66	H2A2B_HUMAN	Histone H2A type 2-B	HIST2H2AB
			2915,579	1,050	R.VGAGAPVYLAAVLEYLTAEILELAGNAAR.D	P16104	H2AX_HUMAN	Histone H2AX (H2a/x) (Histone H2A.X)	H2AFX
2917,63	2916,169	2919,086							
2918,58	2917,122	2920,041							
2934,58	2933,110	2936,045	2933,538	1,040	R.VGAGAPVYMAAVLEYLTAEILELAGNAAR.D	Q6FI13	H2A2A_HUMAN	Histone H2A type 2-A (Histone H2A.2) (Histone H2A/o)	HIST2H2AA3; HIST2H2AA4
			2933,462	1,116	R.VIISAPSADAPMFVMGVNHEKYDNSLK.I	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine 5-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH
2935,57	2934,102	2937,037							

2936,57	2935,104	2938,041	2937,453	0,881	R.GFGFVTYATVEEVDAAAMNARPHKVDGR.V	P09651	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	HNRNPA1
2937,58	2936,111	2939,048	2937,453	0,127	R.GFGFVTYATVEEVDAAAMNARPHKVDGR.V	P09651	ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	HNRNPA1
			2938,357	0,778	K.FISDKDASIVGFFDDSFSEAHSEFLK.A	P30101	PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) [Endoplasmic reticulum resident protein 57] (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	PDIA3
2950,56	2949,080	2952,030							
2951,55	2950,075	2953,027							
2952,53	2951,059	2954,011							
2952,55	2951,078	2954,031							
2953,56	2952,088	2955,041							
2954,55	2953,077	2956,031							
2955,54	2954,059	2957,014							
2957,64	2956,160	2959,118							
2958,63	2957,148	2960,107							
2959,56	2958,079	2961,038							
2960,51	2959,029	2961,990							
2961,51	2960,031	2962,992							
2962,46	2960,982	2963,945							
2962,53	2961,053	2964,016							
2963,46	2961,983	2964,946							
2964,49	2963,012	2965,977							
2965,53	2964,044	2967,010							
2966,01	2964,526	2967,492							
2966,54	2965,060	2968,027							
2967,98	2966,497	2969,465							
2972,55	2971,068	2974,040	2972,526	0,028	R.SLLSNVEGDNAVPMQHNHRPTQPLKGR.T	P00915	CAH1_HUMAN	Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase I) (Carbonic anhydrase B) (CAB) (Carbonic anhydrase I) (CA-I)	CA1
2973,55	2972,063	2975,037	2972,526	1,024	R.SLLSNVEGDNAVPMQHNHRPTQPLKGR.T	P00915	CAH1_HUMAN	Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase I) (Carbonic anhydrase B) (CAB) (Carbonic anhydrase I) (CA-I)	CA1
2974,55	2973,058	2976,033							
2975,55	2974,067	2977,042							
2976,55	2975,058	2978,035							
2977,54	2976,053	2979,030							
2979,58	2978,091	2981,070							
2980,59	2979,097	2982,077							
2981,51	2980,019	2983,000							
2982,53	2981,041	2984,023							
2983,47	2981,974	2984,958							
2984,47	2982,982	2985,967							
2989,55	2988,054	2991,043	2988,520	1,028	R.SLLSNVEGDNAVPMQHNHRPTQPLKGR.T	P00915	CAH1_HUMAN	Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase I) (Carbonic anhydrase B) (CAB) (Carbonic anhydrase I) (CA-I)	CA1
2992,60	2991,104	2994,097							
2997,55	2996,047	2999,045	2997,463	0,083	R.TLSSSTQASIEIDSLYEGIDFYTSITR.A	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8
			2996,493	1,053	K.VADALTNAVAHVDDMPNALSALSDHAHK.L	P69905	HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	HBA1; HBA2
3019,57	3018,061	3021,080							
3052,57	3051,046	3054,099	3052,618	0,046	K.TIDDLKNQILNLTDDNAILLIQIDNAR.L	P13645	K1C10_HUMAN	Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KRT10
			3053,467	0,894	K.EAENPEGEEKEAATLEVERPLPMEVEK.N	P51858	HDGF_HUMAN	Hepatoma-derived growth factor (HDGF) (High mobility group protein 1-like 2) (HMG-112)	HDGF
3053,55	3052,027	3055,081	3053,467	0,087	K.EAENPEGEEKEAATLEVERPLPMEVEK.N	P51858	HDGF_HUMAN	Hepatoma-derived growth factor (HDGF) (High mobility group protein 1-like 2) (HMG-112)	HDGF
			3052,618	0,936	K.TIDDLKNQILNLTDDNAILLIQIDNAR.L	P13645	K1C10_HUMAN	Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)	KRT10
3054,56	3053,033	3056,088	3053,467	1,094	K.EAENPEGEEKEAATLEVERPLPMEVEK.N	P51858	HDGF_HUMAN	Hepatoma-derived growth factor (HDGF) (High mobility group protein 1-like 2) (HMG-112)	HDGF
3055,57	3054,045	3057,101							
3056,58	3055,051	3058,108							
3057,57	3056,044	3059,102							
3068,55	3067,012	3070,080							
3069,54	3068,007	3071,077							
3070,55	3069,016	3072,087							
3071,55	3070,015	3073,087							
3072,54	3071,008	3074,080							
3084,54	3083,002	3086,087	3083,553	0,992	K.YGSGVSGQPPPVAPPEPGVPSSSPSQEPPTKR.E	Q04323	UBXN1_HUMAN	UBX domain-containing protein 1 (SAPK substrate protein 1) (UBA/UBX 33.3 kDa protein)	UBXN1
3085,57	3084,026	3087,112							
3086,54	3085,001	3088,087							
3086,61	3085,065	3088,152							
3087,55	3086,006	3089,094							
3088,55	3087,010	3090,099							
3089,65	3088,105	3091,194							
3090,56	3089,010	3092,101							
3091,54	3089,998	3093,090							
3092,54	3090,997	3094,090	3093,578	1,035	R.SAQSPGAPPGGLEDEVATPAAPRPGFPAVPR.E	O60240	PLIN1_HUMAN	Perilipin-1 (Lipid droplet-associated protein)	PLIN1
3093,57	3092,020	3095,114	3093,578	0,012	R.SAQSPGAPPGGLEDEVATPAAPRPGFPAVPR.E	O60240	PLIN1_HUMAN	Perilipin-1 (Lipid droplet-associated protein)	PLIN1
3100,55	3098,999	3102,100							
3101,55	3099,999	3103,101							
3102,54	3100,988	3104,091							

[illegible]