

SI. LC-MS/MS identification of proteins isolated from membrane protein extracts of RA FLS by immunoprecipitation using anti-KIAA1199 antibody.

	Reference	PepCount	UniquePepCount	CoverPercent	MW	PI	IdentifiedName							
	File, Scan(s)	Sequence	MH+	Diff(MH+)	Charge	Rank	XC	DeltaCn	Sp	RSp	Ions	PI	GroupCount	ProteinCount
\$1-1			30	11	34.81%	38604.07	7.57	sp P07355 ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2						
\$1-2			30	11	34.81%	38604.07	7.57	tr A0A024R5Z7 A0A024R5Z7_HUMAN Annexin OS=Homo sapiens GN=ANXA2 PE=3 SV=1						
\$1-3			30	11	34.81%	38576.02	7.57	tr V9HW65 V9HW65_HUMAN Annexin OS=Homo sapiens GN=HEL-S-270 PE=2 SV=1						
	R16062_1_KIAA,13 942	K.ALLYLCGGDD.-	1097.1939	0.6879		1	1	1.9013	0.3076	748	1 11 18	3.89	1	3
	R16062_1_KIAA,81 10	K.AYTNFDAER.D	1087.1242	-1.6758		2	1	2.268	0.2961	430.9	1 11 16	4.37	1	3
	R16062_1_KIAA,11 816	K.DIISDTSGDFR.K	1226.275	-0.646		2	1	3.1576	0.3734	832	1 14 20	3.93	1	3
	R16062_1_KIAA,11 828	K.DIISDTSGDFR.K	1226.275	-0.752		2	1	3.1305	0.4622	859	1 14 20	3.93	1	3
	R16062_1_KIAA,12 014	K.DIISDTSGDFR.K	1226.275	0.962		2	1	2.3881	0.3634	950.2	1 14 20	3.93	1	3
	R16062_1_KIAA,17 845	K.GLGTDEDSLIEIICSR.T	1778.9331	-1.3739		2	1	3.8729	0.4989	674.4	1 15 30	3.92	1	3
	R16062_1_KIAA,17 856	K.GLGTDEDSLIEIICSR.T	1778.9331	-1.6389		2	1	3.8725	0.4986	650.9	1 14 30	3.92	1	3
	R16062_1_KIAA,17 899	K.GLGTDEDSLIEIICSR.T	1778.9331	0.5091		2	1	2.5057	0.3859	1162.9	1 18 30	3.92	1	3
	R16062_1_KIAA,17 910	K.GLGTDEDSLIEIICSR.T	1778.9331	-0.6069		2	1	3.8163	0.5738	1600.7	1 20 30	3.92	1	3
	R16062_1_KIAA,17 932	K.GLGTDEDSLIEIICSR.T	1778.9331	0.5531		2	1	2.7768	0.4418	1336.4	1 20 30	3.92	1	3
	R16062_1_KIAA,17 943	K.GLGTDEDSLIEIICSR.T	1778.9331	0.7111		2	1	2.5817	0.305	802.4	1 15 30	3.92	1	3
	R16062_1_KIAA,17 804	K.GVDEVTIVNILTNR.S	1543.7474	0.7804		2	1	3.2549	0.4453	1744.9	1 19 26	4.37	1	3
	R16062_1_KIAA,17 812	K.GVDEVTIVNILTNR.S	1543.7474	0.0924		2	1	2.6743	0.3706	851.4	1 15 26	4.37	1	3
	R16062_1_KIAA,17 836	K.GVDEVTIVNILTNR.S	1543.7474	1.3014		2	1	2.8155	0.4081	989.8	1 17 26	4.37	1	3
	R16062_1_KIAA,17 880	K.GVDEVTIVNILTNR.S	1543.7474	0.3204		3	1	4.1475	0.4096	1653.2	1 28 52	4.37	1	3
	R16062_1_KIAA,17	K.GVDEVTIVNILTNR.S	1543.7474	1.9384		2	1	3.1321	0.4616	1645.9	1 19 26	4.37	1	3

	R16062_1_KIAA,12	K.SLYYYIQQDTK.G	907	1422.5639	-0.9931	2	1		2.3264	0.3449	1104	1 14 20	5.55	1	3
	R16062_1_KIAA,12	K.SLYYYIQQDTK.G	907	1422.5639	0.4649	2	1		2.367	0.4125	640.5	1 13 20	5.55	1	3
	R16062_1_KIAA,12	K.SLYYYIQQDTK.G	916	1422.5639	0.4079	2	1		2.8713	0.4141	910.4	1 14 20	5.55	1	3
	R16062_1_KIAA,13	R.AEDGSVIDYELIDQDAR.D	927	1909.9855	-0.7465	2	1		2.751	0.4331	519.3	1 15 32	3.66	1	3
	R16062_1_KIAA,13	R.AEDGSVIDYELIDQDAR.D	882	1909.9855	-0.2795	2	1		3.2203	0.5254	816.7	1 19 32	3.66	1	3
	R16062_1_KIAA,13	R.AEDGSVIDYELIDQDAR.D	907	1909.9855	1.3425	2	1		3.1439	0.4932	830	1 19 32	3.66	1	3
	R16062_1_KIAA,13	R.AEDGSVIDYELIDQDAR.D	918	1909.9855	1.2355	2	1		3.4189	0.4991	1711.7	1 22 32	3.66	1	3
	R16062_1_KIAA,12	R.DALNIETAIK.T	931	1088.2367	0.3977	2	1		2.7248	0.3407	850.2	1 13 18	4.37	1	3
	R16062_1_KIAA,12	R.DALNIETAIK.T	171	1088.2367	2.0377	2	1		2.3828	0.341	890.7	1 14 18	4.37	1	3
	R16062_1_KIAA,10	R.QDIAYFQR.R	308	1112.22	0.926	2	1		2.2605	0.3212	519.2	1 12 16	5.84	1	3
	R16062_1_KIAA,13	R.RAEDGSVIDYELIDQDAR.D	430	2066.1718	0.9038	2	1		2.6999	0.4013	497.8	1 16 34	3.96	1	3
	R16062_1_KIAA,13	R.RAEDGSVIDYELIDQDAR.D	087	2066.1718	1.2268	2	1		2.6453	0.3437	680.5	1 17 34	3.96	1	3
	R16062_1_KIAA,75	R.TNQELQEINR.V	134	1245.3247	0.7747	2	1		2.6509	0.2728	1332.5	1 15 18	4.53	1	3
	R16062_1_KIAA,75	R.TNQELQEINR.V	70	1245.3247	0.7117	2	1		2.6962	0.2478	1197.8	1 15 18	4.53	1	3
\$2-1			25	9	37.81%	35936.83	4.94	sp P08758 ANXA5_HUMAN Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2							
\$2-2			25	9	37.81%	35936.83	4.94	tr V9HWE0 V9HWE0_HUMAN Annexin OS=Homo sapiens GN=HEL-S-7 PE=2 SV=1							
	R16062_1_KIAA,15	K.FITIFGTR.S	102 - 15103	955.1352	0.0882	2	1		2.3288	0.305	380.9	12 10 14	9.75	1	2
	R16062_1_KIAA,15	K.FITIFGTR.S	111	955.1352	0.0352	2	1		2.4588	0.2339	655.1	4 12 14	9.75	1	2
	R16062_1_KIAA,19	K.GLGTDEESILTLTTSR.S	682	1705.8887	0.3327	2	1		2.6333	0.4899	611.1	1 13 30	4.14	1	2
	R16062_1_KIAA,19	K.GLGTDEESILTLTTSR.S	692	1705.8887	0.5297	2	1		3.4593	0.5461	1284.2	1 18 30	4.14	1	2

R16062_1_KIAA,19 760	K.GLGTDEESILTLTTSR.S	1705.8887	2.0777	2	1		3.5778	0.5109	1731.9	123 30	4.14	1	2
R16062_1_KIAA,15 030	K.NFATSLYSM*IK.G	1291.4984	0.3774	2	1		2.5078	0.1523	1191.1	115 20	8.59	1	2
R16062_1_KIAA,15 080	K.NFATSLYSM*IK.G	1291.4984	0.4904	2	1		2.4604	0.239	1083.7	114 20	8.59	1	2
R16062_1_KIAA,15 085	K.NFATSLYSM*IK.G	1291.4984	0.3154	2	1		2.2482	0.2837	720.2	112 20	8.59	1	2
R16062_1_KIAA,10 788	K.VLTEIIASR.T	1002.1901	0.9011	2	1		2.6054	0.3803	1383.3	114 16	5.97	1	2
R16062_1_KIAA,10 795	K.VLTEIIASR.T	1002.1901	0.8571	2	1		2.6476	0.318	1293.5	114 16	5.97	1	2
R16062_1_KIAA,19 046	R.DLLDDLKSELTGK.F	1447.6132	0.6192	2	1		2.6604	0.3643	1284.5	117 24	4.23	1	2
R16062_1_KIAA,19 061	R.DLLDDLKSELTGK.F	1447.6132	-0.4418	2	1		2.695	0.3463	616.1	114 24	4.23	1	2
R16062_1_KIAA,19 071	R.DLLDDLKSELTGK.F	1447.6132	0.8272	2	1		2.5829	0.3049	1109	117 24	4.23	1	2
R16062_1_KIAA,18 936	R.DPDAGIDEAQVEQDAQALFQAGE LK.W	2659.8007	1.1797	3	1		4.6434	0.3989	1411	132 96	3.62	1	2
R16062_1_KIAA,18 947	R.DPDAGIDEAQVEQDAQALFQAGE LK.W	2659.8007	-0.7993	3	1		4.8615	0.5447	1131.9	130 96	3.62	1	2
R16062_1_KIAA,18 950	R.DPDAGIDEAQVEQDAQALFQAGE LK.W	2659.8007	1.0667	3	1		4.1575	0.4387	1226.4	131 96	3.62	1	2
R16062_1_KIAA,19 000	R.DPDAGIDEAQVEQDAQALFQAGE LK.W	2659.8007	0.2617	2	1		4.5825	0.6553	1949.4	125 48	3.62	1	2
R16062_1_KIAA,19 016	R.DPDAGIDEAQVEQDAQALFQAGE LK.W	2659.8007	1.1667	2	1		2.9861	0.5305	1076.4	121 48	3.62	1	2
R16062_1_KIAA,20 298	R.ETSGNLEQLLAVVK.S	1614.8655	0.3715	2	1		2.9096	0.4155	606.5	116 28	4.53	1	2
R16062_1_KIAA,20 309	R.ETSGNLEQLLAVVK.S	1614.8655	0.6735	2	1		2.8967	0.3955	905.3	115 28	4.53	1	2
R16062_1_KIAA,20 471	R.ETSGNLEQLLAVVK.S	1614.8655	2.4365	2	1		2.8476	0.4	794.1	115 28	4.53	1	2
R16062_1_KIAA,15 711	R.SEIDLFNIR.K	1107.2417	0.0697	2	1		2.5099	0.1854	983.2	413 16	4.37	1	2
R16062_1_KIAA,15 721	R.SEIDLFNIR.K	1107.2417	0.2717	2	1		2.5782	0.1865	1063	314 16	4.37	1	2
R16062_1_KIAA,18 256	R.SIPAYLAETLYYAM*K.G	1751.0361	-0.2039	2	1		2.7881	0.4688	577.4	116 28	5.72	1	2
R16062_1_KIAA,18	R.SIPAYLAETLYYAM*K.G	1751.0361	-0.1329	2	1		2.7931	0.5509	423.1	116 28	5.72	1	2

\$3-1	38	8	36.67%	36105.84	8.46	sp P01857 IGHG1_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1
\$3-2	38	8	25.47%	52426.11	8.45	tr A0A087WYC5 A0A087WYC5_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1
\$3-3	38	8	25.58%	51912.59	8.33	tr A0A087X079 A0A087X079_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1
\$3-4	38	8	25.97%	51153.84	7.49	tr A0A087WV47 A0A087WV47_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1
\$3-5	38	8	30.33%	43911.84	6.55	tr A0A0A0MS08 A0A0A0MS08_HUMAN Ig gamma-1 chain C region (Fragment) OS=Homo sapiens GN=IGHG1 PE=1 SV=1
\$3-6	38	8	26.19%	50488.11	8.7	tr A0A087X1C7 A0A087X1C7_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1
\$3-7	38	8	25.64%	51596.34	8.44	tr A8K008 A8K008_HUMAN cDNA FLJ78387 OS=Homo sapiens PE=1 SV=1
\$3-8	38	8	26.02%	51082.9	8.91	tr Q6GMX6 Q6GMX6_HUMAN IGH@ protein OS=Homo sapiens GN=IGH@ PE=1 SV=1
\$3-9	38	8	25.47%	52362.37	8.64	tr Q5EFE5 Q5EFE5_HUMAN Anti-RhD monoclonal T125 gamma1 heavy chain OS=Homo sapiens PE=2 SV=1
\$3-10	38	8	25.64%	51724.53	8.14	tr Q6N089 Q6N089_HUMAN Putative uncharacterized protein DKFZp686P15220 OS=Homo sapiens GN=DKFZp686P15220 PE=1 SV=1
\$3-11	38	8	25.97%	50870.45	7.89	tr S6B291 S6B291_HUMAN IgG H chain OS=Homo sapiens PE=1 SV=1
\$3-12	38	8	25.74%	51715.46	7.88	tr V9HW68 V9HW68_HUMAN Epididymis luminal protein 214 OS=Homo sapiens GN=HEL-214 PE=2 SV=1
\$3-13	38	8	34.77%	38162.08	8.27	tr Q6PYX1 Q6PYX1_HUMAN Hepatitis B virus receptor binding protein (Fragment) OS=Homo sapiens PE=1 SV=1
\$3-14	38	8	25.10%	52852	8.75	tr Q7Z351 Q7Z351_HUMAN Putative uncharacterized protein DKFZp686N02209 OS=Homo sapiens GN=DKFZp686N02209 PE=2 SV=1
\$3-15	38	8	25.21%	52612.6	8.46	tr Q6N094 Q6N094_HUMAN Putative uncharacterized protein DKFZp686O01196 OS=Homo sapiens GN=DKFZp686O01196 PE=2 SV=1
\$3-16	38	8	26.08%	50822.56	8.45	tr A0A087X010 A0A087X010_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1
\$3-17	38	8	25.47%	52109.86	7.49	tr A0A087WYE1 A0A087WYE1_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1
\$3-18	38	8	25.47%	52042.86	8.31	tr Q6MZQ6 Q6MZQ6_HUMAN Putative uncharacterized protein DKFZp686G11190 OS=Homo sapiens GN=DKFZp686G11190 PE=2 SV=1

\$3-19	38	8	25.16%	52758.77	tr Q6N097 Q6N097_HUMAN Putative uncharacterized protein PE=2 SV=1									
\$3-20	38	8	26.08%	50915.61	8.13	tr A0A0G2JNK4 A0A0G2JNK4_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1								
\$3-21	38	8	25.97%	50926.64	8.33	tr Q6N096 Q6N096_HUMAN Putative uncharacterized protein PE=2 SV=1								
\$3-22	38	8	25.58%	52120.99	7.51	tr Q6MZV7 Q6MZV7_HUMAN Putative uncharacterized protein PE=2 SV=1								
R16062_1_KIAA,13 032	K.FNWWYVDGVEVHNAK.T	1678.8284	0.0084	2	1	2.4796	0.361	762.4	116 26	5.32	1	22		
R16062_1_KIAA,13 037	K.FNWWYVDGVEVHNAK.T	1678.8284	0.3344	2	1	2.5702	0.4037	960.2	117 26	5.32	1	22		
R16062_1_KIAA,13 079	K.FNWWYVDGVEVHNAK.T	1678.8284	2.0254	2	1	2.3047	0.4172	489.5	113 26	5.32	1	22		
R16062_1_KIAA,13 434	K.FNWWYVDGVEVHNAK.T	1678.8284	1.4904	2	1	2.6719	0.4252	865.7	116 26	5.32	1	22		
R16062_1_KIAA,13 450	K.FNWWYVDGVEVHNAK.T	1678.8284	-0.5846	2	1	3.5811	0.5896	1005.1	116 26	5.32	1	22		
R16062_1_KIAA,13 471	K.FNWWYVDGVEVHNAK.T	1678.8284	0.6224	2	1	3.0847	0.4418	959.7	117 26	5.32	1	22		
R16062_1_KIAA,13 499	K.FNWWYVDGVEVHNAK.T	1678.8284	0.4734	2	1	2.6174	0.4358	586.3	113 26	5.32	1	22		
R16062_1_KIAA,15 732	K.GFYPSDIAVEWESNGQPENNYK. T	2545.6579	-0.8321	2	1	3.237	0.3584	1188.7	121 42	4	3	26		
R16062_1_KIAA,15 744	K.GFYPSDIAVEWESNGQPENNYK. T	2545.6579	0.1459	2	1	3.2157	0.376	694.7	119 42	4	3	26		
R16062_1_KIAA,15 820	K.GFYPSDIAVEWESNGQPENNYK. T	2545.6579	1.1829	2	1	4.0896	0.5161	1541.9	123 42	4	3	26		
R16062_1_KIAA,15 886	K.GFYPSDIAVEWESNGQPENNYK. T	2545.6579	-2.8691	2	1	3.3734	0.4336	1416.4	120 42	4	3	26		
R16062_1_KIAA,15 897	K.GFYPSDIAVEWESNGQPENNYK. T	2545.6579	1.2169	2	1	3.1724	0.4151	814	120 42	4	3	26		
R16062_1_KIAA,15 997	K.GFYPSDIAVEWESNGQPENNYK. T	2545.6579	-2.8691	2	1	2.9126	0.2407	646.2	117 42	4	3	26		
R16062_1_KIAA,16 239	K.GFYPSDIAVEWESNGQPENNYK. T	2545.6579	-1.8471	2	1	2.6677	0.46	736.1	120 42	4	3	26		
R16062_1_KIAA,12 489	K.NQVSLTCLVK.G	1162.3554	1.1304	2	1	2.3778	0.3172	753.4	112 18	8.22	5	34		

R16062_1_KIAA,11 035	K.STSGGTAALGCLVK.D	1322.484	0.516	2	1	2.6657	0.4955	841.2	115 26	7.94	3	30
R16062_1_KIAA,11 046	K.STSGGTAALGCLVK.D	1322.484	0.393	2	1	2.4749	0.4182	1320.9	119 26	7.94	3	30
R16062_1_KIAA,17 998	K.THTCPPCPAPELLGGPSVFLFPPK .P	2621.0136	-0.2134	3	1	4.3027	0.4413	1646.7	136 92	6.41	2	23
R16062_1_KIAA,18 001	K.THTCPPCPAPELLGGPSVFLFPPK .P	2621.0136	2.4746	3	1	4.4616	0.4912	1449.2	136 92	6.41	2	23
R16062_1_KIAA,18 155	K.THTCPPCPAPELLGGPSVFLFPPK .P	2621.0136	2.1636	3	1	4.1152	0.5475	1058.3	130 92	6.41	2	23
R16062_1_KIAA,18 274	K.THTCPPCPAPELLGGPSVFLFPPK .P	2621.0136	1.4206	3	1	4.5413	0.3761	1462.8	136 92	6.41	2	23
R16062_1_KIAA,16 712	K.THTCPPCPAPELLGGPSVFLFPPK PK.D	2846.3022	2.8522	3	1	5.2416	0.5911	1083.5	139 100	7.76	2	23
R16062_1_KIAA,16 756	K.THTCPPCPAPELLGGPSVFLFPPK PK.D	2846.3022	2.3592	3	1	3.8943	0.4899	1037.1	135 100	7.76	2	23
R16062_1_KIAA,16 865	K.THTCPPCPAPELLGGPSVFLFPPK PK.D	2846.3022	-2.3138	3	1	4.4267	0.5224	706	131 100	7.76	2	23
R16062_1_KIAA,12 985	R.TPEVTCVVVDVSHEDPEVK.F	2140.3272	-0.5408	2	1	2.367	0.3959	560.2	115 36	4.17	2	23
R16062_1_KIAA,12 995	R.TPEVTCVVVDVSHEDPEVK.F	2140.3272	1.0042	2	1	2.4457	0.3006	555.8	115 36	4.17	2	23
R16062_1_KIAA,13 007	R.TPEVTCVVVDVSHEDPEVK.F	2140.3272	-1.3858	2	1	2.6724	0.403	851.8	117 36	4.17	2	23
R16062_1_KIAA,13 013	R.TPEVTCVVVDVSHEDPEVK.F	2140.3272	1.3762	2	1	2.9498	0.5184	1221.1	121 36	4.17	2	23
R16062_1_KIAA,13 066	R.TPEVTCVVVDVSHEDPEVK.F	2140.3272	2.6872	3	1	3.7958	0.4648	1593.5	134 72	4.17	2	23
R16062_1_KIAA,13 440	R.TPEVTCVVVDVSHEDPEVK.F	2140.3272	1.0192	2	1	3.0336	0.569	1086.9	120 36	4.17	2	23
R16062_1_KIAA,18 132	R.VVSVLTVLHQDWLNGK.E	1809.1018	1.1018	2	1	2.4514	0.4444	961.7	116 30	6.71	3	31
R16062_1_KIAA,18 153	R.VVSVLTVLHQDWLNGK.E	1809.1018	0.7948	2	1	2.5641	0.4073	1008.1	117 30	6.71	3	31
R16062_1_KIAA,18 221	R.VVSVLTVLHQDWLNGK.E	1809.1018	1.9848	2	1	3.2725	0.5713	1812.9	121 30	6.71	3	31
R16062_1_KIAA,18 258	R.VVSVLTVLHQDWLNGK.E	1809.1018	2.1968	2	1	3.2131	0.5276	1326.1	119 30	6.71	3	31
R16062_1_KIAA,18 273	R.VVSVLTVLHQDWLNGK.E	1809.1018	-2.5362	2	1	4.0174	0.5921	1429.8	120 30	6.71	3	31
R16062_1_KIAA,18	R.VVSVLTVLHQDWLNGK.E	1809.1018	-2.4042	2	1	3.7172	0.4354	994.5	118 30	6.71	3	31

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R16062_1_KIAA,18 570	R.VVSVLTVLHQDWLNGK.E	1809.1018	-1.3862	2	1		2.8304	0.5929	1186.7	118 30	6.71	3	31	
R16062_1_KIAA,18 605	R.VVSVLTVLHQDWLNGK.E	1809.1018	-1.1742	2	1		3.1467	0.5284	1147	118 30	6.71	3	31	
\$4-1	16	8	31.79%	38714.23	6.57	sp P04083 ANXA1_HUMAN Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2								
						tr Q5TZZ9 Q5TZZ9_HUMAN Annexin OS=Homo sapiens GN=ANXA1 PE=2 SV=1								
\$4-2	16	8	31.79%	38714.23	6.57									
R16062_1_KIAA,11 072	K.AAYLQETGKPLDETLK.K	1777.9965	0.7785	2	1		2.2334	0.2431	407.4	112 30	4.68	1	2	
R16062_1_KIAA,19 230	K.GLGTEDETLIEILASR.T	1703.8728	-0.4642	2	1		3.0458	0.3822	2358.2	121 30	3.92	1	2	
R16062_1_KIAA,19 244	K.GLGTEDETLIEILASR.T	1703.8728	-1.5622	2	1		4.663	0.4276	2287.6	124 30	3.92	1	2	
R16062_1_KIAA,19 263	K.GLGTEDETLIEILASR.T	1703.8728	0.3618	2	1		3.1859	0.4203	2091.8	122 30	3.92	1	2	
R16062_1_KIAA,19 274	K.GLGTEDETLIEILASR.T	1703.8728	1.0718	2	1		3.6598	0.4439	2714.9	124 30	3.92	1	2	
R16062_1_KIAA,19 410	K.GLGTEDETLIEILASR.T	1703.8728	2.0948	2	1		3.1506	0.4943	2114.5	121 30	3.92	1	2	
R16062_1_KIAA,16 632	K.GTDVNVFNTILTTR.S	1551.7263	-1.3467	2	1		3.1184	0.4131	1079.1	116 26	5.84	1	2	
R16062_1_KIAA,16 637	K.GTDVNVFNTILTTR.S	1551.7263	-0.0637	2	1		3.1364	0.5202	858.9	116 26	5.84	1	2	
R16062_1_KIAA,16 658	K.GTDVNVFNTILTTR.S	1551.7263	-1.5257	2	1		2.7999	0.2563	739.8	115 26	5.84	1	2	
R16062_1_KIAA,16 823	K.GTDVNVFNTILTTR.S	1551.7263	-0.3867	2	1		3.1829	0.3685	921.1	118 26	5.84	1	2	
R16062_1_KIAA,16 846	K.GTDVNVFNTILTTR.S	1551.7263	-0.4627	2	1		3.3369	0.5122	847	114 26	5.84	1	2	
R16062_1_KIAA,18 607	K.GVDEATIIDILTK.R	1388.5889	0.7019	2	1		2.4661	0.4782	627	114 24	4.03	1	2	
R16062_1_KIAA,12 033	K.ILVALCGGN.-	917.0787	0.1937	2	1		2.2145	0.3543	685.1	112 16	5.52	1	2	
R16062_1_KIAA,16 365	K.M*YGISLCQAILDETK.G	1759.0084	-0.4496	2	1		3.682	0.5894	1091.1	118 28	4.37	1	2	
R16062_1_KIAA,10 521	K.TPAQFDADEL.R.A	1263.3385	2.0065	2	1		2.3454	0.4779	968.8	114 20	4.03	1	2	
R16062_1_KIAA,11 168	R.SEDFGVNEDLADSDAR.A	1740.7205	0.6615	2	1		3.011	0.4607	1450.8	120 30	3.66	1	2	

\$5-1		12	8	70.75%	15998.35	6.74	sp P68871 HBB_HUMAN Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2							
\$5-2		12	8	70.75%	15998.35	6.74	tr D9YZU5 D9YZU5_HUMAN Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1							
	R16062_1_KIAA,10 178	K.EFTPPVQAAYQK.V	1379.5423	-0.5657	2	1	2.2229	0.1504	464.9	1 14 22	6.1	1	2	
	R16062_1_KIAA,11 116	K.GTFATLSELHCDK.L	1479.6104	-1.6406	2	1	2.3194	0.3027	305.5	2 10 24	5.32	3	4	
	R16062_1_KIAA,11 123	K.GTFATLSELHCDK.L	1479.6104	0.3594	2	1	2.3893	0.4349	434.2	1 12 24	5.32	3	4	
	R16062_1_KIAA,12 498	K.SAVTALWGK.V	933.0864	0.8684	2	1	2.5905	0.4231	810.7	1 13 16	8.47	3	4	
	R16062_1_KIAA,12 521	K.SAVTALWGK.V	933.0864	0.7164	2	1	2.3857	0.3995	1095.1	1 14 16	8.47	3	4	
	R16062_1_KIAA,14 892	K.VLGAFSDGLAHLNLK.G	1670.8908	-0.3942	2	1	2.7099	0.1644	1055.4	1 19 30	5.21	3	5	
	R16062_1_KIAA,10 277	K.VNVDEVGGEALGR.L	1315.415	0.762	2	1	2.9846	0.1859	951.5	1 15 24	4.14	2	3	
	R16062_1_KIAA,10 707	K.VNVDEVGGEALGR.L	1315.415	0.086	2	1	3.2653	0.2788	1280.3	1 18 24	4.14	2	3	
	R16062_1_KIAA,10 734	K.VNVDEVGGEALGR.L	1315.415	1.099	2	1	2.6907	0.1598	1094.6	1 17 24	4.14	2	3	
	R16062_1_KIAA,85 49	K.VVAGVANALAHK.Y	1150.3561	0.2381	2	1	2.3422	0.4164	674.9	1 13 22	8.73	2	4	
	R16062_1_KIAA,15 017	R.FFESFGDLSTPDAM*GNPK.V	2076.2717	-2.1273	2	1	2.478	0.3888	294.4	1 13 36	4.03	3	4	
	R16062_1_KIAA,15 697	R.LLVYPWTQR.F	1275.5235	0.4625	2	1	2.2234	0.3052	665.8	1 11 18	8.75	4	6	
\$6-1		32	6	41.00%	26234.51	8.24	tr Q8TCD0 Q8TCD0_HUMAN Uncharacterized protein OS=Homo sapiens PE=1 SV=1							
\$6-2		32	6	44.75%	24029.93	8.29	tr Q0KKI6 Q0KKI6_HUMAN Immunoglobulin light chain (Fragment) OS=Homo sapiens PE=1 SV=1							
	R16062_1_KIAA,16 535	-.TVAAPSVFIFPPSDEQLK.S	1947.22	-1.248	2	1	2.5905	0.4133	292.4	1 13 34	4.37	4	8	
	R16062_1_KIAA,16 557	-.TVAAPSVFIFPPSDEQLK.S	1947.22	-1.181	2	1	2.2549	0.2349	229.1	1 13 34	4.37	4	8	
	R16062_1_KIAA,16 777	-.TVAAPSVFIFPPSDEQLK.S	1947.22	0.782	2	1	2.4042	0.3821	524.6	1 19 34	4.37	4	8	
	R16062_1_KIAA,16 788	-.TVAAPSVFIFPPSDEQLK.S	1947.22	0.82	2	1	2.4522	0.5211	388.3	1 16 34	4.37	4	8	
	R16062_1_KIAA,17	-.TVAAPSVFIFPPSDEQLK.S	1947.22	0.531	2	1	2.9491	0.4563	756.2	1 21 34	4.37	4	8	

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R16062_1_KIAA,17 206	-.TVAAPSVFIFPPSDEQLK.S	1947.22	0.674	2	1		2.3807	0.3829	237.9	1 13 34	4.37	4	8
R16062_1_KIAA,17 485	-.TVAAPSVFIFPPSDEQLK.S	1947.22	1.737	2	1		2.6139	0.4106	390	1 16 34	4.37	4	8
R16062_1_KIAA,13 302	K.DSTYSLSSTLTLSK.A	1503.6336	0.9196	2	1		2.7028	0.4304	903.4	1 16 26	5.84	3	6
R16062_1_KIAA,13 312	K.DSTYSLSSTLTLSK.A	1503.6336	0.2906	2	1		2.6194	0.4473	718.5	1 15 26	5.84	3	6
R16062_1_KIAA,16 001	K.SGTASVVCLLNNFYPR.E	1799.0141	0.3261	2	1		2.9192	0.5415	550.6	1 13 30	7.94	4	8
R16062_1_KIAA,16 033	K.SGTASVVCLLNNFYPR.E	1799.0141	0.1381	2	1		3.312	0.4871	1199.2	1 18 30	7.94	4	8
R16062_1_KIAA,17 303	K.SGTASVVCLLNNFYPR.E	1799.0141	-0.3619	2	1		2.4085	0.4512	580.2	1 14 30	7.94	4	8
R16062_1_KIAA,17 350	K.SGTASVVCLLNNFYPR.E	1799.0141	-0.1429	2	1		2.8188	0.4831	927.2	1 15 30	7.94	4	8
R16062_1_KIAA,18 804	K.SGTASVVCLLNNFYPR.E	1799.0141	1.6411	2	1		2.9725	0.5376	1033.7	1 17 30	7.94	4	8
R16062_1_KIAA,18 845	K.SGTASVVCLLNNFYPR.E	1799.0141	0.5641	2	1		2.4368	0.4778	1164.4	1 18 30	7.94	4	8
R16062_1_KIAA,18 876	K.SGTASVVCLLNNFYPR.E	1799.0141	2.0111	2	1		2.9342	0.4613	1195.6	1 18 30	7.94	4	8
R16062_1_KIAA,18 922	K.SGTASVVCLLNNFYPR.E	1799.0141	-2.5899	2	1		3.8096	0.4571	1228.7	1 17 30	7.94	4	8
R16062_1_KIAA,19 029	K.SGTASVVCLLNNFYPR.E	1799.0141	-2.6549	2	1		3.1649	0.3967	843.2	1 15 30	7.94	4	8
R16062_1_KIAA,19 259	K.SGTASVVCLLNNFYPR.E	1799.0141	0.8761	2	1		2.7348	0.4147	845.6	1 15 30	7.94	4	8
R16062_1_KIAA,19 266	K.SGTASVVCLLNNFYPR.E	1799.0141	-0.5639	2	1		3.5693	0.5112	830.8	1 16 30	7.94	4	8
R16062_1_KIAA,19 342	K.SGTASVVCLLNNFYPR.E	1799.0141	0.4391	2	1		3.2765	0.4663	1053.3	1 17 30	7.94	4	8
R16062_1_KIAA,19 358	K.SGTASVVCLLNNFYPR.E	1799.0141	0.4801	2	1		3.4313	0.5099	953.8	1 17 30	7.94	4	8
R16062_1_KIAA,70 86	K.VDNALQSGNSQESVTEQDSK.D	2137.1621	1.8861	3	1		3.9621	0.5102	1709.3	1 33 76	3.92	3	6
R16062_1_KIAA,72 95	K.VDNALQSGNSQESVTEQDSK.D	2137.1621	-0.2969	2	1		4.4397	0.5979	1523.1	1 23 38	3.92	3	6
R16062_1_KIAA,72 98	K.VDNALQSGNSQESVTEQDSK.D	2137.1621	1.3441	2	1		2.5383	0.4696	1108.3	1 20 38	3.92	3	6

	R16062_1_KIAA,7309	K.VDNALQSGNSQESVTEQDSK.D	2137.1621	-0.7909	2	1		4.1369	0.6214	1858.9	122 38	3.92	3	6
	R16062_1_KIAA,7311	K.VDNALQSGNSQESVTEQDSK.D	2137.1621	0.5991	2	1		2.7977	0.4484	450.8	117 38	3.92	3	6
	R16062_1_KIAA,9132	K.VYACEVTHQGLSSPVTK.S	1877.0816	-0.5874	2	1		2.836	0.5254	690.8	115 32	6.71	3	6
	R16062_1_KIAA,9134	K.VYACEVTHQGLSSPVTK.S	1877.0816	1.3236	2	1		3.0585	0.5121	845.1	118 32	6.71	3	6
	R16062_1_KIAA,9143	K.VYACEVTHQGLSSPVTK.S	1877.0816	0.5556	2	1		2.9064	0.4781	923.3	117 32	6.71	3	6
	R16062_1_KIAA,10696	R.FSGSGSGTDFTLK.I	1304.3874	-1.4876	2	1		3.2111	0.2331	1179.5	117 24	5.84	1	2
	R16062_1_KIAA,10705	R.FSGSGSGTDFTLK.I	1304.3874	-1.2226	2	1		3.4803	0.2547	1142.3	116 24	5.84	1	2
\$7-1			31	6	42.98%	25645.94	6.15	tr V9HW34 V9HW34_HUMAN Epididymis luminal protein 213 OS=Homo sapiens GN=HEL-213 PE=2 SV=1						
\$7-2			31	6	42.80%	25833.95	6.14	tr Q6PIL8 Q6PIL8_HUMAN IGK@ protein OS=Homo sapiens GN=IGK@ PE=1 SV=1						
\$7-3			31	6	42.98%	25520.68	6.14	tr Q6PJF2 Q6PJF2_HUMAN IGK@ protein OS=Homo sapiens GN=IGK@ PE=1 SV=1						
	R16062_1_KIAA,16535	-.TVAAPSVFIFPPSDEQLK.S	1947.22	-1.248	2	1		2.5905	0.4133	292.4	113 34	4.37	4	8
	R16062_1_KIAA,16557	-.TVAAPSVFIFPPSDEQLK.S	1947.22	-1.181	2	1		2.2549	0.2349	229.1	113 34	4.37	4	8
	R16062_1_KIAA,16777	-.TVAAPSVFIFPPSDEQLK.S	1947.22	0.782	2	1		2.4042	0.3821	524.6	119 34	4.37	4	8
	R16062_1_KIAA,16788	-.TVAAPSVFIFPPSDEQLK.S	1947.22	0.82	2	1		2.4522	0.5211	388.3	116 34	4.37	4	8
	R16062_1_KIAA,17195 - 17196	-.TVAAPSVFIFPPSDEQLK.S	1947.22	0.531	2	1		2.9491	0.4563	756.2	121 34	4.37	4	8
	R16062_1_KIAA,17206	-.TVAAPSVFIFPPSDEQLK.S	1947.22	0.674	2	1		2.3807	0.3829	237.9	113 34	4.37	4	8
	R16062_1_KIAA,17485	-.TVAAPSVFIFPPSDEQLK.S	1947.22	1.737	2	1		2.6139	0.4106	390	116 34	4.37	4	8
	R16062_1_KIAA,13302	K.DSTYLSSTLTLSK.A	1503.6336	0.9196	2	1		2.7028	0.4304	903.4	116 26	5.84	3	6
	R16062_1_KIAA,13312	K.DSTYLSSTLTLSK.A	1503.6336	0.2906	2	1		2.6194	0.4473	718.5	115 26	5.84	3	6
	R16062_1_KIAA,16001	K.SGTASVVCLLNNFYPR.E	1799.0141	0.3261	2	1		2.9192	0.5415	550.6	113 30	7.94	4	8
	R16062_1_KIAA,16	K.SGTASVVCLLNNFYPR.E	1799.0141	0.1381	2	1		3.312	0.4871	1199.2	118 30	7.94	4	8

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R16062_1_KIAA,17303	K.SGTASVVCLLNNFYPR.E	1799.0141	-0.3619	2	1		2.4085	0.4512	580.2	114 30	7.94	4	8
R16062_1_KIAA,17350	K.SGTASVVCLLNNFYPR.E	1799.0141	-0.1429	2	1		2.8188	0.4831	927.2	115 30	7.94	4	8
R16062_1_KIAA,18804	K.SGTASVVCLLNNFYPR.E	1799.0141	1.6411	2	1		2.9725	0.5376	1033.7	117 30	7.94	4	8
R16062_1_KIAA,18845	K.SGTASVVCLLNNFYPR.E	1799.0141	0.5641	2	1		2.4368	0.4778	1164.4	118 30	7.94	4	8
R16062_1_KIAA,18876	K.SGTASVVCLLNNFYPR.E	1799.0141	2.0111	2	1		2.9342	0.4613	1195.6	118 30	7.94	4	8
R16062_1_KIAA,18922	K.SGTASVVCLLNNFYPR.E	1799.0141	-2.5899	2	1		3.8096	0.4571	1228.7	117 30	7.94	4	8
R16062_1_KIAA,19029	K.SGTASVVCLLNNFYPR.E	1799.0141	-2.6549	2	1		3.1649	0.3967	843.2	115 30	7.94	4	8
R16062_1_KIAA,19259	K.SGTASVVCLLNNFYPR.E	1799.0141	0.8761	2	1		2.7348	0.4147	845.6	115 30	7.94	4	8
R16062_1_KIAA,19266	K.SGTASVVCLLNNFYPR.E	1799.0141	-0.5639	2	1		3.5693	0.5112	830.8	116 30	7.94	4	8
R16062_1_KIAA,19342	K.SGTASVVCLLNNFYPR.E	1799.0141	0.4391	2	1		3.2765	0.4663	1053.3	117 30	7.94	4	8
R16062_1_KIAA,19358	K.SGTASVVCLLNNFYPR.E	1799.0141	0.4801	2	1		3.4313	0.5099	953.8	117 30	7.94	4	8
R16062_1_KIAA,7086	K.VDNALQSGNSQESVTEQDSK.D	2137.1621	1.8861	3	1		3.9621	0.5102	1709.3	133 76	3.92	3	6
R16062_1_KIAA,7295	K.VDNALQSGNSQESVTEQDSK.D	2137.1621	-0.2969	2	1		4.4397	0.5979	1523.1	123 38	3.92	3	6
R16062_1_KIAA,7298	K.VDNALQSGNSQESVTEQDSK.D	2137.1621	1.3441	2	1		2.5383	0.4696	1108.3	120 38	3.92	3	6
R16062_1_KIAA,7309	K.VDNALQSGNSQESVTEQDSK.D	2137.1621	-0.7909	2	1		4.1369	0.6214	1858.9	122 38	3.92	3	6
R16062_1_KIAA,7311	K.VDNALQSGNSQESVTEQDSK.D	2137.1621	0.5991	2	1		2.7977	0.4484	450.8	117 38	3.92	3	6
R16062_1_KIAA,9132	K.VYACEVTHQGLSSPVTK.S	1877.0816	-0.5874	2	1		2.836	0.5254	690.8	115 32	6.71	3	6
R16062_1_KIAA,9134	K.VYACEVTHQGLSSPVTK.S	1877.0816	1.3236	2	1		3.0585	0.5121	845.1	118 32	6.71	3	6
R16062_1_KIAA,9143	K.VYACEVTHQGLSSPVTK.S	1877.0816	0.5556	2	1		2.9064	0.4781	923.3	117 32	6.71	3	6
R16062_1_KIAA,13188	R.FSGSGSGTDFLTISR.L	1633.7411	-0.1499	2	1		2.4785	0.4793	434.5	112 30	5.84	2	8

\$8-1		31	6	40.34%	25600.71	5.75	tr A0A087WZW8 A0A087WZW8_HUMAN Protein IGKV3-11 OS=Homo sapiens GN=IGKV3-11 PE=4 SV=1						
	R16062_1_KIAA,16 535	-.TVAAPSVFIFPPSDEQLK.S	1947.22	-1.248	2	1	2.5905	0.4133	292.4	113 34	4.37	4	8
	R16062_1_KIAA,16 557	-.TVAAPSVFIFPPSDEQLK.S	1947.22	-1.181	2	1	2.2549	0.2349	229.1	113 34	4.37	4	8
	R16062_1_KIAA,16 777	-.TVAAPSVFIFPPSDEQLK.S	1947.22	0.782	2	1	2.4042	0.3821	524.6	119 34	4.37	4	8
	R16062_1_KIAA,16 788	-.TVAAPSVFIFPPSDEQLK.S	1947.22	0.82	2	1	2.4522	0.5211	388.3	116 34	4.37	4	8
	R16062_1_KIAA,17 195 - 17196	-.TVAAPSVFIFPPSDEQLK.S	1947.22	0.531	2	1	2.9491	0.4563	756.2	121 34	4.37	4	8
	R16062_1_KIAA,17 206	-.TVAAPSVFIFPPSDEQLK.S	1947.22	0.674	2	1	2.3807	0.3829	237.9	113 34	4.37	4	8
	R16062_1_KIAA,17 485	-.TVAAPSVFIFPPSDEQLK.S	1947.22	1.737	2	1	2.6139	0.4106	390	116 34	4.37	4	8
	R16062_1_KIAA,13 302	K.DSTYSLSSTLTLSK.A	1503.6336	0.9196	2	1	2.7028	0.4304	903.4	116 26	5.84	3	6
	R16062_1_KIAA,13 312	K.DSTYSLSSTLTLSK.A	1503.6336	0.2906	2	1	2.6194	0.4473	718.5	115 26	5.84	3	6
	R16062_1_KIAA,16 001	K.SGTASVVCLLNNFYPR.E	1799.0141	0.3261	2	1	2.9192	0.5415	550.6	113 30	7.94	4	8
	R16062_1_KIAA,16 033	K.SGTASVVCLLNNFYPR.E	1799.0141	0.1381	2	1	3.312	0.4871	1199.2	118 30	7.94	4	8
	R16062_1_KIAA,17 303	K.SGTASVVCLLNNFYPR.E	1799.0141	-0.3619	2	1	2.4085	0.4512	580.2	114 30	7.94	4	8
	R16062_1_KIAA,17 350	K.SGTASVVCLLNNFYPR.E	1799.0141	-0.1429	2	1	2.8188	0.4831	927.2	115 30	7.94	4	8
	R16062_1_KIAA,18 804	K.SGTASVVCLLNNFYPR.E	1799.0141	1.6411	2	1	2.9725	0.5376	1033.7	117 30	7.94	4	8
	R16062_1_KIAA,18 845	K.SGTASVVCLLNNFYPR.E	1799.0141	0.5641	2	1	2.4368	0.4778	1164.4	118 30	7.94	4	8
	R16062_1_KIAA,18 876	K.SGTASVVCLLNNFYPR.E	1799.0141	2.0111	2	1	2.9342	0.4613	1195.6	118 30	7.94	4	8
	R16062_1_KIAA,18 922	K.SGTASVVCLLNNFYPR.E	1799.0141	-2.5899	2	1	3.8096	0.4571	1228.7	117 30	7.94	4	8
	R16062_1_KIAA,19 029	K.SGTASVVCLLNNFYPR.E	1799.0141	-2.6549	2	1	3.1649	0.3967	843.2	115 30	7.94	4	8
	R16062_1_KIAA,19 259	K.SGTASVVCLLNNFYPR.E	1799.0141	0.8761	2	1	2.7348	0.4147	845.6	115 30	7.94	4	8
	R16062_1_KIAA,19	K.SGTASVVCLLNNFYPR.E	1799.0141	-0.5639	2	1	3.5693	0.5112	830.8	116 30	7.94	4	8

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\$9-1	R16062_1_KIAA,19342	K.SGTASVVCLNNFYPR.E	1799.0141	0.4391	2	1		3.2765	0.4663	1053.3	117 30	7.94	48
	R16062_1_KIAA,19358	K.SGTASVVCLNNFYPR.E	1799.0141	0.4801	2	1		3.4313	0.5099	953.8	117 30	7.94	48
	R16062_1_KIAA,7086	K.VDNALQSGNSQESVTEQDSK.D	2137.1621	1.8861	3	1		3.9621	0.5102	1709.3	133 76	3.92	36
	R16062_1_KIAA,7295	K.VDNALQSGNSQESVTEQDSK.D	2137.1621	-0.2969	2	1		4.4397	0.5979	1523.1	123 38	3.92	36
	R16062_1_KIAA,7298	K.VDNALQSGNSQESVTEQDSK.D	2137.1621	1.3441	2	1		2.5383	0.4696	1108.3	120 38	3.92	36
	R16062_1_KIAA,7309	K.VDNALQSGNSQESVTEQDSK.D	2137.1621	-0.7909	2	1		4.1369	0.6214	1858.9	122 38	3.92	36
	R16062_1_KIAA,7311	K.VDNALQSGNSQESVTEQDSK.D	2137.1621	0.5991	2	1		2.7977	0.4484	450.8	117 38	3.92	36
	R16062_1_KIAA,9132	K.VYACEVTHQGLSSPVTK.S	1877.0816	-0.5874	2	1		2.836	0.5254	690.8	115 32	6.71	36
	R16062_1_KIAA,9134	K.VYACEVTHQGLSSPVTK.S	1877.0816	1.3236	2	1		3.0585	0.5121	845.1	118 32	6.71	36
	R16062_1_KIAA,9143	K.VYACEVTHQGLSSPVTK.S	1877.0816	0.5556	2	1		2.9064	0.4781	923.3	117 32	6.71	36
	R16062_1_KIAA,10532	R.LLIYDASNR.A	1065.2048	1.1808	2	1		2.2253	0.3247	948.4	114 16	5.84	22
	sp P01860 IGHG3_HUMAN Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2												
	tr A0A087WXL8 A0A087WXL8_HUMAN Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=1												
	tr A0A075B6N8 A0A075B6N8_HUMAN Ig gamma-3 chain C region (Fragment) OS=Homo sapiens GN=IGHG3 PE=1 SV=1												
	tr A0A087WVW2 A0A087WVW2_HUMAN Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=1												
	tr Q5EBM2 Q5EBM2_HUMAN Uncharacterized protein OS=Homo sapiens PE=1 SV=1												
	tr Q6N030 Q6N030_HUMAN Putative uncharacterized protein												
	8.39DKFZp686I15212 OS=Homo sapiens GN=DKFZp686I15212 PE=1 SV=1												
	tr Q8NF17 Q8NF17_HUMAN FLJ00385 protein (Fragment) OS=Homo sapiens GN=FLJ00385 PE=1 SV=1												
	R16062_1_KIAA,12489	K.NQVSLTCLVK.G	1162.3554	1.1304	2	1		2.3778	0.3172	753.4	112 18	8.22	534
	R16062_1_KIAA,50	K.SCDTPPPCPR.C	1187.2721	-1.7879	2	1		2.9314	0.4783	661.3	114 18	5.55	17

	96	R16062_1_KIAA,53 K.SCDTPPPCPR.C	1187.2721	0.0731	2	1	2.4387	0.4028	597.3	113 18	5.55	1	7
	48	R16062_1_KIAA,53 K.SCDTPPPCPR.C	1187.2721	2.0861	2	1	2.3361	0.5009	650.7	113 18	5.55	1	7
	51	R16062_1_KIAA,11 K.STSGGTAALGCLVK.D	1322.484	0.516	2	1	2.6657	0.4955	841.2	115 26	7.94	3	30
	035	R16062_1_KIAA,11 K.STSGGTAALGCLVK.D	1322.484	0.393	2	1	2.4749	0.4182	1320.9	119 26	7.94	3	30
	046	R16062_1_KIAA,56 K.TPLGDTTHTCPR.C	1356.4605	0.2985	2	1	2.6451	0.5175	662.8	114 22	6.4	1	7
	90	R16062_1_KIAA,17 R.CPAPELLGGPSVFLFPPKPK.D	2152.5571	1.2401	3	1	4.5673	0.53	1249.6	131 76	8.2	1	7
	394	R16062_1_KIAA,17 R.CPAPELLGGPSVFLFPPKPK.D	2152.5571	0.7301	3	1	4.5417	0.6115	1398.2	134 76	8.2	1	7
	405	R16062_1_KIAA,17 R.CPAPELLGGPSVFLFPPKPK.D	2152.5571	2.5651	3	1	4.389	0.6011	792.3	132 76	8.2	1	7
	483	R16062_1_KIAA,18 R.VVSVLTVLHQDWLNGK.E	1809.1018	1.1018	2	1	2.4514	0.4444	961.7	116 30	6.71	3	31
	132	R16062_1_KIAA,18 R.VVSVLTVLHQDWLNGK.E	1809.1018	0.7948	2	1	2.5641	0.4073	1008.1	117 30	6.71	3	31
	153	R16062_1_KIAA,18 R.VVSVLTVLHQDWLNGK.E	1809.1018	1.9848	2	1	3.2725	0.5713	1812.9	121 30	6.71	3	31
	221	R16062_1_KIAA,18 R.VVSVLTVLHQDWLNGK.E	1809.1018	2.1968	2	1	3.2131	0.5276	1326.1	119 30	6.71	3	31
	258	R16062_1_KIAA,18 R.VVSVLTVLHQDWLNGK.E	1809.1018	-2.5362	2	1	4.0174	0.5921	1429.8	120 30	6.71	3	31
	273	R16062_1_KIAA,18 R.VVSVLTVLHQDWLNGK.E	1809.1018	-2.4042	2	1	3.7172	0.4354	994.5	118 30	6.71	3	31
	295	R16062_1_KIAA,18 R.VVSVLTVLHQDWLNGK.E	1809.1018	-1.3862	2	1	2.8304	0.5929	1186.7	118 30	6.71	3	31
	570	R16062_1_KIAA,18 R.VVSVLTVLHQDWLNGK.E	1809.1018	-1.1742	2	1	3.1467	0.5284	1147	118 30	6.71	3	31
	605												
\$10-1	12	6	12.48%	69366.9	5.92	sp P02768 ALBU_HUMAN Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2							
\$10-2	12	6	12.48%	69084.56	5.85	tr Q56G89 Q56G89_HUMAN Serum albumin OS=Homo sapiens PE=2 SV=1							
\$10-3	12	6	12.50%	69267.8	5.91	tr A8K9P0 A8K9P0_HUMAN cDNA FLJ78413, highly similar to Homo sapiens albumin, mRNA OS=Homo sapiens PE=2 SV=1							
\$10-4	12	6	12.30%	70363.15	5.78	tr B4DPP6 B4DPP6_HUMAN cDNA FLJ54371, highly similar to Serum albumin OS=Homo sapiens PE=2 SV=1							

\$10-5			12	6	12.99%	66531.48	5.73	tr F6KPG5 F6KPG5_HUMAN Albumin (Fragment) OS=Homo sapiens PE=2 SV=1						
	R16062_1_KIAA,19562	K.DVFLGM*FLYEYAR.R		1640.8834	-0.2876	2	1	2.8167	0.4499	1155.5	117 24	4.37	1	5
	R16062_1_KIAA,19588	K.DVFLGM*FLYEYAR.R		1640.8834	-0.7836	2	1	3.1188	0.4894	1171.5	117 24	4.37	1	5
	R16062_1_KIAA,19594	K.DVFLGM*FLYEYAR.R		1640.8834	1.4894	2	1	2.6249	0.3842	1113.3	117 24	4.37	1	5
	R16062_1_KIAA,19604	K.DVFLGM*FLYEYAR.R		1640.8834	0.3984	2	1	2.7954	0.5144	693.7	115 24	4.37	1	5
	R16062_1_KIAA,13493	K.LVAASQAALGL.-		1014.2009	0.5919	2	1	2.3672	0.3638	925.9	115 20	5.53	1	5
	R16062_1_KIAA,13500	K.LVAASQAALGL.-		1014.2009	0.5219	2	1	2.9673	0.4726	1505	116 20	5.53	1	5
	R16062_1_KIAA,11158	K.LVNEVTEFAK.T		1150.3065	1.0375	2	1	2.2167	0.4809	562.3	113 18	4.53	1	5
	R16062_1_KIAA,14569	K.QNCELFEQLGEYK.F		1658.784	0.67	2	1	2.4194	0.349	812.1	113 24	4.25	1	5
	R16062_1_KIAA,14649	K.QNCELFEQLGEYK.F		1658.784	1.449	2	1	3.1369	0.4445	660.3	113 24	4.25	1	5
	R16062_1_KIAA,16144	K.VFDEFKPLVEEPQNLIK.Q		2046.3515	0.6605	2	1	2.7895	0.4551	493.2	116 32	4.41	1	5
	R16062_1_KIAA,16173	K.VFDEFKPLVEEPQNLIK.Q		2046.3515	0.6185	2	1	2.5734	0.2411	365.8	114 32	4.41	1	5
	R16062_1_KIAA,6878	K.YICENQDSISSK.L		1444.5197	0.6307	2	1	2.5816	0.2575	624.9	114 22	4.37	1	5
\$11-1			11	6	5.41%	226532.68	5.5	sp P35579 MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4						
\$11-2			11	6	5.41%	226532.68	5.5	tr A0A024R1N1 A0A024R1N1_HUMAN Myosin, heavy polypeptide 9, non-muscle, isoform CRA_a OS=Homo sapiens GN=MYH9 PE=4 SV=1						
	R16062_1_KIAA,14607	K.ANLQIDQINTDLNLER.S		1871.042	0.459	2	1	3.8066	0.5363	1787.4	121 30	4.03	1	2
	R16062_1_KIAA,18427	K.DFSALESQLQDTQELLQEENR.Q		2494.6107	0.4327	2	1	2.9801	0.3968	937.5	120 40	3.77	1	2
	R16062_1_KIAA,18474	K.DFSALESQLQDTQELLQEENR.Q		2494.6107	1.1187	2	1	2.8666	0.4489	550.5	117 40	3.77	1	2
	R16062_1_KIAA,10646	K.IAQLEEQLDNETK.E		1531.6471	0.9501	2	1	2.2806	0.4333	448.9	112 24	4	1	2
	R16062_1_KIAA,10698	K.IAQLEEQLDNETK.E		1531.6471	0.3341	2	1	3.2559	0.4593	1307.7	116 24	4	1	2

\$12-1	R16062_1_KIAA,16 136	K.LQVELDNVTGLLSQSDSK.S	1947.1335	1.4715	2	1		2.616	0.4715	1127.4	1 18 34	4.03	1	2
	R16062_1_KIAA,16 141	K.LQVELDNVTGLLSQSDSK.S	1947.1335	1.0245	2	1		2.7876	0.4715	546.4	1 15 34	4.03	1	2
	R16062_1_KIAA,14 562	R.IAQLEEEEEEEQGNTLINDR.L	2473.5898	0.9478	2	1		2.5673	0.3678	417.1	1 16 40	3.72	1	2
	R16062_1_KIAA,16 114	R.TQLEEELEDELQATEDAK.L	1963.0435	0.2285	2	1		3.8254	0.5727	1495.2	1 20 32	3.71	1	2
	R16062_1_KIAA,16 134	R.TQLEEELEDELQATEDAK.L	1963.0435	-0.3655	2	1		2.9517	0.3391	984.5	1 17 32	3.71	1	2
	R16062_1_KIAA,16 142	R.TQLEEELEDELQATEDAK.L	1963.0435	1.2855	2	1		3.1629	0.3846	1313.6	1 18 32	3.71	1	2
			10	6	79.21%	11022.47	6.03	tr Q4TZM4 Q4TZM4_HUMAN Hemoglobin beta chain (Fragment) OS=Homo sapiens GN=HBB PE=3 SV=1						
	R16062_1_KIAA,11 116	K.GTFATLSELHCDK.L	1479.6104	-1.6406	2	1		2.3194	0.3027	305.5	2 10 24	5.32	3	4
	R16062_1_KIAA,11 123	K.GTFATLSELHCDK.L	1479.6104	0.3594	2	1		2.3893	0.4349	434.2	1 12 24	5.32	3	4
	R16062_1_KIAA,12 498	K.SAVTALWGK.V	933.0864	0.8684	2	1		2.5905	0.4231	810.7	1 13 16	8.47	3	4
	R16062_1_KIAA,12 521	K.SAVTALWGK.V	933.0864	0.7164	2	1		2.3857	0.3995	1095.1	1 14 16	8.47	3	4
	R16062_1_KIAA,15 538	K.VLGAFSNGLAHLDNLK.G	1669.9061	1.8091	2	1		2.632	0.1932	587.5	1 16 30	6.71	1	1
	R16062_1_KIAA,10 277	K.VNVDEVGGEALGR.L	1315.415	0.762	2	1		2.9846	0.1859	951.5	1 15 24	4.14	2	3
\$13-1	R16062_1_KIAA,10 707	K.VNVDEVGGEALGR.L	1315.415	0.086	2	1		3.2653	0.2788	1280.3	1 18 24	4.14	2	3
	R16062_1_KIAA,10 734	K.VNVDEVGGEALGR.L	1315.415	1.099	2	1		2.6907	0.1598	1094.6	1 17 24	4.14	2	3
\$13-2	R16062_1_KIAA,15 017	R.FFESFGDLSTPDAVM*GNPK.V	2076.2717	-2.1273	2	1		2.478	0.3888	294.4	1 13 36	4.03	3	4
	R16062_1_KIAA,15 697	R.LLVVYPWTQR.F	1275.5235	0.4625	2	1		2.2234	0.3052	665.8	1 11 18	8.75	4	6
\$13-3			10	6	17.00%	51511.61	5.37	sp P02679 FIBG_HUMAN Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3						
			10	6	16.70%	52337.57	5.37	tr C9JC84 C9JC84_HUMAN Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=1						
\$13-3			10	6	17.30%	50322.41	5.71	tr C9JEU5 C9JEU5_HUMAN Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=1						
	R16062_1_KIAA,67	K.VAQLEAQCQEPCK.D	1561.7064	0.3294	2	1		2.3324	0.4243	1109.7	1 17 24	4.53	1	3

[illegible]

\$15-2		9	6	3.23%	278118.62	8.42	tr E7ENL6 E7ENL6_HUMAN Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=2						
\$15-3		9	6	2.61%	343669.73	6.26	tr D9ZGF2 D9ZGF2_HUMAN Collagen, type VI, alpha 3 OS=Homo sapiens GN=COL6A3 PE=4 SV=1						
\$15-4		9	6	3.23%	278211.77	8.4	tr B7ZW00 B7ZW00_HUMAN COL6A3 protein OS=Homo sapiens GN=COL6A3 PE=2 SV=1						
	R16062_1_KIAA,14 601	K.LLTPITTLTSEQIQK.L	1686.9716	0.6756	2	1	2.4492	0.334	481.4	1 13 28	6	1	4
	R16062_1_KIAA,14 657	K.LLTPITTLTSEQIQK.L	1686.9716	0.5346	2	1	2.4323	0.3844	593.7	1 17 28	6	1	4
	R16062_1_KIAA,90 95	R.IAVAQYSDDVK.V	1209.3308	0.5008	2	1	2.2047	0.4266	777	1 13 20	4.21	1	4
	R16062_1_KIAA,12 688	R.LQPVLQPLSPGVGGK.R	1587.8881	1.0221	2	1	2.5104	0.4524	831.8	1 17 30	8.75	1	4
	R16062_1_KIAA,12 700	R.LQPVLQPLSPGVGGK.R	1587.8881	0.8671	2	1	2.3391	0.4187	402.8	1 14 30	8.75	1	4
	R16062_1_KIAA,10 860	R.NNLFTSSAGYR.A	1230.3118	0.2868	2	1	2.2869	0.2323	561.8	3 11 20	8.75	1	4
	R16062_1_KIAA,14 431	R.QINVGNALEYVSR.N	1463.6208	-1.0942	2	1	2.2498	0.3571	444.3	1 12 24	6	1	4
	R16062_1_KIAA,14 501	R.QINVGNALEYVSR.N	1463.6208	0.4128	2	1	2.376	0.3774	402.1	1 12 24	6	1	4
	R16062_1_KIAA,19 187	R.VGVVQFSNDVFPEFYLK.T	1989.2585	0.0495	2	1	3.4892	0.5813	1004.1	1 20 32	4.37	1	4
\$16-1		18	5	24.16%	35940.53	7.18	sp P01861 IGHG4_HUMAN Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1						
\$16-2		18	5	24.16%	35940.53	7.18	tr A0A0G2JPD4 A0A0G2JPD4_HUMAN Ig gamma-4 chain C region (Fragment) OS=Homo sapiens GN=IGHG4 PE=1 SV=2						
	R16062_1_KIAA,15 732	K.GFYPSDIAVEWESNGQPENNYK. T	2545.6579	-0.8321	2	1	3.237	0.3584	1188.7	1 21 42	4	3	26
	R16062_1_KIAA,15 744	K.GFYPSDIAVEWESNGQPENNYK. T	2545.6579	0.1459	2	1	3.2157	0.376	694.7	1 19 42	4	3	26
	R16062_1_KIAA,15 820	K.GFYPSDIAVEWESNGQPENNYK. T	2545.6579	1.1829	2	1	4.0896	0.5161	1541.9	1 23 42	4	3	26
	R16062_1_KIAA,15 886	K.GFYPSDIAVEWESNGQPENNYK. T	2545.6579	-2.8691	2	1	3.3734	0.4336	1416.4	1 20 42	4	3	26
	R16062_1_KIAA,15 897	K.GFYPSDIAVEWESNGQPENNYK. T	2545.6579	1.2169	2	1	3.1724	0.4151	814	1 20 42	4	3	26
	R16062_1_KIAA,15 997	K.GFYPSDIAVEWESNGQPENNYK. T	2545.6579	-2.8691	2	1	2.9126	0.2407	646.2	1 17 42	4	3	26
	R16062_1_KIAA,16	K.GFYPSDIAVEWESNGQPENNYK.	2545.6579	-1.8471	2	1	2.6677	0.46	736.1	1 20 42	4	3	26

	R16062_1_KIAA,16	K.THTCPPCPAPELLGGPSVFLFPPK	2846.3022	-2.3138	3	1		4.4267	0.5224	706	131 100	7.76	2	23
	865	PK.D												
	R16062_1_KIAA,76	R.GTLVTVSSASTK.G	1151.2928	0.2358	2	1		2.7321	0.4169	836.4	117 22	8.75	2	2
	37													
	R16062_1_KIAA,12	R.TPEVTCVVVDVSHEDPEVK.F	2140.3272	-0.5408	2	1		2.367	0.3959	560.2	115 36	4.17	2	23
	985													
	R16062_1_KIAA,12	R.TPEVTCVVVDVSHEDPEVK.F	2140.3272	1.0042	2	1		2.4457	0.3006	555.8	115 36	4.17	2	23
	995													
	R16062_1_KIAA,13	R.TPEVTCVVVDVSHEDPEVK.F	2140.3272	-1.3858	2	1		2.6724	0.403	851.8	117 36	4.17	2	23
	007													
	R16062_1_KIAA,13	R.TPEVTCVVVDVSHEDPEVK.F	2140.3272	1.3762	2	1		2.9498	0.5184	1221.1	121 36	4.17	2	23
	013													
	R16062_1_KIAA,13	R.TPEVTCVVVDVSHEDPEVK.F	2140.3272	2.6872	3	1		3.7958	0.4648	1593.5	134 72	4.17	2	23
	066													
	R16062_1_KIAA,13	R.TPEVTCVVVDVSHEDPEVK.F	2140.3272	1.0192	2	1		3.0336	0.569	1086.9	120 36	4.17	2	23
	440													
\$18-1	11	5	16.15%	37654.64	6.08	sp P01876 IGHA1_HUMAN Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2								
\$18-2	11	5	11.54%	53088.19	6.46	tr Q96K68 Q96K68_HUMAN cDNA FLJ14473 fis, clone MAMMA1001080, highly similar to Homo sapiens SNC73 protein (SNC73) mRNA OS=Homo sapiens PE=2 SV=1								
\$18-3	11	5	11.26%	54388.6	6.15	tr Q6N090 Q6N090_HUMAN Putative uncharacterized protein DKFZp686G21220 (Fragment) OS=Homo sapiens GN=DKFZp686G21220 PE=2 SV=1								
\$18-4	11	5	14.84%	40947.28	5.76	tr Q9UP60 Q9UP60_HUMAN SNC73 protein OS=Homo sapiens GN=SNC73 PE=2 SV=1								
\$18-5	11	5	11.26%	54459.59	6.31	tr Q6MZW0 Q6MZW0_HUMAN Putative uncharacterized protein DKFZp686J11235 (Fragment) OS=Homo sapiens GN=DKFZp686J11235 PE=1 SV=1								
\$18-6	11	5	11.56%	53224.24	6.08	tr Q8NCL6 Q8NCL6_HUMAN cDNA FLJ90170 fis, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region OS=Homo sapiens PE=2 SV=1								
	R16062_1_KIAA,49	K.SAVQGPPER.D	941.0238	-0.0222	2	1		2.3424	0.3363	804.7	113 16	5.72	1	6
	33													
	R16062_1_KIAA,82	K.TFTCTAAYPESK.T	1376.487	0.339	2	1		2.5445	0.4546	662.3	114 22	5.66	1	6
	52													
	R16062_1_KIAA,82	K.TFTCTAAYPESK.T	1376.487	0.043	2	1		3.094	0.4182	853	115 22	5.66	1	6
	63 - 8264													
	R16062_1_KIAA,82	K.TFTCTAAYPESK.T	1376.487	0.352	2	1		2.4841	0.5144	700.5	115 22	5.66	1	6
	74													
	R16062_1_KIAA,90	K.TPLTATLSK.S	932.0967	-0.9583	2	1		2.3835	0.3329	763.9	113 16	8.41	1	6

	R16062_1_KIAA,15	132	R.QEPSQGTTTFAVTSILR.V	1837.024	0.624	2	1		2.3027	0.3858	466.5	1 16 32	6	1	6
	R16062_1_KIAA,15	141	R.QEPSQGTTTFAVTSILR.V	1837.024	0.428	2	1		2.2782	0.4184	173.2	3 13 32	6	1	6
	R16062_1_KIAA,10	773	R.WLQGSQEELPR.E	1214.3555	-1.6745	2	1		3.2398	0.4129	1207.8	1 14 18	6	1	6
	R16062_1_KIAA,10	839	R.WLQGSQEELPR.E	1214.3555	-1.6205	2	1		2.2884	0.1936	964.6	1 15 18	6	1	6
	R16062_1_KIAA,10	882	R.WLQGSQEELPR.E	1214.3555	-0.4285	2	1		2.751	0.3897	906.3	1 14 18	6	1	6
	R16062_1_KIAA,10	904	R.WLQGSQEELPR.E	1214.3555	-0.5825	2	1		2.8667	0.3996	889.1	1 12 18	6	1	6
\$19-1		9		5	22.09%	360	53.05	8.57	sp P04406 G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3						
\$19-2		9		5	22.09%	360	53.05	8.57	tr V9HVZ4 V9HVZ4_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=HEL-S-162eP PE=2 SV=1						
\$19-3		9		5	22.09%	360	49.05	8.57	tr Q2TSD0 Q2TSD0_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens PE=2 SV=1						
	R16062_1_KIAA,10	948	K.IISNASCTTNCLAPLAK.V	1835.0796	0.7436	2	1		2.472	0.3564	1180.8	1 18 32	8.06	1	3
	R16062_1_KIAA,11	008	K.IISNASCTTNCLAPLAK.V	1835.0796	-2.2574	2	1		2.3589	0.3568	797.8	1 17 32	8.06	1	3
	R16062_1_KIAA,15	409	K.LISWYDNEFGYSNR.V	1764.8749	0.5189	2	1		2.3639	0.3931	796.8	1 16 26	4.37	1	3
	R16062_1_KIAA,15	580	K.LISWYDNEFGYSNR.V	1764.8749	1.6709	2	1		2.3024	0.3148	363.8	1 14 26	4.37	1	3
	R16062_1_KIAA,16	615	K.LIVINGNPITIFQER.D	1614.8704	0.0734	2	1		2.5766	0.4238	670.6	1 15 26	6	1	3
	R16062_1_KIAA,17	037	K.LIVINGNPITIFQER.D	1614.8704	-0.9176	2	1		2.3524	0.424	414.6	1 13 26	6	1	3
	R16062_1_KIAA,12	074	R.GALQNIIPASTGAAG.A	1412.6169	2.8959	2	1		2.4496	0.3603	450.1	1 16 28	8.75	1	3
	R16062_1_KIAA,12	279	R.VPTANVSVDLTCLR.L	1531.73	0.507	2	1		2.9187	0.5296	853.8	1 15 26	5.8	1	3
	R16062_1_KIAA,12	291	R.VPTANVSVDLTCLR.L	1531.73	0.412	2	1		3.041	0.5333	823.8	1 18 26	5.8	1	3
\$20-1		7		5	24.72%	307	77.91	5.56	sp P02647 APOA1_HUMAN Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1						
\$20-2		7		5	24.72%	307	77.91	5.56	tr A0A024R3E3 A0A024R3E3_HUMAN Apolipoprotein A-I,						

						isoform CRA_a OS=Homo sapiens GN=APOA1 PE=4 SV=1							
	R16062_1_KIAA,15 634	K.LLDNWDSVTSTFSK.L	1613.7498	0.3198	2	1	2.8614	0.5166	1081	1 17 26	4.21	1	2
	R16062_1_KIAA,18 887	K.VSFLSALEEYTK.K	1387.5595	1.3285	2	1	2.3388	0.4546	609.4	1 14 22	4.53	1	2
	R16062_1_KIAA,13 743 - 13744	R.DYVSQFEGSALGK.Q	1401.5031	-1.5779	2	1	2.2299	0.3537	497.9	1 12 24	4.37	1	2
	R16062_1_KIAA,17 562	R.EQLGPVTQEFWDNLEK.E	1934.095	-0.133	2	1	3.0549	0.5699	546	1 16 30	4	1	2
	R16062_1_KIAA,17 578	R.EQLGPVTQEFWDNLEK.E	1934.095	1.783	2	1	2.2553	0.3705	282.8	1 11 30	4	1	2
	R16062_1_KIAA,17 606	R.EQLGPVTQEFWDNLEK.E	1934.095	1.397	2	1	2.348	0.3938	469.1	1 13 30	4	1	2
	R16062_1_KIAA,17 888	R.QGLLPVLESFK.V	1231.4658	0.4218	2	1	3.0087	0.3553	590.4	1 15 20	6	1	2
\$21-1			6	5	17.73%	47650.89	5.33	sp P01011 AACT_HUMAN Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=1 SV=2					
\$21-2			6	5	17.73%	47650.89	5.33	tr A0A024R6P0 A0A024R6P0_HUMAN Serpin peptidase inhibitor, clade A (Alpha-1 antiproteinase, antitrypsin), member 3, isoform CRA_c OS=Homo sapiens GN=SERPINA3 PE=3 SV=1					
\$21-3			6	5	16.74%	50628.29	5.42	tr B3KS79 B3KS79_HUMAN cDNA FLJ35730 fis, clone TESTI2003131, highly similar to ALPHA-1-ANTICHYMOTRYPSIN OS=Homo sapiens PE=2 SV=1					
	R16062_1_KIAA,14 973	K.AVLDFEEGTEASAATAVK.I	1909.0838	0.4238	2	1	2.4444	0.3758	647.4	1 15 36	4	1	3
	R16062_1_KIAA,23 457	K.DLDSQTMMVLVNYIFFK.A	2065.4418	1.0578	2	1	2.3677	0.5001	630.4	1 16 32	4.21	1	3
	R16062_1_KIAA,23 458	K.DLDSQTMMVLVNYIFFK.A	2065.4418	-2.3392	2	1	2.7406	0.4321	817.5	1 16 32	4.21	1	3
	R16062_1_KIAA,17 477	K.ITLLSALVETR.T	1216.4527	0.3427	2	1	2.8412	0.3932	571.4	1 12 20	6	1	3
	R16062_1_KIAA,13 749	R.LYGSEAFATDFQDSAAAK.K	1892.9998	0.6538	2	1	2.3008	0.2794	691	1 16 34	4.03	1	3
	R16062_1_KIAA,78 70	R.NLAVSQVVHK.A	1095.2773	-0.0577	2	1	2.5378	0.36	633.4	2 12 18	8.76	1	3
\$22-1			6	5	3.10%	259210.67	5.49	tr A0A024R462 A0A024R462_HUMAN Fibronectin 1, isoform CRA_n OS=Homo sapiens GN=FN1 PE=4 SV=1					
\$22-2			6	5	3.26%	246697.8	5.72	tr B7ZLE5 B7ZLE5_HUMAN FN1 protein OS=Homo sapiens GN=FN1 PE=2 SV=1					
	R16062_1_KIAA,12 966	R.EESPLLIGQQSTVSDVPR.D	1956.1437	0.6427	2	1	2.4067	0.5093	614.8	1 18 34	4.14	1	2

	R16062_1_KIAA,13006	R.EESPLLIGQQSTVSDVPR.D	1956.1437	0.4687	2	1		2.9904	0.4207	797.7	119 34	4.14	1	2
	R16062_1_KIAA,16346	R.GATYNIIVEALK.D	1292.506	0.445	2	1		2.6761	0.3172	970.1	116 22	6	1	2
	R16062_1_KIAA,6034	R.ISCTIANR.C	935.0541	0.0671	2	1		2.2885	0.3043	754.7	111 14	8.25	1	2
	R16062_1_KIAA,17078	R.NTFAEVTGLSPGVTTYFK.V	1995.22	0.794	2	1		2.7369	0.4965	1317.3	120 34	6	1	2
	R16062_1_KIAA,19683	R.VTWAPPPSIDLTNFLVR.Y	1927.2351	-0.4959	2	1		2.2002	0.2988	194	116 32	5.81	1	2
\$23-1			5	5	18.12%	33922.3	5.46	sp P20774 MIME_HUMAN Mimecan OS=Homo sapiens GN=OGN PE=1 SV=1						
\$23-2			5	5	18.12%	33922.3	5.46	tr A8K0R3 A8K0R3_HUMAN Osteoglycin (Osteoinductive factor, mimecan), isoform CRA_a OS=Homo sapiens GN=OGN PE=2 SV=1						
\$23-3			5	5	18.12%	33922.26	5.33	tr Q7Z532 Q7Z532_HUMAN Osteoglycin OG OS=Homo sapiens PE=2 SV=1						
\$23-4			5	5	15.17%	40553.09	8.08	tr B4DI63 B4DI63_HUMAN cDNA FLJ59205, highly similar to Mimecan OS=Homo sapiens PE=2 SV=1						
	R16062_1_KIAA,13445	K.DFADIPNLR.R	1061.173	0.072	2	1		2.4127	0.4117	612.4	112 16	4.21	1	4
	R16062_1_KIAA,21658	K.LSLEELSLAENQLLK.L	1814.1134	-0.2886	2	1		2.7343	0.365	940.8	118 30	4.25	1	4
	R16062_1_KIAA,20364	R.LDFTGNLIEDIEDGTFSK.L	2015.1632	0.2552	2	1		2.2627	0.3392	301.9	113 34	3.77	1	4
	R16062_1_KIAA,10551	R.LEGNPIVLGK.H	1040.2384	-0.9096	2	1		2.3185	0.285	839.3	115 18	6	1	4
	R16062_1_KIAA,19531	R.RLDFTGNLIEDIEDGTFSK.L	2171.3496	0.1756	3	1		3.9994	0.4778	1405.4	128 72	4.11	1	4
\$24-1			12	4	14.87%	46060.9	7.63	tr Q6N093 Q6N093_HUMAN Putative uncharacterized protein DKFZp686I04196 (Fragment) OS=Homo sapiens GN=DKFZp686I04196 PE=2 SV=1						
\$24-2			12	4	13.19%	51536.19	7.51	tr Q68CN4 Q68CN4_HUMAN Putative uncharacterized protein DKFZp686E23209 OS=Homo sapiens GN=DKFZp686E23209 PE=1 SV=2						
	R16062_1_KIAA,15732	K.GFYPSDIAVEWESNGQPENNYK. T	2545.6579	-0.8321	2	1		3.237	0.3584	1188.7	121 42	4	3	26
	R16062_1_KIAA,15744	K.GFYPSDIAVEWESNGQPENNYK. T	2545.6579	0.1459	2	1		3.2157	0.376	694.7	119 42	4	3	26
	R16062_1_KIAA,15820	K.GFYPSDIAVEWESNGQPENNYK. T	2545.6579	1.1829	2	1		4.0896	0.5161	1541.9	123 42	4	3	26

	R16062_1_KIAA,15	K.GFYPSDIAVEWESNGQPENNYK.	2545.6579	-2.8691	2	1		3.3734	0.4336	1416.4	120 42	4	3	26
	886	T												
	R16062_1_KIAA,15	K.GFYPSDIAVEWESNGQPENNYK.	2545.6579	1.2169	2	1		3.1724	0.4151	814	120 42	4	3	26
	897	T												
	R16062_1_KIAA,15	K.GFYPSDIAVEWESNGQPENNYK.	2545.6579	-2.8691	2	1		2.9126	0.2407	646.2	117 42	4	3	26
	997	T												
	R16062_1_KIAA,16	K.GFYPSDIAVEWESNGQPENNYK.	2545.6579	-1.8471	2	1		2.6677	0.46	736.1	120 42	4	3	26
	239	T												
	R16062_1_KIAA,12	K.NQVSLTCLVK.G	1162.3554	1.1304	2	1		2.3778	0.3172	753.4	112 18	8.22	5	34
	489													
R16062_1_KIAA,11	R.STSESTAALGCLVK.D	1424.5731	-2.5969	2	1		3.363	0.2639	1125.9	119 26	5.72	4	6	
521														
R16062_1_KIAA,16	R.VVSVLTVVHQDWLNGK.E	1795.0751	1.2221	2	1		2.6009	0.4588	568.3	114 30	6.71	2	3	
496														
R16062_1_KIAA,16	R.VVSVLTVVHQDWLNGK.E	1795.0751	-0.3519	2	1		2.591	0.4766	567.2	113 30	6.71	2	3	
926														
R16062_1_KIAA,16	R.VVSVLTVVHQDWLNGK.E	1795.0751	0.3891	2	1		2.6677	0.44	654.6	114 30	6.71	2	3	
934														
\$25-1		6	4	23.93%	24792.57	5.93	tr Q8N355 Q8N355_HUMAN IGL@ protein OS=Homo sapiens GN=IGL@ PE=1 SV=1							
\$25-2		6	4	23.93%	24909.77	6.19	tr Q6GMV8 Q6GMV8_HUMAN Uncharacterized protein OS=Homo sapiens PE=2 SV=1							
	R16062_1_KIAA,45	K.AGVETTPSK.Q	991.0778	0.8108	2	1		2.8256	0.4209	1285.7	116 18	6.05	1	2
	39													
	R16062_1_KIAA,15	K.YAASSYLSLTPEQWK.S	1744.925	-1.278	2	1		3.2108	0.4816	536.1	114 28	6	1	2
	316													
	R16062_1_KIAA,15	K.YAASSYLSLTPEQWK.S	1744.925	-1.378	2	1		3.7386	0.576	535.3	115 28	6	1	2
	328													
	R16062_1_KIAA,92	R.FSGSNSGNTATLTISR.V	1613.7114	0.7294	2	1		2.2685	0.4248	953.3	116 30	9.75	1	2
	62													
	R16062_1_KIAA,92	R.FSGSNSGNTATLTISR.V	1613.7114	0.8554	2	1		2.8972	0.4659	976.7	117 30	9.75	1	2
	73													
	R16062_1_KIAA,61	R.SYSCQVTHEGSTVEK.T	1712.7901	0.5821	2	1		2.3043	0.3286	530	114 28	5.38	1	2
	53													
\$26-1		6	4	13.25%	36688.6	8.44	sp P00338 LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2							
\$26-2		6	4	13.25%	36688.6	8.44	tr V9HWB9 V9HWB9_HUMAN L-lactate dehydrogenase OS=Homo sapiens GN=HEL-S-133P PE=2 SV=1							
	R16062_1_KIAA,19	K.DLADELALVDVIEDK.L	1658.8288	0.4848	2	1		3.1949	0.4604	613.3	114 28	3.66	1	2
	463													
	R16062_1_KIAA,19	K.DLADELALVDVIEDK.L	1658.8288	0.8008	2	1		3.3013	0.4745	1907.5	121 28	3.66	1	2

\$29-1	R16062_1_KIAA,16496	R.VVSVLTVVHQDWLNGK.E	1795.0751	1.2221	2	1		2.6009	0.4588	568.3	114 30	6.71	2	3
	R16062_1_KIAA,16926	R.VVSVLTVVHQDWLNGK.E	1795.0751	-0.3519	2	1		2.591	0.4766	567.2	113 30	6.71	2	3
	R16062_1_KIAA,16934	R.VVSVLTVVHQDWLNGK.E	1795.0751	0.3891	2	1		2.6677	0.44	654.6	114 30	6.71	2	3
\$29-2			5	4	4.34%	151076.53	9.53	sp Q92954 PRG4_HUMAN Proteoglycan 4 OS=Homo sapiens GN=PRG4 PE=1 SV=2						
\$29-3			5	4	4.34%	151076.53	9.53	tr A0A024R930 A0A024R930_HUMAN Proteoglycan 4, isoform CRA_a OS=Homo sapiens GN=PRG4 PE=4 SV=1						
\$29-3			5	4	12.35%	55494.25	9.92	tr B3KQ20 B3KQ20_HUMAN cDNA FLJ32635 fis, clone SYNOV2000178, highly similar to Proteoglycan-4 OS=Homo sapiens PE=2 SV=1						
\$30-1	R16062_1_KIAA,11060	K.DQYYNIDVPSR.T	1370.4491	0.4891	2	1		2.4448	0.2052	439.8	212 20	4.21	1	3
	R16062_1_KIAA,19272	K.GFGGLTGQIVAALSTAK.Y	1591.8336	-0.1364	2	1		2.6401	0.4145	1031.1	117 32	8.75	1	3
	R16062_1_KIAA,16847	R.GLPNVVTSAISLPNIR.K	1651.9322	0.3212	2	1		2.4166	0.4219	512.5	114 30	9.75	1	3
\$30-2	R16062_1_KIAA,19536	R.ITEVWGIPSPIDTVFTR.C	1932.2085	1.4455	2	1		2.2221	0.4241	214.7	112 32	4.37	1	3
	R16062_1_KIAA,19540	R.ITEVWGIPSPIDTVFTR.C	1932.2085	0.4525	2	1		2.646	0.4173	362.3	117 32	4.37	1	3
			5	4	34.69%	16055.42	7.84	sp P02042 HBD_HUMAN Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2						
\$30-2			5	4	34.69%	16055.42	7.84	tr A0N071 A0N071_HUMAN Delta globin OS=Homo sapiens GN=HBD PE=3 SV=1						
\$31-1	R16062_1_KIAA,14892	K.VLGAFSDDLHLNLK.G	1670.8908	-0.3942	2	1		2.7099	0.1644	1055.4	119 30	5.21	3	5
	R16062_1_KIAA,10149	K.VNVDVAVGGEALGR.L	1257.3787	0.4827	2	1		2.798	0.5541	497.2	114 24	4.37	2	3
	R16062_1_KIAA,10181	K.VNVDVAVGGEALGR.L	1257.3787	1.1287	2	1		3.1365	0.5075	1321.3	117 24	4.37	2	3
\$31-2	R16062_1_KIAA,8549	K.VVAGVANALAHK.Y	1150.3561	0.2381	2	1		2.3422	0.4164	674.9	113 22	8.73	2	4
	R16062_1_KIAA,15697	R.LLVVYPWTQR.F	1275.5235	0.4625	2	1		2.2234	0.3052	665.8	111 18	8.75	4	6
			22	3	23.37%	20314.89	6.22	tr S6C4R6 S6C4R6_HUMAN IgG L chain OS=Homo sapiens PE=2 SV=1						
\$31-2			22	3	23.37%	20372.93	5.37	tr S6B2A1 S6B2A1_HUMAN IgG L chain OS=Homo sapiens PE=2 SV=1						

R16062_1_KIAA,16 535	-.TVAAPSVFIFPPSDEQLK.S	1947.22	-1.248	2	1		2.5905	0.4133	292.4	1 13 34	4.37	4	8
R16062_1_KIAA,16 557	-.TVAAPSVFIFPPSDEQLK.S	1947.22	-1.181	2	1		2.2549	0.2349	229.1	1 13 34	4.37	4	8
R16062_1_KIAA,16 777	-.TVAAPSVFIFPPSDEQLK.S	1947.22	0.782	2	1		2.4042	0.3821	524.6	1 19 34	4.37	4	8
R16062_1_KIAA,16 788	-.TVAAPSVFIFPPSDEQLK.S	1947.22	0.82	2	1		2.4522	0.5211	388.3	1 16 34	4.37	4	8
R16062_1_KIAA,17 195 - 17196	-.TVAAPSVFIFPPSDEQLK.S	1947.22	0.531	2	1		2.9491	0.4563	756.2	1 21 34	4.37	4	8
R16062_1_KIAA,17 206	-.TVAAPSVFIFPPSDEQLK.S	1947.22	0.674	2	1		2.3807	0.3829	237.9	1 13 34	4.37	4	8
R16062_1_KIAA,17 485	-.TVAAPSVFIFPPSDEQLK.S	1947.22	1.737	2	1		2.6139	0.4106	390	1 16 34	4.37	4	8
R16062_1_KIAA,15 188	K.LLIYWASTR.E	1123.3291	0.4591	2	1		2.2762	0.1216	807.9	2 12 16	8.75	2	3
R16062_1_KIAA,15 220	K.LLIYWASTR.E	1123.3291	-0.2649	2	1		2.3459	0.3074	757.3	2 12 16	8.75	2	3
R16062_1_KIAA,16 001	K.SGTASVVCLLNNFYPR.E	1799.0141	0.3261	2	1		2.9192	0.5415	550.6	1 13 30	7.94	4	8
R16062_1_KIAA,16 033	K.SGTASVVCLLNNFYPR.E	1799.0141	0.1381	2	1		3.312	0.4871	1199.2	1 18 30	7.94	4	8
R16062_1_KIAA,17 303	K.SGTASVVCLLNNFYPR.E	1799.0141	-0.3619	2	1		2.4085	0.4512	580.2	1 14 30	7.94	4	8
R16062_1_KIAA,17 350	K.SGTASVVCLLNNFYPR.E	1799.0141	-0.1429	2	1		2.8188	0.4831	927.2	1 15 30	7.94	4	8
R16062_1_KIAA,18 804	K.SGTASVVCLLNNFYPR.E	1799.0141	1.6411	2	1		2.9725	0.5376	1033.7	1 17 30	7.94	4	8
R16062_1_KIAA,18 845	K.SGTASVVCLLNNFYPR.E	1799.0141	0.5641	2	1		2.4368	0.4778	1164.4	1 18 30	7.94	4	8
R16062_1_KIAA,18 876	K.SGTASVVCLLNNFYPR.E	1799.0141	2.0111	2	1		2.9342	0.4613	1195.6	1 18 30	7.94	4	8
R16062_1_KIAA,18 922	K.SGTASVVCLLNNFYPR.E	1799.0141	-2.5899	2	1		3.8096	0.4571	1228.7	1 17 30	7.94	4	8
R16062_1_KIAA,19 029	K.SGTASVVCLLNNFYPR.E	1799.0141	-2.6549	2	1		3.1649	0.3967	843.2	1 15 30	7.94	4	8
R16062_1_KIAA,19 259	K.SGTASVVCLLNNFYPR.E	1799.0141	0.8761	2	1		2.7348	0.4147	845.6	1 15 30	7.94	4	8
R16062_1_KIAA,19 266	K.SGTASVVCLLNNFYPR.E	1799.0141	-0.5639	2	1		3.5693	0.5112	830.8	1 16 30	7.94	4	8
R16062_1_KIAA,19	K.SGTASVVCLLNNFYPR.E	1799.0141	0.4391	2	1		3.2765	0.4663	1053.3	1 17 30	7.94	4	8

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	356	R.GVVDSEDLPLNISR.E												
\$34-1		6	3	6.08%	70374.95	5.76	sp P34931 HS71L_HUMAN Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2							
\$34-2		6	3	6.08%	70404.09	5.95	tr Q53FA3 Q53FA3_HUMAN Heat shock 70 kDa protein 1-like (Fragment) OS=Homo sapiens GN=HSPA1L PE=1 SV=1							
\$34-3		6	3	6.08%	70375.9	5.6	tr B2RCQ9 B2RCQ9_HUMAN cDNA, FLJ96225, highly similar to Homo sapiens heat shock 70kDa protein 1-like (HSPA1L), mRNA OS=Homo sapiens PE=2 SV=1							
\$34-4		6	3	5.53%	77561.33	8.2	tr B4DI54 B4DI54_HUMAN cDNA FLJ56386, highly similar to Heat shock 70 kDa protein 1L OS=Homo sapiens PE=2 SV=1							
\$34-5		6	3	7.33%	58332.38	6.09	tr B4DXY3 B4DXY3_HUMAN cDNA FLJ56517, highly similar to Heat shock 70 kDa protein 1L OS=Homo sapiens PE=2 SV=1							
	R16062_1_KIAA,14 993	K.DAGVIAGLNVLR.I	1198.3975	-0.0415	2	1	2.4553	0.1356	723.4	1 14 22	5.84	1	5	
	R16062_1_KIAA,14 463	R.IINEPTAAAIAYGLDK.R	1660.8927	0.3337	2	1	2.5215	0.2627	761.7	1 16 30	4.37	1	5	
	R16062_1_KIAA,14 479	R.IINEPTAAAIAYGLDK.R	1660.8927	0.4237	2	1	2.5849	0.3976	708.9	1 15 30	4.37	1	5	
	R16062_1_KIAA,14 545	R.IINEPTAAAIAYGLDK.R	1660.8927	1.6197	2	1	2.879	0.1941	960.8	1 17 30	4.37	1	5	
	R16062_1_KIAA,73 22	R.VEIIANDQGNR.I ! R.VEILANDQGNR.T	1229.3253	0.1733	2	1	2.7257	0.3648	810.8	1 15 20	4.37	1	5	
	R16062_1_KIAA,73 30	R.VEIIANDQGNR.I ! R.VEILANDQGNR.T	1229.3253	0.1453	2	1	2.4316	0.3158	793.9	1 13 20	4.37	1	5	
\$35-1		6	3	24.57%	20019.72	5.51	sp P02792 FRIL_HUMAN Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2							
	R16062_1_KIAA,14 207	K.LNQALLDLHALGSAR.T	1592.8248	0.6578	2	1	2.2796	0.5239	210.1	1 14 28	6.74	1	1	
	R16062_1_KIAA,15 900	R.DDVALEGVSHFFR.E	1492.6175	0.3775	2	1	2.6014	0.4884	1196.9	1 16 24	4.54	1	1	
	R16062_1_KIAA,15 913	R.DDVALEGVSHFFR.E	1492.6175	0.6375	2	1	2.6544	0.5104	1411.8	1 17 24	4.54	1	1	
	R16062_1_KIAA,16 428	R.LGGPEAGLGEYLFER.L	1608.7764	-1.7066	2	1	2.39	0.2371	556.7	1 13 28	4.25	1	1	
	R16062_1_KIAA,16 481	R.LGGPEAGLGEYLFER.L	1608.7764	-0.2406	2	1	2.7376	0.4981	1140.2	1 18 28	4.25	1	1	
	R16062_1_KIAA,16 579	R.LGGPEAGLGEYLFER.L	1608.7764	0.7424	2	1	2.722	0.4727	646.6	1 14 28	4.25	1	1	
\$36-1		4	3	5.26%	122205.24	5.44	sp P00450 CERU_HUMAN Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1							
\$36-2		4	3	5.26%	122205.24	5.44	tr A5PL27 A5PL27_HUMAN CP protein OS=Homo sapiens							

\$39-3			6	2	6.11%	55928.06	8.54	tr V9HVVY1 V9HVVY1_HUMAN Epididymis secretory sperm binding protein Li 78p OS=Homo sapiens GN=HEL-S-78p PE=2 SV=1								
\$39-4			6	2	6.33%	54253.11	8.3	tr B4E1D3 B4E1D3_HUMAN cDNA FLJ53952, highly similar to Fibrinogen beta chain OS=Homo sapiens PE=2 SV=1								
	R16062_1_KIAA,12 455	K.DNENVVNEYSSELEK.H			1769.8018	0.7828	2	1		2.6633	0.3822	813.9	1 15 28	3.91	1	4
	R16062_1_KIAA,12 470	K.DNENVVNEYSSELEK.H			1769.8018	-0.4922	2	1		2.8103	0.4837	834.6	1 15 28	3.91	1	4
	R16062_1_KIAA,12 484	K.DNENVVNEYSSELEK.H			1769.8018	1.2848	2	1		2.5428	0.4215	1129.1	1 16 28	3.91	1	4
	R16062_1_KIAA,12 488	K.DNENVVNEYSSELEK.H			1769.8018	1.0778	2	1		2.9904	0.4712	1535.1	1 19 28	3.91	1	4
	R16062_1_KIAA,10 273	R.TPCTVSCNIPVVSGK.E			1619.829	0.649	2	1		2.8426	0.518	852.4	1 18 28	7.74	1	4
	R16062_1_KIAA,10 278	R.TPCTVSCNIPVVSGK.E			1619.829	0.723	2	1		2.2383	0.3381	705.6	1 15 28	7.74	1	4
\$40-1			5	2	5.27%	57936.87	7.96	sp P14618 KPYM_HUMAN Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4								
\$40-2			5	2	8.12%	37558	5.97	tr A0A024R609 A0A024R609_HUMAN Pyruvate kinase OS=Homo sapiens GN=PKM2 PE=3 SV=1								
\$40-3			5	2	6.13%	49897.75	7.96	tr B4DNK4 B4DNK4_HUMAN Pyruvate kinase OS=Homo sapiens GN=PKM PE=1 SV=1								
\$40-4			5	2	5.48%	55926.51	7.2	tr B4DRT3 B4DRT3_HUMAN Pyruvate kinase OS=Homo sapiens PE=2 SV=1								
\$40-5			5	2	5.27%	57936.87	7.96	tr V9HWB8 V9HWB8_HUMAN Pyruvate kinase OS=Homo sapiens GN=HEL-S-30 PE=1 SV=1								
\$40-6			5	2	5.27%	58062.05	7.61	tr A0A024R5Z9 A0A024R5Z9_HUMAN Pyruvate kinase OS=Homo sapiens GN=PKM2 PE=3 SV=1								
\$40-7			5	2	5.77%	53045.14	6.39	tr H3BTN5 H3BTN5_HUMAN Pyruvate kinase (Fragment) OS=Homo sapiens GN=PKM PE=1 SV=1								
\$40-8			5	2	9.96%	30720.17	6.46	tr H3BQ34 H3BQ34_HUMAN Pyruvate kinase OS=Homo sapiens GN=PKM PE=1 SV=1								
	R16062_1_KIAA,13 713	K.GVNLPGAAVDLPVSEK.D			1637.8591	0.8411	2	1		2.4388	0.5428	613.3	1 17 32	4.37	1	8
	R16062_1_KIAA,13 733	K.GVNLPGAAVDLPVSEK.D			1637.8591	1.3791	2	1		2.2368	0.2775	529.4	1 15 32	4.37	1	8
	R16062_1_KIAA,11 086	R.LDIDSPPI TAR.N			1198.3511	-0.7019	2	1		2.283	0.1771	693.5	2 13 20	4.21	1	8
	R16062_1_KIAA,11 096	R.LDIDSPPI TAR.N			1198.3511	-0.7219	2	1		2.5744	0.4036	610.3	1 13 20	4.21	1	8
	R16062_1_KIAA,11	R.LDIDSPPI TAR.N			1198.3511	0.3391	2	1		2.5576	0.3581	748	1 14 20	4.21	1	8

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						(Fragment) OS=Homo sapiens PE=2 SV=1													
						tr B7Z5T3 B7Z5T3_HUMAN cDNA FLJ53644, highly similar to													
\$43-4	4	2	10.51%	29018.24	8.76	Four and a half LIM domains protein 1 OS=Homo sapiens PE=2 SV=1													
						tr B7Z6U8 B7Z6U8_HUMAN cDNA FLJ53665, highly similar to													
\$43-5	4	2	10.38%	29499.96	8.67	Four and a half LIM domains protein 1 OS=Homo sapiens PE=2 SV=1													
						tr B7Z5V0 B7Z5V0_HUMAN cDNA FLJ53647, highly similar to													
\$43-6	4	2	9.82%	31224.76	8.79	Four and a half LIM domains protein 1 OS=Homo sapiens PE=2 SV=1													
						tr B7Z4B7 B7Z4B7_HUMAN cDNA FLJ52561, highly similar to													
\$43-7	4	2	10.89%	28097.35	8.7	Four and a half LIM domains protein 1 OS=Homo sapiens PE=2 SV=1													
	R16062_1_KIAA,7990	K.AIVAGDQNVEYK.G	1307.4344	1.2014	2	1	2.2763	0.2395	441.4	1 12 22	4.37	1	7						
	R16062_1_KIAA,8021	K.AIVAGDQNVEYK.G	1307.4344	1.1744	2	1	2.3419	0.4892	962.4	1 17 22	4.37	1	7						
	R16062_1_KIAA,12502	R.FTAVEDQYYCVDCYK.N	1962.0889	1.1589	2	1	2.7645	0.4774	732.7	1 16 28	4.03	1	7						
	R16062_1_KIAA,12509	R.FTAVEDQYYCVDCYK.N	1962.0889	0.9699	2	1	2.9381	0.5614	1308.9	1 18 28	4.03	1	7						
\$44-1	4	2	6.70%	46736.49	5.37	sp P01009 A1AT_HUMAN Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3													
\$44-2	4	2	6.70%	46708.44	5.37	tr A0A024R6I7 A0A024R6I7_HUMAN Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=1													
\$44-3	4	2	23.33%	13097.32	8.93	tr Q9P173 Q9P173_HUMAN PRO2275 OS=Homo sapiens PE=2 SV=1													
\$44-4	4	2	6.70%	46736.49	5.37	tr E9KL23 E9KL23_HUMAN Epididymis secretory sperm binding protein Li 44a OS=Homo sapiens PE=2 SV=1													
\$44-5	4	2	57.14%	4998.76	8.09	tr B2D098 B2D098_HUMAN Alpha-1 antitrypsin Valcamonica variant (Fragment) OS=Homo sapiens PE=4 SV=1													
\$44-6	4	2	7.80%	40234.75	5.26	tr A0A0G2JRN3 A0A0G2JRN3_HUMAN Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=1													
	R16062_1_KIAA,13218	K.SVLGQLGITK.V	1016.2168	0.1788	2	1	2.3081	0.3967	477.6	1 12 18	8.47	1	6						
	R16062_1_KIAA,12631	K.VFSNGADLSGVTEEAPLK.L	1835.0049	0.3799	2	1	3.02	0.3659	941.6	1 18 34	4.14	1	6						
	R16062_1_KIAA,13142	K.VFSNGADLSGVTEEAPLK.L	1835.0049	-0.4871	2	1	2.5149	0.4886	878.1	1 18 34	4.14	1	6						
	R16062_1_KIAA,13148	K.VFSNGADLSGVTEEAPLK.L	1835.0049	-0.1531	2	1	2.6291	0.3745	793.2	1 16 34	4.14	1	6						

\$45-1	3	2	31.48%	11992.34	5.67	sp P01593 KV101_HUMAN Ig kappa chain V-I region AG OS=Homo sapiens PE=1 SV=1								
\$45-2	3	2	31.48%	11842.07	5.11	tr A0A087WZH9 A0A087WZH9_HUMAN Protein IGKV1-33 OS=Homo sapiens GN=IGKV1D-33 PE=4 SV=1								
	R16062_1_KIAA,9375	-.BIZM*TQSPSSLSASVGDR.V ! -.DIQM*TQSPSSLSASVGDR.V	1896.027	1.249	2	1	2.6941	0.1753	1354.9	121 34	5.84	1	2	
	R16062_1_KIAA,14075	K.LLIYDASNLETGVPSR.F ! K.LLIYDASNLETGVPSR.F	1748.9584	-0.3256	2	1	2.8772	0.2138	791.8	117 30	4.37	1	2	
	R16062_1_KIAA,14084	K.LLIYDASNLETGVPSR.F ! K.LLIYDASNLETGVPSR.F	1748.9584	0.5834	2	1	2.6833	0.2237	690.3	116 30	4.37	1	2	
\$46-1	3	2	23.68%	12640.09	7.92	sp P01625 KV402_HUMAN Ig kappa chain V-IV region Len OS=Homo sapiens PE=1 SV=2								
	R16062_1_KIAA,13591	-.DIVM*TQSPDSLAVSLGER.A	1935.1462	0.5732	2	1	3.0165	0.494	1162.6	119 34	4.03	1	1	
	R16062_1_KIAA,15188	K.LLIYWASTR.E	1123.3291	0.4591	2	1	2.2762	0.1216	807.9	212 16	8.75	2	3	
	R16062_1_KIAA,15220	K.LLIYWASTR.E	1123.3291	-0.2649	2	1	2.3459	0.3074	757.3	212 16	8.75	2	3	
\$47-1	3	2	31.19%	11775.11	8.7	sp P01620 KV302_HUMAN Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1								
\$47-2	3	2	31.19%	11788.19	8.72	sp P01622 KV304_HUMAN Ig kappa chain V-III region Ti OS=Homo sapiens PE=1 SV=1								
\$47-3	3	2	31.19%	11746.15	9.07	sp P01623 KV305_HUMAN Ig kappa chain V-III region WOL OS=Homo sapiens PE=1 SV=1								
\$47-4	3	2	31.19%	11830.35	9.34	sp P04206 KV307_HUMAN Ig kappa chain V-III region GOL OS=Homo sapiens PE=1 SV=1								
\$47-5	3	2	31.19%	11646.05	8.56	tr Q9UL78 Q9UL78_HUMAN Myosin-reactive immunoglobulin light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1								
	R16062_1_KIAA,13308	-.EIVLTQSPGTLSPGER.A	1885.1086	-1.2734	2	1	3.8376	0.3449	692.7	119 34	4.53	1	5	
	R16062_1_KIAA,13389	-.EIVLTQSPGTLSPGER.A	1885.1086	-0.2174	2	1	4.421	0.1852	998.1	122 34	4.53	1	5	
	R16062_1_KIAA,13188	R.FSGSGSGTDFLTISR.L	1633.7411	-0.1499	2	1	2.4785	0.4793	434.5	112 30	5.84	2	8	
\$48-1	3	2	8.42%	41654.09	7.16	sp P21810 PGS1_HUMAN Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2								
\$48-2	3	2	8.42%	41655.04	6.6	tr Q53HU6 Q53HU6_HUMAN Biglycan preproprotein variant (Fragment) OS=Homo sapiens PE=2 SV=1								
\$48-3	3	2	9.28%	37618.39	8.08	tr B4DDQ2 B4DDQ2_HUMAN cDNA FLJ55187, highly similar to Biglycan OS=Homo sapiens PE=2 SV=1								

\$51-2		3	2	4.98%	50184.85	9.15	sp Q5VTE0 EF1A3_HUMAN Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1						
\$51-3		3	2	5.78%	42824.19	8.54	tr Q16577 Q16577_HUMAN Elongation factor 1-alpha 1 OS=Homo sapiens GN=PTI-1 PE=2 SV=1						
\$51-4		3	2	4.98%	50140.69	9.1	tr Q6IPS9 Q6IPS9_HUMAN Elongation factor 1-alpha OS=Homo sapiens GN=EEF1A1 PE=2 SV=1						
\$51-5		3	2	5.40%	46269.13	9.08	tr Q9NZS6 Q9NZS6_HUMAN Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1						
\$51-6		3	2	4.98%	50122.66	9.1	tr Q6IPN6 Q6IPN6_HUMAN Elongation factor 1-alpha OS=Homo sapiens GN=EEF1A1 PE=2 SV=1						
\$51-7		3	2	4.98%	50200.79	9.1	tr A8K9C4 A8K9C4_HUMAN Elongation factor 1-alpha OS=Homo sapiens PE=2 SV=1						
\$51-8		3	2	5.22%	47883.07	9.12	tr A0A087WVQ9 A0A087WVQ9_HUMAN Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1						
\$51-9		3	2	4.98%	50184.73	9.14	tr Q6IPT9 Q6IPT9_HUMAN Elongation factor 1-alpha OS=Homo sapiens GN=EEF1A1 PE=2 SV=1						
\$51-10		3	2	4.98%	50112.64	9.1	tr Q53G85 Q53G85_HUMAN Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1						
\$51-11		3	2	5.78%	43024.46	8.94	tr Q96RE1 Q96RE1_HUMAN Elongation factor 1-alpha OS=Homo sapiens GN=EEF1A1L14 PE=2 SV=1						
\$51-12		3	2	4.98%	50110.67	9.1	tr Q53GA1 Q53GA1_HUMAN Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1						
\$51-13		3	2	4.98%	50110.67	9.1	tr Q53GE9 Q53GE9_HUMAN Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1						
\$51-14		3	2	4.98%	50124.65	9.1	tr Q53HR5 Q53HR5_HUMAN Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1						
\$51-15		3	2	4.98%	50198.73	9.04	tr Q53HQ7 Q53HQ7_HUMAN Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1						
\$51-16		3	2	5.82%	42596.1	9.12	tr B4DNE0 B4DNE0_HUMAN cDNA FLJ52573, highly similar to Elongation factor 1-alpha 1 OS=Homo sapiens PE=2 SV=1						
\$51-17		3	2	4.98%	50141.64	8.98	tr Q53HM9 Q53HM9_HUMAN Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1						
	R16062_1_KIAA,9916	K.IGGIGTVPVGR.V	1026.2149	-0.8151	2	1	2.3601	0.3378	696.1	1 14 20	9.75	1	17
	R16062_1_KIAA,9939	K.IGGIGTVPVGR.V	1026.2149	0.6569	2	1	2.5936	0.4662	904	1 14 20	9.75	1	17
	R16062_1_KIAA,11618	K.YYVTIIDAPGHR.D	1405.5829	0.7269	2	1	2.2387	0.2733	660.2	1 12 22	6.74	1	17
\$52-1		3	2	13.17%	22782.62	5.98	sp P04792 HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2						
\$52-2		3	2	13.17%	22782.62	5.98	tr V9HW43 V9HW43_HUMAN Epididymis secretory protein Li 102						

						OS=Homo sapiens GN=HEL-S-102 PE=2 SV=1								
	R16062_1_KIAA,14 494	K.LATQSNEITIPVTFESR.A	1907.1142	0.8632	2	1		2.4414	0.4678	307.9	1 14 32	4.53	1	2
	R16062_1_KIAA,14 891	R.LFDQAFGLPR.L	1164.3381	0.3911	2	1		2.5776	0.3708	998.4	1 14 18	5.84	1	2
	R16062_1_KIAA,14 900	R.LFDQAFGLPR.L	1164.3381	0.8031	2	1		2.8849	0.2327	1136.8	1 15 18	5.84	1	2
\$53-1			3	2	12.78%	25565.39	9.15	sp Q9UIJ7 KAD3_HUMAN GTP:AMP phosphotransferase AK3, mitochondrial OS=Homo sapiens GN=AK3 PE=1 SV=4						
\$53-2			3	2	13.49%	24311.82	8.65	tr Q7Z531 Q7Z531_HUMAN GTP:AMP phosphotransferase AK3, mitochondrial OS=Homo sapiens GN=AK3 PE=2 SV=1						
\$53-3			3	2	12.78%	25620.47	9.3	tr Q7Z4Y4 Q7Z4Y4_HUMAN GTP:AMP phosphotransferase AK3, mitochondrial OS=Homo sapiens GN=AK3 PE=2 SV=1						
\$53-4			3	2	18.47%	18177.75	7.88	tr B3KWD9 B3KWD9_HUMAN cDNA FLJ42834 fis, clone BRCAN2019002, highly similar to GTP:AMP phosphotransferase mitochondrial (EC 2.7.4.10) OS=Homo sapiens PE=2 SV=1						
	R16062_1_KIAA,19 403	K.NLTQYSWLLDGFPR.T	1710.9135	0.6785	2	1		3.1747	0.431	1196.4	1 16 26	5.84	1	4
	R16062_1_KIAA,14 383	K.TVGIDDLTGEPLIQR.E	1627.8211	0.2361	2	1		2.5787	0.3256	298.8	2 12 28	4.03	1	4
	R16062_1_KIAA,14 436	K.TVGIDDLTGEPLIQR.E	1627.8211	1.4961	2	1		2.5752	0.4191	595.3	1 17 28	4.03	1	4
\$54-1			3	2	5.10%	56559.96	5.26	sp P06576 ATPB_HUMAN ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3						
\$54-2			3	2	7.46%	38138.71	5.37	tr H0YH81 H0YH81_HUMAN ATP synthase subunit beta (Fragment) OS=Homo sapiens GN=ATP5B PE=1 SV=1						
\$54-3			3	2	10.00%	28392.5	5.85	tr F8W0P7 F8W0P7_HUMAN ATP synthase subunit beta, mitochondrial (Fragment) OS=Homo sapiens GN=ATP5B PE=1 SV=2						
\$54-4			3	2	6.07%	48113.19	4.95	tr Q0QEN7 Q0QEN7_HUMAN ATP synthase subunit beta (Fragment) OS=Homo sapiens GN=ATP5B PE=2 SV=1						
\$54-5			3	2	5.10%	56559.96	5.26	tr V9HW31 V9HW31_HUMAN ATP synthase subunit beta OS=Homo sapiens GN=HEL-S-271 PE=1 SV=1						
	R16062_1_KIAA,14 249	R.FTQAGSEVSALLGR.I	1436.5953	0.4393	2	1		3.3736	0.515	952.2	1 15 26	6	1	5
	R16062_1_KIAA,14 258	R.FTQAGSEVSALLGR.I	1436.5953	0.7043	2	1		2.6827	0.5096	952.6	1 15 26	6	1	5
	R16062_1_KIAA,17 352	R.VALTGLTVAEYFR.D	1440.6687	0.4877	2	1		2.7325	0.4673	664.7	1 13 24	5.97	1	5
\$55-1			3	2	1.10%	280738.8	5.7	sp P21333 FLNA_HUMAN Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4						

\$55-2			3	2	1.11%	277505.36	5.7	tr Q60FE6 Q60FE6_HUMAN Filamin A OS=Homo sapiens GN=FLNA PE=2 SV=1								
\$55-3			3	2	1.11%	278226.18	5.71	tr Q60FE5 Q60FE5_HUMAN Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1								
\$55-4			3	2	1.25%	245850.76	5.65	tr A0A087WWY3 A0A087WWY3_HUMAN Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=1								
\$55-5			3	2	1.11%	276550.17	5.69	tr Q5HY54 Q5HY54_HUMAN Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=1								
\$55-6			3	2	1.25%	245866.76	5.65	tr A6NDY9 A6NDY9_HUMAN Filamin A OS=Homo sapiens GN=FLNA PE=2 SV=4								
	R16062_1_KIAA,10 930	R.GAGTGGLGLAVEGPSEAK.M		1571.7144	0.3294	2	1		2.2376	0.3841	680.3	1 16 34	4.53	1	6	
	R16062_1_KIAA,19 446	R.LIALLEVLSQK.K		1227.5186	-0.1704	2	1		2.3087	0.5758	785.3	1 14 20	6	1	6	
	R16062_1_KIAA,19 502	R.LIALLEVLSQK.K		1227.5186	-0.8554	2	1		2.209	0.282	612.3	1 14 20	6	1	6	
\$56-1			2	2	22.88%	12766.4	9.15	tr A0N5G5 A0N5G5_HUMAN Rheumatoid factor D5 light chain (Fragment) OS=Homo sapiens GN=V<kappa>3 PE=2 SV=1								
	R16062_1_KIAA,13 699	-.EIVLTQSPATLSLSPGER.A		1899.1352	0.5292	2	1		2.9155	0.4558	853.7	1 17 34	4.53	1	1	
	R16062_1_KIAA,10 532	R.LLIYDASNR.A		1065.2048	1.1808	2	1		2.2253	0.3247	948.4	1 14 16	5.84	2	2	
\$57-1			2	2	11.43%	27745.18	4.73	sp P63104 1433Z_HUMAN 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1								
\$57-2			2	2	16.67%	19072.44	4.48	tr B0AZS6 B0AZS6_HUMAN 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1								
\$57-3			2	2	22.40%	13985.51	4.29	tr B7Z2E6 B7Z2E6_HUMAN 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1								
\$57-4			2	2	11.43%	27745.18	4.73	tr D0PNI1 D0PNI1_HUMAN Epididymis luminal protein 4 OS=Homo sapiens GN=YWHAZ PE=2 SV=1								
\$57-5			2	2	21.54%	14636.33	4.37	tr H0YB80 H0YB80_HUMAN 14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens GN=YWHAZ PE=1 SV=1								
\$57-6			2	2	26.42%	11810.06	4.14	3-monooxygenasea/tryptophan 5-monooxygenase activation protein zeta (Fragment) OS=Homo sapiens PE=2 SV=1								
	R16062_1_KIAA,17 112	K.DSTLIM*QLLR.D		1206.4382	0.6502	2	1		2.2301	0.1672	887.6	1 12 18	5.84	1	6	
	R16062_1_KIAA,14 637	K.GIVDQSQQAYQEAFEISK.K		2042.1919	-0.5201	2	1		2.5191	0.4315	607	1 16 34	4.14	1	6	
\$58-1			2	2	6.40%	45205.2	6.13	sp P00738 HPT_HUMAN Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1								

\$58-2			2	2	11.40%	25457.89	6.06	tr Q6PEJ8 Q6PEJ8_HUMAN HP protein OS=Homo sapiens GN=HP PE=2 SV=1									
\$58-3			2	2	9.25%	31407.82	8.48	tr A0A087WU08 A0A087WU08_HUMAN Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1									
\$58-4			2	2	7.49%	38451.68	6.26	tr A0A0C4DGL8 A0A0C4DGL8_HUMAN Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1									
\$58-5			2	2	9.25%	31381.78	8.48	tr Q6NSB4 Q6NSB4_HUMAN HP protein OS=Homo sapiens GN=HP PE=2 SV=1									
\$58-6			2	2	11.40%	25471.92	6.24	tr B3KP77 B3KP77_HUMAN cDNA FLJ31310 fis, clone LIVER1000165, highly similar to Haptoglobin OS=Homo sapiens PE=2 SV=1									
\$58-7			2	2	5.88%	49105.84	6.17	tr H0Y300 H0Y300_HUMAN Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=4									
\$58-8			2	2	7.12%	40668.96	5.54	tr J3QLC9 J3QLC9_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=1 SV=1									
\$58-9			2	2	6.44%	44929.88	6.13	tr J3QR68 J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=1 SV=1									
	R16062_1_KIAA,11010	K.SCAVAEYGVYVK.V		1346.504	0.169	2	1		2.3154	0.4719	556.9	112 22	5.72	1	9		
	R16062_1_KIAA,11634	K.YVM*LPVADQDQCIR.H		1724.9537	0.5137	2	1		2.5392	0.3567	854.6	116 26	4.21	1	9		
\$59-1			2	2	2.42%	129314.11	9.08	sp P08123 CO1A2_HUMAN Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=7									
\$59-2			2	2	2.42%	129150.98	9.13	tr A0A087WTA8 A0A087WTA8_HUMAN Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=1									
	R16062_1_KIAA,5385	R.GEAGAAGPAGPAGPR.G		1236.3195	0.5645	2	1		2.4946	0.3982	926.4	117 28	6	1	2		
	R16062_1_KIAA,8343	R.GETGPSGPVGPAGAVGPR.G		1563.6972	0.2442	2	1		3.0171	0.398	978.3	119 34	6	1	2		
\$60-1			2	2	10.83%	25599.64	8.83	tr S6BGF5 S6BGF5_HUMAN IgG H chain OS=Homo sapiens PE=2 SV=1									
	R16062_1_KIAA,7637	R.GTLVTVSSASTK.G		1151.2928	0.2358	2	1		2.7321	0.4169	836.4	117 22	8.75	2	2		
	R16062_1_KIAA,11521	R.STSESTAALGCLVK.D		1424.5731	-2.5969	2	1		3.363	0.2639	1125.9	119 26	5.72	4	6		
\$61-1			4	1	13.33%	13282.83	8.62	tr A2NYQ9 A2NYQ9_HUMAN Anti-folate binding protein (Fragment) OS=Homo sapiens GN=HuVH8B VH PE=2 SV=1									
	R16062_1_KIAA,11454	-.QVQLVESGGGLVQPGR.S		1624.8237	-0.2783	2	1		2.9155	0.4606	1459.8	119 30	6	1	1		
	R16062_1_KIAA,11466	-.QVQLVESGGGLVQPGR.S		1624.8237	-0.6543	2	1		3.1665	0.429	1225.3	120 30	6	1	1		

	R16062_1_KIAA,11 511	-.QVQLVESGGGLVQPGR.S	1624.8237	0.3777	2	1		3.7845	0.4187	1810.9	121 30	6	1	1
	R16062_1_KIAA,11 539	-.QVQLVESGGGLVQPGR.S	1624.8237	0.4107	2	1		3.1884	0.4102	1354.6	118 30	6	1	1
\$62-1			4	1	7.35%	22876.37	9.73	sp P46782 RS5_HUMAN 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4						
\$62-2			4	1	7.35%	22876.37	9.73	tr A0A024R4Q8 A0A024R4Q8_HUMAN Ribosomal protein S5, isoform CRA_a OS=Homo sapiens GN=RPS5 PE=3 SV=1						
\$62-3			4	1	6.67%	25333.23	9.78	tr M0R0R2 M0R0R2_HUMAN 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1						
\$62-4			4	1	7.50%	22390.83	9.59	tr M0R0F0 M0R0F0_HUMAN 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1						
\$62-5			4	1	11.19%	14762.75	8.66	tr M0QZN2 M0QZN2_HUMAN 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1						
\$62-6			4	1	7.35%	22964.49	9.76	tr Q53G25 Q53G25_HUMAN Ribosomal protein S5 variant (Fragment) OS=Homo sapiens PE=2 SV=1						
	R16062_1_KIAA,19 311	K.TIAECLADELINAAK.G	1632.8311	0.1901	2	1		3.0252	0.5113	1303.4	118 28	4.14	1	6
	R16062_1_KIAA,19 324	K.TIAECLADELINAAK.G	1632.8311	-0.3689	2	1		3.2939	0.4453	974.5	118 28	4.14	1	6
	R16062_1_KIAA,19 340	K.TIAECLADELINAAK.G	1632.8311	1.3791	2	1		2.7191	0.2968	1609.2	118 28	4.14	1	6
	R16062_1_KIAA,19 356	K.TIAECLADELINAAK.G	1632.8311	1.4571	2	1		3.2179	0.2962	1479.9	119 28	4.14	1	6
\$63-1			4	1	5.53%	22110.34	8.27	sp Q06830 PRDX1_HUMAN Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1						
\$63-2			4	1	5.56%	21891.93	5.66	sp P32119 PRDX2_HUMAN Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5						
\$63-3			4	1	6.43%	18975.75	6.42	tr A0A0A0MSI0 A0A0A0MSI0_HUMAN Peroxiredoxin-1 (Fragment) OS=Homo sapiens GN=PRDX1 PE=1 SV=1						
\$63-4			4	1	5.56%	21891.93	5.66	tr V9HW12 V9HW12_HUMAN Epididymis secretory sperm binding protein Li 2a OS=Homo sapiens GN=HEL-S-2a PE=2 SV=1						
\$63-5			4	1	6.01%	20107.19	8.9	tr B4DF70 B4DF70_HUMAN cDNA FLJ60461, highly similar to Peroxiredoxin-2 (EC 1.11.1.15) OS=Homo sapiens PE=2 SV=1						
\$63-6			4	1	5.53%	22200.51	8.58	tr B2R4P2 B2R4P2_HUMAN cDNA, FLJ92164, highly similar to Homo sapiens peroxiredoxin 1 (PRDX1), mRNA OS=Homo sapiens PE=2 SV=1						
\$63-7			4	1	11.34%	10676.1	8.79	tr A0A0A0MRQ5 A0A0A0MRQ5_HUMAN Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1						
	R16062_1_KIAA,11	R.QITVNDLPVGR.S	1212.381	0.168	2	1		2.3237	0.3005	616.9	111 20	5.84	1	7

	432	R16062_1_KIAA,11	R.QITVNDLPVGR.S	1212.381	-0.485	2	1		2.7165	0.3418	1220.6	1 16 20	5.84	1	7
	472	R16062_1_KIAA,11	R.QITVNDLPVGR.S	1212.381	0.985	2	1		2.8559	0.3889	826.2	1 15 20	5.84	1	7
	524	R16062_1_KIAA,11	R.QITVNDLPVGR.S	1212.381	0.515	2	1		2.6238	0.372	753.5	1 13 20	5.84	1	7
\$64-1	533	R16062_1_KIAA,11	R.QITVNDLPVGR.S	1212.381	13.22%	13437.2	9.43	sp P01771 HV310_HUMAN Ig heavy chain V-III region HIL OS=Homo sapiens PE=1 SV=1							
	785	R16062_1_KIAA,12	-.QVKLVQAGGGVVQPGR.S	1593.856	-0.632	2	1		2.2298	0.2525	394.3	3 13 30	11	1	1
	817	R16062_1_KIAA,12	-.QVKLVQAGGGVVQPGR.S	1593.856	-0.418	2	1		2.8817	0.217	699.5	3 15 30	11	1	1
	861	R16062_1_KIAA,12	-.QVKLVQAGGGVVQPGR.S	1593.856	-0.424	2	1		2.9304	0.2442	596.9	3 15 30	11	1	1
\$65-1				3	1	7.77%	11367.28	11.36	sp P62805 H4_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2						
\$65-2				3	1	18.60%	4915.8	10.92	tr Q6B823 Q6B823_HUMAN Histone H4 (Fragment) OS=Homo sapiens PE=3 SV=1						
\$65-3				3	1	7.77%	11367.28	11.36	tr B2R4R0 B2R4R0_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4L PE=2 SV=1						
\$65-4				3	1	7.77%	11314.23	11.04	tr Q0VAS5 Q0VAS5_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4H PE=2 SV=1						
	655	R16062_1_KIAA,13	K.VFLENVIR.D	990.1811	0.4381	2	1		2.2759	0.2887	634.7	2 12 14	5.97	1	4
	672 - 13673	R16062_1_KIAA,13	K.VFLENVIR.D	990.1811	-0.0549	2	1		2.5114	0.3316	598.7	6 12 14	5.97	1	4
	686	R16062_1_KIAA,13	K.VFLENVIR.D	990.1811	0.3571	2	1		2.3892	0.3359	659.5	2 12 14	5.97	1	4
\$66-1				2	1	10.00%	13352.93	5.72	tr A0A068LKQ0 A0A068LKQ0_HUMAN Ig heavy chain variable region (Fragment) OS=Homo sapiens PE=4 SV=1						
	25	R16062_1_KIAA,87	-.EVQLVQSGAEVK.K	1287.4447	-0.0633	2	1		2.8872	0.2047	648.4	1 14 22	4.53	1	1
	83	R16062_1_KIAA,88	-.EVQLVQSGAEVK.K	1287.4447	0.9987	2	1		2.38	0.1118	917.3	1 15 22	4.53	1	1
\$67-1				2	1	13.91%	12626.09	8.93	tr A2J1N6 A2J1N6_HUMAN Rheumatoid factor RF-ET9 (Fragment) OS=Homo sapiens PE=2 SV=1						
	454	R16062_1_KIAA,10	-.LVESGGGLVKPGGSLR.L	1526.7632	0.4632	2	1		2.3532	0.2813	688.4	1 16 30	8.75	1	1
	467	R16062_1_KIAA,10	-.LVESGGGLVKPGGSLR.L	1526.7632	0.2432	2	1		2.4754	0.267	803.8	1 17 30	8.75	1	1

\$68-1		2	1	14.07%	14538.35	8.93	tr A2N2G5 A2N2G5_HUMAN VH87-2 protein (Fragment) OS=Homo sapiens GN=VH87-2 PE=2 SV=1								
	R16062_1_KIAA,14008														
	R16062_1_KIAA,19025														
\$69-1		2	1	11.90%	13950.15	10.31	sp P33778 H2B1B_HUMAN Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2								
\$69-2		2	1	11.90%	13906.09	10.31	sp P62807 H2B1C_HUMAN Histone H2B type 1-C/E/F/G/I OS=Homo sapiens GN=HIST1H2BC PE=1 SV=4								
\$69-3		2	1	11.90%	13936.11	10.31	sp P58876 H2B1D_HUMAN Histone H2B type 1-D OS=Homo sapiens GN=HIST1H2BD PE=1 SV=2								
\$69-4		2	1	11.90%	13892.06	10.31	sp Q93079 H2B1H_HUMAN Histone H2B type 1-H OS=Homo sapiens GN=HIST1H2BH PE=1 SV=3								
\$69-5		2	1	11.90%	13904.12	10.31	sp P06899 H2B1J_HUMAN Histone H2B type 1-J OS=Homo sapiens GN=HIST1H2BJ PE=1 SV=3								
\$69-6		2	1	11.90%	13890.09	10.31	sp O60814 H2B1K_HUMAN Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3								
\$69-7		2	1	11.90%	13952.16	10.31	sp Q99880 H2B1L_HUMAN Histone H2B type 1-L OS=Homo sapiens GN=HIST1H2BL PE=1 SV=3								
\$69-8		2	1	11.90%	13989.22	10.31	sp Q99879 H2B1M_HUMAN Histone H2B type 1-M OS=Homo sapiens GN=HIST1H2BM PE=1 SV=3								
\$69-9		2	1	11.90%	13922.09	10.31	sp Q99877 H2B1N_HUMAN Histone H2B type 1-N OS=Homo sapiens GN=HIST1H2BN PE=1 SV=3								
\$69-10		2	1	11.90%	13906.09	10.31	sp P23527 H2B1O_HUMAN Histone H2B type 1-O OS=Homo sapiens GN=HIST1H2BO PE=1 SV=3								
\$69-11		2	1	11.90%	13920.12	10.31	sp Q16778 H2B2E_HUMAN Histone H2B type 2-E OS=Homo sapiens GN=HIST2H2BE PE=1 SV=3								
\$69-12		2	1	11.90%	13920.11	10.31	sp Q5QNW6 H2B2F_HUMAN Histone H2B type 2-F OS=Homo sapiens GN=HIST2H2BF PE=1 SV=3								
\$69-13		2	1	11.90%	13908.06	10.31	sp Q8N257 H2B3B_HUMAN Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3								
\$69-14		2	1	11.90%	13944.15	10.37	sp P57053 H2BFS_HUMAN Histone H2B type F-S OS=Homo sapiens GN=H2BFS PE=1 SV=2								
\$69-15		2	1	11.90%	13906.09	10.31	tr B2R4S9 B2R4S9_HUMAN Histone H2B OS=Homo sapiens GN=HIST1H2BE PE=2 SV=1								
\$69-16		2	1	11.90%	13922.09	10.31	tr A0A024RCJ9 A0A024RCJ9_HUMAN Histone H2B OS=Homo sapiens PE=3 SV=1								
\$69-17		2	1	9.04%	18803.85	10.53	tr U3KQK0 U3KQK0_HUMAN Histone H2B OS=Homo sapiens GN=HIST1H2BN PE=1 SV=1								
\$69-1		2	1	11.90%	13936.11	10.31	tr A0A024QZZ7 A0A024QZZ7_HUMAN Histone H2B OS=Homo								

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\$71-8		2	1	22.22%	10079.62	5.5	tr E9PS23 E9PS23_HUMAN Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=1 SV=6								
\$71-9		2	1	16.39%	13923.21	8.86	tr E9PQB7 E9PQB7_HUMAN Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=1 SV=1								
	R16062_1_KIAA,16166	K.EILVGDIVGQTVDDPYATFVK.M	2167.4008	0.8078	2	1		3.5271	0.5457	1205	121 38	3.84	1	9	
	R16062_1_KIAA,16219	K.EILVGDIVGQTVDDPYATFVK.M	2167.4008	0.8388	2	1		3.7862	0.5517	921.9	121 38	3.84	1	9	
\$72-1		2	1	6.31%	24722.05	8.35	sp P04179 SODM_HUMAN Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens GN=SOD2 PE=1 SV=2								
\$72-2		2	1	6.31%	24750.1	8.35	tr A0A0C4DFU2 A0A0C4DFU2_HUMAN Superoxide dismutase OS=Homo sapiens GN=SOD2 PE=1 SV=1								
\$72-3		2	1	8.64%	18261.81	8.48	tr A0A0C4DG56 A0A0C4DG56_HUMAN Superoxide dismutase OS=Homo sapiens GN=SOD2 PE=1 SV=1								
\$72-4		2	1	6.60%	23638.65	7.34	tr Q4ZJ1 Q4ZJ1_HUMAN Superoxide dismutase (Fragment) OS=Homo sapiens GN=SOD2 PE=2 SV=1								
\$72-5		2	1	6.67%	23224.19	6.87	tr Q7Z7M6 Q7Z7M6_HUMAN Superoxide dismutase (Fragment) OS=Homo sapiens GN=SOD2 PE=2 SV=1								
\$72-6		2	1	6.57%	23672.68	6.87	tr Q7Z7M4 Q7Z7M4_HUMAN Superoxide dismutase (Fragment) OS=Homo sapiens GN=SOD2 PE=2 SV=1								
\$72-7		2	1	7.37%	21104.8	9.24	tr F5GYZ5 F5GYZ5_HUMAN Superoxide dismutase [Mn], mitochondrial (Fragment) OS=Homo sapiens GN=SOD2 PE=1 SV=1								
\$72-8		2	1	7.65%	20019.63	9.36	tr F5H4R2 F5H4R2_HUMAN Superoxide dismutase [Mn], mitochondrial (Fragment) OS=Homo sapiens GN=SOD2 PE=1 SV=1								
\$72-9		2	1	6.57%	23558.61	6.9	tr Q7Z7M7 Q7Z7M7_HUMAN Superoxide dismutase (Fragment) OS=Homo sapiens GN=SOD2 PE=2 SV=1								
\$72-10		2	1	12.61%	12130.54	8.05	tr F5H3C5 F5H3C5_HUMAN Superoxide dismutase [Mn], mitochondrial (Fragment) OS=Homo sapiens GN=SOD2 PE=1 SV=1								
	R16062_1_KIAA,12225	K.GDVTAQIALQPALK.F	1425.6556	-0.6684	2	1		2.3033	0.2726	606	113 26	5.84	1	10	
	R16062_1_KIAA,12242	K.GDVTAQIALQPALK.F	1425.6556	0.9096	2	1		2.4271	0.2746	649.6	213 26	5.84	1	10	
\$73-1		2	1	7.47%	26922.76	5.09	sp O00299 CLIC1_HUMAN Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4								
\$73-2		2	1	7.47%	26922.76	5.09	tr Q5SRT3 Q5SRT3_HUMAN Chloride intracellular channel protein OS=Homo sapiens GN=CLIC1 PE=2 SV=2								
\$73-3		2	1	7.47%	27014.86	5.09	tr Q53FB0 Q53FB0_HUMAN Chloride intracellular channel protein (Fragment) OS=Homo sapiens PE=2 SV=1								

	R16062_1_KIAA,15 960	K.LAALNPESNTAGLDIFAK.F	1846.074	0.565	2	1		2.7533	0.372	619.7	1 16 34	4.37	1	3
	R16062_1_KIAA,15 970	K.LAALNPESNTAGLDIFAK.F	1846.074	0.823	2	1		2.8014	0.4263	645.2	1 17 34	4.37	1	3
\$74-1			2	1	4.23%	39594.9	9.1	sp P51991 ROA3_HUMAN Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2						
\$74-2			2	1	4.49%	37028.98	8.46	tr B4DDB6 B4DDB6_HUMAN Heterogeneous nuclear ribonucleoprotein A3, isoform CRA_a OS=Homo sapiens GN=HNRPA3 PE=2 SV=1						
\$74-3			2	1	4.95%	34189.15	8.18	tr B4E3E6 B4E3E6_HUMAN cDNA FLJ58832, highly similar to Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens PE=2 SV=1						
\$74-4			2	1	5.95%	29356.68	8.5	tr Q65ZQ3 Q65ZQ3_HUMAN FBRNP OS=Homo sapiens GN=D10S102 PE=2 SV=1						
	R16062_1_KIAA,17 267	K.LFIGGLSFETDDSLR.E	1771.9488	0.7728	2	1		2.6808	0.2659	1177.3	1 19 30	4.03	1	4
	R16062_1_KIAA,17 346	K.LFIGGLSFETDDSLR.E	1771.9488	0.2908	2	1		2.8108	0.3798	937.9	1 17 30	4.03	1	4
\$75-1			2	1	3.26%	37540.16	6.36	sp P37837 TALDO_HUMAN Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2						
\$75-2			2	1	3.46%	35328.83	9.07	tr F2Z393 F2Z393_HUMAN Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=1						
	R16062_1_KIAA,13 063	K.LLGELLQDNAK.L	1214.3937	-0.8883	2	1		2.5668	0.3047	680	1 13 20	4.37	1	2
	R16062_1_KIAA,13 077	K.LLGELLQDNAK.L	1214.3937	-0.2713	2	1		2.8913	0.4608	1220.1	1 16 20	4.37	1	2
\$76-1			2	1	5.02%	35882.74	5.84	sp P09525 ANXA4_HUMAN Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4						
\$76-2			2	1	4.98%	36085.01	5.84	tr Q6LES2 Q6LES2_HUMAN Annexin (Fragment) OS=Homo sapiens GN=ANXA4 PE=2 SV=1						
\$76-3			2	1	5.35%	33551.92	5.64	tr Q6P452 Q6P452_HUMAN Annexin OS=Homo sapiens GN=ANXA4 PE=1 SV=1						
\$76-4			2	1	7.11%	25420.97	6.03	tr Q59FK3 Q59FK3_HUMAN Annexin (Fragment) OS=Homo sapiens PE=2 SV=1						
\$76-5			2	1	14.29%	12747.68	8.52	tr Q6MZI0 Q6MZI0_HUMAN Annexin (Fragment) OS=Homo sapiens GN=DKFZp686H02120 PE=2 SV=1						
\$76-6			2	1	5.28%	34459.16	5.65	tr B4DE02 B4DE02_HUMAN Annexin OS=Homo sapiens PE=2 SV=1						
\$76-7			2	1	4.98%	36056.95	5.65	tr V9HW59 V9HW59_HUMAN Annexin OS=Homo sapiens GN=HEL-S-274 PE=2 SV=1						

\$76-8	2	1	5.35%	33613.96	5.64	tr B4DDZ4 B4DDZ4_HUMAN Annexin OS=Homo sapiens PE=2 SV=1									
R16062_1_KIAA,19 476		K.SETSGSFEDALLAIVK.C	1667.8389	0.4089	2	1		3.0374	0.3639	1025.2	1 16 30	4.14	1	8	
R16062_1_KIAA,19 530		K.SETSGSFEDALLAIVK.C	1667.8389	0.6169	2	1		2.9033	0.4402	789.3	1 16 30	4.14	1	8	
\$77-1	2	1	3.79%	34364.47	5.41	sp Q8NHW5 RLA0L_HUMAN 60S acidic ribosomal protein P0-like OS=Homo sapiens GN=RPLP0P6 PE=5 SV=1									
\$77-2	2	1	3.79%	34273.51	5.72	sp P05388 RLA0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1									
\$77-3	2	1	7.23%	18270.39	9.65	tr G3V210 G3V210_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1									
\$77-4	2	1	3.79%	34273.51	5.72	tr A0A024RBS2 A0A024RBS2_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=3 SV=1									
\$77-5	2	1	3.79%	34301.53	5.72	tr Q53HW2 Q53HW2_HUMAN 60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens PE=2 SV=1									
\$77-6	2	1	3.79%	34239.49	5.72	tr A8K4Z4 A8K4Z4_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens PE=2 SV=1									
\$77-7	2	1	4.86%	27187.55	9.11	tr F8VU65 F8VU65_HUMAN 60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens GN=RPLP0 PE=1 SV=1									
\$77-8	2	1	7.84%	16680.51	9.39	tr F8VPE8 F8VPE8_HUMAN 60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens GN=RPLP0 PE=1 SV=1									
\$77-9	2	1	4.72%	27298.65	8.36	tr Q6NSF2 Q6NSF2_HUMAN RPLP0 protein OS=Homo sapiens GN=RPLP0 PE=2 SV=1									
\$77-1 0	2	1	4.51%	28538.63	4.69	tr B4E3D5 B4E3D5_HUMAN cDNA FLJ51469, highly similar to 60S acidic ribosomal protein P0 OS=Homo sapiens PE=2 SV=1									
\$77-1 1	2	1	4.27%	30456.11	5.9	tr F8VWS0 F8VWS0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1									
\$77-1 2	2	1	4.92%	26901.25	9.05	tr F8VW21 F8VW21_HUMAN 60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens GN=RPLP0 PE=1 SV=1									
R16062_1_KIAA,17 427		K.TSFFQALGITTK.I	1314.5117	0.3797	2	1		2.4005	0.5168	999.2	1 14 22	8.41	1	12	
R16062_1_KIAA,17 482		K.TSFFQALGITTK.I	1314.5117	0.3687	2	1		3.2542	0.5068	895.2	1 14 22	8.41	1	12	
\$78-1	2	1	4.89%	29995.51	10.61	sp P62424 RL7A_HUMAN 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2									
\$78-2	2	1	6.81%	21544.69	11.02	tr Q5T8U3 Q5T8U3_HUMAN 60S ribosomal protein L7a (Fragment) OS=Homo sapiens GN=RPL7A PE=1 SV=1									
\$78-3	2	1	8.61%	16539.45	10.01	tr Q5T8U2 Q5T8U2_HUMAN 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=1									
\$78-4	2	1	9.15%	15636.38	10.06	tr Q9BY74 Q9BY74_HUMAN Ribosomal protein L7a (Fragment)									

						OS=Homo sapiens GN=RP-L7a PE=2 SV=1								
	R16062_1_KIAA,11 410	R.AGVNTVTTLVENK.K	1346.5121	0.3131	2	1		2.798	0.5118	718.5	1 14 24	6.05	1	4
	R16062_1_KIAA,11 431	R.AGVNTVTTLVENK.K	1346.5121	1.0751	2	1		3.273	0.4627	1057.9	1 16 24	6.05	1	4
\$79-1			2	1	4.27%	31121.92	4.9	sp P29692 EF1D_HUMAN Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5						
\$79-2			2	1	7.23%	18157.05	4.97	tr E9PPR1 E9PPR1_HUMAN Elongation factor 1-delta (Fragment) OS=Homo sapiens GN=EEF1D PE=1 SV=1						
\$79-3			2	1	6.06%	21824.3	5.38	tr E9PQ49 E9PQ49_HUMAN Elongation factor 1-delta (Fragment) OS=Homo sapiens GN=EEF1D PE=1 SV=6						
\$79-4			2	1	4.60%	28821.32	4.93	tr E9PK01 E9PK01_HUMAN Elongation factor 1-delta (Fragment) OS=Homo sapiens GN=EEF1D PE=1 SV=1						
\$79-5			2	1	6.42%	20819.11	4.9	tr E9PL71 E9PL71_HUMAN Elongation factor 1-delta (Fragment) OS=Homo sapiens GN=EEF1D PE=1 SV=1						
\$79-6			2	1	9.23%	14179.82	6.84	tr E9PMW7 E9PMW7_HUMAN Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=1						
\$79-7			2	1	5.88%	22490.13	5.38	tr E9PI39 E9PI39_HUMAN Elongation factor 1-delta (Fragment) OS=Homo sapiens GN=EEF1D PE=1 SV=1						
\$79-8			2	1	1.90%	69282.71	6.76	tr A0A087X1X7 A0A087X1X7_HUMAN Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=1						
\$79-9			2	1	7.14%	18401.26	4.82	tr E9PL12 E9PL12_HUMAN Elongation factor 1-delta (Fragment) OS=Homo sapiens GN=EEF1D PE=1 SV=1						
\$79-1 0			2	1	2.18%	60882.77	7.48	tr Q9BW34 Q9BW34_HUMAN EEF1D protein (Fragment) OS=Homo sapiens GN=EEF1D PE=2 SV=2						
\$79-1 1			2	1	1.85%	71450.24	6.02	tr B2RAR6 B2RAR6_HUMAN cDNA, FLJ95068, highly similar to Homo sapiens eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1						
\$79-1 2			2	1	1.85%	71422.19	6.02	tr D3DWK1 D3DWK1_HUMAN Eukaryotic translation elongation factor 1 delta (Guanine nucleotide exchange protein), isoform CRA_b OS=Homo sapiens GN=EEF1D PE=3 SV=1						
\$79-1 3			2	1	8.76%	15001.89	8.85	tr E9PIZ1 E9PIZ1_HUMAN Elongation factor 1-delta (Fragment) OS=Homo sapiens GN=EEF1D PE=1 SV=1						
\$79-1 4			2	1	1.90%	69395.87	6.76	tr Q71RH4 Q71RH4_HUMAN FP1047 OS=Homo sapiens PE=2 SV=1						
\$79-1 5			2	1	1.85%	71418.3	6.23	tr Q9H7G6 Q9H7G6_HUMAN cDNA: FLJ20897 fis, clone ADKA03573 OS=Homo sapiens PE=2 SV=1						
\$79-1 6			2	1	1.72%	76570.37	6.61	tr E9PRY8 E9PRY8_HUMAN Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=1						
\$79-1			2	1	5.71%	22836.7	9.05	tr H0YCK7 H0YCK7_HUMAN Elongation factor 1-delta						

7							(Fragment) OS=Homo sapiens GN=EEF1D PE=1 SV=1								
\$79-1							tr E9PN91 E9PN91_HUMAN Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=1								
8		2	1	11.32%	11615.91	6.28									
	R16062_1_KIAA,15679	R.GVVQELQQAISK.L	1300.4866	0.2096	2	1		2.5926	0.4084	894.8	1 14 22	6	1	18	
	R16062_1_KIAA,15740	R.GVVQELQQAISK.L	1300.4866	0.1206	2	1		2.2135	0.3556	635.4	1 12 22	6	1	18	
\$80-1		2	1	3.50%	32922.77	5.45	sp P52907 CAZA1_HUMAN F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3								
\$80-2		2	1	3.50%	32949.08	5.57	sp P47755 CAZA2_HUMAN F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3								
\$80-3		2	1	3.50%	32922.77	5.45	tr A0A024R0E5 A0A024R0E5_HUMAN Capping protein (Actin filament) muscle Z-line, alpha 1, isoform CRA_a OS=Homo sapiens GN=CAPZA1 PE=4 SV=1								
\$80-4		2	1	3.50%	32949.08	5.57	tr A4D0V4 A4D0V4_HUMAN Capping protein (Actin filament) muscle Z-line, alpha 2 OS=Homo sapiens GN=CAPZA2 PE=2 SV=1								
\$80-5		2	1	3.50%	32967.11	5.57	tr Q53GC7 Q53GC7_HUMAN Capping protein (Actin filament) muscle Z-line, alpha 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1								
\$80-6		2	1	5.75%	20080.88	6.07	tr A0A0D9SET8 A0A0D9SET8_HUMAN F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=1								
\$80-7		2	1	6.85%	16698.71	5	tr C9JUG7 C9JUG7_HUMAN F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=1								
\$80-8		2	1	3.50%	32967.11	5.57	tr Q53GE2 Q53GE2_HUMAN Capping protein (Actin filament) muscle Z-line, alpha 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1								
\$80-9		2	1	3.50%	32908.74	5.44	tr A8K0T9 A8K0T9_HUMAN cDNA FLJ75422, highly similar to Homo sapiens capping protein (actin filament) muscle Z-line, alpha 1, mRNA OS=Homo sapiens PE=2 SV=1								
\$80-10		2	1	5.75%	19963.56	5.14	tr F8W9N7 F8W9N7_HUMAN F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=1								
	R16062_1_KIAA,13638	R.LLLNNDNLLR.E	1198.3975	-0.4025	2	1		2.3746	0.3255	874.3	1 14 18	5.84	1	10	
	R16062_1_KIAA,13669	R.LLLNNDNLLR.E	1198.3975	-1.5415	2	1		2.6166	0.1714	1184.2	1 15 18	5.84	1	10	
\$81-1		2	1	8.25%	22119.27	7.13	sp P30043 BLVRB_HUMAN Flavin reductase (NADPH) OS=Homo sapiens GN=BLVRB PE=1 SV=3								
\$81-2		2	1	10.43%	17160.36	6.27	tr M0R192 M0R192_HUMAN Flavin reductase (NADPH) OS=Homo sapiens GN=BLVRB PE=1 SV=1								
\$81-3		2	1	8.25%	22119.27	7.13	tr V9HWI1 V9HWI1_HUMAN Epididymis secretory protein Li 10								

[illegible]

[illegible]

	R16062_1_KIAA,12 622	K.LVILANNCPALR.K	1354.6172	0.7672	2	1	2.4734	0.2941	868.8	1 14 22	8.25	1	4
\$94-1			1	1	3.25%	51676.43	6.55	sp P02790 HEMO_HUMAN Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2					
	R16062_1_KIAA,18 249	K.LYLVQGTQVYVFLTK.G	1773.1078	-0.7042	2	1	3.2723	0.4053	628.4	1 15 28	8.5	1	1
\$95-1			1	1	3.14%	43810.07	9.47	sp P51888 PRELP_HUMAN Prolargin OS=Homo sapiens GN=PRELP PE=1 SV=1					
\$95-2			1	1	5.31%	26038.22	9.27	tr Q7Z4B2 Q7Z4B2_HUMAN MSTP161 OS=Homo sapiens GN=MST161 PE=2 SV=1					
\$95-3			1	1	3.14%	43783.05	9.47	tr Q6FHG6 Q6FHG6_HUMAN PRELP protein (Fragment) OS=Homo sapiens GN=PRELP PE=2 SV=1					
	R16062_1_KIAA,11 369	K.NQLEEVPSALPR.N	1353.5063	0.2793	2	1	2.6933	0.5067	1327.1	1 17 22	4.53	1	3
\$96-1			1	1	8.90%	21258.59	6.16	sp P60953 CDC42_HUMAN Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2					
\$96-2			1	1	8.90%	21258.59	6.16	tr A0A024RAE4 A0A024RAE4_HUMAN Cell division cycle 42 (GTP binding protein, 25kDa), isoform CRA_a OS=Homo sapiens GN=CDC42 PE=3 SV=1					
\$96-3			1	1	8.90%	21272.62	6.73	tr A0A024R9T1 A0A024R9T1_HUMAN HCG39634, isoform CRA_a OS=Homo sapiens GN=hCG_39634 PE=3 SV=1					
\$96-4			1	1	7.20%	26528.26	7.52	tr B4E1U9 B4E1U9_HUMAN cDNA FLJ54776, highly similar to Cell division control protein 42 homolog OS=Homo sapiens PE=2 SV=1					
\$96-5			1	1	7.30%	26519.18	6.89	tr B7ZAY4 B7ZAY4_HUMAN cDNA, FLJ79348, highly similar to Cell division control protein 42 homolog OS=Homo sapiens PE=2 SV=1					
\$96-6			1	1	7.30%	26579.19	6.44	tr B4DMH5 B4DMH5_HUMAN cDNA FLJ55107, highly similar to Cell division control protein 42 homolog OS=Homo sapiens PE=2 SV=1					
	R16062_1_KIAA,19 951	K.NVFDEAILAALEPPEPK.K	1854.0929	0.9249	3	1	4.1327	0.5197	1150.2	1 30 64	4	1	6
\$97-1			1	1	2.17%	85697.56	5.9	sp P06396 GELS_HUMAN Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1					
\$97-2			1	1	2.27%	82525.62	5.43	tr A0A0A0MS51 A0A0A0MS51_HUMAN Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1					
\$97-3			1	1	2.22%	84745.33	5.57	tr A0A0A0MT01 A0A0A0MT01_HUMAN Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1					
\$97-4			1	1	2.22%	84766.38	5.57	tr B7Z6N2 B7Z6N2_HUMAN cDNA FLJ56154, highly similar to Gelsolin OS=Homo sapiens PE=2 SV=1					
\$97-5			1	1	2.47%	75751.99	5.56	tr B7Z4U6 B7Z4U6_HUMAN cDNA FLJ55803, highly similar to					

\$97-6																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			</
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\$100-6		1	1	5.69%	14052.6	11.34	tr B4DEB1 B4DEB1_HUMAN Histone H3 OS=Homo sapiens GN=H3F3A PE=1 SV=1										
\$100-7		1	1	5.15%	15430.11	11.27	tr Q5TEC6 Q5TEC6_HUMAN Histone H3 OS=Homo sapiens GN=HIST2H3PS2 PE=1 SV=1										
\$100-8		1	1	5.15%	15327.92	11.27	tr B2R4P9 B2R4P9_HUMAN Histone H3 OS=Homo sapiens GN=H3F3A PE=2 SV=1										
\$100-9		1	1	5.15%	15313.85	11.26	tr B2R6Y1 B2R6Y1_HUMAN Histone H3 OS=Homo sapiens PE=2 SV=1										
\$100-10		1	1	4.64%	16621.42	11.84	tr K7ES00 K7ES00_HUMAN Histone H3.3 (Fragment) OS=Homo sapiens GN=H3F3B PE=1 SV=1										
\$100-11		1	1	5.30%	14914.48	11.29	tr K7EK07 K7EK07_HUMAN Histone H3 (Fragment) OS=Homo sapiens GN=H3F3B PE=1 SV=1										
\$100-12		1	1	7.61%	10334.07	11.82	tr K7EMV3 K7EMV3_HUMAN Histone H3 OS=Homo sapiens GN=H3F3B PE=1 SV=1										
\$100-13		1	1	6.19%	12918.21	11.92	tr B4E380 B4E380_HUMAN Histone H3 OS=Homo sapiens PE=2 SV=1										
\$100-14		1	1	6.19%	12808.02	11.49	tr K7EP01 K7EP01_HUMAN Histone H3.3 OS=Homo sapiens GN=H3F3B PE=1 SV=1										
	R16062_1_KIAA,10 159	K.STELLIR.K	831.9803	0.4573	2	1		2.2893	0.2375	557.5	4 10 12	5.72	1	14			
\$101-1		1	1	52.17%	2564.98	4.68	tr A8CGI2 A8CGI2_HUMAN Ubiquitin C (Fragment) OS=Homo sapiens GN=UBC PE=2 SV=1										
	R16062_1_KIAA,10 387	K.TITLEVEPSDTI.-	1318.4523	-0.4787	2	1		2.5963	0.1048	429.2	12 11 22	3.57	1	1			
\$102-1		1	1	3.45%	28870.18	6.59	sp P00915 CAH1_HUMAN Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2										
\$102-2		1	1	3.45%	28870.18	6.59	tr V9HWE3 V9HWE3_HUMAN Carbonic anhydrase I, isoform CRA_a OS=Homo sapiens GN=HEL-S-11 PE=2 SV=1										
\$102-3		1	1	5.06%	19697.03	8.06	tr H0YBE2 H0YBE2_HUMAN Carbonic anhydrase 1 (Fragment) OS=Homo sapiens GN=CA1 PE=1 SV=1										
\$102-4		1	1	6.57%	15041.25	8.74	tr E5RJI8 E5RJI8_HUMAN Carbonic anhydrase 1 (Fragment) OS=Homo sapiens GN=CA1 PE=1 SV=6										
\$102-5		1	1	4.64%	21402.04	7.1	tr E5RFE7 E5RFE7_HUMAN Carbonic anhydrase 1 (Fragment) OS=Homo sapiens GN=CA1 PE=1 SV=1										
\$102-6		1	1	3.59%	27753.85	6.11	tr E5RHP7 E5RHP7_HUMAN Carbonic anhydrase 1 (Fragment) OS=Homo sapiens GN=CA1 PE=1 SV=1										
\$102-7		1	1	5.14%	19236.32	6.75	tr E5RH81 E5RH81_HUMAN Carbonic anhydrase 1 (Fragment) OS=Homo sapiens GN=CA1 PE=1 SV=6										
\$102-8		1	1	10.34%	9406.94	9.57	tr E5RJF6 E5RJF6_HUMAN Carbonic anhydrase 1 (Fragment) OS=Homo sapiens GN=CA1 PE=1 SV=1										
	R16062_1_KIAA,12	K.VLDALQAIK.T	971.176	-0.24	2	1		2.3457	0.3349	712.7	1 13 16	5.81	1	8			

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2							GN=TPSB2 PE=1 SV=2												
\$108-3			1	1	4.96%	31282.12	6.62	tr J3QTS8 J3QTS8_HUMAN Tryptase alpha/beta-1 OS=Homo sapiens GN=TPSAB1 PE=1 SV=1											
\$108-4			1	1	4.96%	31296.19	6.85	tr Q6NZY1 Q6NZY1_HUMAN TPSB2 protein OS=Homo sapiens GN=TPSB2 PE=2 SV=1											
\$108-5			1	1	5.09%	30488.1	6.62	tr Q6B051 Q6B051_HUMAN Tryptase alpha/beta 1 OS=Homo sapiens GN=TPSAB1 PE=2 SV=1											
\$108-6			1	1	5.09%	30713.46	6.18	tr Q86TM8 Q86TM8_HUMAN TPSAB1 protein OS=Homo sapiens GN=TPSAB1 PE=2 SV=1											
\$108-7			1	1	4.96%	31418.28	6.82	tr A0A087WUI4 A0A087WUI4_HUMAN Tryptase beta-2 OS=Homo sapiens GN=TPSB2 PE=1 SV=1											
\$108-8			1	1	4.79%	32576.47	6.82	tr A0A087X1U0 A0A087X1U0_HUMAN Tryptase beta-2 OS=Homo sapiens GN=TPSB2 PE=1 SV=1											
\$108-9			1	1	5.09%	30517.08	6.62	tr Q6FHB8 Q6FHB8_HUMAN TPSB2 protein (Fragment) OS=Homo sapiens GN=TPSB2 PE=2 SV=1											
\$108-10			1	1	5.09%	30491.1	6.58	tr Q96RZ6 Q96RZ6_HUMAN Tryptase I OS=Homo sapiens GN=tryptaseC PE=3 SV=1											
\$108-11			1	1	5.07%	30869.65	6.37	tr Q86UA5 Q86UA5_HUMAN TPSAB1 protein (Fragment) OS=Homo sapiens GN=TPSAB1 PE=2 SV=1											
\$108-12			1	1	6.57%	23895.27	5.96	tr A0A0C4DGM1 A0A0C4DGM1_HUMAN Tryptase alpha/beta-1 (Fragment) OS=Homo sapiens GN=TPSAB1 PE=1 SV=1											
	R16062_1_KIAA,6796	R.DSCQGDSGGPLVCK.V		1480.5471	0.5371	2	1		2.5367	0.3999	756.9	1 16 26	4.21	1	12				
\$109-1			1	1	3.14%	54305.86	5.55	sp P04004 VTNC_HUMAN Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1											
\$109-2			1	1	3.14%	54305.86	5.55	tr D9ZGG2 D9ZGG2_HUMAN Vitronectin OS=Homo sapiens GN=VTN PE=4 SV=1											
\$109-3			1	1	7.01%	23605.07	4.53	tr B7Z553 B7Z553_HUMAN cDNA FLJ51266, highly similar to Vitronectin OS=Homo sapiens PE=2 SV=1											
	R16062_1_KIAA,18194	R.DVWGIEGPIDAAFTR.I		1647.8126	0.4856	2	1		2.2114	0.2747	466.4	1 14 28	4.03	1	3				
\$110-1			1	1	2.97%	75873.42	5.42	sp P08133 ANXA6_HUMAN Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3											
\$110-2			1	1	3.66%	61852.41	5.36	tr B7Z582 B7Z582_HUMAN Annexin OS=Homo sapiens PE=2 SV=1											
\$110-3			1	1	6.06%	36962.98	5.62	tr E7EMC6 E7EMC6_HUMAN Annexin OS=Homo sapiens GN=ANXA6 PE=1 SV=1											
\$110-4			1	1	6.06%	36998.98	5.69	tr Q6ZP35 Q6ZP35_HUMAN Annexin OS=Homo sapiens PE=2 SV=1											
	R16062_1_KIAA,16773	R.EDAQVA AEILEIADTPSGDK.T		2073.2011	0.8011	2	1		2.606	0.4502	972.6	1 21 38	3.71	1	4				

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6						CRA_i OS=Homo sapiens GN=TPM1 PE=2 SV=1
\$117-7	1	1	4.03%	28747.31	4.78	tr H7BYY1 H7BYY1_HUMAN Tropomyosin 1 (Alpha), isoform CRA_m OS=Homo sapiens GN=TPM1 PE=1 SV=1
\$117-8	1	1	3.64%	31753.14	4.85	tr B7Z596 B7Z596_HUMAN Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=1
\$117-9	1	1	4.03%	28521.96	4.67	tr V9HW56 V9HW56_HUMAN Epididymis secretory protein Li 108 OS=Homo sapiens GN=HEL-S-108 PE=2 SV=1
\$117-10	1	1	3.07%	37453.09	4.67	tr Q6ZN40 Q6ZN40_HUMAN Tropomyosin 1 (Alpha), isoform CRA_f OS=Homo sapiens GN=TPM1 PE=1 SV=1
\$117-11	1	1	4.31%	27175.7	4.71	tr Q5HYB6 Q5HYB6_HUMAN Epididymis luminal protein 189 OS=Homo sapiens GN=DKFZp686J1372 PE=1 SV=1
\$117-12	1	1	3.52%	32866.03	4.69	tr A0A0K0K1I0 A0A0K0K1I0_HUMAN Epididymis secretory protein Li 265 OS=Homo sapiens GN=HEL-S-265 PE=2 SV=1
\$117-13	1	1	3.30%	34402.47	5.35	tr Q59GR8 Q59GR8_HUMAN TPM1 protein variant (Fragment) OS=Homo sapiens PE=2 SV=1
\$117-14	1	1	5.59%	20621.09	4.61	tr K7ENT6 K7ENT6_HUMAN Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens GN=TPM4 PE=1 SV=1
\$117-15	1	1	3.52%	32677.74	4.7	tr A0A024R5W6 A0A024R5W6_HUMAN Tropomyosin 1 (Alpha), isoform CRA_a OS=Homo sapiens GN=TPM1 PE=3 SV=1
\$117-16	1	1	3.52%	33026.07	4.65	tr A7XZE4 A7XZE4_HUMAN Beta tropomyosin isoform OS=Homo sapiens GN=TPM2b PE=2 SV=1
\$117-17	1	1	10.53%	11017.31	4.8	tr D6R904 D6R904_HUMAN Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1
\$117-18	1	1	3.51%	33222.68	4.73	tr J3KN67 J3KN67_HUMAN Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1
\$117-19	1	1	5.88%	19306.65	4.76	tr K7ERG3 K7ERG3_HUMAN Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens GN=TPM4 PE=1 SV=1
\$117-20	1	1	4.03%	28579.97	4.74	tr H0YK48 H0YK48_HUMAN Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=1
\$117-21	1	1	6.33%	17833.02	4.8	tr B4DTK3 B4DTK3_HUMAN cDNA FLJ57891, highly similar to Tropomyosin beta chain OS=Homo sapiens PE=2 SV=1
\$117-22	1	1	14.71%	8014.11	4.82	tr H0YL80 H0YL80_HUMAN Tropomyosin alpha-1 chain (Fragment) OS=Homo sapiens GN=TPM1 PE=1 SV=1
\$117-23	1	1	1.38%	82419.73	4.9	tr M1VPF4 M1VPF4_HUMAN Tyrosine-protein kinase receptor OS=Homo sapiens GN=TPM3-ROS1 PE=2 SV=1
\$117-24	1	1	4.08%	28385.68	4.74	tr D9YZV7 D9YZV7_HUMAN Tropomyosin 1 (Alpha) isoform 6 OS=Homo sapiens GN=TPM1 PE=3 SV=1
\$117-25	1	1	5.32%	21833.55	4.78	tr B4DGC2 B4DGC2_HUMAN cDNA FLJ56690, highly similar to Tropomyosin beta chain OS=Homo sapiens PE=2 SV=1
\$117-26	1	1	4.12%	28420.27	4.89	tr Q15657 Q15657_HUMAN Tropomyosin isoform OS=Homo sapiens PE=2 SV=1

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	R16062_1_KIAA,12 069	R.KIQDLNLSRQAK.A	1414.636	-0.68	2	1	2.811	0.1702	284.6	5 12 22	9.99	1	2
\$119- 1	1	1	1.36%	74139.71	6.57	sp P02545 LMNA_HUMAN Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1							
\$119- 2	1	1	1.85%	55638.35	6.24	tr Q3BDU5 Q3BDU5_HUMAN Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1							
\$119- 3	1	1	1.94%	53197.58	6.03	tr Q8N519 Q8N519_HUMAN LMNA protein OS=Homo sapiens PE=2 SV=1							
\$119- 4	1	1	4.95%	20796.48	6.04	tr H0YAB0 H0YAB0_HUMAN Prelamin-A/C (Fragment) OS=Homo sapiens GN=LMNA PE=1 SV=1							
\$119- 5	1	1	1.88%	55043.76	6.51	tr Q5I6Y5 Q5I6Y5_HUMAN Lamin A/C transcript variant 1 OS=Homo sapiens GN=LMNA PE=2 SV=1							
\$119- 6	1	1	1.57%	65116.95	6.4	tr W8QEH3 W8QEH3_HUMAN Lamin A/C OS=Homo sapiens GN=LMNA PE=3 SV=1							
\$119- 7	1	1	1.83%	55762.49	6.55	tr Q5TCI8 Q5TCI8_HUMAN Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1							
	R16062_1_KIAA,11 764	R.LADALQELR.A	1029.1724	1.0134	2	1	2.8909	0.2881	1200.8	1 15 16	4.37	1	7
\$120- 1	1	1	7.84%	35619.67	8.42	sp Q9H7P6 MB12B_HUMAN Multivesicular body subunit 12B OS=Homo sapiens GN=MVB12B PE=1 SV=2							
\$120- 2	1	1	7.84%	35619.67	8.42	tr A0A024R8B8 A0A024R8B8_HUMAN Chromosome 9 open reading frame 28, isoform CRA_a OS=Homo sapiens GN=C9orf28 PE=4 SV=1							
\$120- 3	1	1	8.22%	33830.34	5.69	tr B7Z1P9 B7Z1P9_HUMAN cDNA FLJ53722 OS=Homo sapiens PE=2 SV=1							
\$120- 4	1	1	11.68%	24052.64	9.69	tr B7Z4X0 B7Z4X0_HUMAN cDNA FLJ55114 OS=Homo sapiens PE=2 SV=1							
\$120- 5	1	1	13.30%	21225.17	8.72	tr Q9H7N7 Q9H7N7_HUMAN FLJ00031 protein (Fragment) OS=Homo sapiens GN=FLJ00031 PE=2 SV=1							
	R16062_1_KIAA,15 795	R.NHDSSQPTTPSQSSAASTPAPNL PR.H	2549.6528	0.5638	2	1	2.3006	0.1551	191.5	3 12 48	6.74	1	5
\$121- 1	1	1	2.06%	66248.64	8.22	sp Q5JTV8 TOIP1_HUMAN Torsin-1A-interacting protein 1 OS=Homo sapiens GN=TOR1AIP1 PE=1 SV=2							
\$121- 2	1	1	4.05%	33639.61	7.9	tr H0Y4R4 H0Y4R4_HUMAN Torsin-1A-interacting protein 1 (Fragment) OS=Homo sapiens GN=TOR1AIP1 PE=1 SV=1							
\$121- 3	1	1	2.60%	52406.24	6.59	tr A0A0A0MSK5 A0A0A0MSK5_HUMAN Torsin-1A-interacting protein 1 OS=Homo sapiens GN=TOR1AIP1 PE=1 SV=1							
\$121- 4	1	1	2.00%	67822.29	7.71	tr J3KN66 J3KN66_HUMAN Torsin-1A-interacting protein 1 OS=Homo sapiens GN=TOR1AIP1 PE=1 SV=1							
	R16062_1_KIAA,15 553	R.SQPAILLTAAAR.D	1254.5042	-0.3248	2	1	2.3921	0.3108	558.3	1 15 22	9.47	1	4

\$122-1		1	1	17.48%	11536.25	6.19	tr Q562M3 Q562M3_HUMAN Actin-like protein (Fragment) OS=Homo sapiens GN=ACT PE=3 SV=1								
	R16062_1_KIAA,12304	R.VAPEEHPVLLTQAPLNPK.A	1954.2589	0.3749	2	1		2.2019	0.1597	420.2	116 34	5.4	1	1	
\$123-1		1	1	1.35%	103057.69	5.25	sp P12814 ACTN1_HUMAN Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2								
\$123-2		1	1	1.32%	104854.22	5.27	sp O43707 ACTN4_HUMAN Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2								
\$123-3		1	1	1.35%	103057.69	5.25	tr A0A024R694 A0A024R694_HUMAN Actinin, alpha 1, isoform CRA_a OS=Homo sapiens GN=ACTN1 PE=4 SV=1								
\$123-4		1	1	2.25%	61575.38	5.05	tr B4DFY0 B4DFY0_HUMAN cDNA FLJ53313, highly similar to Alpha-actinin-1 OS=Homo sapiens PE=2 SV=1								
\$123-5		1	1	1.46%	94783.8	5.47	tr B7Z565 B7Z565_HUMAN cDNA FLJ54739, highly similar to Alpha-actinin-1 OS=Homo sapiens PE=2 SV=1								
\$123-6		1	1	13.95%	10195.33	5.41	tr Q5ZEZ4 Q5ZEZ4_HUMAN Alpha-actinin 1 (Fragment) OS=Homo sapiens GN=ACTN1 PE=2 SV=1								
\$123-7		1	1	4.04%	34320.38	5.14	tr H7C5W8 H7C5W8_HUMAN Alpha-actinin-1 (Fragment) OS=Homo sapiens GN=ACTN1 PE=1 SV=1								
\$123-8		1	1	4.78%	28762.32	4.94	tr H0YJW3 H0YJW3_HUMAN Alpha-actinin-1 (Fragment) OS=Homo sapiens GN=ACTN1 PE=1 SV=1								
\$123-9		1	1	1.46%	94825.88	5.47	tr H9KV75 H9KV75_HUMAN Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=1								
\$123-10		1	1	1.89%	73619.77	5.16	tr Q96BG6 Q96BG6_HUMAN ACTN4 protein (Fragment) OS=Homo sapiens GN=ACTN4 PE=2 SV=2								
\$123-11		1	1	5.80%	24263.23	5.37	tr H0YJ11 H0YJ11_HUMAN Alpha-actinin-1 (Fragment) OS=Homo sapiens GN=ACTN1 PE=1 SV=1								
\$123-12		1	1	2.30%	59564.47	4.82	tr F5GXS2 F5GXS2_HUMAN Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2								
\$123-13		1	1	3.51%	39001.7	5.1	tr H7C144 H7C144_HUMAN Alpha-actinin-4 (Fragment) OS=Homo sapiens GN=ACTN4 PE=1 SV=1								
\$123-14		1	1	2.54%	54281.13	4.98	tr B3KUX9 B3KUX9_HUMAN cDNA FLJ40884 fis, clone UTERU2000607, highly similar to Alpha-actinin-1 OS=Homo sapiens PE=2 SV=1								
\$123-15		1	1	3.88%	35411.97	5.01	tr A1L0V1 A1L0V1_HUMAN ACTN1 protein (Fragment) OS=Homo sapiens GN=ACTN1 PE=2 SV=1								
\$123-16		1	1	2.01%	67142.84	5.83	tr B7Z2W3 B7Z2W3_HUMAN cDNA FLJ54432, highly similar to Alpha-actinin-1 OS=Homo sapiens PE=2 SV=1								
	R16062_1_KIAA,19609	R.VGWEQLLTTIAR.T	1387.6091	0.0821	2	1		2.4487	0.3763	707.1	113 22	5.97	1	16	
\$124-1		1	1	7.28%	28048.49	8.25	sp P35270 SPRE_HUMAN Sepiapterin reductase OS=Homo sapiens GN=SPR PE=1 SV=1								

\$124-2	tr B4DSF0 B4DSF0_HUMAN cDNA FLJ56734, moderately similar													
	11 to Sepiapterin reductase (EC 1.1.1.153) OS=Homo sapiens PE=2 SV=1													
R16062_1_KIAA,20222	R.VPADLGAEAGLQQLLGALR.E	1893.1771	0.6201	2	1	3.4054	0.5128	1101.3	120 36	4.37	1	2		