

Mascot Search Results

User : Joe Gray

Email : joe.gray@ncl.ac.uk

Search title : JG_3_0001.dat - SpecView

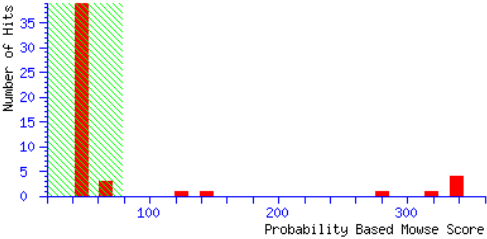
Database : MSDB 20060831 (3239079 sequences; 1079594700 residues)

Timestamp : 12 Jan 2007 at 12:24:13 GMT

Top Score : 338 for **AAA51748**, HUMAPOAIV NID: - Homo sapiens

Probability Based Mowse Score

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 78 are significant (p<0.05).



Protein Summary Report

		Help
	Significance threshold p<	Max. number of hits

Index

Accession	Mass	Score	Description
1. AAA51748	43358	338	HUMAPOAIV NID: - Homo sapiens
2. CAB58685	43507	335	SEQUENCE 1 FROM PATENT W09315198.- unidentified.
3. AAQ91809	45371	332	AY422950 NID: - Homo sapiens
4. AAA96731	45353	332	HUMAPOA4A NID: - Homo sapiens
5. LPHUA4	45307	315	apolipoprotein A-IV precursor [validated] - human
6. Q13784_HUMAN	28141	280	APOA4 protein (Fragment).- Homo sapiens (Human).
7. A47141	46510	139	apolipoprotein A-IV I isoform - baboon (fragment)
8. S29565	49846	119	apolipoprotein A-IV - crab-eating macaque
9. C87410	70844	64	iolC protein [imported] - Caulobacter crescentus
10. Q3SQM9_NITWN	41297	62	Acyl-CoA dehydrogenase (EC 1.3.99.2).- Nitrobacter winogradskyi (strain Nb-255 / ATCC 25391).
11. I54248	10612	62	apolipoprotein A-IV - chimpanzee (fragment)
12. Q6WAZ7_TRYCR	82415	56	C71 surface protein.- Trypanosoma cruzi.
13. Q3XUS9_9PROT	61027	56	Coenzyme B12-binding:Radical SAM.- Magnetococcus sp. MC-1.
14. Q4USB5_XANC8	13788	56	HrpB2 protein.- Xanthomonas campestris pv. campestris (strain 8004).
15. Q4D9P5_TRYCR	126270	54	DNA-directed RNA polymerase III subunit, putative (EC 2.7.7.6).- Trypanosoma cruzi.
16. C83690	22489	53	hypothetical protein BH0323 [imported] - Bacillus halodurans (strain C-125)
17. Q56EH5_9CAUD	36302	52	Hypothetical protein PHG310RF188c.- Aeromonas phage 31.
18. Q4MZD6_THEPA	62104	52	Hypothetical protein.- Theileria parva.
19. Q4JCL5_SULAC	24648	52	Conserved protein.- Sulfolobus acidocaldarius.
20. Q8SPT5_MACMU	16793	51	Growth differentiation factor 9 (Fragment).- Macaca mulatta (Rhesus macaque).
21. A44277	64504	51	nonstructural protein NS1 - bluetongue virus (serotype 2)
22. T50803	83475	51	hypothetical protein T30N20_210 - Arabidopsis thaliana
23. Q94BQ3_ARATH	83778	51	Hypothetical protein At5g10940.- Arabidopsis thaliana (Mouse-ear cress).
24. Q6Q539_YEAST	24211	50	YDR226W.- Saccharomyces cerevisiae (Baker's yeast).
25. Q2BL66_9GAMM	52033	50	Argininosuccinate lyase.- Oceanospirillum sp. MED92.

26.	Q4IVR0_AZ0VI	36505	50	Regulatory protein, ArsR.- Azotobacter vinelandii AvOP.
27.	Q1RSK3_MEDTR	105088	50	Zinc finger, RING-type; Transcription factor jumonji, jmjC.- Medicago truncatula (Barrel medic).
28.	Q1ZTR3_9VIBR	31022	50	Putative putative phospholipid biosynthesis acyltransferase.- Vibrio angustum S14.
29.	Q390G0_BURSS	100380	50	ATP-dependent transcriptional regulator, MaltT-like, LuxR family.- Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760 / NCIB 9086 / R18194))
30.	Q8TA35_HETGL	25472	50	Dorsal gland cell protein Hgg-26 (Fragment).- Heterodera glycines (Soybean cyst nematode worm).
31.	Q7XUX8_ORYSA	41458	50	OSJNBa0027G07.11 protein.- Oryza sativa (japonica cultivar-group).
32.	Q6IQ22_HUMAN	11751	50	RAB12, member RAS oncogene family.- Homo sapiens (Human).
33.	AH3404	20696	49	hypothetical protein BMEI1222 [imported] - Brucella melitensis (strain 16M)
34.	AAN43115	54614	49	AE005674 NID: - Shigella flexneri 2a str. 301
35.	Q2RNF9_RHORT	80918	49	Malate dehydrogenase (EC 1.1.1.40) (EC 2.3.1.8).- Rhodospirillum rubrum (strain ATCC 11170 / NCIB 8255).
36.	T08180	65798	49	PF20 protein, microtubule-associated - Chlamydomonas reinhardtii
37.	Q7V0J9_PROMP	38698	48	Possible dTDP-glucose 4,6-dehydratase (EC 4.2.1.46).- Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
38.	Q5Z147_CHICK	101099	48	Hypothetical protein.- Gallus gallus (Chicken).
39.	Q4DLZ9_TRYCR	19461	48	Protein tyrosine phosphatase-like protein, putative.- Trypanosoma cruzi.
40.	Q39YY1_GEOMG	16521	48	Putative PAS/PAC sensor protein.- Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210).
41.	Q9TUL8_HORSE	42919	48	Matrix metalloproteinase-2 (Fragment).- Equus caballus (Horse).
42.	Q3M485_ANAVT	42516	48	Hydrogenase formation HypD protein.- Anabaena variabilis (strain ATCC 29413 / PCC 7937).
43.	Q5NVL1_PONPY	79482	48	Hypothetical protein DKFZp459N0220 (Fragment).- Pongo pygmaeus (Orangutan).
44.	Q4AI58_9CHLB	37062	48	Cell shape determining protein MreB/Mrl.- Chlorobium phaeobacteroides BS1.
45.	Q2HUK6_MEDTR	39508	47	Mitochondrial substrate carrier.- Medicago truncatula (Barrel medic).
46.	Q5ZF44_MEDTR	39616	47	Mitochondrial phosphate translocator.- Medicago truncatula (Barrel medic).
47.	Q5R9R8_PONPY	72095	47	Hypothetical protein DKFZp469P0412.- Pongo pygmaeus (Orangutan).
48.	Q4CFZ5_CLOTM	11661	47	Hypothetical protein.- Clostridium thermocellum ATCC 27405.
49.	Q2DM63_9DELT	19010	47	Hypothetical protein precursor.- Geobacter uraniumreducens Rf4.
50.	Q7P987_RICSI	73246	47	Propionyl-CoA carboxylase alpha chain.- Rickettsia sibirica 246.

Results List

1.	AAA51748	Mass: 43358	Score: 338	Expect: 5.1e-28	Queries matched: 31
HUMAPOAIV NID: - Homo sapiens					
	Observed	Mr(expt)	Mr(calc)	Delta	Start End Miss Peptide
	975.4483	974.4410	974.5032	-0.0623	236 - 244 0 R.ISASAEELR.Q
	983.4562	982.4489	982.5447	-0.0958	247 - 255 0 R.LAPLAEDVR.G
	1076.4495	1075.4422	1075.5338	-0.0916	331 - 339 0 K.VNSFFSTFK.E
	1083.4282	1082.4209	1082.5284	-0.1075	181 - 189 0 R.LTPYADEFK.V
	1104.4679	1103.4606	1103.5611	-0.1005	115 - 123 0 R.LEPYADQLR.T
	1132.5159	1131.5087	1131.6149	-0.1062	135 - 143 1 R.RQLTPYAQR.M
	1196.4419	1195.4346	1195.5509	-0.1163	287 - 296 0 R.VEPYGENFNK.A
	1215.5637	1214.5564	1214.6441	-0.0877	297 - 306 0 K.ALVQQMEQLR.T
	1231.5737	1230.5665	1230.6390	-0.0726	297 - 306 0 K.ALVQQMEQLR.T + Oxidation (M)
	1235.5752	1234.5679	1234.6669	-0.0990	93 - 103 0 R.LLPHANEVSQK.I
	1258.5780	1257.5707	1257.6677	-0.0970	192 - 201 1 K.IDQTVEELRR.S
	1287.5711	1286.5638	1286.6579	-0.0940	124 - 134 0 R.TQVNTQAEQLR.R
	1300.6026	1299.5954	1299.6782	-0.0829	170 - 180 1 K.IDQNVEELKGR.L
	1310.5953	1309.5880	1309.6918	-0.1038	181 - 191 1 R.LTPYADEFKVK.I
	1311.6184	1310.6111	1310.6982	-0.0871	60 - 70 0 K.LVPFATELHER.L
	1319.5820	1318.5747	1318.6557	-0.0810	329 - 339 1 R.DKVNSFFSTFK.E
	1350.5619	1349.5546	1349.6463	-0.0917	202 - 213 0 R.SLAPYAQDTQEK.L
	1352.5712	1351.5639	1351.6520	-0.0881	286 - 296 1 R.RVEPYGENFNK.A
	1407.6373	1406.6300	1406.7041	-0.0741	46 - 58 0 K.LGEVNTYAGDLQK.K
	1439.7198	1438.7125	1438.7932	-0.0807	59 - 70 1 K.KLVPFATELHER.L
	1443.6886	1442.6813	1442.7590	-0.0776	124 - 135 1 R.TQVNTQAEQLRR.Q
	1558.7275	1557.7202	1557.7973	-0.0771	214 - 226 0 K.LNHQLEGLTFQMK.K
	1574.7196	1573.7123	1573.7922	-0.0799	214 - 226 0 K.LNHQLEGLTFQMK.K + Oxidation (M)
	1634.7576	1633.7503	1633.8311	-0.0808	32 - 45 0 K.SELTQQLNALFQDK.L
	1805.8453	1804.8380	1804.9107	-0.0727	309 - 325 0 K.LGPHAGDVEGHSFLEK.D
	1927.9091	1926.9019	1926.9435	-0.0416	268 - 284 0 K.SLAELGGHLDQQVEEFR.R
	1993.9450	1992.9377	1992.9864	-0.0487	150 - 167 0 R.ENADSLQASLRPHADELK.A
	2084.0093	2083.0020	2083.0446	-0.0426	268 - 285 1 K.SLAELGGHLDQQVEEFR.R
	2193.1061	2192.0988	2192.1185	-0.0197	150 - 169 1 R.ENADSLQASLRPHADELKAK.I
	2362.2237	2361.2164	2361.2400	-0.0236	147 - 167 1 R.VLRENADSLQASLRPHADELK.A
	2890.4720	2889.4647	2889.4330	0.0317	202 - 226 1 R.SLAPYAQDTQEKLNHGLEGLTFQMK.K
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 976.4208, 980.4021, 1065.9443, 1218.5811, 1297.5441, 1336.3908, 1427.4641, 1485.7681, 1499.7430, 1508.6825, 1585.8063, 1656.7520, 1707.7763, 1834.8681, 1976.9265, 2045.0624, 2067.6716, 2069.7862, 2211.0997					
2.	CAB58685	Mass: 43507	Score: 335	Expect: 1e-27	Queries matched: 31
SEQUENCE 1 FROM PATENT W09315198.- unidentified.					
	Observed	Mr(expt)	Mr(calc)	Delta	Start End Miss Peptide

975.4483	974.4410	974.5032	-0.0623	237	-	245	0	R.ISASAEELR.Q
983.4562	982.4489	982.5447	-0.0958	248	-	256	0	R.LAPLAEDVR.G
1076.4495	1075.4422	1075.5338	-0.0916	332	-	340	0	K.VNSFFSTFK.E
1083.4282	1082.4209	1082.5284	-0.1075	182	-	190	0	R.LTPYADEFK.V
1104.4679	1103.4606	1103.5611	-0.1005	116	-	124	0	R.LEPYADQLR.T
1132.5159	1131.5087	1131.6149	-0.1062	136	-	144	1	R.RQLTPYAQR.M
1196.4419	1195.4346	1195.5509	-0.1163	288	-	297	0	R.VEPYGENFNK.A
1215.5637	1214.5564	1214.6441	-0.0877	298	-	307	0	K.ALVQQMEQLR.Q
1231.5737	1230.5665	1230.6390	-0.0726	298	-	307	0	K.ALVQQMEQLR.Q + Oxidation (M)
1235.5752	1234.5679	1234.6669	-0.0990	94	-	104	0	R.LLPHANEVSQK.I
1258.5780	1257.5707	1257.6677	-0.0970	193	-	202	1	K.IDQTVEELRR.S
1287.5711	1286.5638	1286.6579	-0.0940	125	-	135	0	R.TQVNTQAEQLR.R
1300.6026	1299.5954	1299.6782	-0.0829	171	-	181	1	K.IDQNVEELKGR.L
1310.5953	1309.5880	1309.6918	-0.1038	182	-	192	1	R.LTPYADEFKVK.I
1311.6184	1310.6111	1310.6982	-0.0871	61	-	71	0	K.LVPFATELHER.L
1319.5820	1318.5747	1318.6557	-0.0810	330	-	340	1	R.DKVNSTFFSTFK.E
1350.5619	1349.5546	1349.6463	-0.0917	203	-	214	0	R.SLAPYAQDTQEK.L
1352.5712	1351.5639	1351.6520	-0.0881	287	-	297	1	R.RVEPYGENFNK.A
1407.6373	1406.6300	1406.7041	-0.0741	47	-	59	0	K.LGEVNTYAGDLQK.K
1439.7198	1438.7125	1438.7932	-0.0807	60	-	71	1	K.KLVPFATELHER.L
1443.6886	1442.6813	1442.7590	-0.0776	125	-	136	1	R.TQVNTQAEQLRR.Q
1558.7275	1557.7202	1557.7973	-0.0771	215	-	227	0	K.LNHQLEGLTFQMK.K
1574.7196	1573.7123	1573.7922	-0.0799	215	-	227	0	K.LNHQLEGLTFQMK.K + Oxidation (M)
1634.7576	1633.7503	1633.8311	-0.0808	33	-	46	0	K.SELTQQLNALFQDK.L
1805.8453	1804.8380	1804.9107	-0.0727	310	-	326	0	K.LGPHAGDVEGHLSFLEK.D
1927.9091	1926.9019	1926.9435	-0.0416	269	-	285	0	K.SLAELGGHLDQQVEEFR.R
1993.9450	1992.9377	1992.9864	-0.0487	151	-	168	0	R.ENADSLQASLRPHADELK.A
2084.0093	2083.0020	2083.0446	-0.0426	269	-	286	1	K.SLAELGGHLDQQVEEFR.R
2193.1061	2192.0988	2192.1185	-0.0197	151	-	170	1	R.ENADSLQASLRPHADELKAK.I
2362.2237	2361.2164	2361.2400	-0.0236	148	-	168	1	R.VLRENADSLQASLRPHADELK.A
2890.4720	2889.4647	2889.4330	0.0317	203	-	227	1	R.SLAPYAQDTQEKLNHQLEGLTFQMK.K
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 976.4208, 980.4021, 1065.9443, 1218.5811, 1297.5441, 1336.3908, 1427.4641, 1485.7681, 1499.7430, 1508.6825, 1585.8063, 1656.7520, 1707.7763, 1834.8681, 1976.9265, 2045.0624, 2067.6716, 2069.7862, 2211.0997								

3. [AAQ91809](#) Mass: 45371 Score: **332** Expect: 2e-27 Queries matched: 31

AY422950 NID: - Homo sapiens								
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
975.4483	974.4410	974.5032	-0.0623	256	-	264	0	R.ISASAEELR.Q
983.4562	982.4489	982.5447	-0.0958	267	-	275	0	R.LAPLAEDVR.G
1076.4495	1075.4422	1075.5338	-0.0916	351	-	359	0	K.VNSFFSTFK.E
1083.4282	1082.4209	1082.5284	-0.1075	201	-	209	0	R.LTPYADEFK.V
1104.4679	1103.4606	1103.5611	-0.1005	135	-	143	0	R.LEPYADQLR.T
1132.5159	1131.5087	1131.6149	-0.1062	155	-	163	1	R.RQLTPYAQR.M
1196.4419	1195.4346	1195.5509	-0.1163	307	-	316	0	R.VEPYGENFNK.A
1215.5637	1214.5564	1214.6441	-0.0877	317	-	326	0	K.ALVQQMEQLR.Q
1231.5737	1230.5665	1230.6390	-0.0726	317	-	326	0	K.ALVQQMEQLR.Q + Oxidation (M)
1235.5752	1234.5679	1234.6669	-0.0990	113	-	123	0	R.LLPHANEVSQK.I
1258.5780	1257.5707	1257.6677	-0.0970	212	-	221	1	K.IDQTVEELRR.S
1287.5711	1286.5638	1286.6579	-0.0940	144	-	154	0	R.TQVNTQAEQLR.R
1300.6026	1299.5954	1299.6782	-0.0829	190	-	200	1	K.IDQNVEELKGR.L
1310.5953	1309.5880	1309.6918	-0.1038	201	-	211	1	R.LTPYADEFKVK.I
1311.6184	1310.6111	1310.6982	-0.0871	80	-	90	0	K.LVPFATELHER.L
1319.5820	1318.5747	1318.6557	-0.0810	349	-	359	1	R.DKVNSTFFSTFK.E
1350.5619	1349.5546	1349.6463	-0.0917	222	-	233	0	R.SLAPYAQDTQEK.L
1352.5712	1351.5639	1351.6520	-0.0881	306	-	316	1	R.RVEPYGENFNK.A
1407.6373	1406.6300	1406.7041	-0.0741	66	-	78	0	K.LGEVNTYAGDLQK.K
1439.7198	1438.7125	1438.7932	-0.0807	79	-	90	1	K.KLVPFATELHER.L
1443.6886	1442.6813	1442.7590	-0.0776	144	-	155	1	R.TQVNTQAEQLRR.Q
1558.7275	1557.7202	1557.7973	-0.0771	234	-	246	0	K.LNHQLEGLTFQMK.K
1574.7196	1573.7123	1573.7922	-0.0799	234	-	246	0	K.LNHQLEGLTFQMK.K + Oxidation (M)
1634.7576	1633.7503	1633.8311	-0.0808	52	-	65	0	K.SELTQQLNALFQDK.L
1805.8453	1804.8380	1804.9107	-0.0727	329	-	345	0	K.LGPHAGDVEGHLSFLEK.D
1927.9091	1926.9019	1926.9435	-0.0416	288	-	304	0	K.SLAELGGHLDQQVEEFR.R
1993.9450	1992.9377	1992.9864	-0.0487	170	-	187	0	R.ENADSLQASLRPHADELK.A
2084.0093	2083.0020	2083.0446	-0.0426	288	-	305	1	K.SLAELGGHLDQQVEEFR.R
2193.1061	2192.0988	2192.1185	-0.0197	170	-	189	1	R.ENADSLQASLRPHADELKAK.I
2362.2237	2361.2164	2361.2400	-0.0236	167	-	187	1	R.VLRENADSLQASLRPHADELK.A
2890.4720	2889.4647	2889.4330	0.0317	222	-	246	1	R.SLAPYAQDTQEKLNHQLEGLTFQMK.K
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 976.4208, 980.4021, 1065.9443, 1218.5811, 1297.5441, 1336.3908, 1427.4641, 1485.7681, 1499.7430, 1508.6825, 1585.8063, 1656.7520, 1707.7763, 1834.8681, 1976.9265, 2045.0624, 2067.6716, 2069.7862, 2211.0997								

4. [AAA96731](#) Mass: 45353 Score: 332 Expect: 2e-27 Queries matched: 31

HUMAPOA4A NID: - Homo sapiens

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
975.4483	974.4410	974.5032	-0.0623	256	- 264	0	R.ISASAEELR.Q
983.4562	982.4489	982.5447	-0.0958	267	- 275	0	R.LAPLAEDVR.G
1076.4495	1075.4422	1075.5338	-0.0916	351	- 359	0	K.VNSFFSTFK.E
1083.4282	1082.4209	1082.5284	-0.1075	201	- 209	0	R.LTPYADEFK.V
1104.4679	1103.4606	1103.5611	-0.1005	135	- 143	0	R.LEPYADQLR.T
1132.5159	1131.5087	1131.6149	-0.1062	155	- 163	1	R.RQLTPYAQR.M
1196.4419	1195.4346	1195.5509	-0.1163	307	- 316	0	R.VEPYGENFNK.A
1215.5637	1214.5564	1214.6441	-0.0877	317	- 326	0	K.ALVQQMEQLR.T
1231.5737	1230.5665	1230.6390	-0.0726	317	- 326	0	K.ALVQQMEQLR.T + Oxidation (M)
1235.5752	1234.5679	1234.6669	-0.0990	113	- 123	0	R.LLPANEVSQK.I
1258.5780	1257.5707	1257.6677	-0.0970	212	- 221	1	K.IDQTVEELRR.S
1287.5711	1286.5638	1286.6579	-0.0940	144	- 154	0	R.TQVNTQAEQLR.R
1300.6026	1299.5954	1299.6782	-0.0829	190	- 200	1	K.IDQNVEELKGR.L
1310.5953	1309.5880	1309.6918	-0.1038	201	- 211	1	R.LTPYADEFKVK.I
1311.6184	1310.6111	1310.6982	-0.0871	80	- 90	0	K.LVPFATELHER.L
1319.5820	1318.5747	1318.6557	-0.0810	349	- 359	1	R.DKVSFFSTFK.E
1350.5619	1349.5546	1349.6463	-0.0917	222	- 233	0	R.SLAPYAQDTQEK.L
1352.5712	1351.5639	1351.6520	-0.0881	306	- 316	1	R.RVEPYGENFNK.A
1407.6373	1406.6300	1406.7041	-0.0741	66	- 78	0	K.LGEVNTYAGDLQK.K
1439.7198	1438.7125	1438.7932	-0.0807	79	- 90	1	K.KLVPFATELHER.L
1443.6886	1442.6813	1442.7590	-0.0776	144	- 155	1	R.TQVNTQAEQLRR.Q
1558.7275	1557.7202	1557.7973	-0.0771	234	- 246	0	K.LNHQLEGLTFQMK.K
1574.7196	1573.7123	1573.7922	-0.0799	234	- 246	0	K.LNHQLEGLTFQMK.K + Oxidation (M)
1634.7576	1633.7503	1633.8311	-0.0808	52	- 65	0	K.SELTQQLNALFQDK.L
1805.8453	1804.8380	1804.9107	-0.0727	329	- 345	0	K.LGPHAGDVEGHLSFLEK.D
1927.9091	1926.9019	1926.9435	-0.0416	288	- 304	0	K.SLAELGGHLDQQVEEFR.R
1993.9450	1992.9377	1992.9864	-0.0487	170	- 187	0	R.ENADSLQASLRPHADELK.A
2084.0093	2083.0020	2083.0446	-0.0426	288	- 305	1	K.SLAELGGHLDQQVEEFR.R
2193.1061	2192.0988	2192.1185	-0.0197	170	- 189	1	R.ENADSLQASLRPHADELKAK.I
2362.2237	2361.2164	2361.2400	-0.0236	167	- 187	1	R.VLRENADSLQASLRPHADELK.A
2890.4720	2889.4647	2889.4330	0.0317	222	- 246	1	R.SLAPYAQDTQEKLNHGLEGLTFQMK.K

No match to: 854.9449, 860.9786, 876.9413, 959.3966, 976.4208, 980.4021, 1065.9443, 1218.5811, 1297.5441, 1336.3908, 1427.4641, 1485.7681, 1499.7430, 1508.6825, 1585.8063, 1656.7520, 1707.7763, 1834.8681, 1976.9265, 2045.0624, 2067.6716, 2069.7862, 2211.0997

5. [LPHUA4](#) Mass: 45307 Score: 315 Expect: 1e-25 Queries matched: 30

apolipoprotein A-IV precursor [validated] - human

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
975.4483	974.4410	974.5032	-0.0623	256	- 264	0	R.ISASAEELR.Q
983.4562	982.4489	982.5447	-0.0958	267	- 275	0	R.LAPLAEDVR.G
1076.4495	1075.4422	1075.5338	-0.0916	351	- 359	0	K.VNSFFSTFK.E
1083.4282	1082.4209	1082.5284	-0.1075	201	- 209	0	R.LTPYADEFK.V
1104.4679	1103.4606	1103.5611	-0.1005	135	- 143	0	R.LEPYADQLR.T
1196.4419	1195.4346	1195.5509	-0.1163	307	- 316	0	R.VEPYGENFNK.A
1215.5637	1214.5564	1214.6441	-0.0877	317	- 326	0	K.ALVQQMEQLR.Q
1231.5737	1230.5665	1230.6390	-0.0726	317	- 326	0	K.ALVQQMEQLR.Q + Oxidation (M)
1235.5752	1234.5679	1234.6669	-0.0990	113	- 123	0	R.LLPANEVSQK.I
1258.5780	1257.5707	1257.6676	-0.0970	276	- 287	1	R.GNLKGNTGLQK.S
1287.5711	1286.5638	1286.6579	-0.0940	144	- 154	0	R.TQVNTQAEQLR.R
1300.6026	1299.5954	1299.6782	-0.0829	190	- 200	1	K.IDQNVEELKGR.L
1310.5953	1309.5880	1309.6918	-0.1038	201	- 211	1	R.LTPYADEFKVK.I
1311.6184	1310.6111	1310.6982	-0.0871	80	- 90	0	K.LVPFATELHER.L
1319.5820	1318.5747	1318.6557	-0.0810	349	- 359	1	R.DKVSFFSTFK.E
1350.5619	1349.5546	1349.6463	-0.0917	222	- 233	0	R.SLAPYAQDTQEK.L
1352.5712	1351.5639	1351.6520	-0.0881	306	- 316	1	R.RVEPYGENFNK.A
1407.6373	1406.6300	1406.7041	-0.0741	66	- 78	0	K.LGEVNTYAGDLQK.K
1439.7198	1438.7125	1438.7932	-0.0807	79	- 90	1	K.KLVPFATELHER.L
1443.6886	1442.6813	1442.7590	-0.0776	144	- 155	1	R.TQVNTQAEQLRR.Q
1558.7275	1557.7202	1557.7973	-0.0771	234	- 246	0	K.LNHQLEGLTFQMK.K
1574.7196	1573.7123	1573.7922	-0.0799	234	- 246	0	K.LNHQLEGLTFQMK.K + Oxidation (M)
1634.7576	1633.7503	1633.8311	-0.0808	52	- 65	0	K.SELTQQLNALFQDK.L
1805.8453	1804.8380	1804.9107	-0.0727	329	- 345	0	K.LGPHAGDVEGHLSFLEK.D
1927.9091	1926.9019	1926.9435	-0.0416	288	- 304	0	K.SLAELGGHLDQQVEEFR.R
1993.9450	1992.9377	1992.9864	-0.0487	170	- 187	0	R.ENADSLQASLRPHADELK.A
2084.0093	2083.0020	2083.0446	-0.0426	288	- 305	1	K.SLAELGGHLDQQVEEFR.R
2193.1061	2192.0988	2192.1185	-0.0197	170	- 189	1	R.ENADSLQASLRPHADELKAK.I
2362.2237	2361.2164	2361.2400	-0.0236	167	- 187	1	R.VLRENADSLQASLRPHADELK.A
2890.4720	2889.4647	2889.4330	0.0317	222	- 246	1	R.SLAPYAQDTQEKLNHGLEGLTFQMK.K

No match to: 854.9449, 860.9786, 876.9413, 959.3966, 976.4208, 980.4021, 1065.9443, 1132.5159, 1218.5811, 1297.5441, 1336.3908, 1427.4641, 1485.7681, 1499.7430, 1508.6825, 1585.8063, 1656.7520, 1707.7763, 1834.8681, 1976.9265, 2045.0624, 2067.6716, 2069.7862, 2211.0997

6.

Q13784_HUMAN

Mass: 28141

Score: 280

Expect: 3.2e-22

Queries matched: 25

APOA4 protein (Fragment).- Homo sapiens (Human).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
975.4483	974.4410	974.5032	-0.0623	122	- 130	0	R.ISASAEELR.Q
983.4562	982.4489	982.5447	-0.0958	133	- 141	0	R.LAPLAEDVR.G
1076.4495	1075.4422	1075.5338	-0.0916	217	- 225	0	K.VNSFFSTFK.E
1083.4282	1082.4209	1082.5284	-0.1075	67	- 75	0	R.LTPYADEFK.V
1104.4679	1103.4606	1103.5611	-0.1005	1	- 9	0	-.LEPYADQLR.T
1196.4419	1195.4346	1195.5509	-0.1163	173	- 182	0	R.VEPYGENFNK.A
1215.5637	1214.5564	1214.6441	-0.0877	183	- 192	0	K.ALVQQMEQLR.Q
1231.5737	1230.5665	1230.6390	-0.0726	183	- 192	0	K.ALVQQMEQLR.Q + Oxidation (M)
1258.5780	1257.5707	1257.6676	-0.0970	142	- 153	1	R.GNLKGNTEGLQK.S
1287.5711	1286.5638	1286.6579	-0.0940	10	- 20	0	R.TQVNTQAEQLR.R
1300.6026	1299.5954	1299.6782	-0.0829	56	- 66	1	K.IDQNVEELKGR.L
1310.5953	1309.5880	1309.6918	-0.1038	67	- 77	1	R.LTPYADEFKVK.I
1319.5820	1318.5747	1318.6557	-0.0810	215	- 225	1	R.DKVSFFSTFK.E
1350.5619	1349.5546	1349.6463	-0.0917	88	- 99	0	R.SLAPYAQDTQEK.L
1352.5712	1351.5639	1351.6520	-0.0881	172	- 182	1	R.RVEPYGENFNK.A
1443.6886	1442.6813	1442.7590	-0.0776	10	- 21	1	R.TQVNTQAEQLRR.Q
1558.7275	1557.7202	1557.7973	-0.0771	100	- 112	0	K.LNHQLEGLTFQMK.K
1574.7196	1573.7123	1573.7922	-0.0799	100	- 112	0	K.LNHQLEGLTFQMK.K + Oxidation (M)
1805.8453	1804.8380	1804.9107	-0.0727	195	- 211	0	K.LGPHAGDVEGHLSFLEK.D
1927.9091	1926.9019	1926.9435	-0.0416	154	- 170	0	K.SLAELGGHLDQQVEEFR.R
1993.9450	1992.9377	1992.9864	-0.0487	36	- 53	0	R.ENADSLQASLRPHADELK.A
2084.0093	2083.0020	2083.0446	-0.0426	154	- 171	1	K.SLAELGGHLDQQVEEFR.R
2193.1061	2192.0988	2192.1185	-0.0197	36	- 55	1	R.ENADSLQASLRPHADELKAK.I
2362.2237	2361.2164	2361.2400	-0.0236	33	- 53	1	R.VLRENADSLQASLRPHADELK.A
2890.4720	2889.4647	2889.4330	0.0317	88	- 112	1	R.SLAPYAQDTQEKLNHGLEGLTFQMK.K

No match to: 854.9449, 860.9786, 876.9413, 959.3966, 976.4208, 980.4021, 1065.9443, 1132.5159, 1218.5811, 1235.5752, 1297.5441, 1311.6184, 1336.3908, 1407.6373, 1427.4641, 1439.7198, 1485.7681, 1499.7430, 1508.6825, 1585.8063, 1634.7576, 1656.7520, 1707.7763, 1834.8681, 1976.9265, 2045.0624, 2067.6716, 2069.7862, 2211.0997

7.

A47141

Mass: 46510

Score: 139

Expect: 4.1e-08

Queries matched: 18

apolipoprotein A-IV I isoform - baboon (fragment)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
975.4483	974.4410	974.5032	-0.0623	240	- 248	0	R.ISASAEELR.Q
1076.4495	1075.4422	1075.5338	-0.0916	335	- 343	0	K.VNSFFSTFK.E
1083.4282	1082.4209	1082.5284	-0.1075	185	- 193	0	R.LTPYADEFK.V
1132.5159	1131.5087	1131.6149	-0.1062	139	- 147	1	R.RQLTPYAQR.M
1196.4419	1195.4346	1195.5509	-0.1163	291	- 300	0	R.VEPYGENFNK.A
1215.5637	1214.5564	1214.6441	-0.0877	301	- 310	0	K.ALVQQMEQLR.Q
1231.5737	1230.5665	1230.6390	-0.0726	301	- 310	0	K.ALVQQMEQLR.Q + Oxidation (M)
1235.5752	1234.5679	1234.6669	-0.0990	97	- 107	0	R.LLPHANEVSQK.I
1258.5780	1257.5707	1257.6677	-0.0970	196	- 205	1	K.IDQTVEELRR.S
1300.6026	1299.5954	1299.6782	-0.0829	174	- 184	1	K.IDQNVEELKGR.L
1310.5953	1309.5880	1309.6918	-0.1038	185	- 195	1	R.LTPYADEFKVK.I
1311.6184	1310.6111	1310.6982	-0.0871	64	- 74	0	K.LVPFATELHER.L
1319.5820	1318.5747	1318.6557	-0.0810	333	- 343	1	R.DKVSFFSTFK.E
1407.6373	1406.6300	1406.7041	-0.0741	50	- 62	0	K.LGEVNTYAGDLQK.K
1439.7198	1438.7125	1438.7932	-0.0807	63	- 74	1	K.KLVPFATELHER.L
1634.7576	1633.7503	1633.8311	-0.0808	36	- 49	0	K.SELTQQLNALFQDK.L
1656.7520	1655.7447	1655.8817	-0.1370	218	- 231	1	K.LNHQLEGLAFQMKK.N
1805.8453	1804.8380	1804.9107	-0.0727	313	- 329	0	K.LGPHAGDVEGHLSFLEK.D

No match to: 854.9449, 860.9786, 876.9413, 959.3966, 976.4208, 980.4021, 983.4562, 1065.9443, 1104.4679, 1218.5811, 1287.5711, 1297.5441, 1336.3908, 1350.5619, 1352.5712, 1427.4641, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1585.8063, 1707.7763, 1834.8681, 1927.9091, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2211.0997, 2362.2237, 2890.4720

8.

S29565

Mass: 49846

Score: 119

Expect: 4.1e-06

Queries matched: 17

apolipoprotein A-IV - crab-eating macaque

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
975.4483	974.4410	974.5032	-0.0623	256	- 264	0	R.ISASAEELR.Q
1076.4495	1075.4422	1075.5338	-0.0916	351	- 359	0	K.VNSFFSTFK.E
1083.4282	1082.4209	1082.5284	-0.1075	201	- 209	0	R.LTPYADEFK.V
1132.5159	1131.5087	1131.6149	-0.1062	155	- 163	1	R.RQLTPYAQR.M
1196.4419	1195.4346	1195.5509	-0.1163	307	- 316	0	R.VEPYGENFNK.A
1215.5637	1214.5564	1214.6441	-0.0877	317	- 326	0	K.ALVQQMEQLR.Q
1231.5737	1230.5665	1230.6390	-0.0726	317	- 326	0	K.ALVQQMEQLR.Q + Oxidation (M)
1235.5752	1234.5679	1234.6669	-0.0990	113	- 123	0	R.LLPHANEVSQK.I
1258.5780	1257.5707	1257.6677	-0.0970	212	- 221	1	K.IDQTVEELRR.S

1310.5953	1309.5880	1309.6918	-0.1038	201	-	211	1	R.LTPYADEFKVK.I
1311.6184	1310.6111	1310.6982	-0.0871	80	-	90	0	K.LVPFATELHER.L
1319.5820	1318.5747	1318.6557	-0.0810	349	-	359	1	R.DKVNSFFSTFK.E
1407.6373	1406.6300	1406.7041	-0.0741	66	-	78	0	K.LGEVNTYAGDLQK.K
1439.7198	1438.7125	1438.7932	-0.0807	79	-	90	1	K.KLVPFATELHER.L
1634.7576	1633.7503	1633.8311	-0.0808	52	-	65	0	K.SELTQQLNALFQDK.L
1656.7520	1655.7447	1655.8817	-0.1370	234	-	247	1	K.LNHQLEGLAFQMKK.N
1805.8453	1804.8380	1804.9107	-0.0727	329	-	345	0	K.LGPHAGDVEGHSFLEK.D
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 976.4208, 980.4021, 983.4562, 1065.9443, 1104.4679, 1218.5811, 1287.5711, 1297.5441, 1300.6026, 1336.3908, 1350.5619, 1352.5712, 1427.4641, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1585.8063, 1707.7763, 1834.8681, 1927.9091, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2211.0997, 2362.2237, 2890.4720								

9. [C87410](#) Mass: 70844 Score: 64 Expect: 1.3 Queries matched: 12

iolC protein [imported] - Caulobacter crescentus								
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
976.4208	975.4135	975.5059	-0.0924	236	-	244	0	R.ASDALLVCK.R + Carbamidomethyl (C)
1132.5159	1131.5087	1131.6070	-0.0983	236	-	245	1	R.ASDALLVCKR.G + Carbamidomethyl (C)
1215.5637	1214.5564	1214.6553	-0.0990	487	-	496	1	R.QLLRLADACR.K + Carbamidomethyl (C)
1258.5780	1257.5707	1257.6400	-0.0693	63	-	73	1	R.VGADHMGFRIR.E
1439.7198	1438.7125	1438.7721	-0.0596	103	-	113	1	R.DRVNFPLIFYR.E
1499.7430	1498.7357	1498.7674	-0.0317	57	-	70	1	K.TGLLTRVGADHMGFR.F + Oxidation (M)
1585.8063	1584.7990	1584.7817	0.0173	549	-	562	0	R.EIEIAIAENDPLCR.G
1707.7763	1706.7690	1706.8012	-0.0322	343	-	356	0	R.EDAELEHIHWATTR.E
1805.8453	1804.8380	1804.8703	-0.0323	184	-	199	1	K.DAGENRFVENQQVTAK.L
1976.9265	1975.9192	1975.9864	-0.0672	341	-	356	1	R.LREDAELEHIHWATTR.E
2084.0093	2083.0020	2083.0181	-0.0161	74	-	92	1	R.EQLEREGVDVAGVLSDPDR.L
2362.2237	2361.2164	2361.2592	-0.0429	162	-	183	1	K.AAGGRVAFDIDYRPVLWGLTGK.D
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1196.4419, 1218.5811, 1231.5737, 1235.5752, 1287.5711, 1297.5441, 1300.6026, 1310.5953, 1311.6184, 1319.5820, 1336.3908, 1350.5619, 1352.5712, 1407.6373, 1427.4641, 1443.6886, 1485.7681, 1508.6825, 1558.7275, 1574.7196, 1634.7576, 1656.7520, 1834.8681, 1927.9091, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2193.1061, 2211.0997, 2890.4720								

10. [Q3SQM9_NITWN](#) Mass: 41297 Score: 62 Expect: 1.8 Queries matched: 10

Acyl-CoA dehydrogenase (EC 1.3.99.2).- Nitrobacter winogradskyi (strain Nb-255 / ATCC 25391).								
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
975.4483	974.4410	974.4781	-0.0371	57	-	66	0	R.NDVGGSALSR.L
976.4208	975.4135	975.4807	-0.0672	232	-	241	0	R.IAMAGLDGGR.L + Oxidation (M)
983.4562	982.4489	982.4906	-0.0417	259	-	266	1	K.ALGYMKER.K + Oxidation (M)
1076.4495	1075.4422	1075.4869	-0.0447	200	-	208	0	K.MGWNAQPTR.A + Oxidation (M)
1300.6026	1299.5954	1299.6968	-0.1015	44	-	56	0	R.EAAALGIGGICIR.N + Carbamidomethyl (C)
1319.5820	1318.5747	1318.6629	-0.0881	187	-	199	1	R.GTPGVSFGANERK.M
1439.7198	1438.7125	1438.6432	0.0693	307	-	319	0	R.EDTNATMLCAVAK.R + Carbamidomethyl (C); Oxidation (M)
1574.7196	1573.7123	1573.8140	-0.1017	23	-	35	1	R.KIAPFALQWDEEK.H
1834.8681	1833.8608	1833.9155	-0.0547	223	-	241	1	R.IGAEGAGFRIAMAGLDGGR.L + Oxidation (M)
1976.9265	1975.9192	1975.9686	-0.0494	200	-	216	1	K.MGWNAQPTRAVIFENAR.V + Oxidation (M)
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 980.4021, 1065.9443, 1083.4282, 1104.4679, 1132.5159, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1310.5953, 1311.6184, 1336.3908, 1350.5619, 1352.5712, 1407.6373, 1427.4641, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1585.8063, 1634.7576, 1656.7520, 1707.7763, 1805.8453, 1927.9091, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2211.0997, 2362.2237, 2890.4720								

11. [I54248](#) Mass: 10612 Score: 62 Expect: 2.2 Queries matched: 7

apolipoprotein A-IV - chimpanzee (fragment)								
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
1076.4495	1075.4422	1075.5338	-0.0916	46	-	54	0	K.VNSFFSTFK.E
1196.4419	1195.4346	1195.5509	-0.1163	2	-	11	0	R.VEPYGENFNK.A
1215.5637	1214.5564	1214.6441	-0.0877	12	-	21	0	K.ALVQQMEQLR.T
1231.5737	1230.5665	1230.6390	-0.0726	12	-	21	0	K.ALVQQMEQLR.T + Oxidation (M)
1319.5820	1318.5747	1318.6557	-0.0810	44	-	54	1	R.DKVNSFFSTFK.E
1352.5712	1351.5639	1351.6520	-0.0881	1	-	11	1	- .RVEPYGENFNK.A
1805.8453	1804.8380	1804.9107	-0.0727	24	-	40	0	K.LGPHAGDVEGHSFLEK.D
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1083.4282, 1104.4679, 1132.5159, 1218.5811, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1310.5953, 1311.6184, 1336.3908, 1350.5619, 1407.6373, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1585.8063, 1634.7576, 1656.7520, 1707.7763, 1834.8681, 1927.9091, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2211.0997, 2362.2237, 2890.4720								

12. [Q6WAZ7_TRYCR](#) Mass: 82415 Score: 56 Expect: 7.6 Queries matched: 12

C71 surface protein.- Trypanosoma cruzi.								
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
975.4483	974.4410	974.5145	-0.0735	674	-	682	1	K.NVDSKGISR.F
1132.5159	1131.5087	1131.5996	-0.0909	87	-	96	1	K.NGRETLSSLR.V
1215.5637	1214.5564	1214.5567	-0.0003	683	-	695	0	R.FYIGDGGSAGSK.E
1235.5752	1234.5679	1234.5975	-0.0296	450	-	462	0	K.GGGESSLGMVSVR.L
1287.5711	1286.5638	1286.6255	-0.0616	633	-	642	1	K.ELRSNWEPEK.T
1300.6026	1299.5954	1299.5080	0.0874	322	-	332	0	K.LMMMTACDDGR.R + Carbamidomethyl (C)

1508.6825	1507.6753	1507.7266	-0.0513	217	-	232	0	R.LFGAVGNVNDGSSGK.K
1585.8063	1584.7990	1584.7532	0.0459	539	-	554	0	K.GTNGVATGYADGVTFR.G
1634.7576	1633.7503	1633.8861	-0.1358	380	-	393	1	K.DVMLVTLVPVSNRK.G
1656.7520	1655.7447	1655.7824	-0.0377	592	-	607	0	K.GDNPIPLVGATMDDK.N
1805.8453	1804.8380	1804.8447	-0.0067	148	-	164	0	K.TQVLVECPAGNNSCVSK.K + Carbamidomethyl (C)
2362.2237	2361.2164	2361.1052	0.1112	484	-	507	1	R.VSELCPSPGTAKNPSAGSGCSTVR.I + Carbamidomethyl (C)
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1196.4419, 1218.5811, 1231.5737, 1258.5780, 1297.5441, 1310.5953, 1311.6184, 1319.5820, 1336.3908, 1350.5619, 1352.5712, 1407.6373, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1558.7275, 1574.7196, 1707.7763, 1834.8681, 1927.9091, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2211.0997, 2890.4720								

13. [Q3XUS9_9PROT](#) Mass: 61027 Score: 56 Expect: 8.1 Queries matched: 11

Coenzyme B12-binding:Radical SAM.- Magnetococcus sp. MC-1.

observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1076.4495	1075.4422	1075.5406	-0.0984	1	-	9	0 -.MDMLLVNPK.H + Oxidation (M)
1218.5811	1217.5738	1217.6139	-0.0401	294	-	305	0 R.IGAESGSDEILK.D
1235.5752	1234.5679	1234.6094	-0.0415	236	-	245	1 R.DELFFHSGKR.V
1258.5780	1257.5707	1257.5416	0.0290	284	-	293	1 R.MEQCGCRFLR.I + Oxidation (M)
1287.5711	1286.5638	1286.6830	-0.1192	212	-	222	1 R.SAKDILDEIQR.I
1407.6373	1406.6300	1406.7153	-0.0853	178	-	190	0 K.ATYGQEVQVLSGR.G
1508.6825	1507.6753	1507.7531	-0.0779	426	-	437	1 R.DQDRFLVQNAFR.L
1574.7196	1573.7123	1573.8199	-0.1076	294	-	308	1 R.IGAESGSDEILKDIK.K
1585.8063	1584.7990	1584.8088	-0.0098	232	-	243	1 R.IFFRDELFFHSGK.G
1634.7576	1633.7503	1633.8675	-0.1172	291	-	305	1 R.FLRIGAESGSDEILK.D
1927.9091	1926.9019	1926.8426	0.0593	191	-	207	1 R.GCSFKCTFCYNVVSQK.W + Carbamidomethyl (C)
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1083.4282, 1104.4679, 1132.5159, 1196.4419, 1215.5637, 1231.5737, 1297.5441, 1300.6026, 1310.5953, 1311.6184, 1319.5820, 1336.3908, 1350.5619, 1352.5712, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1558.7275, 1656.7520, 1707.7763, 1805.8453, 1834.8681, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2211.0997, 2362.2237, 2890.4720							

14. [Q4USB5_XANC8](#) Mass: 13788 Score: 56 Expect: 8.3 Queries matched: 7

HrpB2 protein.- Xanthomonas campestris pv. campestris (strain 8004).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
975.4483	974.4410	974.4855	-0.0445	52	-	60	0 R.VGEPISMISR.M
1196.4419	1195.4346	1195.4961	-0.0615	61	-	70	0 R.MVDMQNDGVR.A + 2 Oxidation (M)
1350.5619	1349.5546	1349.6206	-0.0660	86	-	97	0 K.MGLEEIAAEEMK.L
1558.7275	1557.7202	1557.7245	-0.0043	71	-	85	0 R.AMTEHVDAFGANAPK.M
1574.7196	1573.7123	1573.7194	-0.0072	71	-	85	0 R.AMTEHVDAFGANAPK.M + Oxidation (M)
1993.9450	1992.9377	1992.9220	0.0158	35	-	51	0 R.FQALMQSSCLPPAMQR.V + Carbamidomethyl (C); 2 Oxidation (M)
2890.4720	2889.4647	2889.3346	0.1301	71	-	97	1 R.AMTEHVDAFGANAPKMGLEEIAAEEMK.L
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1132.5159, 1215.5637, 1218.5811, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1310.5953, 1311.6184, 1319.5820, 1336.3908, 1352.5712, 1407.6373, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1585.8063, 1634.7576, 1656.7520, 1707.7763, 1805.8453, 1834.8681, 1927.9091, 1976.9265, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2211.0997, 2362.2237							

15. [Q4D9P5_TRYCR](#) Mass: 126270 Score: 54 Expect: 13 Queries matched: 15

DNA-directed RNA polymerase III subunit, putative (EC 2.7.7.6).- Trypanosoma cruzi.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
975.4483	974.4410	974.5032	-0.0623	810	-	819	0 K.ALNSDGIASK.G
983.4562	982.4489	982.4542	-0.0053	691	-	699	0 R.NTFQSAMGK.Q
1083.4282	1082.4209	1082.4927	-0.0718	768	-	776	1 R.CSLDRGYGR.C + Carbamidomethyl (C)
1218.5811	1217.5738	1217.6040	-0.0302	886	-	896	1 R.VPEPGDKFSSR.H
1310.5953	1309.5880	1309.6700	-0.0820	407	-	417	1 K.AFNVKQLMESK.L + Oxidation (M)
1352.5712	1351.5639	1351.6442	-0.0803	730	-	740	1 R.TKAMDLTHYEK.L + Oxidation (M)
1439.7198	1438.7125	1438.7213	-0.0088	336	-	346	1 R.HKALYVCFMVR.R + Carbamidomethyl (C); Oxidation (M)
1508.6825	1507.6753	1507.7381	-0.0628	157	-	169	0 R.ECPLDPGGYFIIK.G + Carbamidomethyl (C)
1558.7275	1557.7202	1557.8548	-0.1346	1108	-	1121	0 K.LLLQELQGMGISTR.L
1574.7196	1573.7123	1573.8133	-0.1011	170	-	183	1 K.GVEKVCLVQEQQSK.N
1805.8453	1804.8380	1804.9028	-0.0648	901	-	917	0 K.GVVGLITDGVNMPFNEK.G + Oxidation (M)
1927.9091	1926.9019	1927.0012	-0.0993	369	-	385	0 R.FETTGTLMGLLFEDLLK.Q
1993.9450	1992.9377	1993.0488	-0.1111	130	-	147	1 K.IGTIPIMLKSSSCNLFGR.T + Carbamidomethyl (C)
2045.0624	2044.0551	2044.1060	-0.0509	121	-	138	1 K.RPCTETDIKIGTIPIMLK.S + Oxidation (M)
2084.0093	2083.0020	2083.1023	-0.1003	368	-	385	1 K.RFETTGTLMGLLFEDLLK.Q
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 976.4208, 980.4021, 1065.9443, 1076.4495, 1104.4679, 1132.5159, 1196.4419, 1215.5637, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1311.6184, 1319.5820, 1336.3908, 1350.5619, 1407.6373, 1427.4641, 1443.6886, 1485.7681, 1499.7430, 1585.8063, 1634.7576, 1656.7520, 1707.7763, 1834.8681, 1976.9265, 2067.6716, 2069.7862, 2193.1061, 2211.0997, 2362.2237, 2890.4720							

16. [C83690](#) Mass: 22489 Score: 53 Expect: 16 Queries matched: 7

hypothetical protein BH0323 [imported] - Bacillus halodurans (strain C-125)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1235.5752	1234.5679	1234.6346	-0.0667	90	-	99	0 R.LNPFDFNQLK.T
1300.6026	1299.5954	1299.6935	-0.0981	127	-	137	1 K.DGKHVTEFIVR.E
1310.5953	1309.5880	1309.6374	-0.0494	80	-	89	1 K.EHREEIIDNR.L
1834.8681	1833.8608	1833.9049	-0.0441	46	-	59	1 K.LKFHDHLDENYIYK.C

1927.9091	1926.9019	1926.9184	-0.0165	102	-	117	0	K.EDHILTHINIDEHEGR.R
2084.0093	2083.0020	2083.0195	-0.0175	102	-	118	1	K.EDHILTHINIDEHEGRR.V
2211.0997	2210.0924	2210.1081	-0.0157	60	-	78	1	K.CFVIDDPVILNKWYSAAEK.K
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1132.5159, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1258.5780, 1287.5711, 1297.5441, 1311.6184, 1319.5820, 1336.3908, 1350.5619, 1352.5712, 1407.6373, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1585.8063, 1634.7576, 1656.7520, 1707.7763, 1805.8453, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2193.1061, 2362.2237, 2890.4720								

17. [Q56EH5_9CAUD](#) Mass: 36302 Score: 52 Expect: 20 Queries matched: 8

Hypothetical protein PHG31ORF188c.- Aeromonas phage 31.								
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
1287.5711	1286.5638	1286.6111	-0.0473	247	-	257	0	K.INMHIDCSGIK.H + Carbamidomethyl (C)
1311.6184	1310.6111	1310.6176	-0.0065	10	-	20	0	K.VEISDCVYQQK.K
1407.6373	1406.6300	1406.7306	-0.1006	236	-	246	1	R.YNLDFPNRIK.I
1439.7198	1438.7125	1438.7126	-0.0001	10	-	21	1	K.VEISDCVYQQK.K
1656.7520	1655.7447	1655.8487	-0.1040	244	-	257	1	R.QIKINMHIDCSGIK.H + Carbamidomethyl (C)
1707.7763	1706.7690	1706.8185	-0.0495	264	-	277	0	K.ITGYPEECEIILDR.N + Carbamidomethyl (C)
2193.1061	2192.0988	2191.9336	0.1652	161	-	177	1	K.QCVEVMDRYMDDSIIEFR.V + Carbamidomethyl (C)
2362.2237	2361.2164	2361.0728	0.1435	147	-	168	1	R.SGTFDSGSAGIFAKQCVEVMR.Y + Carbamidomethyl (C)
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1132.5159, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1235.5752, 1258.5780, 1297.5441, 1300.6026, 1310.5953, 1319.5820, 1336.3908, 1350.5619, 1352.5712, 1427.4641, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1585.8063, 1634.7576, 1805.8453, 1834.8681, 1927.9091, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2211.0997, 2890.4720								

18. [Q4MZD6_THEPA](#) Mass: 62104 Score: 52 Expect: 20 Queries matched: 13

Hypothetical protein.- Theileria parva.								
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
1132.5159	1131.5087	1131.6175	-0.1089	415	-	424	0	K.ALELDPTFVK.A
1231.5737	1230.5665	1230.5591	0.0074	311	-	320	0	R.YDDAILCYQK.S
1258.5780	1257.5707	1257.5845	-0.0139	301	-	310	1	R.LAACYTKMER.Y + Carbamidomethyl (C); Oxidation (M)
1287.5711	1286.5638	1286.4875	0.0763	178	-	188	0	R.DGLMACMGNNR.N + Carbamidomethyl (C); 2 Oxidation (M)
1350.5619	1349.5546	1349.6649	-0.1103	76	-	87	1	K.GLCEYKLGNPEK.A
1407.6373	1406.6300	1406.6863	-0.0563	76	-	87	1	K.GLCEYKLGNPEK.A + Carbamidomethyl (C)
1485.7681	1484.7608	1484.6783	0.0825	139	-	150	1	R.KYQEQQPEYASK.L
1558.7275	1557.7202	1557.7054	0.0148	508	-	520	0	K.ISENPMTMAEYLK.D + 2 Oxidation (M)
1656.7520	1655.7447	1655.8049	-0.0602	449	-	463	1	K.GLKVDPPNNECLQGR.N
1805.8453	1804.8380	1804.8375	0.0005	261	-	275	1	K.AAVYLEMGDYKCIK.T + Carbamidomethyl (C); Oxidation (M)
1993.9450	1992.9377	1993.0012	-0.0635	396	-	414	1	R.AAALLKCEYPSALADCNK.A
2045.0624	2044.0551	2043.9214	0.1337	452	-	469	1	K.VDPNNECLQGRNNCLNK.I
2069.7862	2068.7789	2068.8869	-0.1080	42	-	60	0	R.SGAYASMYMYNEALADANK.C
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1196.4419, 1215.5637, 1218.5811, 1235.5752, 1297.5441, 1300.6026, 1310.5953, 1311.6184, 1319.5820, 1336.3908, 1352.5712, 1427.4641, 1439.7198, 1443.6886, 1499.7430, 1508.6825, 1574.7196, 1585.8063, 1634.7576, 1707.7763, 1834.8681, 1927.9091, 1976.9265, 2067.6716, 2084.0093, 2193.1061, 2211.0997, 2362.2237, 2890.4720								

19. [Q4JCL5_SULAC](#) Mass: 24648 Score: 52 Expect: 22 Queries matched: 8

Conserved protein.- Sulfolobus acidocaldarius.								
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
983.4562	982.4489	982.4793	-0.0304	210	-	219	0	R.VSIACSGFLS.-
1132.5159	1131.5087	1131.5706	-0.0619	49	-	58	1	K.AMKNLENANK.R
1215.5637	1214.5564	1214.6295	-0.0731	81	-	91	0	R.GDLFIHTIDGK.I
1310.5953	1309.5880	1309.6877	-0.0997	144	-	155	0	K.YSSLIVLSESGR.K
1311.6184	1310.6111	1310.6765	-0.0653	199	-	209	0	K.NVLETHQVICR.V
1319.5820	1318.5747	1318.6564	-0.0817	98	-	107	1	R.QMRPPKNYNR.F + Oxidation (M)
1499.7430	1498.7357	1498.8442	-0.1085	92	-	103	1	K.IIFVDRQMRPPK.N
1927.9091	1926.9019	1927.0852	-0.1833	108	-	124	1	R.FVGLMEQLLLEGGIPPK.G + Oxidation (M)
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1196.4419, 1218.5811, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1336.3908, 1350.5619, 1352.5712, 1407.6373, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1508.6825, 1558.7275, 1574.7196, 1585.8063, 1634.7576, 1656.7520, 1707.7763, 1805.8453, 1834.8681, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2211.0997, 2362.2237, 2890.4720								

20. [Q8SPT5_MACMU](#) Mass: 16793 Score: 51 Expect: 24 Queries matched: 7

Growth differentiation factor 9 (Fragment).- Macaca mulatta (Rhesus macaque).								
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
975.4483	974.4410	974.5297	-0.0888	34	-	41	1	K.FSSKTLHR.A
980.4021	979.3948	979.4653	-0.0705	23	-	30	0	K.CVCNLMIK.E + Carbamidomethyl (C)
1350.5619	1349.5546	1349.6505	-0.0959	23	-	33	1	K.CVCNLMIKEPK.F + Carbamidomethyl (C); Oxidation (M)
1407.6373	1406.6300	1406.6720	-0.0420	23	-	33	1	K.CVCNLMIKEPK.F + 2 Carbamidomethyl (C); Oxidation (M)
1443.6886	1442.6813	1442.6356	0.0457	79	-	90	0	R.SIHMSINFCTCMK.D + 2 Oxidation (M)
1656.7520	1655.7447	1655.7582	-0.0135	78	-	90	1	K.RSIHMSINFCTCMK.D + Carbamidomethyl (C); 2 Oxidation (M)
2890.4720	2889.4647	2889.4801	-0.0154	5	-	30	1	K.SVLLYTINNVSFSFAVKCVCNLMIK.E + Carbamidomethyl (C)
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 976.4208, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1132.5159, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1310.5953, 1311.6184, 1319.5820, 1336.3908, 1352.5712, 1427.4641, 1439.7198, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1585.8063, 1634.7576, 1707.7763, 1805.8453, 1834.8681, 1927.9091, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2211.0997, 2362.2237								

21.	A44277	Mass: 64504	Score: 51	Expect: 25	Queries matched: 13
nonstructural protein NS1 - bluetongue virus (serotype 2)					
Observed	Mr(expt)	Mr(calc)	Delta	Start	End Miss Peptide
975.4483	974.4410	974.4781	-0.0371	124 - 132	0 K.QSALANSER.V
983.4562	982.4489	982.4099	0.0390	115 - 123	0 K.SGMMDEAVK.Q + Oxidation (M)
1218.5811	1217.5738	1217.5573	0.0165	503 - 512	0 R.AYATMFEMVR.C
1258.5780	1257.5707	1257.5304	0.0403	36 - 45	0 R.NCLFNMGMCVK.Q + 2 Carbamidomethyl (C); Oxidation (M)
1287.5711	1286.5638	1286.6653	-0.1014	347 - 357	0 K.QIPTCSVIDVR.A + Carbamidomethyl (C)
1300.6026	1299.5954	1299.5886	0.0068	35 - 45	1 K.RNCLFNMGMCVK.Q + Oxidation (M)
1350.5619	1349.5546	1349.6584	-0.1038	334 - 343	1 R.KHTCQLCYLK.H + 2 Carbamidomethyl (C)
1352.5712	1351.5639	1351.6554	-0.0915	104 - 114	1 R.CGAQLLEDYRK.S + Carbamidomethyl (C)
1574.7196	1573.7123	1573.7493	-0.0371	335 - 346	1 K.HTCQLCYLKHSK.Q + 2 Carbamidomethyl (C)
1585.8063	1584.7990	1584.7467	0.0524	201 - 213	1 R.QINTCPYTGyrGR.V + Carbamidomethyl (C)
1834.8681	1833.8608	1833.8575	0.0032	267 - 281	0 R.VPTGEFPLHQMLMR.R + 3 Oxidation (M)
1927.9091	1926.9019	1926.9951	-0.0932	251 - 266	1 R.VGYAEIIRYVQQLFGR.V
1993.9450	1992.9377	1993.1222	-0.1845	214 - 229	0 R.VFQVMFLPIQLINFLR.M + Oxidation (M)
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 976.4208, 980.4021, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1132.5159, 1196.4419, 1215.5637, 1231.5737, 1235.5752, 1297.5441, 1310.5953, 1311.6184, 1319.5820, 1336.3908, 1407.6373, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1634.7576, 1656.7520, 1707.7763, 1805.8453, 1976.9265, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2211.0997, 2362.2237, 2890.4720					
22.	T50803	Mass: 83475	Score: 51	Expect: 27	Queries matched: 11
hypothetical protein T30N20_210 - Arabidopsis thaliana					
Observed	Mr(expt)	Mr(calc)	Delta	Start	End Miss Peptide
975.4483	974.4410	974.4062	0.0348	402 - 408	0 R.HECLCTR.A + 2 Carbamidomethyl (C)
1104.4679	1103.4606	1103.5546	-0.0940	30 - 38	0 R.MQFHSSLVR.R
1297.5441	1296.5368	1296.5694	-0.0326	19 - 29	0 R.SQDPSHEVDQR.M
1350.5619	1349.5546	1349.6880	-0.1334	642 - 651	1 R.WFIWEKQTGR.L
1585.8063	1584.7990	1584.8042	-0.0051	723 - 735	1 R.NRENPLSVELMQR.F
1634.7576	1633.7503	1633.8246	-0.0743	725 - 737	1 R.ENPLSVELMQRFR.M + Oxidation (M)
1927.9091	1926.9019	1926.9622	-0.0603	84 - 100	0 K.LLHSIDTGHTANIFCTK.F + Carbamidomethyl (C)
2193.1061	2192.0988	2192.0796	0.0192	610 - 629	1 R.YVGHCNVGTDIKQASFLGQR.G
2211.0997	2210.0924	2210.0967	-0.0043	153 - 173	0 K.LAVEGPNPNVWSASEDTGLR.Q
2362.2237	2361.2164	2360.9942	0.2222	736 - 754	1 R.FRMQEFAEGNFHPFECTQS.- + Carbamidomethyl (C)
2890.4720	2889.4647	2889.4555	0.0092	220 - 245	1 K.SCDISATRPHELLVGGSDAFARLYDR.R + Carbamidomethyl (C)
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1132.5159, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1300.6026, 1310.5953, 1311.6184, 1319.5820, 1336.3908, 1352.5712, 1407.6373, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1656.7520, 1707.7763, 1805.8453, 1834.8681, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093					
23.	Q94BQ3_ARATH	Mass: 83778	Score: 51	Expect: 28	Queries matched: 11
Hypothetical protein At5g10940.- Arabidopsis thaliana (Mouse-ear cross).					
Observed	Mr(expt)	Mr(calc)	Delta	Start	End Miss Peptide
975.4483	974.4410	974.4062	0.0348	405 - 411	0 R.HECLCTR.A + 2 Carbamidomethyl (C)
1104.4679	1103.4606	1103.5546	-0.0940	30 - 38	0 R.MQFHSSLVR.R
1297.5441	1296.5368	1296.5694	-0.0326	19 - 29	0 R.SQDPSHEVDQR.M
1350.5619	1349.5546	1349.6880	-0.1334	645 - 654	1 R.WFIWEKQTGR.L
1585.8063	1584.7990	1584.8042	-0.0051	726 - 738	1 R.NRENPLSVELMQR.F
1634.7576	1633.7503	1633.8246	-0.0743	728 - 740	1 R.ENPLSVELMQRFR.M + Oxidation (M)
1927.9091	1926.9019	1926.9622	-0.0603	84 - 100	0 K.LLHSIDTGHTANIFCTK.F + Carbamidomethyl (C)
2193.1061	2192.0988	2192.0796	0.0192	613 - 632	1 R.YVGHCNVGTDIKQASFLGQR.G
2211.0997	2210.0924	2210.0967	-0.0043	153 - 173	0 K.LAVEGPNPNVWSASEDTGLR.Q
2362.2237	2361.2164	2360.9942	0.2222	739 - 757	1 R.FRMQEFAEGNFHPFECTQS.- + Carbamidomethyl (C)
2890.4720	2889.4647	2889.4555	0.0092	220 - 245	1 K.SCDISATRPHELLVGGSDAFARLYDR.R + Carbamidomethyl (C)
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1132.5159, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1300.6026, 1310.5953, 1311.6184, 1319.5820, 1336.3908, 1352.5712, 1407.6373, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1656.7520, 1707.7763, 1805.8453, 1834.8681, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093					
24.	Q6Q539_YEAST	Mass: 24211	Score: 50	Expect: 30	Queries matched: 7
YDR226W.- Saccharomyces cerevisiae (Baker's yeast).					
Observed	Mr(expt)	Mr(calc)	Delta	Start	End Miss Peptide
1076.4495	1075.4422	1075.5145	-0.0723	168 - 177	1 R.SDDNADALKK.R
1104.4679	1103.4606	1103.4917	-0.0311	76 - 85	0 K.DELTNNPACK.N
1218.5811	1217.5738	1217.6114	-0.0376	147 - 156	1 K.IFNPPKEDMK.D
1439.7198	1438.7125	1438.7139	-0.0014	30 - 42	0 R.FHAAHLATGDMRL.S
1443.6886	1442.6813	1442.8092	-0.1279	43 - 56	1 R.SQIAKGTQLGLEAK.K
1993.9450	1992.9377	1993.0309	-0.0931	179 - 195	1 R.LAAYHAQTEPIVDYFKK.T
2193.1061	2192.0988	2192.0571	0.0417	76 - 95	1 K.DELTNNPACKNGFILDGFPK.T
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1083.4282, 1132.5159, 1196.4419, 1215.5637, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1310.5953, 1311.6184, 1319.5820, 1336.3908, 1350.5619, 1352.5712, 1407.6373, 1427.4641, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1585.8063, 1634.7576, 1656.7520, 1707.7763, 1805.8453, 1834.8681, 1927.9091, 1976.9265, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2211.0997, 2362.2237, 2890.4720					

25.	Q2BL66_9GAMM	Mass: 52033	Score: 50	Expect: 31	Queries matched: 9
Argininosuccinate lyase.- Oceanospirillum sp. MED92.					
Observed	Mr(expt)	Mr(calc)	Delta	Start	End Miss Peptide
1218.5811	1217.5738	1217.5822	-0.0084	357 - 366	1 K.EENMREAAALR.G
1231.5737	1230.5665	1230.5087	0.0577	183 - 191	1 R.DFSRFEDCR.E + Carbamidomethyl (C)
1407.6373	1406.6300	1406.6361	-0.0060	1 - 12	1 -.MSDKTNQQWGR.F
1656.7520	1655.7447	1655.8518	-0.1071	367 - 381	1 R.GFSTATDLADYLVRK.G
1707.7763	1706.7690	1706.8483	-0.0793	341 - 356	1 K.GCLRAFADMVPALEAK.E + Oxidation (M)
1805.8453	1804.8380	1804.9691	-0.1311	300 - 315	1 K.SGRVFGHLSLLTLMK.S + Oxidation (M)
1976.9265	1975.9192	1975.9374	-0.0182	324 - 340	1 K.DNQEDKEPLFDAIDTVK.G
2045.0624	2044.0551	2044.0775	-0.0224	194 - 213	0 R.ANIMPLGAAALAGTTYPIQR.D + Oxidation (M)
2211.0997	2210.0924	2210.0863	0.0060	237 - 255	0 R.DFAIEFCSASSILLMHLTR.M + Carbamidomethyl (C)
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1132.5159, 1196.4419, 1215.5637, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1310.5953, 1311.6184, 1319.5820, 1336.3908, 1350.5619, 1352.5712, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1585.8063, 1634.7576, 1834.8681, 1927.9091, 1993.9450, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2362.2237, 2890.4720					
26.	Q4IVR0_AZ0VI	Mass: 36505	Score: 50	Expect: 31	Queries matched: 8
Regulatory protein, ArsR.- Azotobacter vinelandii AvOP.					
Observed	Mr(expt)	Mr(calc)	Delta	Start	End Miss Peptide
975.4483	974.4410	974.5297	-0.0887	313 - 320	0 R.NGFQIQIR.H
1076.4495	1075.4422	1075.5219	-0.0797	211 - 219	0 R.ECLENVELK.L
1132.5159	1131.5087	1131.5019	0.0068	129 - 137	1 R.DFFSRMADK.F + Oxidation (M)
1215.5637	1214.5564	1214.6771	-0.1207	84 - 96	0 R.ALPAAGFAGTILR.A
1218.5811	1217.5738	1217.6438	-0.0700	260 - 270	0 R.GGSLLLLTELCR.H + Carbamidomethyl (C)
1310.5953	1309.5880	1309.5166	0.0714	11 - 22	0 R.DDDCDELAALCK.A
1976.9265	1975.9192	1975.8615	0.0577	11 - 29	1 R.DDDCDELAALCKAGGDPLR.L
2193.1061	2192.0988	2192.1048	-0.0060	134 - 152	1 R.MADKFQAQQDLIAGLPQYR.D
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 976.4208, 980.4021, 983.4562, 1065.9443, 1083.4282, 1104.4679, 1196.4419, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1311.6184, 1319.5820, 1336.3908, 1350.5619, 1352.5712, 1407.6373, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1585.8063, 1634.7576, 1656.7520, 1707.7763, 1805.8453, 1834.8681, 1927.9091, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2211.0997, 2362.2237, 2890.4720					
27.	Q1RSK3_MEDTR	Mass: 105088	Score: 50	Expect: 32	Queries matched: 14
Zinc finger, RING-type; Transcription factor jumonji, jmjC.- Medicago truncatula (Barrel medic).					
Observed	Mr(expt)	Mr(calc)	Delta	Start	End Miss Peptide
980.4021	979.3948	979.4467	-0.0519	664 - 671	0 R.TNVEMMQK.T
983.4562	982.4489	982.3922	0.0567	34 - 42	0 R.CTAMSMPDK.T
1196.4419	1195.4346	1195.4961	-0.0615	422 - 431	0 K.NVEEMVSGCR.T + Carbamidomethyl (C); Oxidation (M)
1215.5637	1214.5564	1214.4986	0.0578	680 - 690	0 K.ESHGDPDICS.R
1231.5737	1230.5665	1230.6092	-0.0427	702 - 712	0 K.INGLDLESQK.A
1310.5953	1309.5880	1309.5860	0.0020	292 - 301	0 R.EQCFEVELEK.K + Carbamidomethyl (C)
1319.5820	1318.5747	1318.6703	-0.0956	43 - 53	1 K.TVCEKHYIAK.K
1350.5619	1349.5546	1349.6802	-0.1256	764 - 773	1 K.VTEYLKMHWK.E + Oxidation (M)
1352.5712	1351.5639	1351.6013	-0.0374	207 - 216	1 K.DVTWCLKCDR.R + 2 Carbamidomethyl (C)
1485.7681	1484.7608	1484.7511	0.0097	620 - 632	0 K.IYISYGISDELGR.G
1508.6825	1507.6753	1507.6516	0.0236	239 - 250	1 K.ICPACRGICNCK.I + 4 Carbamidomethyl (C)
1834.8681	1833.8608	1833.8493	0.0115	354 - 369	0 R.EATLHQSEEPQTEHAK.T
2211.0997	2210.0924	2210.0235	0.0689	528 - 546	0 K.AIDCLDGSEIDIELNQFMK.G + Carbamidomethyl (C)
2362.2237	2361.2164	2361.1787	0.0377	645 - 663	1 R.DMVYLLVHSSEVQLKDWQR.T + Oxidation (M)
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1132.5159, 1218.5811, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1311.6184, 1336.3908, 1407.6373, 1427.4641, 1439.7198, 1443.6886, 1499.7430, 1558.7275, 1574.7196, 1585.8063, 1634.7576, 1656.7520, 1707.7763, 1805.8453, 1927.9091, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2890.4720					
28.	Q1ZTR3_9VIBR	Mass: 31022	Score: 50	Expect: 33	Queries matched: 8
Putative putative phospholipid biosynthesis acyltransferase.- Vibrio angustum S14.					
Observed	Mr(expt)	Mr(calc)	Delta	Start	End Miss Peptide
1132.5159	1131.5087	1131.5416	-0.0330	113 - 121	0 R.LPQCDCLVK.A + 2 Carbamidomethyl (C)
1350.5619	1349.5546	1349.5769	-0.0223	144 - 155	0 R.DPESLLDSCSER.L
1407.6373	1406.6300	1406.5984	0.0317	144 - 155	0 R.DPESLLDSCSER.L + Carbamidomethyl (C)
1558.7275	1557.7202	1557.8514	-0.1312	156 - 170	0 R.LGSGNVLLVFPEGTR.T
2084.0093	2083.0020	2083.0069	-0.0049	228 - 247	1 K.DKIEVGFSFIESSDSTAAR.K
2193.1061	2192.0988	2192.0167	0.0821	136 - 155	1 K.AAGYIPNRDPESLLDSCSER.L
2211.0997	2210.0924	2210.1881	-0.0957	93 - 112	0 R.NCLIVANHPSLIDYVLIASR.L
2890.4720	2889.4647	2889.4177	0.0470	144 - 170	1 R.DPESLLDSCSERLGSNGNVLLVFPEGTR.T
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1310.5953, 1311.6184, 1319.5820, 1336.3908, 1352.5712, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1574.7196, 1585.8063, 1634.7576, 1656.7520, 1707.7763, 1805.8453, 1834.8681, 1927.9091, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2362.2237					
29.	Q390G0_BURS3	Mass: 100380	Score: 50	Expect: 33	Queries matched: 13
ATP-dependent transcriptional regulator, Malt-like, LuxR family.- Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760 / NCIB 9086 / R18194))					
Observed	Mr(expt)	Mr(calc)	Delta	Start	End Miss Peptide

	975.4483	974.4410	974.5185	-0.0775	412	-	419	0	R.TVLDWVSR.L
	976.4208	975.4135	975.4985	-0.0850	907	-	916	0	R.SGLALDASSR.T
	980.4021	979.3948	979.4579	-0.0631	673	-	681	0	R.VACMATGVR.L + Carbamidomethyl (C); Oxidation (M)
	1132.5159	1131.5087	1131.5771	-0.0684	488	-	497	0	R.SIESLELGER.V
	1287.5711	1286.5638	1286.6805	-0.1167	289	-	299	0	R.HFLLCTAVLDR.M
	1311.6184	1310.6111	1310.6805	-0.0693	635	-	645	0	R.FMQTAAVLQFR.S
	1634.7576	1633.7503	1633.8320	-0.0817	620	-	634	0	R.FDIAMQACSLGPLLR.F
	1656.7520	1655.7447	1655.8599	-0.1152	673	-	688	1	R.VACMATGVRHLHVSAGK.L + Carbamidomethyl (C)
	1707.7763	1706.7690	1706.8484	-0.0794	620	-	634	0	R.FDIAMQACSLGPLLR.F + Carbamidomethyl (C); Oxidation (M)
	1927.9091	1926.9019	1926.9808	-0.0789	433	-	449	0	R.IAHVWALALSMQMV DAR.R + Oxidation (M)
	2045.0624	2044.0551	2044.0800	-0.0249	479	-	497	1	R.SLIAGLSDRSIESLELGER.V
	2084.0093	2083.0020	2083.0819	-0.0799	433	-	450	1	R.IAHVWALALSMQMV DAR.R + Oxidation (M)
	2362.2237	2361.2164	2361.1230	0.0934	1	-	23	1	-.MTSSDSRQAAGPADADGIEVLVR.T + Oxidation (M)
	No match to: 854.9449, 860.9786, 876.9413, 959.3966, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1235.5752, 1258.5780, 1297.5441, 1300.6026, 1310.5953, 1319.5820, 1336.3908, 1350.5619, 1352.5712, 1407.6373, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1585.8063, 1805.8453, 1834.8681, 1976.9265, 1993.9450, 2067.6716, 2069.7862, 2193.1061, 2211.0997, 2890.4720								
30.	Q8TA35_HETGL Mass: 25472 Score: 50 Expect: 34 Queries matched: 7								
	Dorsal gland cell protein Hgg-26 (Fragment).- Heterodera glycinis (Soybean cyst nematode worm).								
	Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
	1083.4282	1082.4209	1082.5145	-0.0936	157	-	165	0	R.AADFYININR.L
	1132.5159	1131.5087	1131.5270	-0.0183	82	-	89	1	K.LCEEYKYK.F + Carbamidomethyl (C)
	1196.4419	1195.4346	1195.4993	-0.0647	217	-	227	0	R.STSWDESVQGT.-
	1352.5712	1351.5639	1351.6004	-0.0365	216	-	227	1	R.RSTSWDESVQGT.-
	1927.9091	1926.9019	1926.9257	-0.0239	150	-	165	1	K.TDLEMVRAADFYININR.L
	2084.0093	2083.0020	2082.9528	0.0492	196	-	215	1	R.DSASKSPYPPGTSEMGTS LR.R + Oxidation (M)
	2890.4720	2889.4647	2889.4184	0.0463	157	-	180	1	R.AADFYININRLINDDYIDNVYEIVK.V
	No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1104.4679, 1215.5637, 1218.5811, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1310.5953, 1311.6184, 1319.5820, 1336.3908, 1350.5619, 1407.6373, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1585.8063, 1634.7576, 1656.7520, 1707.7763, 1805.8453, 1834.8681, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2193.1061, 2211.0997, 2362.2237								
31.	Q7XUX8_ORYSA Mass: 41458 Score: 50 Expect: 36 Queries matched: 9								
	OSJNBa0027G07.11 protein.- Oryza sativa (japonica cultivar-group).								
	Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
	1218.5811	1217.5738	1217.5564	0.0174	206	-	215	0	K.EDDAVWVQDLK.L
	1350.5619	1349.5546	1349.5427	0.0119	313	-	324	0	R.GWQNNGCCPLCR.R
	1407.6373	1406.6300	1406.5642	0.0659	313	-	324	0	R.GWQNNGCCPLCR.R + Carbamidomethyl (C)
	1443.6886	1442.6813	1442.7187	-0.0374	326	-	338	0	R.ETETALHLVATCR.Y
	1585.8063	1584.7990	1584.8347	-0.0357	291	-	302	1	K.CKFHAWLIQNR.V + Carbamidomethyl (C)
	1656.7520	1655.7447	1655.8413	-0.0966	325	-	338	1	R.RETETALHLVATCR.Y + Carbamidomethyl (C)
	1993.9450	1992.9377	1992.9608	-0.0231	62	-	79	1	K.NMAAAGRMTLESLEQLDK.Q + Oxidation (M)
	2211.0997	2210.0924	2210.0823	0.0101	104	-	123	1	K.TCMTPTSGGLGLVNLNLDK.F + Carbamidomethyl (C); Oxidation (M)
	2362.2237	2361.2164	2361.2032	0.0132	99	-	120	1	K.VNLTKTCMPTSGGLGLVNLNLDK.F + Carbamidomethyl (C); Oxidation (M)
	No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1132.5159, 1196.4419, 1215.5637, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1310.5953, 1311.6184, 1319.5820, 1336.3908, 1352.5712, 1407.6373, 1427.4641, 1439.7198, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1634.7576, 1707.7763, 1805.8453, 1834.8681, 1927.9091, 1976.9265, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2890.4720								
32.	Q6IQ22_HUMAN Mass: 11751 Score: 50 Expect: 36 Queries matched: 6								
	RAB12, member RAS oncogene family.- Homo sapiens (Human).								
	Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
	983.4562	982.4489	982.5308	-0.0819	2	-	10	1	M.DPGAALQRR.A
	1218.5811	1217.5738	1217.6727	-0.0990	73	-	85	1	K.STVGKGATATLGR.A
	1300.6026	1299.5954	1299.6142	-0.0188	86	-	97	0	R.ASWRPGSCSPSR.G
	1336.3908	1335.3835	1335.5111	-0.1276	62	-	72	0	R.FTDDTFCEACK.S + Carbamidomethyl (C)
	1508.6825	1507.6753	1507.7895	-0.1142	101	-	114	1	R.VSSSLGVFRGWASR.-
	2069.7862	2068.7789	2068.8540	-0.0751	56	-	72	1	K.TSLMERFTDDTFCEACK.S + Carbamidomethyl (C); Oxidation (M)
	No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1132.5159, 1196.4419, 1215.5637, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1310.5953, 1311.6184, 1319.5820, 1350.5619, 1352.5712, 1407.6373, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1558.7275, 1574.7196, 1585.8063, 1634.7576, 1656.7520, 1707.7763, 1805.8453, 1834.8681, 1927.9091, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2084.0093, 2193.1061, 2211.0997, 2362.2237, 2890.4720								
33.	AH3404 Mass: 20696 Score: 49 Expect: 37 Queries matched: 8								
	hypothetical protein BMEI1222 [imported] - Brucella melitensis (strain 16M)								
	Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
	1083.4282	1082.4209	1082.4485	-0.0276	6	-	14	0	R.GSCQMTDLR.F + Carbamidomethyl (C); Oxidation (M)
	1215.5637	1214.5564	1214.6441	-0.0877	176	-	186	1	K.SLMQPRIGQSV.-
	1231.5737	1230.5665	1230.6390	-0.0726	176	-	186	1	K.SLMQPRIGQSV.- + Oxidation (M)
	1235.5752	1234.5679	1234.6202	-0.0523	130	-	139	0	R.TEMVIWAMVR.Q
	1258.5780	1257.5707	1257.6564	-0.0858	50	-	61	0	R.AELAADISLEAR.G
	1310.5953	1309.5880	1309.5867	0.0013	4	-	14	1	K.SRGSCQMTDLR.F + Carbamidomethyl (C)
	1407.6373	1406.6300	1406.7162	-0.0862	129	-	139	1	R.RTEMVIWAMVR.Q + Oxidation (M)
	1558.7275	1557.7202	1557.8402	-0.1200	97	-	111	0	R.ADVVSFQVPSPATLK.F

Hypothetical protein.- Gallus gallus (Chicken).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
976.4208	975.4135	975.4695	-0.0560	605	- 612	0	R.MTETPELR.S
1104.4679	1103.4606	1103.4805	-0.0199	558	- 566	0	R.LECEEPEAK.G + Carbamidomethyl (C)
1196.4419	1195.4346	1195.5399	-0.1053	926	- 935	1	R.CAIEADMKM.K + Carbamidomethyl (C)
1231.5737	1230.5665	1230.6091	-0.0427	151	- 160	1	K.LEEEEEAEVKR.K
1311.6184	1310.6111	1310.5772	0.0340	442	- 456	0	K.ECLGSGAGSTAGSSK.D
1350.5619	1349.5546	1349.6570	-0.1025	138	- 148	0	R.LEELCNEIMIK.K + Oxidation (M)
1407.6373	1406.6300	1406.6785	-0.0485	138	- 148	0	R.LEELCNEIMIK.K + Carbamidomethyl (C); Oxidation (M)
1439.7198	1438.7125	1438.6721	0.0403	441	- 456	1	K.KECLGSGAGSTAGSSK.D
1443.6886	1442.6813	1442.7616	-0.0803	86	- 98	0	K.GEVVETVEDVIVR.K
1485.7681	1484.7608	1484.6678	0.0930	125	- 137	0	K.DAELIQAGHMDNR.L + Oxidation (M)
1508.6825	1507.6753	1507.8194	-0.1441	788	- 800	1	K.AIMLVWRAANHR.Y
1993.9450	1992.9377	1992.9099	0.0279	63	- 79	0	K.HCASQYSELLETETPK.R + Carbamidomethyl (C)
2211.0997	2210.0924	2210.0572	0.0352	25	- 44	1	K.LCLASSVMRSGDQNWVSVSR.A + Oxidation (M)
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1132.5159, 1215.5637, 1218.5811, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1310.5953, 1319.5820, 1336.3908, 1352.5712, 1427.4641, 1499.7430, 1558.7275, 1574.7196, 1585.8063, 1634.7576, 1656.7520, 1707.7763, 1805.8453, 1834.8681, 1927.9091, 1976.9265, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2362.2237, 2890.4720							

39. [Q4DLZ9_TRYCR](#) Mass: 19461 Score: 48 Expect: 51 Queries matched: 7

Protein tyrosine phosphatase-like protein, putative.- Trypanosoma cruzi.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1350.5619	1349.5546	1349.6431	-0.0885	1	- 12	1	- .MEANGTLVECKR.G
1407.6373	1406.6300	1406.6646	-0.0346	1	- 12	1	- .MEANGTLVECKR.G + Carbamidomethyl (C)
1443.6886	1442.6813	1442.6572	0.0242	160	- 172	0	R.HQESNEGLICAR.C
1485.7681	1484.7608	1484.6605	0.1003	51	- 63	0	R.ACGPTYNAEVFEK.Q + Carbamidomethyl (C)
1558.7275	1557.7202	1557.8085	-0.0883	143	- 155	0	K.GAINQVQLNWLMR.Y + Oxidation (M)
2045.0624	2044.0551	2043.9908	0.0643	156	- 172	1	R.YKPRHQESNEGLICAR.C + Carbamidomethyl (C)
2362.2237	2361.2164	2361.2766	-0.0602	22	- 42	1	R.FLIIDAPSPSSVPAYMKLLQR.H + Oxidation (M)
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1132.5159, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1310.5953, 1311.6184, 1319.5820, 1336.3908, 1352.5712, 1427.4641, 1439.7198, 1499.7430, 1508.6825, 1574.7196, 1585.8063, 1634.7576, 1656.7520, 1707.7763, 1805.8453, 1834.8681, 1927.9091, 1976.9265, 1993.9450, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2211.0997, 2890.4720							

40. [Q39YY1_GEOMG](#) Mass: 16521 Score: 48 Expect: 53 Queries matched: 7

Putative PAS/PAC sensor protein.- Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1215.5637	1214.5564	1214.6441	-0.0877	84	- 96	0	K.LLSAPALCSAGGR.I
1319.5820	1318.5747	1318.6551	-0.0803	1	- 11	1	- .MPDTTNDKLLR.L + Oxidation (M)
1350.5619	1349.5546	1349.6067	-0.0521	108	- 121	0	R.DCEGAMAGSGAIIR.D
1352.5712	1351.5639	1351.6078	-0.0439	72	- 83	0	R.VMETGETHYGTK.L
1407.6373	1406.6300	1406.6282	0.0018	108	- 121	0	R.DCEGAMAGSGAIIR.D + Carbamidomethyl (C)
1508.6825	1507.6753	1507.7089	-0.0336	71	- 83	1	R.RVMETGETHYGTK.L
1585.8063	1584.7990	1584.8511	-0.0521	12	- 26	0	R.LIAEGVPDAVIFADR.E
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1132.5159, 1196.4419, 1218.5811, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1310.5953, 1311.6184, 1336.3908, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1558.7275, 1574.7196, 1634.7576, 1656.7520, 1707.7763, 1805.8453, 1834.8681, 1927.9091, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2211.0997, 2362.2237, 2890.4720							

41. [Q9TUL8_HORSE](#) Mass: 42919 Score: 48 Expect: 54 Queries matched: 8

Matrix metalloproteinase-2 (Fragment).- Equus caballus (Horse).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1132.5159	1131.5087	1131.4502	0.0584	135	- 144	0	K.EYTSCTDTGR.S
1310.5953	1309.5880	1309.6931	-0.1051	1	- 10	1	- .NYNFFPRKPK.W
1407.6373	1406.6300	1406.5891	0.0409	68	- 79	0	R.WEHDGYPFDGK.D
1634.7576	1633.7503	1633.6137	0.1366	265	- 277	0	K.MWCATTANYDDDR.K + Carbamidomethyl (C); Oxidation (M)
1993.9450	1992.9377	1992.9475	-0.0098	51	- 67	1	R.FSRIHDGEADIMINFR.W + Oxidation (M)
2069.7862	2068.7789	2068.9352	-0.1563	117	- 134	1	K.YGNADGEYCKFPFLFNGK.E
2084.0093	2083.0020	2082.8993	0.1027	145	- 162	1	R.SDGFLWCSTTYNFDKDGK.Y
2890.4720	2889.4647	2889.2824	0.1823	163	- 188	1	K.YGFCPHEALFTMGGNADGQPCFKPFR.F
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1311.6184, 1319.5820, 1336.3908, 1350.5619, 1352.5712, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1585.8063, 1656.7520, 1707.7763, 1805.8453, 1834.8681, 1927.9091, 1976.9265, 2045.0624, 2067.6716, 2193.1061, 2211.0997, 2362.2237							

42. [Q3M485_ANAVT](#) Mass: 42516 Score: 48 Expect: 55 Queries matched: 9

Hydrogenase formation HypD protein.- Anabaena variabilis (strain ATCC 29413 / PCC 7937).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1258.5780	1257.5707	1257.6928	-0.1222	372	- 383	1	K.QAAEKPKVTISS.-
1311.6184	1310.6111	1310.6142	-0.0031	3	- 12	1	K.YVDEFREPEK.A
1508.6825	1507.6753	1507.7704	-0.0952	117	- 129	0	R.MVYSPLDSLQIAR.N + Oxidation (M)
1558.7275	1557.7202	1557.7431	-0.0229	33	- 46	0	K.IMEVCGGHTSIFK.Y
1574.7196	1573.7123	1573.7381	-0.0258	33	- 46	0	K.IMEVCGGHTSIFK.Y + Oxidation (M)
1927.9091	1926.9019	1927.0097	-0.1079	257	- 273	1	K.QGNQIALEAMHKVFAVR.E + Oxidation (M)

1993.9450	1992.9377	1993.0025	-0.0648	30	-	46	1	K.HIKIMEVCGGHTHSIFK.Y + Carbamidomethyl (C)
2084.0093	2083.0020	2083.0520	-0.0500	117	-	134	1	R.MVYSPLDSLQIARNHPDK.E
2193.1061	2192.0988	2192.1259	-0.0271	110	-	129	1	K.ATGADIRMVYSPLDSLQIAR.N + Oxidation (M)
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1132.5159, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1235.5752, 1287.5711, 1297.5441, 1300.6026, 1310.5953, 1319.5820, 1336.3908, 1350.5619, 1352.5712, 1407.6373, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1585.8063, 1634.7576, 1656.7520, 1707.7763, 1805.8453, 1834.8681, 1976.9265, 2045.0624, 2067.6716, 2069.7862, 2211.0997, 2362.2237, 2890.4720								

43. [Q5NVL1_PONPY](#) Mass: 79482 Score: 48 Expect: 58 Queries matched: 11

Hypothetical protein DKFZp459N0220 (Fragment).- Pongo pygmaeus (Orangutan).								
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
975.4483	974.4410	974.4855	-0.0445	58	-	65	0	K.LAEMLDQR.Q
1104.4679	1103.4606	1103.5094	-0.0489	552	-	561	0	K.ASQEDANEIK.S
1132.5159	1131.5087	1131.5957	-0.0871	659	-	668	1	R.DKVQLMAAEK.K
1287.5711	1286.5638	1286.5812	-0.0174	9	-	21	0	R.AAGEPGTSMPPKEK.K + Oxidation (M)
1311.6184	1310.6111	1310.6726	-0.0615	642	-	651	1	K.EMKLLLDMYR.S
1319.5820	1318.5747	1318.6364	-0.0617	552	-	563	1	K.ASQEDANEIKSK.R
1443.6886	1442.6813	1442.6823	-0.0010	8	-	21	1	K.RAAGEPGTSMPPKEK.K + Oxidation (M)
1634.7576	1633.7503	1633.7795	-0.0292	515	-	530	0	R.SGSALLQSQSSTEDPK.D
1656.7520	1655.7447	1655.8492	-0.1045	478	-	491	0	R.HLTSSLQNHNHQLK.G
1927.9091	1926.9019	1927.0162	-0.1144	306	-	324	1	K.VYGAGSSLYGGTITINARK.F
2211.0997	2210.0924	2210.1668	-0.0744	478	-	496	1	R.HLTSSLQNHNHQLKGEVLR.Y
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1235.5752, 1258.5780, 1297.5441, 1300.6026, 1310.5953, 1336.3908, 1350.5619, 1352.5712, 1407.6373, 1427.4641, 1439.7198, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1585.8063, 1707.7763, 1805.8453, 1834.8681, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2362.2237, 2890.4720								

44. [Q4AI58_9CHLB](#) Mass: 37062 Score: 48 Expect: 58 Queries matched: 8

Cell shape determining protein MreB/Mrl.- Chlorobium phaeobacteroides BS1.								
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
1235.5752	1234.5679	1234.6669	-0.0990	309	-	319	0	K.LSVHVAEDPLR.A
1300.6026	1299.5954	1299.6975	-0.1021	331	-	340	1	K.NFDKFTFLIR.-
1311.6184	1310.6111	1310.6652	-0.0541	285	-	297	0	R.TGIYLAGGGSMLR.G + Oxidation (M)
1350.5619	1349.5546	1349.6860	-0.1315	251	-	262	1	K.EIASCLDKSISK.I + Carbamidomethyl (C)
1439.7198	1438.7125	1438.8031	-0.0906	28	-	40	0	K.VIVDEPSIVALER.N
1585.8063	1584.7990	1584.9086	-0.1096	259	-	273	1	K.SISKIEAAVLNALEK.T
1707.7763	1706.7690	1706.8913	-0.1222	236	-	250	1	R.DMLTGIPKEVTVNYK.E
1976.9265	1975.9192	1976.0466	-0.1274	10	-	27	0	K.EIAIDLGTANTIIINYDK.V
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1132.5159, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1258.5780, 1287.5711, 1297.5441, 1310.5953, 1319.5820, 1336.3908, 1352.5712, 1407.6373, 1427.4641, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1634.7576, 1656.7520, 1805.8453, 1834.8681, 1927.9091, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2211.0997, 2362.2237, 2890.4720								

45. [Q2HUJ6_MEDTR](#) Mass: 39508 Score: 47 Expect: 65 Queries matched: 8

Mitochondrial substrate carrier.- Medicago truncatula (Barrel medic).								
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
1076.4495	1075.4422	1075.4790	-0.0368	104	-	112	0	K.CNMQIDPAK.Y + Carbamidomethyl (C)
1258.5780	1257.5707	1257.6942	-0.1235	201	-	211	1	K.VRVQTQPGFAR.G
1310.5953	1309.5880	1309.6158	-0.0278	104	-	114	1	K.CNMQIDPAKYK.S
1311.6184	1310.6111	1310.7234	-0.1122	220	-	231	1	K.FVKSEGALGLYK.G
1350.5619	1349.5546	1349.6761	-0.1215	52	-	64	1	R.GTGSGRFMIPSPK.E + Oxidation (M)
1574.7196	1573.7123	1573.8028	-0.0905	248	-	260	0	K.FASFETIVEQIYK.H
1707.7763	1706.7690	1706.8450	-0.0760	135	-	150	0	R.GWVPTLLGYSAQGACK.F + Carbamidomethyl (C)
2084.0093	2083.0020	2083.0812	-0.0792	333	-	351	0	R.IVMIGTLTGAQWGIYDAFK.V
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1083.4282, 1104.4679, 1132.5159, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1235.5752, 1287.5711, 1297.5441, 1300.6026, 1319.5820, 1336.3908, 1352.5712, 1407.6373, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1585.8063, 1634.7576, 1656.7520, 1805.8453, 1834.8681, 1927.9091, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2193.1061, 2211.0997, 2362.2237, 2890.4720								

46. [Q5ZF44_MEDTR](#) Mass: 39616 Score: 47 Expect: 66 Queries matched: 8

Mitochondrial phosphate translocator.- Medicago truncatula (Barrel medic).								
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
1076.4495	1075.4422	1075.4790	-0.0368	104	-	112	0	K.CNMQIDPAK.Y + Carbamidomethyl (C)
1258.5780	1257.5707	1257.6942	-0.1235	201	-	211	1	K.VRVQTQPGFAR.G
1310.5953	1309.5880	1309.6158	-0.0278	104	-	114	1	K.CNMQIDPAKYK.S
1311.6184	1310.6111	1310.7234	-0.1122	220	-	231	1	K.FVKSEGALGLYK.G
1350.5619	1349.5546	1349.6761	-0.1215	52	-	64	1	R.GTGSGRFMIPSPK.E + Oxidation (M)
1574.7196	1573.7123	1573.8028	-0.0905	248	-	260	0	K.FASFETIVEQIYK.H
1707.7763	1706.7690	1706.8450	-0.0760	135	-	150	0	R.GWVPTLLGYSAQGACK.F + Carbamidomethyl (C)
2084.0093	2083.0020	2083.0812	-0.0792	333	-	351	0	R.IVMIGTLTGAQWGIYDAFK.V
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1083.4282, 1104.4679, 1132.5159, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1235.5752, 1287.5711, 1297.5441, 1300.6026, 1319.5820, 1336.3908, 1352.5712, 1407.6373, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1585.8063, 1634.7576, 1656.7520, 1805.8453, 1834.8681, 1927.9091, 1976.9265, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2193.1061, 2211.0997, 2362.2237, 2890.4720								

47. [Q5R9R8_PONPY](#) Mass: 72095 Score: 47 Expect: 66 Queries matched: 12

Hypothetical protein DKFZp469P0412.- Pongo pygmaeus (Orangutan).									
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide		
976.4208	975.4135	975.4985	-0.0850	56	- 63	1	K.ENRSLETK.Y		
1297.5441	1296.5368	1296.6383	-0.1015	38	- 48	0	R.YMATVVENLNK.A + Oxidation (M)		
1300.6026	1299.5954	1299.5942	0.0011	351	- 361	0	R.EPEQLGEDVER.R		
1311.6184	1310.6111	1310.5383	0.0728	465	- 474	0	K.VYHMDMEAQR.K + 2 Oxidation (M)		
1407.6373	1406.6300	1406.6434	-0.0134	465	- 475	1	K.VYHMDMEAQRK.N		
1439.7198	1438.7125	1438.6333	0.0792	465	- 475	1	K.VYHMDMEAQRK.N + 2 Oxidation (M)		
1585.8063	1584.7990	1584.7462	0.0528	580	- 592	1	R.RECLSSMVTMFPK.V + Carbamidomethyl (C)		
1656.7520	1655.7447	1655.8413	-0.0966	66	- 79	1	R.HLQMQATKELSSQR.L		
1834.8681	1833.8608	1833.9519	-0.0911	395	- 411	0	R.RPHLPMSPSTQQSALGK.Q		
1976.9265	1975.9192	1975.9210	-0.0018	294	- 307	1	R.RQLWLIEEEEMWQQR.Q + Oxidation (M)		
2084.0093	2083.0020	2082.9453	0.0566	344	- 361	1	K.EQESPGRPEQLGEDVER.R		
2193.1061	2192.0988	2192.0605	0.0383	529	- 546	1	R.QEVINHVVQIMKEMEASYK.A + Oxidation (M)		
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1132.5159, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1310.5953, 1319.5820, 1336.3908, 1350.5619, 1352.5712, 1427.4641, 1443.6886, 1485.7681, 1499.7430, 1508.6825, 1558.7275, 1574.7196, 1634.7576, 1707.7763, 1805.8453, 1927.9091, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2211.0997, 2362.2237, 2890.4720									

48. [Q4CFZ5_CLOTM](#) Mass: 11661 Score: 47 Expect: 68 Queries matched: 6

Hypothetical protein.- Clostridium thermocellum ATCC 27405.									
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide		
1352.5712	1351.5639	1351.6805	-0.1166	41	- 51	0	K.VYNQDVVQLMK.R + Oxidation (M)		
1508.6825	1507.6753	1507.7816	-0.1064	41	- 52	1	K.VYNQDVVQLMKR.L + Oxidation (M)		
1558.7275	1557.7202	1557.8038	-0.0836	16	- 29	1	K.YAKSVLGSELYSNK.I		
1707.7763	1706.7690	1706.8661	-0.0971	38	- 51	1	K.ENKVYNQDVVQLMK.R		
1834.8681	1833.8608	1833.9988	-0.1380	19	- 34	1	K.SVLGSELYSNKIFIHK.I		
1976.9265	1975.9192	1975.9239	-0.0047	68	- 84	0	R.CEIPPVDIVITMGCNMK.Y + 2 Carbamidomethyl (C)		
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 975.4483, 976.4208, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1104.4679, 1132.5159, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1235.5752, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1310.5953, 1311.6184, 1319.5820, 1336.3908, 1350.5619, 1407.6373, 1427.4641, 1439.7198, 1443.6886, 1485.7681, 1499.7430, 1574.7196, 1585.8063, 1634.7576, 1656.7520, 1805.8453, 1927.9091, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2211.0997, 2362.2237, 2890.4720									

49. [Q2DM63_9DELT](#) Mass: 19010 Score: 47 Expect: 69 Queries matched: 7

Hypothetical protein precursor.-			Geobacter uraniumreducens Rf4.															
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide											
975.4483	974.4410	974.4967	-0.0557	159	- 166	1	K.EMANKNIR.-											
1132.5159	1131.5087	1131.5780	-0.0693	142	- 151	1	K.MQGCLPEVKK.L											
1231.5737	1230.5665	1230.6464	-0.0799	140	- 150	1	R.VKMQGCLPEVK.K											
1352.5712	1351.5639	1351.6111	-0.0472	152	- 163	1	K.LAGDMEKEMANK.N + Oxidation (M)											
1485.7681	1484.7608	1484.7398	0.0210	93	- 105	0	K.DEVVAVYADLYTK.D											
1499.7430	1498.7357	1498.8467	-0.1110	127	- 139	1	K.ASELNERLISVLR.V											
2890.4720	2889.4647	2889.5098	-0.0451	2	- 27	1	M.KAAISGLLFLSVYLPSCFASDLSQR.A + Carbamidomethyl (C)											
No match to:			854.9449,	860.9786,	876.9413,	959.3966,	976.4208,	980.4021,	983.4562,	1065.9443,	1076.4495,	1083.4282,	1104.4679,	1196.4419,	1215.5637,	1218.5811,	1235.5752,	1258.5780,
			1287.5711,	1297.5441,	1300.6026,	1310.5953,	1311.6184,	1319.5820,	1336.3908,	1350.5619,	1407.6373,	1427.4641,	1439.7198,	1443.6886,	1508.6825,	1558.7275,	1574.7196,	1585.8063,
			1634.7576,	1656.7520,	1707.7763,	1805.8453,	1834.8681,	1927.9091,	1976.9265,	1993.9450,	2045.0624,	2067.6716,	2069.7862,	2084.0093,	2193.1061,	2211.0997,	2362.2237	

50. [Q7P987_RICSI](#) Mass: 73246 Score: 47 Expect: 71 Queries matched: 10

Propionyl-CoA carboxylase alpha chain.- Rickettsia sibirica 246.									
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide		
975.4483	974.4410	974.5073	-0.0663	500	- 507	0	R.WVVTIDDK.L		
976.4208	975.4135	975.4668	-0.0533	163	- 173	1	K.AAAGGGGRGMR.V + Oxidation (M)		
1104.4679	1103.4606	1103.5645	-0.1039	632	- 640	0	K.MENLILAE.R + Oxidation (M)		
1235.5752	1234.5679	1234.6478	-0.0799	580	- 590	0	R.ISELEALMVSK.V + Oxidation (M)		
1350.5619	1349.5546	1349.6074	-0.0528	287	- 296	0	K.NFYFLEMNTR.L + Oxidation (M)		
1443.6886	1442.6813	1442.7477	-0.0664	482	- 495	0	R.ASLISGNINNQANK.I		
1558.7275	1557.7202	1557.8514	-0.1312	359	- 372	1	R.IIAYSEPAKSPNIR.I		
1707.7763	1706.7690	1706.7933	-0.0243	174	- 189	0	R.VVNNPAEMANAFESAK.L + Oxidation (M)		
1976.9265	1975.9192	1975.9958	-0.0766	614	- 631	0	K.EGQEVTVGQEIMILTAMK.M		
2890.4720	2889.4647	2889.5157	-0.0510	126	- 153	1	K.IAIEAGVSTVPGYMGINDVKQAIDIAK.E + Oxidation (M)		
No match to: 854.9449, 860.9786, 876.9413, 959.3966, 980.4021, 983.4562, 1065.9443, 1076.4495, 1083.4282, 1132.5159, 1196.4419, 1215.5637, 1218.5811, 1231.5737, 1258.5780, 1287.5711, 1297.5441, 1300.6026, 1310.5953, 1311.6184, 1319.5820, 1336.3908, 1352.5712, 1407.6373, 1427.4641, 1439.7198, 1485.7681, 1499.7430, 1508.6825, 1574.7196, 1585.8063, 1634.7576, 1656.7520, 1805.8453, 1834.8681, 1927.9091, 1993.9450, 2045.0624, 2067.6716, 2069.7862, 2084.0093, 2193.1061, 2211.0997, 2362.2237									

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Variable modifications : Carbamidomethyl (C),Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 100 ppm
Peptide Charge State : 1+

Max Missed Cleavages : 1
Number of queries : 54

Mascot: <http://www.matrixscience.com/>