

MATRIX

SCIENCE

Mascot Search Results

User : Joe Gray

Email : joe.gray@ncl.ac.uk

Search title : DIP_2_0001.dat - SpecView

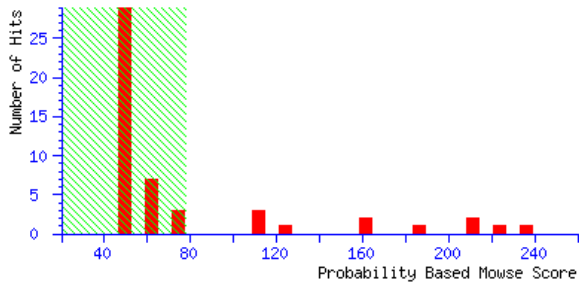
Database : MSDB 20060831 (3239079 sequences; 1079594700 residues)

Timestamp : 8 Jan 2007 at 11:34:53 GMT

Top Score : 236 for CAA00975, APOA1 PROTEIN (FRAGMENT).- Homo sapiens (Human).

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.	CAA00975	28061	236	APOA1 PROTEIN (FRAGMENT).- Homo sapiens (Human).
2.	AAA51747	28944	218	HUMAPOAIC NID: - Homo sapiens
3.	LPHUA1	30759	208	apolipoprotein A-I precursor [validated] - human
4.	AAX42892	30872	207	AY890956 NID: - synthetic construct
5.	AAA35545	30745	192	HUMAPOAIP NID: - Homo sapiens
6.	CAA03490	23205	160	SEQUENCE 10 FROM PATENT W09637608.- unidentified.
7.	1AV1A	23389	160	apolipoprotein a-i lipid-binding domain mutant N-TERMINAL MET, DEL(1-43), chain A - human
8.	Q8HZ97_PANTR	22075	130	Apolipoprotein A-I (Fragment).- Pan troglodytes (Chimpanzee).
9.	Q8HZ95_PONPY	22116	113	Apolipoprotein A-I (Fragment).- Pongo pygmaeus (Orangutan).
10.	A26529	30700	107	apolipoprotein A-I precursor - crab-eating macaque
11.	JS0079	30716	107	apolipoprotein A-I precursor - baboon
12.	CAD61352	18392	74	Sequence 2 from Patent W002083898 precursor.- Homo sapiens (Human).
13.	Q31VN4_SHIBS	15504	69	Hypothetical protein yrfH.- Shigella boydii serotype 4 (strain Sb227).
14.	Q8ZLJ5_SALTY	15511	68	Heat shock protein.- Salmonella typhimurium.
15.	H86004	15486	61	ribosome-associated heat shock protein yrfH [similarity] - Escherichia coli (strain 0157:H7, substrain EDL933)

16.	H97327	17433	59	transcription regulator, MarR/EmrR family [imported] - Clostridium acetobutylicum
17.	Q57IX7_SALCH	15557	59	Heat shock protein, predicted small RNA-binding protein.- Salmonella choleraesuis.
18.	Q5PLY1_SALPA	15465	58	Heat shock protein.- Salmonella paratyphi-a.
19.	Q7SD03_NEUCR	189062	57	Hypothetical protein NCU03060.1.- Neurospora crassa.
20.	Q5ZVU0_LEGPH	41536	56	L-lysine dehydrogenase.- Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 / ATCC 33152 / DSM 7513).
21.	B72212	20862	56	translation elongation factor P - Thermotoga maritima (strain MSB8)
22.	Q19Y36_9CAUD	12275	55	Gp24.- Mycobacteriophage Wildcat.
23.	Q2WWQ7_9GAMM	12361	53	Hypothetical protein.- Shewanella sp. W3-18-1.
24.	Q2ZS56_SHEPU	12333	53	Hypothetical protein.- Shewanella putrefaciens CN-32.
25.	Q833F6_ENTFA	106075	53	Tape measure protein, putative.- Enterococcus faecalis (Streptococcus faecalis).
26.	AAL97589	22480	53	AE010023 NID: - Streptococcus pyogenes MGAS8232
27.	Q8I4X5_PLAF7	188045	53	Hypothetical protein.- Plasmodium falciparum (isolate 3D7).
28.	Q8K6Y4_STRP3	28197	53	Putative 1-acylglycerol-3-phosphate O-acyltransferase.- Streptococcus pyogenes serotype M3.
29.	Q84QB8_ORYSA	42907	52	Putative receptor ser/thr protein.- Oryza sativa (japonica cultivar-group).
30.	AAM79212	22460	52	AE014074 NID: - Streptococcus pyogenes MGAS315
31.	AAN72830	253967	52	AY157993 NID: - Tomato black ring virus
32.	AAK33806	22479	51	AE006538 NID: - Streptococcus pyogenes M1 GAS
33.	Q8T530_PLAFA	14687	51	Erythrocyte membrane protein 1 (Fragment).- Plasmodium falciparum.
34.	Q8GJA6_CAMJE	53327	51	Hypothetical protein Cjp49.- Campylobacter jejuni.
35.	Q2YVH6_STAAB	9035	51	Hypothetical protein.- Staphylococcus aureus (strain bovine RF122).
36.	Q9AH95_STRPN	24847	51	Wze (Tyrosine-protein kinase Wze) (EC 2.7.1.112).- Streptococcus pneumoniae.
37.	Q1RUA7_MEDTR	7463	51	Hypothetical protein.- Medicago truncatula (Barrel medic).
38.	Q54RC0_DICDI	45292	51	Hypothetical protein.- Dictyostelium discoideum AX4.
39.	Q8D787_VIBVU	11586	51	Hypothetical protein.- Vibrio vulnificus.
40.	Q88180_MOUSE	65724	51	Guanine Nucleotide Regulatory Protein.- Mus musculus (Mouse).
41.	Q9FG41_ARATH	73235	50	Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:T25011.- Arabidopsis thaliana (Mouse-ear cress).
42.	Q1IF78_9PSED	98036	50	Hypothetical protein.- Pseudomonas entomophila L48.
43.	Q4YWP1_PLABE	30166	50	Hypothetical protein (Fragment).- Plasmodium berghei.
44.	T35704	16760	50	peptidylprolyl isomerase (EC 5.2.1.8) SC7H1.09 [similarity] - Streptomyces coelicolor
45.	Q57U85_9TRYP	49924	50	Orotidine-5-phosphate decarboxylase/orotate phosphoribosyltransferase, putative (EC 2.4.2.10) (EC 4.1.1.23).- Trypanosoma brucei.
46.	Q4JCP4_SULAC	27674	49	Conserved protein.- Sulfolobus acidocaldarius.
47.	Q9Y355_HUMAN	7429	49	Apolipoprotein A1 (Fragment).- Homo sapiens (Human).
48.	C32055	17279	49	nifX protein - Azotobacter vinelandii
49.	Q5ZWH6_LEGPH	79435	49	Hypothetical protein.- Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 / ATCC 33152 / DSM 7513).
50.	1DM9A	11873	49	hypothetical 15.5 kd protein in mrca-pcka intergenic region, chain A - bacteria

Results List

1.	CAA00975	Mass: 28061	Score: 236	Expect: 8.1e-18	Queries matched: 22
APOA1 PROTEIN (FRAGMENT).- Homo sapiens (Human).					
	Observed	Mr(expt)	Mr(calc)	Delta	Start End Miss Peptide
	781.4592	780.4520	780.4242	0.0278	154 - 160 0 R.AHVDALR.T
	831.4419	830.4346	830.4286	0.0060	189 - 195 0 R.LAEYHAK.A
	873.4641	872.4568	872.4352	0.0217	124 - 131 0 R.AELQEGAR.Q
	1012.6155	1011.6083	1011.5713	0.0370	207 - 215 0 K.AKPALEDLR.Q
	1157.6270	1156.6198	1156.6200	-0.0002	178 - 188 1 R.LEALKENGGAR.L
	1226.5773	1225.5700	1225.5364	0.0336	1 - 10 0 -.DEPPQSPWDR.V
	1230.7044	1229.6971	1229.7019	-0.0048	216 - 226 0 R.QGLLPVLESFK.V
	1235.6798	1234.6726	1234.6809	-0.0083	13 - 23 0 K.DLATVYVDVLK.D
	1252.6795	1251.6722	1251.6135	0.0587	97 - 106 0 K.VQPYLDDFQK.K
	1283.6177	1282.6105	1282.5652	0.0453	108 - 116 0 K.WQEEMELYR.Q
	1299.6059	1298.5987	1298.5601	0.0386	108 - 116 0 K.WQEEMELYR.Q + Oxidation (M)
	1301.6870	1300.6797	1300.6411	0.0385	161 - 171 0 R.THLAPYSDEL.R.Q
	1318.6687	1317.6615	1317.6347	0.0268	141 - 151 1 K.LSPLGEEMRDR.A + Oxidation (M)
	1380.7520	1379.7447	1379.7085	0.0362	97 - 107 1 K.VQPYLDDFQKK.W
	1386.7403	1385.7330	1385.7078	0.0252	227 - 238 0 K.VSFLSALEEYTK.K

1400.6846	1399.6774	1399.6619	0.0155	28	-	40	0	R.DYVSQFEGSALGK.Q
1427.7243	1426.7170	1426.6551	0.0620	107	-	116	1	K.KWQEEMELYSR.Q + Oxidation (M)
1462.8779	1461.8706	1461.8442	0.0264	11	-	23	1	R.VKDLATVYVDVLK.D
1467.8310	1466.8238	1466.7841	0.0397	119	-	131	1	K.VEPLRAELQEGAR.Q
1612.8208	1611.8135	1611.7780	0.0355	46	-	59	0	K.LLDNWDSTSTFSK.L
1815.9168	1814.9096	1814.8434	0.0661	24	-	40	1	K.DSGRDYVSQFEGSALGK.Q
2202.1952	2201.1880	2201.1116	0.0763	60	-	77	1	K.LREQLGPVTQEFWDNLEK.E
No match to: 712.2679, 825.1370, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 876.3626, 877.0567, 1158.6512, 1213.7102, 1224.6023, 1238.8028, 1240.5956, 1242.5818, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1298.6028, 1315.6103, 1334.6603, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1690.6642, 1706.9716, 1723.9839								

2. [AAA51747](#) Mass: 28944 Score: 218 Expect: 5.1e-16 Queries matched: 21

HUMAPOAIC NID: - Homo sapiens								
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
781.4592	780.4520	780.4242	0.0278	160	-	166	0	R.AHVDALR.T
831.4419	830.4346	830.4286	0.0060	195	-	201	0	R.LAEYHAK.A
873.4641	872.4568	872.4352	0.0217	130	-	137	0	R.AELQEGAR.Q
1012.6155	1011.6083	1011.5713	0.0370	213	-	221	0	K.AKPAEDLR.Q
1157.6270	1156.6198	1156.6200	-0.0002	184	-	194	1	R.LEALKENGGAR.L
1230.7044	1229.6971	1229.7019	-0.0048	222	-	232	0	R.QGLLPVLESFK.V
1235.6798	1234.6726	1234.6809	-0.0083	19	-	29	0	K.DLATVYVDVLK.D
1252.6795	1251.6722	1251.6135	0.0587	103	-	112	0	K.VQPYLDDFQK.K
1283.6177	1282.6105	1282.5652	0.0453	114	-	122	0	K.WQEEMELYSR.Q
1299.6059	1298.5987	1298.5601	0.0386	114	-	122	0	K.WQEEMELYSR.Q + Oxidation (M)
1301.6870	1300.6797	1300.6411	0.0385	167	-	177	0	R.THLAPYSDEL.R.Q
1318.6687	1317.6615	1317.6347	0.0268	147	-	157	1	K.LSPLGEEMRDR.A + Oxidation (M)
1380.7520	1379.7447	1379.7085	0.0362	103	-	113	1	K.VQPYLDDFQKK.W
1386.7403	1385.7330	1385.7078	0.0252	233	-	244	0	K.VSFLSALEEYTK.K
1400.6846	1399.6774	1399.6619	0.0155	34	-	46	0	R.DYVSQFEGSALGK.Q
1427.7243	1426.7170	1426.6551	0.0620	113	-	122	1	K.KWQEEMELYSR.Q + Oxidation (M)
1462.8779	1461.8706	1461.8442	0.0264	17	-	29	1	R.VKDLATVYVDVLK.D
1467.8310	1466.8238	1466.7841	0.0397	125	-	137	1	K.VEPLRAELQEGAR.Q
1612.8208	1611.8135	1611.7780	0.0355	52	-	65	0	K.LLDNWDSTSTFSK.L
1815.9168	1814.9096	1814.8434	0.0661	30	-	46	1	K.DSGRDYVSQFEGSALGK.Q
2202.1952	2201.1880	2201.1116	0.0763	66	-	83	1	K.LREQLGPVTQEFWDNLEK.E
No match to: 712.2679, 825.1370, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 876.3626, 877.0567, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1238.8028, 1240.5956, 1242.5818, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1298.6028, 1315.6103, 1334.6603, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1690.6642, 1706.9716, 1723.9839								

3. [LPHUA1](#) Mass: 30759 Score: 208 Expect: 5.1e-15 Queries matched: 21

apolipoprotein A-I precursor [validated] - human								
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
781.4592	780.4520	780.4242	0.0278	178	-	184	0	R.AHVDALR.T
831.4419	830.4346	830.4286	0.0060	213	-	219	0	R.LAEYHAK.A
873.4641	872.4568	872.4352	0.0217	148	-	155	0	R.AELQEGAR.Q
1012.6155	1011.6083	1011.5713	0.0370	231	-	239	0	K.AKPAEDLR.Q
1157.6270	1156.6198	1156.6200	-0.0002	202	-	212	1	R.LEALKENGGAR.L
1230.7044	1229.6971	1229.7019	-0.0048	240	-	250	0	R.QGLLPVLESFK.V
1235.6798	1234.6726	1234.6809	-0.0083	37	-	47	0	K.DLATVYVDVLK.D
1252.6795	1251.6722	1251.6135	0.0587	121	-	130	0	K.VQPYLDDFQK.K
1283.6177	1282.6105	1282.5652	0.0453	132	-	140	0	K.WQEEMELYSR.Q
1299.6059	1298.5987	1298.5601	0.0386	132	-	140	0	K.WQEEMELYSR.Q + Oxidation (M)
1301.6870	1300.6797	1300.6411	0.0385	185	-	195	0	R.THLAPYSDEL.R.Q
1318.6687	1317.6615	1317.6347	0.0268	165	-	175	1	K.LSPLGEEMRDR.A + Oxidation (M)
1380.7520	1379.7447	1379.7085	0.0362	121	-	131	1	K.VQPYLDDFQKK.W
1386.7403	1385.7330	1385.7078	0.0252	251	-	262	0	K.VSFLSALEEYTK.K
1400.6846	1399.6774	1399.6619	0.0155	52	-	64	0	R.DYVSQFEGSALGK.Q
1427.7243	1426.7170	1426.6551	0.0620	131	-	140	1	K.KWQEEMELYSR.Q + Oxidation (M)
1462.8779	1461.8706	1461.8442	0.0264	35	-	47	1	R.VKDLATVYVDVLK.D
1467.8310	1466.8238	1466.7841	0.0397	143	-	155	1	K.VEPLRAELQEGAR.Q

1612.8208 1611.8135 1611.7780 0.0355 70 - 83 0 K.LLDNWDSTSTFSK.L
 1815.9168 1814.9096 1814.8434 0.0661 48 - 64 1 K.DSGRDYVSQFEGSALGK.Q
 2202.1952 2201.1880 2201.1116 0.0763 84 - 101 1 K.LREQLGPVTQEFWDNLEK.E

No match to: 712.2679, 825.1370, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 876.3626, 877.0567, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1238.8028, 1240.5956, 1242.5818, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1298.6028, 1315.6103, 1334.6603, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1690.6642, 1706.9716, 1723.9839

4. [AAX42892](#) Mass: 30872 Score: **207** Expect: 6.5e-15 Queries matched: 21

AY890956 NID: - synthetic construct

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4592	780.4520	780.4242	0.0278	178	- 184	0	R.AHVDALR.T
831.4419	830.4346	830.4286	0.0060	213	- 219	0	R.LAEYHAK.A
873.4641	872.4568	872.4352	0.0217	148	- 155	0	R.AELQEGAR.Q
1012.6155	1011.6083	1011.5713	0.0370	231	- 239	0	K.AKPALEDLR.Q
1157.6270	1156.6198	1156.6200	-0.0002	202	- 212	1	R.LEALKENGGAR.L
1230.7044	1229.6971	1229.7019	-0.0048	240	- 250	0	R.QGLLPVLESFK.V
1235.6798	1234.6726	1234.6809	-0.0083	37	- 47	0	K.DLATVYVDVLK.D
1252.6795	1251.6722	1251.6135	0.0587	121	- 130	0	K.VQPYLDDFQK.K
1283.6177	1282.6105	1282.5652	0.0453	132	- 140	0	K.WQEEMELYR.Q
1299.6059	1298.5987	1298.5601	0.0386	132	- 140	0	K.WQEEMELYR.Q + Oxidation (M)
1301.6870	1300.6797	1300.6411	0.0385	185	- 195	0	R.THLAPYSDEL.R.Q
1318.6687	1317.6615	1317.6347	0.0268	165	- 175	1	K.LSPLGEEMRDR.A + Oxidation (M)
1380.7520	1379.7447	1379.7085	0.0362	121	- 131	1	K.VQPYLDDFQKK.W
1386.7403	1385.7330	1385.7078	0.0252	251	- 262	0	K.VSFLSALEEYTK.K
1400.6846	1399.6774	1399.6619	0.0155	52	- 64	0	R.DYVSQFEGSALGK.Q
1427.7243	1426.7170	1426.6551	0.0620	131	- 140	1	K.KWQEEMELYR.Q + Oxidation (M)
1462.8779	1461.8706	1461.8442	0.0264	35	- 47	1	R.VKDLATVYVDVLK.D
1467.8310	1466.8238	1466.7841	0.0397	143	- 155	1	K.VEPLRAELQEGAR.Q
1612.8208	1611.8135	1611.7780	0.0355	70	- 83	0	K.LLDNWDSTSTFSK.L
1815.9168	1814.9096	1814.8434	0.0661	48	- 64	1	K.DSGRDYVSQFEGSALGK.Q
2202.1952	2201.1880	2201.1116	0.0763	84	- 101	1	K.LREQLGPVTQEFWDNLEK.E

No match to: 712.2679, 825.1370, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 876.3626, 877.0567, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1238.8028, 1240.5956, 1242.5818, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1298.6028, 1315.6103, 1334.6603, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1690.6642, 1706.9716, 1723.9839

5. [AAA35545](#) Mass: 30745 Score: **192** Expect: 2e-13 Queries matched: 20

HUMAPOAIP NID: - Homo sapiens

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4592	780.4520	780.4242	0.0278	178	- 184	0	R.AHVDALR.T
831.4419	830.4346	830.4286	0.0060	213	- 219	0	R.LAEYHAK.A
873.4641	872.4568	872.4352	0.0217	148	- 155	0	R.AELQEGAR.Q
1012.6155	1011.6083	1011.5713	0.0370	231	- 239	0	K.AKPALEDLR.Q
1157.6270	1156.6198	1156.6200	-0.0002	202	- 212	1	R.LEALKENGGAR.L
1230.7044	1229.6971	1229.7019	-0.0048	240	- 250	0	R.QGLLPVLESFK.V
1235.6798	1234.6726	1234.6809	-0.0083	37	- 47	0	K.DLATVYVDVLK.D
1252.6795	1251.6722	1251.6135	0.0587	121	- 130	0	K.VQPYLDDFQK.K
1283.6177	1282.6105	1282.5652	0.0453	132	- 140	0	K.WQEEMELYR.Q
1299.6059	1298.5987	1298.5601	0.0386	132	- 140	0	K.WQEEMELYR.Q + Oxidation (M)
1301.6870	1300.6797	1300.6411	0.0385	185	- 195	0	R.THLAPYSDEL.R.Q
1318.6687	1317.6615	1317.6347	0.0268	165	- 175	1	K.LSPLGEEMRDR.A + Oxidation (M)
1380.7520	1379.7447	1379.7085	0.0362	121	- 131	1	K.VQPYLDDFQKK.W
1386.7403	1385.7330	1385.7078	0.0252	251	- 262	0	K.VSFLSALEEYTK.K
1400.6846	1399.6774	1399.6619	0.0155	52	- 64	0	R.DYVSQFEGSALGK.Q
1427.7243	1426.7170	1426.6551	0.0620	131	- 140	1	K.KWQEEMELYR.Q + Oxidation (M)
1462.8779	1461.8706	1461.8442	0.0264	35	- 47	1	R.VKDLATVYVDVLK.D
1612.8208	1611.8135	1611.7780	0.0355	70	- 83	0	K.LLDNWDSTSTFSK.L
1815.9168	1814.9096	1814.8434	0.0661	48	- 64	1	K.DSGRDYVSQFEGSALGK.Q
2202.1952	2201.1880	2201.1116	0.0763	84	- 101	1	K.LREQLGPVTQEFWDNLEK.E

No match to: 712.2679, 825.1370, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 876.3626, 877.0567, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1238.8028, 1240.5956, 1242.5818, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1298.6028, 1315.6103, 1334.6603, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1467.8310, 1690.6642, 1706.9716, 1723.9839

6. [CAA03490](#) Mass: 23205 Score: **160** Expect: 3.2e-10 Queries matched: 17

SEQUENCE 10 FROM PATENT W09637608.- unidentified.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4592	780.4520	780.4242	0.0278	111	- 117	0	R.AHVDALR.T
831.4419	830.4346	830.4286	0.0060	146	- 152	0	R.LAEYHAK.A
873.4641	872.4568	872.4352	0.0217	81	- 88	0	R.AELQEGAR.Q
1012.6155	1011.6083	1011.5713	0.0370	164	- 172	0	K.AKPALEDLR.Q
1157.6270	1156.6198	1156.6200	-0.0002	135	- 145	1	R.LEALKENGGAR.L
1226.5773	1225.5700	1225.5986	-0.0286	107	- 117	1	R.DCARAHVDALR.T
1230.7044	1229.6971	1229.7019	-0.0048	173	- 183	0	R.QGLLPVLESFK.V
1252.6795	1251.6722	1251.6135	0.0587	54	- 63	0	K.VQPYLDDFQK.K
1283.6177	1282.6105	1282.6200	-0.0096	107	- 117	1	R.DCARAHVDALR.T + Carbamidomethyl (C)
1299.6059	1298.5987	1298.5601	0.0386	65	- 73	0	K.WQEEMELR.Q + Oxidation (M)
1301.6870	1300.6797	1300.6411	0.0385	118	- 128	0	R.THLAPYSDEL.R.Q
1380.7520	1379.7447	1379.7085	0.0362	54	- 64	1	K.VQPYLDDFQKK.W
1386.7403	1385.7330	1385.7078	0.0252	184	- 195	0	K.VSFLSALEEYTK.K
1427.7243	1426.7170	1426.6551	0.0620	64	- 73	1	K.KWQEEMELR.Q + Oxidation (M)
1467.8310	1466.8238	1466.7841	0.0397	76	- 88	1	K.VEPLRAELQEGAR.Q
1612.8208	1611.8135	1611.7780	0.0355	3	- 16	0	K.LLDNWDVTSTFSK.L
2202.1952	2201.1880	2201.1116	0.0763	17	- 34	1	K.LREQLGPVTQEFWDNLEK.E

No match to: 712.2679, 825.1370, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 876.3626, 877.0567, 1158.6512, 1213.7102, 1224.6023, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1298.6028, 1315.6103, 1318.6687, 1334.6603, 1400.6846, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1462.8779, 1690.6642, 1706.9716, 1723.9839, 1815.9168

7. [1AV1A](#) Mass: 23389 Score: **160** Expect: 3.2e-10 Queries matched: 17

apolipoprotein a-i lipid-binding domain mutant N-TERMINAL MET, DEL(1-43), chain A - human

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4592	780.4520	780.4242	0.0278	112	- 118	0	R.AHVDALR.T
831.4419	830.4346	830.4286	0.0060	147	- 153	0	R.LAEYHAK.A
873.4641	872.4568	872.4352	0.0217	82	- 89	0	R.AELQEGAR.Q
1012.6155	1011.6083	1011.5713	0.0370	165	- 173	0	K.AKPALEDLR.Q
1157.6270	1156.6198	1156.6200	-0.0002	136	- 146	1	R.LEALKENGGAR.L
1230.7044	1229.6971	1229.7019	-0.0048	174	- 184	0	R.QGLLPVLESFK.V
1252.6795	1251.6722	1251.6135	0.0587	55	- 64	0	K.VQPYLDDFQK.K
1283.6177	1282.6105	1282.5652	0.0453	66	- 74	0	K.WQEEMELR.Q
1299.6059	1298.5987	1298.5601	0.0386	66	- 74	0	K.WQEEMELR.Q + Oxidation (M)
1301.6870	1300.6797	1300.6411	0.0385	119	- 129	0	R.THLAPYSDEL.R.Q
1318.6687	1317.6615	1317.6347	0.0268	99	- 109	1	K.LSPLGEEMRDR.A + Oxidation (M)
1380.7520	1379.7447	1379.7085	0.0362	55	- 65	1	K.VQPYLDDFQKK.W
1386.7403	1385.7330	1385.7078	0.0252	185	- 196	0	K.VSFLSALEEYTK.K
1427.7243	1426.7170	1426.6551	0.0620	65	- 74	1	K.KWQEEMELR.Q + Oxidation (M)
1467.8310	1466.8238	1466.7841	0.0397	77	- 89	1	K.VEPLRAELQEGAR.Q
1612.8208	1611.8135	1611.7780	0.0355	4	- 17	0	K.LLDNWDVTSTFSK.L
2202.1952	2201.1880	2201.1116	0.0763	18	- 35	1	K.LREQLGPVTQEFWDNLEK.E

No match to: 712.2679, 825.1370, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 876.3626, 877.0567, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1298.6028, 1315.6103, 1334.6603, 1400.6846, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1462.8779, 1690.6642, 1706.9716, 1723.9839, 1815.9168

8. [Q8HZ97_PANTR](#) Mass: 22075 Score: **130** Expect: 3.2e-07 Queries matched: 14

Apolipoprotein A-I (Fragment).- Pan troglodytes (Chimpanzee).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4592	780.4520	780.4242	0.0278	141	- 147	0	R.AHVDALR.T
831.4419	830.4346	830.4286	0.0060	176	- 182	0	R.LAEYHAK.A
873.4641	872.4568	872.4352	0.0217	111	- 118	0	R.AELQEGAR.Q
1157.6270	1156.6198	1156.6200	-0.0002	165	- 175	1	R.LEALKENGGAR.L
1252.6795	1251.6722	1251.6135	0.0587	84	- 93	0	K.VQPYLDDFQK.K

1283.6177	1282.6105	1282.5652	0.0453	95 - 103	0	K.WQEEMELLYR.Q
1299.6059	1298.5987	1298.5601	0.0386	95 - 103	0	K.WQEEMELLYR.Q + Oxidation (M)
1301.6870	1300.6797	1300.6411	0.0385	148 - 158	0	R.THLAPYSDEL.R.Q
1380.7520	1379.7447	1379.7085	0.0362	84 - 94	1	K.VQPYLDDFQK.K.W
1400.6846	1399.6774	1399.6619	0.0155	15 - 27	0	R.DYVSQFEGSALGK.Q
1427.7243	1426.7170	1426.6551	0.0620	94 - 103	1	K.KWQEEMELLYR.Q + Oxidation (M)
1612.8208	1611.8135	1611.7780	0.0355	33 - 46	0	K.LLDNWDSTSTFSK.L
1815.9168	1814.9096	1814.8434	0.0661	11 - 27	1	K.DSGRDYVSQFEGSALGK.Q
2202.1952	2201.1880	2201.1116	0.0763	47 - 64	1	K.LREQLGPTQEFWDNLEK.E

No match to: 712.2679, 825.1370, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 876.3626, 877.0567, 1012.6155, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1298.6028, 1315.6103, 1318.6687, 1334.6603, 1386.7403, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1462.8779, 1467.8310, 1690.6642, 1706.9716, 1723.9839

9. [Q8HZ95_PONPY](#) Mass: 22116 Score: **113** Expect: 1.6e-05 Queries matched: 13

Apolipoprotein A-I (Fragment). - Pongo pygmaeus (Orangutan).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4592	780.4520	780.4242	0.0278	141 - 147	0		R.AHVDALR.T
831.4419	830.4346	830.4286	0.0060	176 - 182	0		R.LAEYHAK.A
873.4641	872.4568	872.4352	0.0217	111 - 118	0		R.AELQEGAR.Q
1157.6270	1156.6198	1156.6200	-0.0002	165 - 175	1		R.LEALKENGGAR.L
1252.6795	1251.6722	1251.6135	0.0587	84 - 93	0		K.VQPYLDDFQK.K
1283.6177	1282.6105	1282.5652	0.0453	95 - 103	0		K.WQEEMELLYR.Q
1299.6059	1298.5987	1298.5601	0.0386	95 - 103	0		K.WQEEMELLYR.Q + Oxidation (M)
1315.6103	1314.6030	1314.6568	-0.0538	148 - 158	0		R.THLAPYTDLR.Q
1380.7520	1379.7447	1379.7085	0.0362	84 - 94	1		K.VQPYLDDFQK.K.W
1400.6846	1399.6774	1399.6619	0.0155	15 - 27	0		R.DYVSQFEGSALGK.Q
1427.7243	1426.7170	1426.6551	0.0620	94 - 103	1		K.KWQEEMELLYR.Q + Oxidation (M)
1815.9168	1814.9096	1814.8434	0.0661	11 - 27	1		K.DSGRDYVSQFEGSALGK.Q
2202.1952	2201.1880	2201.1116	0.0763	47 - 64	1		K.LREQLGPTQEFWDNLEK.E

No match to: 712.2679, 825.1370, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 876.3626, 877.0567, 1012.6155, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1298.6028, 1301.6870, 1318.6687, 1334.6603, 1386.7403, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839

10. [A26529](#) Mass: 30700 Score: **107** Expect: 6.5e-05 Queries matched: 14

apolipoprotein A-I precursor - crab-eating macaque

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4592	780.4520	780.4242	0.0278	178 - 184	0		R.AHVDALR.T
831.4419	830.4346	830.4286	0.0060	213 - 219	0		R.LAEYHAK.A
1012.6155	1011.6083	1011.5713	0.0370	231 - 239	0		K.AKPALEDLR.Q
1157.6270	1156.6198	1156.6200	-0.0002	202 - 212	1		R.LEALKENGGAR.L
1230.7044	1229.6971	1229.7019	-0.0048	240 - 250	0		R.QGLLPVLESFK.V
1252.6795	1251.6722	1251.6135	0.0587	121 - 130	0		K.VQPYLDDFQK.K
1283.6177	1282.6105	1282.5652	0.0453	132 - 140	0		K.WQEEMELLYR.Q
1299.6059	1298.5987	1298.5601	0.0386	132 - 140	0		K.WQEEMELLYR.Q + Oxidation (M)
1301.6870	1300.6797	1300.6411	0.0385	185 - 195	0		R.THLAPYSDEL.R.Q
1380.7520	1379.7447	1379.7085	0.0362	121 - 131	1		K.VQPYLDDFQK.K.W
1386.7403	1385.7330	1385.7078	0.0252	251 - 262	0		K.VSFLSALEEYTK.K
1400.6846	1399.6774	1399.6619	0.0155	52 - 64	0		K.DYVSQFEGSALGK.Q
1427.7243	1426.7170	1426.6551	0.0620	131 - 140	1		K.KWQEEMELLYR.Q + Oxidation (M)
2202.1952	2201.1880	2201.1116	0.0763	84 - 101	1		K.LREQLGPTQEFWDNLEK.E

No match to: 712.2679, 825.1370, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1298.6028, 1315.6103, 1318.6687, 1334.6603, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168

11. [JS0079](#) Mass: 30716 Score: **107** Expect: 6.5e-05 Queries matched: 14

apolipoprotein A-I precursor - baboon

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4592	780.4520	780.4242	0.0278	178 - 184	0		R.AHVDALR.T
831.4419	830.4346	830.4286	0.0060	213 - 219	0		R.LAEYHAK.A
1012.6155	1011.6083	1011.5713	0.0370	231 - 239	0		K.AKPALEDLR.Q

1157.6270	1156.6198	1156.6200	-0.0002	202 - 212	1	R.LEALKENGGAR.L
1230.7044	1229.6971	1229.7019	-0.0048	240 - 250	0	R.QGLLPVLESFK.V
1252.6795	1251.6722	1251.6135	0.0587	121 - 130	0	K.VQPYLDDFQK.K
1283.6177	1282.6105	1282.5652	0.0453	132 - 140	0	K.WQEEMELYR.Q
1299.6059	1298.5987	1298.5601	0.0386	132 - 140	0	K.WQEEMELYR.Q + Oxidation (M)
1301.6870	1300.6797	1300.6411	0.0385	185 - 195	0	R.THLAPYSDEL.R.Q
1380.7520	1379.7447	1379.7085	0.0362	121 - 131	1	K.VQPYLDDFQKK.W
1386.7403	1385.7330	1385.7078	0.0252	251 - 262	0	K.VSFLSALEEYTK.K
1400.6846	1399.6774	1399.6619	0.0155	52 - 64	0	K.DYVSQFEGSALGK.Q
1427.7243	1426.7170	1426.6551	0.0620	131 - 140	1	K.KWQEEMELYR.Q + Oxidation (M)
2202.1952	2201.1880	2201.1116	0.0763	84 - 101	1	K.LREQLGPVTQEFWDNLEK.E

No match to: 712.2679, 825.1370, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1298.6028, 1315.6103, 1318.6687, 1334.6603, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168

12. [CAD61352](#) Mass: 18392 Score: 74 Expect: 0.14 Queries matched: 9

Sequence 2 from Patent W002083898 precursor.- Homo sapiens (Human).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1235.6798	1234.6726	1234.6809	-0.0083	37 - 47	0		K.DLATVYVDVLK.D
1252.6795	1251.6722	1251.6135	0.0587	121 - 130	0		K.VQPYLDDFQK.K
1283.6177	1282.6105	1282.5652	0.0453	132 - 140	0		K.WQEEMELYR.Q
1299.6059	1298.5987	1298.5601	0.0386	132 - 140	0		K.WQEEMELYR.Q + Oxidation (M)
1380.7520	1379.7447	1379.7085	0.0362	121 - 131	1		K.VQPYLDDFQKK.W
1400.6846	1399.6774	1399.6619	0.0155	52 - 64	0		R.DYVSQFEGSALGK.Q
1427.7243	1426.7170	1426.6551	0.0620	131 - 140	1		K.KWQEEMELYR.Q + Oxidation (M)
1462.8779	1461.8706	1461.8442	0.0264	35 - 47	1		R.VKDLATVYVDVLK.D
1815.9168	1814.9096	1814.8434	0.0661	48 - 64	1		K.DSGRDYVSQFEGSALGK.Q

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1238.8028, 1240.5956, 1242.5818, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1298.6028, 1301.6870, 1315.6103, 1318.6687, 1334.6603, 1386.7403, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 2202.1952

13. [Q31VN4_SHIBS](#) Mass: 15504 Score: 69 Expect: 0.44 Queries matched: 10

Hypothetical protein yrfH.- Shigella boydii serotype 4 (strain Sb227).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
852.4849	851.4776	851.3993	0.0783	96 - 102	1		R.EKMAMAR.K + Oxidation (M)
873.4641	872.4568	872.4253	0.0316	36 - 42	0		K.VHYNGQR.S
1158.6512	1157.6440	1157.6345	0.0094	11 - 19	1		R.LDKWLWAAR.F
1240.5956	1239.5884	1239.6553	-0.0669	14 - 22	1		K.WLWAARFYK.T
1257.6582	1256.6509	1256.7452	-0.0943	65 - 75	1		R.TVIVKAITEQR.R
1257.7440	1256.7367	1256.7452	-0.0085	65 - 75	1		R.TVIVKAITEQR.R
1258.5811	1257.5738	1257.6677	-0.0939	59 - 69	1		R.QGNDERTVIVK.A
1283.6177	1282.6105	1282.7244	-0.1140	3 - 13	1		K.EKPAVEVRLDK.W
1400.6846	1399.6774	1399.7320	-0.0546	36 - 47	1		K.VHYNGQRSKPSK.I
1408.7587	1407.7515	1407.7292	0.0222	103 - 114	1		R.KLNALTMPHPDR.R + Oxidation (M)

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 833.3959, 841.0980, 853.5010, 861.0837, 876.3626, 877.0567, 1012.6155, 1157.6270, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1242.5818, 1252.6795, 1274.6199, 1282.5765, 1298.6028, 1299.6059, 1301.6870, 1315.6103, 1318.6687, 1334.6603, 1380.7520, 1386.7403, 1402.7407, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168, 2202.1952

14. [Q8ZLJ5_SALTY](#) Mass: 15511 Score: 68 Expect: 0.5 Queries matched: 10

Heat shock protein.- Salmonella typhimurium.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
833.3959	832.3886	832.4225	-0.0339	96 - 102	1		R.EKMAQAR.K
873.4641	872.4568	872.4253	0.0316	36 - 42	0		K.VHYNGQR.S
1158.6512	1157.6440	1157.6345	0.0094	11 - 19	1		R.LDKWLWAAR.F
1224.6023	1223.5950	1223.5638	0.0313	25 - 35	1		R.AMAREMIEGK.V + 2 Oxidation (M)
1240.5956	1239.5884	1239.6553	-0.0669	14 - 22	1		K.WLWAARFYK.T
1257.6582	1256.6509	1256.7452	-0.0943	65 - 75	1		R.TVIVKAITEQR.R
1257.7440	1256.7367	1256.7452	-0.0085	65 - 75	1		R.TVIVKAITEQR.R

1258.5811 1257.5738 1257.6677 -0.0939 59 - 69 1 R.QGNDERTVIVK.A
 1400.6846 1399.6774 1399.7320 -0.0546 36 - 47 1 K.VHYNGQRSKPSK.I
 1408.7587 1407.7515 1407.7292 0.0222 103 - 114 1 R.KLNALTMPPDR.R + Oxidation (M)
No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 841.0980, 852.4849, 853.5010, 861.0837, 876.3626, 877.0567, 1012.6155, 1157.6270,
 1213.7102, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1242.5818, 1252.6795, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1301.6870, 1315.6103,
 1318.6687, 1334.6603, 1380.7520, 1386.7403, 1402.7407, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839,
 1815.9168, 2202.1952

15. [H86004](#) Mass: 15486 Score: 61 Expect: 2.7 Queries matched: 9

ribosome-associated heat shock protein yrfH [similarity] - Escherichia coli (strain 0157:H7, substrain EDL933)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
873.4641	872.4568	872.4253	0.0316	36	-	42	0 K.VHYNGQR.S
1158.6512	1157.6440	1157.6345	0.0094	11	-	19	1 R.LDKWLWAAR.F
1240.5956	1239.5884	1239.6553	-0.0669	14	-	22	1 K.WLWAARFYK.T
1257.6582	1256.6509	1256.7452	-0.0943	65	-	75	1 R.TVIVKAITEQR.R
1257.7440	1256.7367	1256.7452	-0.0085	65	-	75	1 R.TVIVKAITEQR.R
1258.5811	1257.5738	1257.6677	-0.0939	59	-	69	1 R.QGNDERTVIVK.A
1283.6177	1282.6105	1282.7244	-0.1140	3	-	13	1 K.EKPAVEVRLDK.W
1400.6846	1399.6774	1399.7320	-0.0546	36	-	47	1 K.VHYNGQRSKPSK.I
1408.7587	1407.7515	1407.7292	0.0222	103	-	114	1 R.KLNALTMPPDR.R + Oxidation (M)

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 876.3626, 877.0567, 1012.6155, 1157.6270,
 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1242.5818, 1252.6795, 1274.6199, 1282.5765, 1298.6028, 1299.6059, 1301.6870, 1315.6103,
 1318.6687, 1334.6603, 1380.7520, 1386.7403, 1402.7407, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839,
 1815.9168, 2202.1952

16. [H97327](#) Mass: 17433 Score: 59 Expect: 3.9 Queries matched: 7

transcription regulator, MarR/EmrR family [imported] - Clostridium acetobutylicum

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
832.3588	831.3515	831.3835	-0.0320	2	-	8	0 M.NNNTQNK.T
1158.6512	1157.6440	1157.5352	0.1087	121	-	129	1 K.EKESAFYER.I
1213.7102	1212.7029	1212.6138	0.0891	123	-	132	1 K.ESAFYERIAK.W
1224.6023	1223.5950	1223.5928	0.0022	70	-	80	1 K.SIAMDRSSVSR.L + Oxidation (M)
1230.7044	1229.6971	1229.7091	-0.0120	76	-	86	1 R.SSVSRLVNQLK.N
1318.6687	1317.6615	1317.6021	0.0593	2	-	12	1 M.NNNTQNKTDNR.I
1422.7041	1421.6968	1421.7700	-0.0732	81	-	92	1 R.LVNQLKNMGYVK.S + Oxidation (M)

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270,
 1226.5773, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059,
 1301.6870, 1315.6103, 1334.6603, 1380.7520, 1386.7403, 1400.6846, 1402.7407, 1408.7587, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642,
 1706.9716, 1723.9839, 1815.9168, 2202.1952

17. [Q57IX7_SALCH](#) Mass: 15557 Score: 59 Expect: 4.2 Queries matched: 10

Heat shock protein, predicted small RNA-binding protein.- Salmonella choleraesuis.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
833.3959	832.3886	832.4225	-0.0339	96	-	102	1 R.EKMAQAR.K
873.4641	872.4568	872.4253	0.0316	36	-	42	0 K.VHYNGQR.S
1158.6512	1157.6440	1157.6345	0.0094	11	-	19	1 R.LDKWLWAAR.F
1240.5956	1239.5884	1239.6553	-0.0669	14	-	22	1 K.WLWAARFYK.T
1257.6582	1256.6509	1256.7452	-0.0943	65	-	75	1 R.TVIVKAITEQR.R
1257.7440	1256.7367	1256.7452	-0.0085	65	-	75	1 R.TVIVKAITEQR.R
1258.5811	1257.5738	1257.6677	-0.0939	59	-	69	1 R.QGNDERTVIVK.A
1400.6846	1399.6774	1399.7320	-0.0546	36	-	47	1 K.VHYNGQRSKPSK.I
1408.7587	1407.7515	1407.7292	0.0222	103	-	114	1 R.KLNALTMPPDR.R
1424.7200	1423.7128	1423.7242	-0.0114	103	-	114	1 R.KLNALTMPPDR.R + Oxidation (M)

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 841.0980, 852.4849, 853.5010, 861.0837, 876.3626, 877.0567, 1012.6155, 1157.6270,
 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1242.5818, 1252.6795, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1301.6870,
 1315.6103, 1318.6687, 1334.6603, 1380.7520, 1386.7403, 1402.7407, 1422.7041, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839,
 1815.9168, 2202.1952

18. [Q5PLY1_SALPA](#) Mass: 15465 Score: 58 Expect: 4.8 Queries matched: 9

Heat shock protein.- Salmonella paratyphi-a.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
833.3959	832.3886	832.4225	-0.0339	96	-	102	1 R.EKMAQAR.K
873.4641	872.4568	872.4253	0.0316	36	-	42	0 K.VHYNGQR.S
1158.6512	1157.6440	1157.6345	0.0094	11	-	19	1 R.LDKWLWAAR.F
1240.5956	1239.5884	1239.6553	-0.0669	14	-	22	1 K.WLWAARFYK.T
1257.6582	1256.6509	1256.7452	-0.0943	65	-	75	1 R.TVIVKAITEQR.R
1257.7440	1256.7367	1256.7452	-0.0085	65	-	75	1 R.TVIVKAITEQR.R
1258.5811	1257.5738	1257.6677	-0.0939	59	-	69	1 R.QGNDERTVIVK.A
1400.6846	1399.6774	1399.7320	-0.0546	36	-	47	1 K.VHYNGQRSKPSK.I
1408.7587	1407.7515	1407.7292	0.0222	103	-	114	1 R.KLNALTMPHPDR.R + Oxidation (M)
No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 841.0980, 852.4849, 853.5010, 861.0837, 876.3626, 877.0567, 1012.6155, 1157.6270, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1242.5818, 1252.6795, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1301.6870, 1315.6103, 1318.6687, 1334.6603, 1380.7520, 1386.7403, 1402.7407, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168, 2202.1952							

19. [Q7SD03_NEUCR](#) Mass: 189062 Score: 57 Expect: 6.6 Queries matched: 20

Hypothetical protein NCU03060.1.- Neurospora crassa.							
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
831.4419	830.4346	830.4359	-0.0013	138	-	144	0 R.SSRPTQR.R
1012.6155	1011.6083	1011.5461	0.0622	1618	-	1626	1 R.DIDRGAPIR.H
1157.6270	1156.6198	1156.5948	0.0249	1171	-	1180	1 R.AVDANNERLR.E
1224.6023	1223.5950	1223.6220	-0.0269	813	-	822	0 K.MLDILGDYLR.V + Oxidation (M)
1226.5773	1225.5700	1225.5947	-0.0247	1533	-	1542	1 R.LQRMFGDLCK.K + Oxidation (M)
1230.7044	1229.6971	1229.6615	0.0356	913	-	922	1 K.QTIEEEVVKR.A
1235.6798	1234.6726	1234.7172	-0.0447	1319	-	1329	0 R.SEYLLSVLLAK.H
1242.5818	1241.5745	1241.5896	-0.0151	1464	-	1473	1 K.ANMERIMYSK.E
1258.5811	1257.5738	1257.5845	-0.0107	1464	-	1473	1 K.ANMERIMYSK.E + Oxidation (M)
1274.6199	1273.6126	1273.5795	0.0332	1464	-	1473	1 K.ANMERIMYSK.E + 2 Oxidation (M)
1283.6177	1282.6105	1282.6162	-0.0057	1533	-	1542	1 R.LQRMFGDLCK.K + Carbamidomethyl (C); Oxidation (M)
1298.6028	1297.5955	1297.6989	-0.1035	1181	-	1192	1 R.EEEARAGKPLAK.K
1318.6687	1317.6615	1317.5684	0.0930	1099	-	1108	0 R.EEQEELEEQR.A
1402.7407	1401.7335	1401.6120	0.1214	659	-	670	1 K.GPTDEEQDEARR.I
1408.7587	1407.7515	1407.6590	0.0925	97	-	110	0 R.SAQSNVVSASSSR.T
1422.7041	1421.6968	1421.7667	-0.0698	490	-	501	0 K.TVQSVSFLSWLR.N
1424.7200	1423.7128	1423.6983	0.0145	550	-	561	1 R.DYELFVDGNPKK.T
1612.8208	1611.8135	1611.8580	-0.0445	1357	-	1373	1 R.RGEASSISGSPAPLGVK.K
1815.9168	1814.9096	1814.8758	0.0337	1557	-	1572	1 K.KPSRQDLEDGEIASDR.D
2202.1952	2201.1880	2200.9847	0.2032	1276	-	1292	1 R.DDPELQMHDKFFLEEHR.V + Oxidation (M)
No match to: 712.2679, 781.4592, 825.1370, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1158.6512, 1213.7102, 1238.8028, 1240.5956, 1252.6795, 1257.6582, 1257.7440, 1282.5765, 1299.6059, 1301.6870, 1315.6103, 1334.6603, 1380.7520, 1386.7403, 1400.6846, 1427.7243, 1462.8779, 1467.8310, 1690.6642, 1706.9716, 1723.9839							

20. [Q5ZVU0_LEGPH](#) Mass: 41536 Score: 56 Expect: 7.6 Queries matched: 9

L-lysine dehydrogenase.- Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 / ATCC 33152 / DSM 7513).							
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
832.3588	831.3515	831.4061	-0.0546	257	-	263	1 R.YPGHCKK.M
1224.6023	1223.5950	1223.6584	-0.0633	2	-	12	0 M.IICVGLSSFTK.E + Carbamidomethyl (C)
1242.5818	1241.5745	1241.6880	-0.1135	363	-	372	1 K.FKLSHVLENR.F
1298.6028	1297.5955	1297.6774	-0.0819	1	-	12	0 -.MIICVGLSSFTK.E
1299.6059	1298.5987	1298.7095	-0.1108	365	-	375	1 K.LSHVLENRFGK.Y
1402.7407	1401.7335	1401.6090	0.1244	15	-	27	0 K.DCMYNYMITGAGK.I
1424.7200	1423.7128	1423.7744	-0.0617	2	-	14	1 M.IICVGLSSFTKEK.D
1612.8208	1611.8135	1611.8364	-0.0229	1	-	14	1 -.MIICVGLSSFTKEK.D + Carbamidomethyl (C)
1723.9839	1722.9766	1723.0495	-0.0728	59	-	74	1 R.LLTALPEIKTVALDVK.D
No match to: 712.2679, 781.4592, 825.1370, 831.4419, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1158.6512, 1213.7102, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1240.5956, 1252.6795, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1283.6177, 1301.6870, 1315.6103, 1318.6687, 1334.6603, 1380.7520, 1386.7403, 1400.6846, 1408.7587, 1422.7041, 1427.7243, 1462.8779, 1467.8310, 1690.6642, 1706.9716, 1815.9168, 2202.1952							

21. [B72212](#) Mass: 20862 Score: 56 Expect: 8.3 Queries matched: 7

translation elongation factor P - *Thermotoga maritima* (strain MSB8)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
----------	----------	----------	-------	-------	-----	------	---------

781.4592	780.4520	780.3766	0.0754	178	-	184	0 R.TGEYVGR.A
831.4419	830.4346	830.4974	-0.0628	33	-	40	1 R.GSGLIRTK.L
852.4849	851.4776	851.4137	0.0640	178	-	185	1 R.TGEYVGRA.-
1230.7044	1229.6971	1229.6451	0.0520	28	-	38	1 K.HFMGRGSLIR.T
1252.6795	1251.6722	1251.6207	0.0515	174	-	184	1 K.VDTRTGEYVGR.A
1274.6199	1273.6126	1273.6601	-0.0474	22	-	32	1 R.VLEASKHFMGR.G
1380.7520	1379.7447	1379.7336	0.0111	160	-	171	0 K.ITVPYFIEVGDK.I

No match to: 712.2679, 825.1370, 832.3588, 833.3959, 841.0980, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1257.6582, 1257.7440, 1258.5811, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1301.6870, 1315.6103, 1318.6687, 1334.6603, 1386.7403, 1400.6846, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168, 2202.1952

22. [Q19Y36_9CAUD](#) Mass: 12275 Score: 55 Expect: 11 Queries matched: 6

Gp24.- Mycobacteriophage Wildcat.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
----------	----------	----------	-------	-------	-----	------	---------

853.5010	852.4937	852.4857	0.0080	63	-	69	1 R.KLFNFGK.S
1226.5773	1225.5700	1225.6302	-0.0602	35	-	45	0 K.SSVANLELEHK.A
1235.6798	1234.6726	1234.6193	0.0532	70	-	80	0 K.SPVFTTEDLAR.A
1282.5765	1281.5692	1281.6465	-0.0773	83	-	92	1 R.VVYFERAQR.L
1386.7403	1385.7330	1385.7554	-0.0224	5	-	17	0 K.AIVQLPDGSYVPK.H
1462.8779	1461.8706	1461.7576	0.1130	70	-	82	1 K.SPVFTTEDLARAR.V

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 833.3959, 841.0980, 852.4849, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1158.6512, 1213.7102, 1224.6023, 1230.7044, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1283.6177, 1298.6028, 1299.6059, 1301.6870, 1315.6103, 1318.6687, 1334.6603, 1380.7520, 1400.6846, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168, 2202.1952

23. [Q2WWQ7_9GAMM](#) Mass: 12361 Score: 53 Expect: 15 Queries matched: 7Hypothetical protein.- *Shewanella* sp. W3-18-1.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
----------	----------	----------	-------	-------	-----	------	---------

833.3959	832.3886	832.4225	-0.0339	32	-	38	1 R.NKQMGK.Y
852.4849	851.4776	851.4977	-0.0201	65	-	71	1 K.KHQLAQK.E
853.5010	852.4937	852.4341	0.0596	42	-	48	0 K.SLDYSLR.R
1230.7044	1229.6971	1229.6364	0.0607	23	-	33	1 K.VSADLEQARNK.Q
1257.6582	1256.6509	1256.6765	-0.0255	39	-	48	1 K.YIKSLDYSLR.R
1257.7440	1256.7367	1256.6765	0.0602	39	-	48	1 K.YIKSLDYSLR.R
2202.1952	2201.1880	2201.0375	0.1504	2	-	21	0 M.TTDIDLQSAIAALDEYGYDK.K

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 841.0980, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1258.5811, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1301.6870, 1315.6103, 1318.6687, 1334.6603, 1380.7520, 1386.7403, 1400.6846, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168

24. [Q2ZS56_SHEPU](#) Mass: 12333 Score: 53 Expect: 15 Queries matched: 7Hypothetical protein.- *Shewanella putrefaciens* CN-32.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
----------	----------	----------	-------	-------	-----	------	---------

833.3959	832.3886	832.4225	-0.0339	32	-	38	1 R.NKQMGK.Y
852.4849	851.4776	851.4977	-0.0201	65	-	71	1 K.KHQLAQK.E
853.5010	852.4937	852.4341	0.0596	42	-	48	0 K.SLDYSLR.R
1230.7044	1229.6971	1229.6364	0.0607	23	-	33	1 K.VSADLEQARNK.Q
1257.6582	1256.6509	1256.6765	-0.0255	39	-	48	1 K.YIKSLDYSLR.R
1257.7440	1256.7367	1256.6765	0.0602	39	-	48	1 K.YIKSLDYSLR.R
2202.1952	2201.1880	2201.0375	0.1504	2	-	21	0 M.TTDIDLQSAIAALDEYGYDK.K

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 841.0980, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1258.5811, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1301.6870, 1315.6103, 1318.6687, 1334.6603, 1380.7520, 1386.7403, 1400.6846, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168

25. [Q833F6_ENTFA](#) Mass: 106075 Score: 53 Expect: 16 Queries matched: 13Tape measure protein, putative.- *Enterococcus faecalis* (*Streptococcus faecalis*).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1230.7044	1229.6971	1229.7053	-0.0082	566	-	576	0 K.MIAENVVITLK.N
1235.6798	1234.6726	1234.7146	-0.0420	844	-	855	1 K.IKGALGIHSPSR.W
1252.6795	1251.6722	1251.6467	0.0255	548	-	558	1 K.NAFKMVVNAMK.A
1257.6582	1256.6509	1256.5495	0.1014	442	-	452	0 K.EAFSNAGTWMK.E + Oxidation (M)
1258.5811	1257.5738	1257.6353	-0.0615	753	-	763	0 K.DGIINGWENLK.Q
1274.6199	1273.6126	1273.7176	-0.1050	255	-	266	1 K.TGLANMKTAVR.G
1315.6103	1314.6030	1314.6244	-0.0214	471	-	481	0 K.EFFSGLWNSTK.E
1386.7403	1385.7330	1385.7514	-0.0184	234	-	247	1 K.EGGGGLKSLEQIAK.D
1402.7407	1401.7335	1401.7463	-0.0128	128	-	141	0 K.GVQLIASSTNDLGK.S
1408.7587	1407.7515	1407.8166	-0.0651	654	-	664	0 K.LFFTLLWIDIK.Y
1422.7041	1421.6968	1421.7184	-0.0215	248	-	261	1 K.DSTAGIKTGLANMK.T + Oxidation (M)
1427.7243	1426.7170	1426.7204	-0.0034	453	-	465	1 K.EVPGNAADWVKNK.W
1467.8310	1466.8238	1466.7564	0.0673	846	-	858	1 K.GALGIHSPSRWMMR.D
No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1238.8028, 1240.5956, 1242.5818, 1257.7440, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1301.6870, 1318.6687, 1334.6603, 1380.7520, 1400.6846, 1424.7200, 1462.8779, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168, 2202.1952							

26. [AAL97589](#) Mass: 22480 Score: 53 Expect: 17 Queries matched: 7

AE010023 NID: - Streptococcus pyogenes MGAS8232							
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1157.6270	1156.6198	1156.5434	0.0764	101	-	109	0 K.MIEEYLTSR.D + Oxidation (M)
1158.6512	1157.6440	1157.6516	-0.0077	54	-	64	1 K.NLARTSSKPGK.T
1235.6798	1234.6726	1234.7033	-0.0308	43	-	53	1 K.SSFINTILGRK.N
1301.6870	1300.6797	1300.6009	0.0788	128	-	137	0 K.EDIQMYDFLK.Y
1380.7520	1379.7447	1379.7700	-0.0253	138	-	149	0 K.YYDIPVIVVATK.A
1386.7403	1385.7330	1385.6826	0.0503	174	-	185	0 K.SDTFIVFSSVER.I
1467.8310	1466.8238	1466.7405	0.0833	65	-	76	0 K.TQLLNFFNIDDK.L
No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1315.6103, 1318.6687, 1334.6603, 1400.6846, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168, 2202.1952							

27. [Q8I4X5_PLAF7](#) Mass: 188045 Score: 53 Expect: 17 Queries matched: 18

Hypothetical protein.- Plasmodium falciparum (isolate 3D7).							
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
832.3588	831.3515	831.4086	-0.0571	1008	-	1014	1 K.DDVNKNK.N
833.3959	832.3886	832.3311	0.0575	234	-	240	0 K.DNNDNNK.D
853.5010	852.4937	852.4817	0.0120	223	-	229	1 K.INKVHDK.I
1012.6155	1011.6083	1011.5475	0.0608	1336	-	1343	1 K.HIRNHAHK.D
1157.6270	1156.6198	1156.5764	0.0434	1097	-	1106	0 K.STVFSNFDLK.E
1213.7102	1212.7029	1212.7077	-0.0048	756	-	765	1 K.IDIIEQLNK.S
1226.5773	1225.5700	1225.6091	-0.0391	1138	-	1147	0 K.NLNSNYFINK.I
1242.5818	1241.5745	1241.6768	-0.1022	130	-	140	0 K.LVIDTFHVGNK.S
1252.6795	1251.6722	1251.6394	0.0329	916	-	925	1 K.FNLTSCLKNR.K + Carbamidomethyl (C)
1257.6582	1256.6509	1256.6724	-0.0215	1107	-	1116	1 K.ENLDRQIEK.N
1257.7440	1256.7367	1256.6724	0.0643	1107	-	1116	1 K.ENLDRQIEK.N
1283.6177	1282.6105	1282.5578	0.0527	1197	-	1206	0 K.EYNNNTYNTHK.Y
1334.6603	1333.6530	1333.7354	-0.0823	1262	-	1272	1 K.EINNKSITFLR.Q
1380.7520	1379.7447	1379.7296	0.0151	615	-	626	0 K.LQYLNASTIK.F
1408.7587	1407.7515	1407.6816	0.0699	74	-	84	0 K.NVEEYINVICR.I + Carbamidomethyl (C)
1422.7041	1421.6968	1421.6786	0.0182	1399	-	1410	0 K.ENTNDVNTFIQK.E
1467.8310	1466.8238	1466.7477	0.0761	821	-	832	1 K.QEENEEHALTIR.N
2202.1952	2201.1880	2201.0461	0.1419	975	-	993	1 K.INIPDDNNNNNNNKISFK.S
No match to: 712.2679, 781.4592, 825.1370, 831.4419, 841.0980, 852.4849, 861.0837, 873.4641, 876.3626, 877.0567, 1158.6512, 1224.6023, 1230.7044, 1235.6798, 1238.8028, 1240.5956, 1258.5811, 1274.6199, 1282.5765, 1298.6028, 1299.6059, 1301.6870, 1315.6103, 1318.6687, 1386.7403, 1400.6846, 1402.7407, 1424.7200, 1427.7243, 1462.8779, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168							

28. [Q8K6Y4_STRP3](#) Mass: 28197 Score: 53 Expect: 17 Queries matched: 10

Putative 1-acylglycerol-3-phosphate O-acyltransferase.- Streptococcus pyogenes serotype M3.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
832.3588	831.3515	831.4279	-0.0764	2	-	7	0 M.FYAYLR.G
1012.6155	1011.6083	1011.5575	0.0508	59	-	66	1 K.QFIFMAKK.E
1318.6687	1317.6615	1317.5983	0.0632	174	-	185	0 R.MNDEGIAEVANR.I
1334.6603	1333.6530	1333.5932	0.0599	174	-	185	0 R.MNDEGIAEVANR.I + Oxidation (M)
1408.7587	1407.7515	1407.6890	0.0625	138	-	150	0 K.IMPAAAYQGPM SVK.G + Oxidation (M)
1422.7041	1421.6968	1421.7990	-0.1021	119	-	132	1 R.HSQEVKGGVAVIAK.M
1424.7200	1423.7128	1423.6839	0.0289	138	-	150	0 K.IMPAAAYQGPM SVK.G + 2 Oxidation (M)
1467.8310	1466.8238	1466.7299	0.0938	106	-	118	1 K.SNRSLLMFPGSR.H + Oxidation (M)
1723.9839	1722.9766	1722.9245	0.0521	67	-	79	1 K.ELFTNRLFAWWIK.M
1815.9168	1814.9096	1814.8814	0.0282	44	-	58	0 R.TFWDPVYMAFAARPK.Q + Oxidation (M)
No match to: 712.2679, 781.4592, 825.1370, 831.4419, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1157.6270, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1301.6870, 1315.6103, 1380.7520, 1386.7403, 1400.6846, 1402.7407, 1427.7243, 1462.8779, 1612.8208, 1690.6642, 1706.9716, 2202.1952							

29. [Q84QB8_ORYSA](#) Mass: 42907 Score: 52 Expect: 19 Queries matched: 11

Putative receptor ser/thr protein.- Oryza sativa (japonica cultivar-group).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
873.4641	872.4568	872.4967	-0.0399	184	-	191	0 K.ASNILLDK.K
1157.6270	1156.6198	1156.6175	0.0022	147	-	155	1 R.CIPLNWQKR.A
1224.6023	1223.5950	1223.4998	0.0953	54	-	63	0 R.NFHMMNCVGR.G + Oxidation (M)
1240.5956	1239.5884	1239.4947	0.0937	54	-	63	0 R.NFHMMNCVGR.G + 2 Oxidation (M)
1257.6582	1256.6509	1256.7088	-0.0579	72	-	83	1 K.GNLKDGQTQIAIK.K
1257.7440	1256.7367	1256.7088	0.0279	72	-	83	1 K.GNLKDGQTQIAIK.K
1258.5811	1257.5738	1257.6061	-0.0323	16	-	28	0 R.GNQNGSAAVTSR.S
1301.6870	1300.6797	1300.6710	0.0087	145	-	154	1 R.SRCIPLNWQK.R + Carbamidomethyl (C)
1400.6846	1399.6774	1399.7460	-0.0686	205	-	216	0 K.LFPDTTITHISTR.V
1706.9716	1705.9644	1705.7963	0.1681	50	-	63	1 K.LATRNFMHMMNCVGR.G + Carbamidomethyl (C)
2202.1952	2201.1880	2201.1844	0.0036	197	-	216	1 K.IGDFGLAKLFPDTTITHISTR.V
No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 876.3626, 877.0567, 1012.6155, 1158.6512, 1213.7102, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1242.5818, 1252.6795, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1315.6103, 1318.6687, 1334.6603, 1380.7520, 1386.7403, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1723.9839, 1815.9168							

30. [AAM79212](#) Mass: 22460 Score: 52 Expect: 21 Queries matched: 7

AE014074 NID: - Streptococcus pyogenes MGAS315

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1157.6270	1156.6198	1156.5434	0.0764	101	-	109	0 K.MIEEYLTSR.D + Oxidation (M)
1158.6512	1157.6440	1157.6516	-0.0077	54	-	64	1 K.NLARTSSKPGK.T
1235.6798	1234.6726	1234.7033	-0.0308	43	-	53	1 K.SSFINTILGRK.N
1301.6870	1300.6797	1300.6009	0.0788	128	-	137	0 K.EDIQMYDFLK.Y
1380.7520	1379.7447	1379.7700	-0.0253	138	-	149	0 K.YYDIPVIVVATK.A
1386.7403	1385.7330	1385.6826	0.0503	174	-	185	0 K.SDTFIVFSSVER.I
1467.8310	1466.8238	1466.7405	0.0833	65	-	76	0 K.TQLLNFFNIDDK.L
No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1315.6103, 1318.6687, 1334.6603, 1400.6846, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168, 2202.1952							

31. [AAN72830](#) Mass: 253967 Score: 52 Expect: 22 Queries matched: 21

AY157993 NID: - Tomato black ring virus

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
832.3588	831.3515	831.4095	-0.0580	2205	-	2211	0 K.VPCMVAR.Q + Carbamidomethyl (C)
852.4849	851.4776	851.4137	0.0639	19	-	25	0 K.YNNSLNK.Y
853.5010	852.4937	852.4705	0.0232	753	-	759	0 K.DLVELHK.R
873.4641	872.4568	872.5153	-0.0585	1416	-	1424	0 R.VVGMLVAGK.D
1012.6155	1011.6083	1011.5396	0.0687	1269	-	1276	1 R.MTRHQALR.F
1224.6023	1223.5950	1223.5063	0.0887	2010	-	2019	0 R.FMHMSEQGNK.A + Oxidation (M)
1240.5956	1239.5884	1239.6459	-0.0575	1495	-	1505	1 K.EPAVLTKDDPR.C
1242.5818	1241.5745	1241.6438	-0.0692	1476	-	1486	0 K.TNMVPVPESLR.V

1258.5811	1257.5738	1257.6387	-0.0649	1476	-	1486	0	K.TNMVPVPESLR.V + Oxidation (M)
1274.6199	1273.6126	1273.6423	-0.0297	2205	-	2214	1	K.VPCMVARQWK.S + Carbamidomethyl (C)
1282.5765	1281.5692	1281.6573	-0.0880	419	-	430	1	R.ANVFMKAMAGVK.N + Oxidation (M)
1298.6028	1297.5955	1297.6522	-0.0567	419	-	430	1	R.ANVFMKAMAGVK.N + 2 Oxidation (M)
1301.6870	1300.6797	1300.6735	0.0062	127	-	138	1	R.REVAEASAEALR.L
1318.6687	1317.6615	1317.6104	0.0511	639	-	650	1	K.IGAACHSMRMGK.E + Carbamidomethyl (C)
1334.6603	1333.6530	1333.6448	0.0082	1689	-	1700	0	R.LPCQVGTNPYSR.E
1380.7520	1379.7447	1379.6074	0.1373	2009	-	2019	1	K.RFMHMSEQNK.A + Oxidation (M)
1386.7403	1385.7330	1385.7336	-0.0006	1475	-	1486	1	K.KTNMVPVPESLR.V + Oxidation (M)
1427.7243	1426.7170	1426.6762	0.0408	788	-	800	0	K.SNFMSTLDNALAK.H + Oxidation (M)
1462.8779	1461.8706	1461.7252	0.1454	50	-	61	1	K.KYNVLSSFFSDR.V
1723.9839	1722.9766	1722.8664	0.1103	771	-	783	1	R.RCEPVWIYLFQQR.H + Carbamidomethyl (C)
1815.9168	1814.9096	1814.8747	0.0349	1675	-	1688	1	K.TCAFTQFLQHNHR.L + Carbamidomethyl (C)

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 833.3959, 841.0980, 861.0837, 876.3626, 877.0567, 1157.6270, 1158.6512, 1213.7102, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1252.6795, 1257.6582, 1257.7440, 1283.6177, 1299.6059, 1315.6103, 1400.6846, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 2202.1952

32. [AAK33806](#) Mass: 22479 Score: 51 Expect: 23 Queries matched: 7

AE006538 NID: - Streptococcus pyogenes M1 GAS

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1157.6270	1156.6198	1156.5434	0.0764	101	- 109	0	K.MIEEYLTSR.D + Oxidation (M)
1158.6512	1157.6440	1157.6516	-0.0077	54	- 64	1	K.NLARTSSKPGK.T
1235.6798	1234.6726	1234.7033	-0.0308	43	- 53	1	K.SSFINTILGRK.N
1301.6870	1300.6797	1300.6009	0.0788	128	- 137	0	K.EDIQMYDFLK.Y
1380.7520	1379.7447	1379.7700	-0.0253	138	- 149	0	K.YYDIPVIVVATK.A
1386.7403	1385.7330	1385.6826	0.0503	174	- 185	0	K.SDTFIVFSSVER.I
1467.8310	1466.8238	1466.7405	0.0833	65	- 76	0	K.TQLLNFFNIDDK.L

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1315.6103, 1318.6687, 1334.6603, 1400.6846, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168, 2202.1952

33. [Q8T530_PLAFA](#) Mass: 14687 Score: 51 Expect: 25 Queries matched: 6

Erythrocyte membrane protein 1 (Fragment).- Plasmodium falciparum.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
831.4419	830.4346	830.4498	-0.0152	25	-	31	0	K.LQLQDSLK.N
1012.6155	1011.6083	1011.5097	0.0985	37	-	45	0	K.IHSEVTNGR.T
1282.5765	1281.5692	1281.6717	-0.1024	8	-	18	1	R.GKDLFIGYNQK.D
1298.6028	1297.5955	1297.6738	-0.0783	37	-	48	1	K.IHSEVTNGRTGK.N
1301.6870	1300.6797	1300.5684	0.1113	58	-	68	0	K.GDTDGNYQLR.E
1427.7243	1426.7170	1426.6510	0.0660	82	-	95	1	K.AITCGAGEGDRYSK.Y

No match to: 712.2679, 781.4592, 825.1370, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1157.6270, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1283.6177, 1299.6059, 1315.6103, 1318.6687, 1334.6603, 1380.7520, 1386.7403, 1400.6846, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168, 2202.1952

34. [Q8GJA6_CAMJE](#) Mass: 53327 Score: 51 Expect: 26 Queries matched: 10

Hypothetical protein Cjp49.- Campylobacter jejuni.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1230.7044	1229.6971	1229.6404	0.0567	107	- 116	1	K.IHFNTKDDIK.D
1235.6798	1234.6726	1234.6227	0.0498	320	- 330	0	K.NTMEANTILTK.L
1283.6177	1282.6105	1282.6293	-0.0188	156	- 166	0	K.STLYLDIDITK.K
1299.6059	1298.5987	1298.6441	-0.0454	278	- 287	1	K.NLKNFVDFMR.K + Oxidation (M)
1318.6687	1317.6615	1317.6962	-0.0348	168	- 178	0	K.DLSDMILNIIR.K + Oxidation (M)
1400.6846	1399.6774	1399.7558	-0.0784	191	- 202	0	K.IDILNNESLELK.Q
1422.7041	1421.6968	1421.6575	0.0393	113	- 123	1	K.DDIKDFWNDVR.S
1427.7243	1426.7170	1426.7667	-0.0497	52	- 63	1	K.ENPTEKNLEILK.K
1612.8208	1611.8135	1611.6987	0.1148	29	- 41	1	K.DWKMDFSNQENAK.D
1706.9716	1705.9644	1705.9402	0.0241	400	- 413	1	K.NKIPLNAYIIQEYK.K

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1298.6028, 1301.6870, 1315.6103, 1334.6603, 1380.7520, 1386.7403, 1402.7407, 1408.7587, 1424.7200, 1462.8779, 1467.8310, 1690.6642, 1723.9839, 1815.9168, 2202.1952

35. [Q2YVH6_STAAB](#) Mass: 9035 Score: 51 Expect: 26 Queries matched: 7

Hypothetical protein.- Staphylococcus aureus (strain bovine RF122).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
832.3588	831.3515	831.4252	-0.0737	2	-	7	0 M.HHHFVR.C
1224.6023	1223.5950	1223.6081	-0.0130	51	-	60	1 R.DCISTFLNR.L
1334.6603	1333.6530	1333.6826	-0.0295	2	-	11	1 M.HHHFVRCLTK.Y + Carbamidomethyl (C)
1380.7520	1379.7447	1379.7812	-0.0365	61	-	72	0 R.LQLQIGGYVVK.L
1402.7407	1401.7335	1401.6711	0.0624	48	-	58	1 K.YERDCISTFLR.N
1408.7587	1407.7515	1407.7016	0.0499	1	-	11	1 -.MHHFVRCLTK.Y
1424.7200	1423.7128	1423.6965	0.0163	1	-	11	1 -.MHHFVRCLTK.Y + Oxidation (M)

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1158.6512, 1213.7102, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1301.6870, 1315.6103, 1318.6687, 1386.7403, 1400.6846, 1422.7041, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168, 2202.1952

36. [Q9AH95_STRPN](#) Mass: 24847 Score: 51 Expect: 26 Queries matched: 7

Wze (Tyrosine-protein kinase Wze) (EC 2.7.1.112).- Streptococcus pneumoniae.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1158.6512	1157.6440	1157.6478	-0.0038	1	-	10	1 -.MPTLEIAQKK.L
1252.6795	1251.6722	1251.5917	0.0805	134	-	143	0 K.NFNMIETLR.K
1299.6059	1298.5987	1298.5567	0.0420	215	-	226	0 K.YGAYGSYGNYGK.K
1380.7520	1379.7447	1379.6867	0.0580	134	-	144	1 K.NFNMIETLRK.Y
1422.7041	1421.6968	1421.7514	-0.0546	63	-	75	1 R.AGYKTLIDGDTR.Q
1427.7243	1426.7170	1426.6516	0.0654	215	-	227	1 K.YGAYGSYGNYGKK.-
1467.8310	1466.8238	1466.7518	0.0720	50	-	62	0 K.TTTSINIAWSFAR.A

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1301.6870, 1315.6103, 1318.6687, 1334.6603, 1386.7403, 1400.6846, 1402.7407, 1408.7587, 1424.7200, 1462.8779, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168, 2202.1952

37. [Q1RUA7_MEDTR](#) Mass: 7463 Score: 51 Expect: 26 Queries matched: 5

Hypothetical protein.- Medicago truncatula (Barrel medic).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
852.4849	851.4776	851.4211	0.0565	12	-	18	0 K.LPTCQYK.C
873.4641	872.4568	872.4286	0.0282	19	-	26	0 K.CGSTPRPR.H
1252.6795	1251.6722	1251.6897	-0.0174	1	-	11	0 -.MLDIPPLNVPK.L + Oxidation (M)
1318.6687	1317.6615	1317.6888	-0.0274	47	-	58	0 R.QTVSATSELLNR.C
1706.9716	1705.9644	1705.8392	0.1252	12	-	26	1 K.LPTCQYKCGSTPRPR.H

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 833.3959, 841.0980, 853.5010, 861.0837, 876.3626, 877.0567, 1012.6155, 1157.6270, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1301.6870, 1315.6103, 1334.6603, 1380.7520, 1386.7403, 1400.6846, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1723.9839, 1815.9168, 2202.1952

38. [Q54RC0_DICDI](#) Mass: 45292 Score: 51 Expect: 28 Queries matched: 9

Hypothetical protein.- Dictyostelium discoideum AX4.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4592	780.4520	780.4718	-0.0199	86	-	91	1 K.KPRQPR.Q
831.4419	830.4346	830.4035	0.0311	320	-	327	0 R.NPFGGSPR.N
876.3626	875.3553	875.3621	-0.0067	123	-	130	0 R.GEDSPSER.D
1224.6023	1223.5950	1223.5279	0.0672	273	-	283	1 R.NSGDRDQGGYR.G
1226.5773	1225.5700	1225.5587	0.0112	160	-	170	1 R.EGGFNRGGYNR.G
1252.6795	1251.6722	1251.5592	0.1130	278	-	288	1 R.DQGGYRGTDQR.E
1299.6059	1298.5987	1298.5751	0.0235	215	-	226	1 R.EGGYNRGGYGNR.D
1422.7041	1421.6968	1421.6422	0.0546	356	-	368	0 R.NPSEDVSTNAFNK.Q
1706.9716	1705.9644	1705.8019	0.1624	356	-	370	1 R.NPSEDVSTNAFNKQR.K

No match to: 712.2679, 825.1370, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 877.0567, 1012.6155, 1157.6270, 1158.6512, 1213.7102, 1230.7044, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1301.6870, 1315.6103, 1318.6687, 1334.6603, 1380.7520, 1386.7403, 1400.6846, 1402.7407, 1408.7587, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1723.9839, 1815.9168, 2202.1952

39. [Q8D787_VIBVU](#) Mass: 11586 Score: 51 Expect: 28 Queries matched: 6

Hypothetical protein.- *Vibrio vulnificus*.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
831.4419	830.4346	830.4432	-0.0086	68	-	75	0 R.AAIGICQR.A
1318.6687	1317.6615	1317.6711	-0.0096	1	-	11	0 -.MILENKPNSTR.Q + Oxidation (M)
1334.6603	1333.6530	1333.7201	-0.0671	38	-	50	1 K.AQTNSTVTISGKK.D
1386.7403	1385.7330	1385.6074	0.1256	21	-	30	0 K.QCDFIYFHEK.T + Carbamidomethyl (C)
1400.6846	1399.6774	1399.7605	-0.0831	68	-	80	1 R.AAIGICQRALQEK.D
1723.9839	1722.9766	1722.8610	0.1156	76	-	90	1 R.ALQEKDFTVDASLMR.I

No match to: 712.2679, 781.4592, 825.1370, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1301.6870, 1315.6103, 1380.7520, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1815.9168, 2202.1952

40. [O88180_MOUSE](#) Mass: 65724 Score: 50 Expect: 29 Queries matched: 12

Guanine Nucleotide Regulatory Protein.- *Mus musculus* (Mouse).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1226.5773	1225.5700	1225.6376	-0.0676	408	-	418	1 K.YKDMGTVVLGK.L + Oxidation (M)
1230.7044	1229.6971	1229.5750	0.1221	75	-	85	0 R.MEWGAPVEPSK.D
1235.6798	1234.6726	1234.6458	0.0267	251	-	261	0 K.HFTILDAPGHK.S
1240.5956	1239.5884	1239.6169	-0.0285	557	-	567	0 R.TAGTICLETFK.D + Carbamidomethyl (C)
1258.5811	1257.5738	1257.6612	-0.0874	547	-	556	1 K.QDQVCJARLR.T + Carbamidomethyl (C)
1298.6028	1297.5955	1297.6561	-0.0606	295	-	306	1 K.GGQTRHAMLAK.T
1315.6103	1314.6030	1314.6527	-0.0497	2	-	14	1 M.AAAEAAEAEARQK.H
1318.6687	1317.6615	1317.5983	0.0632	1	-	13	0 -.MAAAEAAEAEARQK.K
1334.6603	1333.6530	1333.5932	0.0599	1	-	13	0 -.MAAAEAAEAEARQK.K + Oxidation (M)
1386.7403	1385.7330	1385.6761	0.0569	74	-	85	1 K.RMEWGAPVEPSK.D
1402.7407	1401.7335	1401.6710	0.0624	74	-	85	1 K.RMEWGAPVEPSK.D + Oxidation (M)
1422.7041	1421.6968	1421.8242	-0.1273	395	-	407	1 R.SIDGPIRLPIVDK.Y

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1158.6512, 1213.7102, 1224.6023, 1238.8028, 1242.5818, 1252.6795, 1257.6582, 1257.7440, 1274.6199, 1282.5765, 1283.6177, 1299.6059, 1301.6870, 1380.7520, 1400.6846, 1408.7587, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168, 2202.1952

41. [Q9FG41_ARATH](#) Mass: 73235 Score: 50 Expect: 32 Queries matched: 12

Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:T25011.- *Arabidopsis thaliana* (Mouse-ear cress).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
831.4419	830.4346	830.4385	-0.0039	542	-	548	0 R.DLEDIVK.K
1158.6512	1157.6440	1157.5717	0.0723	263	-	271	1 R.DKNLYNYTK.V
1224.6023	1223.5950	1223.6583	-0.0633	398	-	408	1 R.ISDSMFVKVLGK.V
1230.7044	1229.6971	1229.7053	-0.0082	384	-	394	0 R.ELQALLISCLK.Q
1240.5956	1239.5884	1239.5917	-0.0034	395	-	404	1 K.QERISDSMFK.V
1298.6028	1297.5955	1297.6778	-0.0823	265	-	274	1 K.NLYNYTKVQR.H
1301.6870	1300.6797	1300.7000	-0.0203	64	-	74	1 K.LYRHSSNGVIR.F
1334.6603	1333.6530	1333.7241	-0.0711	286	-	296	1 K.DFVIESKEIVR.K
1402.7407	1401.7335	1401.7649	-0.0315	22	-	33	1 K.GLEKIVEQLSMR.Q
1408.7587	1407.7515	1407.7721	-0.0207	13	-	25	1 R.EVLATPSHKGLEK.I
1424.7200	1423.7128	1423.6799	0.0329	1	-	12	1 -.MEESSNLMLKAR.E + Oxidation (M)
1690.6642	1689.6569	1689.7780	-0.1211	321	-	335	1 K.DDGAEYVRGLCDHLK.T

No match to: 712.2679, 781.4592, 825.1370, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1213.7102, 1226.5773, 1235.6798, 1238.8028, 1242.5818, 1252.6795, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1283.6177, 1299.6059, 1315.6103, 1318.6687, 1380.7520, 1386.7403, 1400.6846, 1422.7041, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1706.9716, 1723.9839, 1815.9168, 2202.1952

42. [Q1IF78_9PSED](#) Mass: 98036 Score: 50 Expect: 33 Queries matched: 12

Hypothetical protein.- *Pseudomonas entomophila* L48.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
----------	----------	----------	-------	-------	-----	------	---------

832.3588	831.3515	831.4086	-0.0571	157 - 163	1	R.VDKEEGR.K
833.3959	832.3886	832.4265	-0.0379	401 - 407	0	R.MPYAVPR.R
1158.6512	1157.6440	1157.6842	-0.0402	690 - 699	1	K.LGEQLMLVKK.Q
1230.7044	1229.6971	1229.7165	-0.0194	145 - 156	0	K.VCVVISTVAALR.V
1235.6798	1234.6726	1234.6921	-0.0195	816 - 825	1	K.DSRLIVEYK.G
1282.5765	1281.5692	1281.6750	-0.1058	849 - 860	1	K.SAGKGLYLMAQK.K + Oxidation (M)
1298.6028	1297.5955	1297.6150	-0.0195	324 - 334	0	R.HLIDTDNVDEK.A
1334.6603	1333.6530	1333.6448	0.0082	100 - 110	0	K.MQTLEAFQNP.R.H
1422.7041	1421.6968	1421.7514	-0.0546	12 - 24	1	R.ALGSLEKYLDASR.L
1427.7243	1426.7170	1426.7779	-0.0609	867 - 879	1	R.GVREQLLAVIENS.-
1690.6642	1689.6569	1689.8065	-0.1497	562 - 575	0	R.LCVMEQGELELVDR.G + Carbamidomethyl (C)
1706.9716	1705.9644	1705.9879	-0.0235	673 - 687	1	R.GFSLSQLKGGFILR.R

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1213.7102, 1224.6023, 1226.5773, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1283.6177, 1299.6059, 1301.6870, 1315.6103, 1318.6687, 1380.7520, 1386.7403, 1400.6846, 1402.7407, 1408.7587, 1424.7200, 1462.8779, 1467.8310, 1612.8208, 1723.9839, 1815.9168, 2202.1952

43. [Q4YWP1_PLABE](#) Mass: 30166 Score: 50 Expect: 34 Queries matched: 9

Hypothetical protein (Fragment).- Plasmodium berghei.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
831.4419	830.4346	830.4861	-0.0516	221 - 227	1	K.KDTNLLK.S	
832.3588	831.3515	831.4160	-0.0645	231 - 237	0	K.MNPITEK.K	
1274.6199	1273.6126	1273.6012	0.0114	202 - 211	0	K.YISYVNDLCK.M + Carbamidomethyl (C)	
1282.5765	1281.5692	1281.6573	-0.0881	1 - 11	1	-.KIYANCLICGK.L + Carbamidomethyl (C)	
1334.6603	1333.6530	1333.7241	-0.0711	156 - 166	1	K.INENVDYVKKI.E	
1400.6846	1399.6774	1399.6772	0.0002	65 - 75	0	K.YYFDPLNNNLK.K	
1402.7407	1401.7335	1401.6962	0.0373	201 - 211	1	K.KYISYVNDLCK.M + Carbamidomethyl (C)	
1422.7041	1421.6968	1421.6820	0.0148	84 - 95	1	K.MLKNSVNEENTK.I + Oxidation (M)	
1424.7200	1423.7128	1423.6255	0.0872	167 - 177	0	K.EFSEYLNHEK.K	

No match to: 712.2679, 781.4592, 825.1370, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1257.6582, 1257.7440, 1258.5811, 1283.6177, 1298.6028, 1299.6059, 1301.6870, 1315.6103, 1318.6687, 1380.7520, 1386.7403, 1408.7587, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168, 2202.1952

44. [T35704](#) Mass: 16760 Score: 50 Expect: 34 Queries matched: 8

peptidylprolyl isomerase (EC 5.2.1.8) SC7H1.09 [similarity] - Streptomyces coelicolor

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
832.3588	831.3515	831.4272	-0.0757	1 - 7	0	-.MAENVLR.G	
873.4641	872.4568	872.4716	-0.0147	131 - 138	0	R.VTIAADQR.S	
1158.6512	1157.6440	1157.6305	0.0135	35 - 45	1	R.VPGFVVRGGDR.L	
1257.6582	1256.6509	1256.6837	-0.0328	128 - 138	1	R.LDRVTIAADQR.S	
1257.7440	1256.7367	1256.6837	0.0530	128 - 138	1	R.LDRVTIAADQR.S	
1386.7403	1385.7330	1385.7377	-0.0047	144 - 157	0	R.ALWPGGGTAMVTLI.-	
1402.7407	1401.7335	1401.7326	0.0009	144 - 157	0	R.ALWPGGGTAMVTLI.- + Oxidation (M)	
1408.7587	1407.7515	1407.6465	0.1049	23 - 34	1	R.GGFCDGTVFHRR.V + Carbamidomethyl (C)	

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 876.3626, 877.0567, 1012.6155, 1157.6270, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1258.5811, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1301.6870, 1315.6103, 1318.6687, 1334.6603, 1380.7520, 1400.6846, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168, 2202.1952

45. [Q57U85_9TRYP](#) Mass: 49924 Score: 50 Expect: 36 Queries matched: 9

Orotidine-5-phosphate decarboxylase/ototate phosphoribosyltransferase, putative (EC 2.4.2.10) (EC 4.1.1.23).- Trypanosoma brucei.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1224.6023	1223.5950	1223.5670	0.0281	88 - 99	0	R.GDIADTAEAYAK.S	
1230.7044	1229.6971	1229.6478	0.0493	127 - 137	1	K.YSSKGVFVLCK.T	
1235.6798	1234.6726	1234.7332	-0.0606	294 - 303	1	R.RLVTHPLIMR.L	
1252.6795	1251.6722	1251.6645	0.0077	131 - 141	1	K.GVFVLCKTSNK.G + Carbamidomethyl (C)	
1258.5811	1257.5738	1257.6751	-0.1013	15 - 25	0	K.TTLLCIGLDPR.A + Carbamidomethyl (C)	
1318.6687	1317.6615	1317.6710	-0.0096	26 - 38	1	R.ADTAAAVLECKR.I	
1334.6603	1333.6530	1333.6626	-0.0095	357 - 368	1	K.GLIEGDFQKQDR.V	
1380.7520	1379.7447	1379.6681	0.0767	87 - 99	1	K.RGDIADTAEAYAK.S	

1400.6846 1399.6774 1399.7857 -0.1083 13 - 25 1 R.AKTTLLCIGLDPR.A

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1158.6512, 1213.7102, 1226.5773, 1238.8028, 1240.5956, 1242.5818, 1257.6582, 1257.7440, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1301.6870, 1315.6103, 1386.7403, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168, 2202.1952

46. [Q4JCP4_SULAC](#) Mass: 27674 Score: 49 Expect: 37 Queries matched: 8

Conserved protein.- *Sulfolobus acidocaldarius*.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
----------	----------	----------	-------	-------	-----	------	---------

833.3959	832.3886	832.4403	-0.0517	169	-	176	0 K.ALTSGQTR.F
1274.6199	1273.6126	1273.7354	-0.1227	165	-	176	1 K.LSLKALTSGQTR.F
1298.6028	1297.5955	1297.6666	-0.0711	106	-	116	0 K.LFDQFLTASTR.E
1299.6059	1298.5987	1298.7081	-0.1095	219	-	230	0 K.EVVTTALLESNPK.T
1318.6687	1317.6615	1317.5811	0.0803	13	-	23	0 R.GFNFFVENCNK.D
1400.6846	1399.6774	1399.6442	0.0332	93	-	104	0 K.LTYCAYNNPDVK.K
1690.6642	1689.6569	1689.7627	-0.1059	127	-	140	1 R.RDEVEVNECQEVK.L
1815.9168	1814.9096	1814.9447	-0.0352	214	-	230	1 K.CDGLKEVVTTALLESNPK.T

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1257.6582, 1257.7440, 1258.5811, 1282.5765, 1283.6177, 1301.6870, 1315.6103, 1334.6603, 1380.7520, 1386.7403, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1706.9716, 1723.9839, 2202.1952

47. [Q9Y355_HUMAN](#) Mass: 7429 Score: 49 Expect: 37 Queries matched: 5

Apolipoprotein A1 (Fragment).- *Homo sapiens (Human)*.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
----------	----------	----------	-------	-------	-----	------	---------

781.4592	780.4520	780.4242	0.0278	14	-	20	0 R.AHVDALR.T
831.4419	830.4346	830.4286	0.0060	49	-	55	0 R.LAEYHAK.A
1157.6270	1156.6198	1156.6200	-0.0002	38	-	48	1 R.LEALKENGGAR.L
1301.6870	1300.6797	1300.6411	0.0385	21	-	31	0 R.THLAPYSDEL.R.Q
1318.6687	1317.6615	1317.6347	0.0268	1	-	11	1 -.LSPLGEEMRDR.A + Oxidation (M)

No match to: 712.2679, 825.1370, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1158.6512, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1252.6795, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1315.6103, 1334.6603, 1380.7520, 1386.7403, 1400.6846, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168, 2202.1952

48. [C32055](#) Mass: 17279 Score: 49 Expect: 38 Queries matched: 6

nifX protein - *Azotobacter vinelandii*

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
----------	----------	----------	-------	-------	-----	------	---------

832.3588	831.3515	831.4021	-0.0506	140	-	146	1 R.TRGPDMDR.R
852.4849	851.4776	851.4137	0.0639	22	-	29	0 K.VAFASSDR.E
1213.7102	1212.7029	1212.6900	0.0129	97	-	107	0 R.QLMAIGVQPIK.V + Oxidation (M)
1252.6795	1251.6722	1251.6247	0.0475	41	-	51	0 R.SFAIYGVNPER.S
1274.6199	1273.6126	1273.6051	0.0076	30	-	40	0 R.ELVDQHFQSSR.S
2202.1952	2201.1880	2201.1175	0.0704	2	-	21	1 M.SSPTRQLQVLDSDDGTLLK.V

No match to: 712.2679, 781.4592, 825.1370, 831.4419, 833.3959, 841.0980, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1157.6270, 1158.6512, 1224.6023, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1240.5956, 1242.5818, 1257.6582, 1257.7440, 1258.5811, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1301.6870, 1315.6103, 1318.6687, 1334.6603, 1380.7520, 1386.7403, 1400.6846, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168

49. [Q5ZWH6_LEGPH](#) Mass: 79435 Score: 49 Expect: 38 Queries matched: 12

Hypothetical protein.- *Legionella pneumophila* subsp. *pneumophila* (strain Philadelphia 1 / ATCC 33152 / DSM 7513).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
----------	----------	----------	-------	-------	-----	------	---------

1157.6270	1156.6198	1156.6451	-0.0254	647	-	656	0 K.SLERPEVSLK.Y
1224.6023	1223.5950	1223.7060	-0.1109	333	-	342	1 R.HDILNLMIKK.L
1235.6798	1234.6726	1234.6669	0.0056	322	-	332	1 K.QLALFASDSKR.H
1240.5956	1239.5884	1239.6036	-0.0152	539	-	547	1 K.DNKFWDFR.N
1252.6795	1251.6722	1251.7121	-0.0399	332	-	341	1 K.RHDILNLMIK.K
1299.6059	1298.5987	1298.6771	-0.0784	72	-	81	1 R.KNLFDFVFNR.T
1386.7403	1385.7330	1385.7164	0.0166	507	-	517	1 K.TINHRSFIENR.K
1400.6846	1399.6774	1399.7248	-0.0474	73	-	83	1 K.NLFDVFVNRK.T

1408.7587 1407.7515 1407.7245 0.0270 456 - 467 0 R.ELNATTYLINEK.K
1422.7041 1421.6968 1421.7952 -0.0983 353 - 365 1 K.LASVMPYATTKIK.I
1427.7243 1426.7170 1426.7107 0.0063 49 - 59 0 R.FIFTFSLFCFR.A
1815.9168 1814.9096 1814.7693 0.1402 193 - 208 0 K.DENESSSTVGEEYIEK.L
No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 873.4641, 876.3626, 877.0567, 1012.6155, 1158.6512, 1213.7102, 1226.5773, 1230.7044, 1238.8028, 1242.5818, 1257.6582, 1257.7440, 1258.5811, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1301.6870, 1315.6103, 1318.6687, 1334.6603, 1380.7520, 1402.7407, 1424.7200, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 2202.1952

50. [1DM9A](#) **Mass:** 11873 **Score:** 49 **Expect:** 40 **Queries matched:** 7

hypothetical 15.5 kd protein in mrca-pcka intergenic region, chain A - bacteria

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
873.4641	872.4568	872.4253	0.0316	32	-	38	0 K.VHYNGQR.S
1158.6512	1157.6440	1157.6345	0.0094	7	-	15	1 R.LDKWLWAAR.F
1240.5956	1239.5884	1239.6553	-0.0669	10	-	18	1 K.WLWAARFYK.T
1257.6582	1256.6509	1256.7452	-0.0943	61	-	71	1 R.TVIVKAITEQR.R
1257.7440	1256.7367	1256.7452	-0.0085	61	-	71	1 R.TVIVKAITEQR.R
1258.5811	1257.5738	1257.6677	-0.0939	55	-	65	1 R.QGNDERTVIVK.A
1400.6846	1399.6774	1399.7320	-0.0546	32	-	43	1 K.VHYNGQRSKPSK.I
No match to: 712.2679, 781.4592, 825.1370, 831.4419, 832.3588, 833.3959, 841.0980, 852.4849, 853.5010, 861.0837, 876.3626, 877.0567, 1012.6155, 1157.6270, 1213.7102, 1224.6023, 1226.5773, 1230.7044, 1235.6798, 1238.8028, 1242.5818, 1252.6795, 1274.6199, 1282.5765, 1283.6177, 1298.6028, 1299.6059, 1301.6870, 1315.6103, 1318.6687, 1334.6603, 1380.7520, 1386.7403, 1402.7407, 1408.7587, 1422.7041, 1424.7200, 1427.7243, 1462.8779, 1467.8310, 1612.8208, 1690.6642, 1706.9716, 1723.9839, 1815.9168, 2202.1952							

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 : 53

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