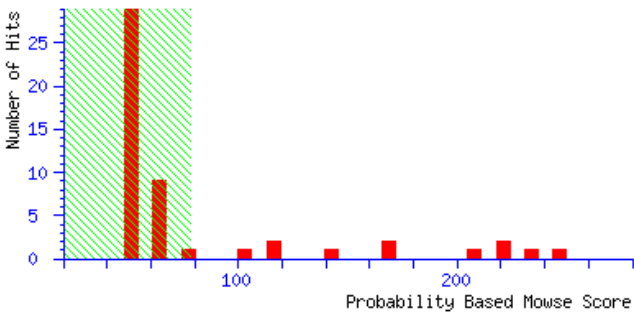


Mascot Search Results

User : Joe Gray
Email : joe.gray@ncl.ac.uk
Search title : DIP_1_0001.dat - SpecView
Database : MSDB 20060831 (3239079 sequences; 1079594700 residues)
Timestamp : 8 Jan 2007 at 11:27:46 GMT
Top Score : 247 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	247	APOA1 PROTEIN (FRAGMENT).- Homo sapiens (Human).
2.	AAA51747	28944	229	HUMAPOAIC NID: - Homo sapiens
3.	LPHUA1	30759	220	apolipoprotein A-I precursor [validated] - human
4.	AAX42892	30872	220	AY890956 NID: - synthetic construct
5.	AAA35545	30745	204	HUMAPOAIP NID: - Homo sapiens
6.	CAA03490	23205	169	SEQUENCE 10 FROM PATENT W09637608.- unidentified.
7.	1AV1A	23389	168	apolipoprotein a-i lipid-binding domain mutant N-TERMINAL MET, DEL(1-43), chain A - human
8.	Q8HZ97_PANTR	22075	137	Apolipoprotein A-I (Fragment).- Pan troglodytes (Chimpanzee).
9.	A26529	30700	115	apolipoprotein A-I precursor - crab-eating macaque
10.	JS0079	30716	115	apolipoprotein A-I precursor - baboon

11.	Q8HZ95_PONPY	22116	105	Apolipoprotein A-I (Fragment).- Pongo pygmaeus (Orangutan).
12.	CAD61352	18392	77	Sequence 2 from Patent WO02083898 precursor.- Homo sapiens (Human).
13.	T47237	87729	64	myosin II heavy chain [imported] - Naegleria fowleri (fragment)
14.	Q676V0_HP62	73294	64	Putative replication protein E1.- Human papillomavirus type 62.
15.	Q8TV91_METKA	29481	63	Predicted transcriptional regulator containing a DNA-binding HTH domain.- Methanopyrus kandleri.
16.	002568_9BILA	17537	62	Enolase (Fragment).- Cerebratulus cf. lacteus.
17.	H87687	130186	62	helicase, UvrD/Rep family [imported] - Caulobacter crescentus
18.	Q6DU55_PRUPE	67223	60	S-locus-like receptor protein kinase (Fragment).- Prunus persica (Peach).
19.	Q7MS71_WOLSU	44173	59	Hypothetical protein hydC.- Wolinella succinogenes.
20.	Q4IBZ3_GIBZE	31681	58	Hypothetical protein.- Gibberella zeae (Fusarium graminearum).
21.	E96933	18193	57	hypothetical protein CAC0275 [imported] - Clostridium acetobutylicum
22.	Q3KQC8_XENLA	28985	57	Hypothetical protein.- Xenopus laevis (African clawed frog).
23.	Q9N0V7_RABIT	60174	56	Cystathionine beta-synthase (EC 4.2.1.22).- Oryctolagus cuniculus (Rabbit).
24.	Q5NCF0_MOUSE	19181	56	Novel Sybindin-like family domain-containing protein.- Mus musculus (Mouse).
25.	AAL97589	22480	56	AE010023 NID: - Streptococcus pyogenes MGAS8232
26.	CAA40001	3140	55	BSDCIA NID: - Bacillus subtilis
27.	Q219J6_RHOPB	54585	55	Transcriptional regulator, XRE family.- Rhodopseudomonas palustris (strain BisB18).
28.	Q4LAF2_STAHI	57597	55	Type I restriction-modification system DNA methylase.- Staphylococcus haemolyticus (strain JCSC1435).
29.	AAM79212	22460	55	AE014074 NID: - Streptococcus pyogenes MGAS315
30.	AAK33806	22479	54	AE006538 NID: - Streptococcus pyogenes M1 GAS
31.	Q4WN94_ASPFU	42187	54	Actin binding protein, putative.- Aspergillus fumigatus (Sartorya fumigata).
32.	Q2RK76_MOOTA	45037	54	UDP-N-acetylglucosamine 1-carboxyvinyltransferase.- Moorella thermoacetica (strain ATCC 39073).
33.	Q8GC31_LEUCI	47411	53	Putative mobilization protein.- Leuconostoc citreum.
34.	Q16V40_AEDAE	22771	53	Hypothetical protein.- Aedes aegypti (Yellowfever mosquito).
35.	Q1EPB8_MUSAC	14866	53	Hypothetical protein.- Musa acuminata (Banana).
36.	Q3WCG3_9ACTO	35265	53	Pyruvate dehydrogenase (Lipoamide) (EC 1.2.4.1).- Frankia sp. EAN1pec.
37.	Q1RUA7_MEDTR	7463	53	Hypothetical protein.- Medicago truncatula (Barrel medic).
38.	Q9C902_ARATH	86001	52	Protein kinase, putative; 19229-23534 (Hypothetical protein At3g06620).- Arabidopsis thaliana (Mouse-ear cress).
39.	Q9TSS5_BOSIN	10093	52	BoLA-DRB3 protein (Fragment).- Bos indicus (Zebu).
40.	Q5VU61_HUMAN	26265	52	Tropomyosin 3.- Homo sapiens (Human).
41.	S11390	29003	52	tropomyosin 5 - mouse
42.	Q54L29_DICDI	11417	52	Hypothetical protein.- Dictyostelium discoideum AX4.
43.	Q5ZUP2_LEGPH	50366	51	Hypothetical protein.- Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 / ATCC 33152 / DSM 7513).
44.	A25530	29015	51	tropomyosin, fibroblast - human
45.	Q4HE11_CAMCO	31370	51	Hypothetical protein.- Campylobacter coli RM2228.
46.	Q8XVL4_RALSO	63203	51	Probable prolyl-trna synthetase protein (EC 6.1.1.15).- Ralstonia solanacearum (Pseudomonas solanacearum).
47.	Q22LV9_TETTH	52292	51	Hypothetical protein.- Tetrahymena thermophila SB210.
48.	Q9Y355_HUMAN	7429	51	Apolipoprotein A1 (Fragment).- Homo sapiens (Human).
49.	T35704	16760	51	peptidylprolyl isomerase (EC 5.2.1.8) SC7H1.09 [similarity] - Streptomyces coelicolor
50.	Q9KJG9_STRLI	16717	51	Peptidyl-prolyl cis-trans isomerase.- Streptomyces lividans.

Results List

1. [CAA00975](#) Mass: 28061 Score: **247** Expect: 6.5e-19 Queries matched: 23

APOA1 PROTEIN (FRAGMENT).- Homo sapiens (Human).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4409	780.4336	780.4242	0.0094	154	- 160	0	R.AHVDALR.T
831.3855	830.3783	830.4286	-0.0503	189	- 195	0	R.LAEYHAK.A
873.4259	872.4186	872.4352	-0.0165	124	- 131	0	R.AELQEGAR.Q
1012.5758	1011.5686	1011.5713	-0.0027	207	- 215	0	K.AKPALEDLR.Q

1157.6034	1156.5962	1156.6200	-0.0238	178 - 188	1	R.LEALKENGGAR.L
1226.5318	1225.5245	1225.5364	-0.0118	1 - 10	0	-.DEPPQSPWDR.V
1230.6543	1229.6470	1229.7019	-0.0549	216 - 226	0	R.QGLLPVLESFK.V
1235.5913	1234.5840	1234.6809	-0.0969	13 - 23	0	K.DLATVYVDVLK.D
1252.6284	1251.6211	1251.6135	0.0076	97 - 106	0	K.VQPYLDDFQK.K
1283.5580	1282.5508	1282.5652	-0.0144	108 - 116	0	K.WQEEMELYSR.Q
1299.5558	1298.5485	1298.5601	-0.0116	108 - 116	0	K.WQEEMELYSR.Q + Oxidation (M)
1301.6318	1300.6245	1300.6411	-0.0166	161 - 171	0	R.THLAPYSDEL.R
1307.6958	1306.6885	1306.6187	0.0698	78 - 88	1	K.ETEGRLRQEMSK.D
1318.6086	1317.6013	1317.6347	-0.0334	141 - 151	1	K.LSPLGEEMRDR.A + Oxidation (M)
1323.6033	1322.5960	1322.6136	-0.0176	78 - 88	1	K.ETEGRLRQEMSK.D + Oxidation (M)
1380.6922	1379.6849	1379.7085	-0.0236	97 - 107	1	K.VQPYLDDFQKK.W
1386.6862	1385.6789	1385.7078	-0.0289	227 - 238	0	K.VSFLSALEEYTK.K
1400.6222	1399.6149	1399.6619	-0.0470	28 - 40	0	R.DYVSQFEGSALGK.Q
1462.8200	1461.8127	1461.8442	-0.0315	11 - 23	1	R.VKDLATVYVDVLK.D
1467.7784	1466.7712	1466.7841	-0.0129	119 - 131	1	K.VEPLRAELQEGAR.Q
1612.7497	1611.7424	1611.7780	-0.0356	46 - 59	0	K.LLDNWDSVTSTFSK.L
1815.8328	1814.8255	1814.8434	-0.0179	24 - 40	1	K.DSGRDYVSQFEGSALGK.Q
2202.0786	2201.0713	2201.1116	-0.0403	60 - 77	1	K.LREQLGPTQEFWDNLEK.E

No match to: 832.3686, 852.4759, 855.0295, 861.0514, 877.0207, 893.0028, 1158.5981, 1179.5649, 1213.6598, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1308.6351, 1316.5630, 1317.6197, 1408.7039, 1475.7529, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1993.9556, 2383.9341

2. [AAA51747](#) Mass: 28944 Score: **229** Expect: 4.1e-17 Queries matched: 22

HUMAPOAIC NID: - Homo sapiens

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4409	780.4336	780.4242	0.0094	160 - 166	0		R.AHVDALR.T
831.3855	830.3783	830.4286	-0.0503	195 - 201	0		R.LAEYHAK.A
873.4259	872.4186	872.4352	-0.0165	130 - 137	0		R.AELQEGAR.Q
1012.5758	1011.5686	1011.5713	-0.0027	213 - 221	0		K.AKPALEDLR.Q
1157.6034	1156.5962	1156.6200	-0.0238	184 - 194	1		R.LEALKENGGAR.L
1230.6543	1229.6470	1229.7019	-0.0549	222 - 232	0		R.QGLLPVLESFK.V
1235.5913	1234.5840	1234.6809	-0.0969	19 - 29	0		K.DLATVYVDVLK.D
1252.6284	1251.6211	1251.6135	0.0076	103 - 112	0		K.VQPYLDDFQK.K
1283.5580	1282.5508	1282.5652	-0.0144	114 - 122	0		K.WQEEMELYSR.Q
1299.5558	1298.5485	1298.5601	-0.0116	114 - 122	0		K.WQEEMELYSR.Q + Oxidation (M)
1301.6318	1300.6245	1300.6411	-0.0166	167 - 177	0		R.THLAPYSDEL.R
1307.6958	1306.6885	1306.6187	0.0698	84 - 94	1		K.ETEGRLRQEMSK.D
1318.6086	1317.6013	1317.6347	-0.0334	147 - 157	1		K.LSPLGEEMRDR.A + Oxidation (M)
1323.6033	1322.5960	1322.6136	-0.0176	84 - 94	1		K.ETEGRLRQEMSK.D + Oxidation (M)
1380.6922	1379.6849	1379.7085	-0.0236	103 - 113	1		K.VQPYLDDFQKK.W
1386.6862	1385.6789	1385.7078	-0.0289	233 - 244	0		K.VSFLSALEEYTK.K
1400.6222	1399.6149	1399.6619	-0.0470	34 - 46	0		R.DYVSQFEGSALGK.Q
1462.8200	1461.8127	1461.8442	-0.0315	17 - 29	1		R.VKDLATVYVDVLK.D
1467.7784	1466.7712	1466.7841	-0.0129	125 - 137	1		K.VEPLRAELQEGAR.Q
1612.7497	1611.7424	1611.7780	-0.0356	52 - 65	0		K.LLDNWDSVTSTFSK.L
1815.8328	1814.8255	1814.8434	-0.0179	30 - 46	1		K.DSGRDYVSQFEGSALGK.Q
2202.0786	2201.0713	2201.1116	-0.0403	66 - 83	1		K.LREQLGPTQEFWDNLEK.E

No match to: 832.3686, 852.4759, 855.0295, 861.0514, 877.0207, 893.0028, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1308.6351, 1316.5630, 1317.6197, 1408.7039, 1475.7529, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1993.9556, 2383.9341

3. [LPHUA1](#) Mass: 30759 Score: **220** Expect: 3.2e-16 Queries matched: 22

apolipoprotein A-I precursor [validated] - human

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
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781.4409	780.4336	780.4242	0.0094	178 - 184	0	R.AHVDALR.T
831.3855	830.3783	830.4286	-0.0503	213 - 219	0	R.LAEYHAK.A
873.4259	872.4186	872.4352	-0.0165	148 - 155	0	R.AELQEGAR.Q
1012.5758	1011.5686	1011.5713	-0.0027	231 - 239	0	K.AKPALEDLR.Q
1157.6034	1156.5962	1156.6200	-0.0238	202 - 212	1	R.LEALKENGGA.L
1230.6543	1229.6470	1229.7019	-0.0549	240 - 250	0	R.QGLLPVLESF.V
1235.5913	1234.5840	1234.6809	-0.0969	37 - 47	0	K.DLATVYVDVLK.D
1252.6284	1251.6211	1251.6135	0.0076	121 - 130	0	K.VQPYLDDFQK.K
1283.5580	1282.5508	1282.5652	-0.0144	132 - 140	0	K.WQEEMELYR.Q
1299.5558	1298.5485	1298.5601	-0.0116	132 - 140	0	K.WQEEMELYR.Q + Oxidation (M)
1301.6318	1300.6245	1300.6411	-0.0166	185 - 195	0	R.THLAPYSDEL.R
1307.6958	1306.6885	1306.6187	0.0698	102 - 112	1	K.ETEGLRQEMSK.D
1318.6086	1317.6013	1317.6347	-0.0334	165 - 175	1	K.LSPLGEEMRDR.A + Oxidation (M)
1323.6033	1322.5960	1322.6136	-0.0176	102 - 112	1	K.ETEGLRQEMSK.D + Oxidation (M)
1380.6922	1379.6849	1379.7085	-0.0236	121 - 131	1	K.VQPYLDDFQK.W
1386.6862	1385.6789	1385.7078	-0.0289	251 - 262	0	K.VSFLSALEEYTK.K
1400.6222	1399.6149	1399.6619	-0.0470	52 - 64	0	R.DYVSQFEGSALGK.Q
1462.8200	1461.8127	1461.8442	-0.0315	35 - 47	1	R.VKDLATVYVDVLK.D
1467.7784	1466.7712	1466.7841	-0.0129	143 - 155	1	K.VEPLRAELQEGAR.Q
1612.7497	1611.7424	1611.7780	-0.0356	70 - 83	0	K.LLDNWDSVTSTFSK.L
1815.8328	1814.8255	1814.8434	-0.0179	48 - 64	1	K.DSGRDYVSQFEGSALGK.Q
2202.0786	2201.0713	2201.1116	-0.0403	84 - 101	1	K.LREQLGPTQEFWDNLEK.E

No match to: 832.3686, 852.4759, 855.0295, 861.0514, 877.0207, 893.0028, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1308.6351, 1316.5630, 1317.6197, 1408.7039, 1475.7529, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1993.9556, 2383.9341

4. [AAX42892](#) Mass: 30872 Score: **220** Expect: 3.2e-16 Queries matched: 22

AY890956 NID: - synthetic construct

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4409	780.4336	780.4242	0.0094	178 - 184	0		R.AHVDALR.T
831.3855	830.3783	830.4286	-0.0503	213 - 219	0		R.LAEYHAK.A
873.4259	872.4186	872.4352	-0.0165	148 - 155	0		R.AELQEGAR.Q
1012.5758	1011.5686	1011.5713	-0.0027	231 - 239	0		K.AKPALEDLR.Q
1157.6034	1156.5962	1156.6200	-0.0238	202 - 212	1		R.LEALKENGGA.L
1230.6543	1229.6470	1229.7019	-0.0549	240 - 250	0		R.QGLLPVLESF.V
1235.5913	1234.5840	1234.6809	-0.0969	37 - 47	0		K.DLATVYVDVLK.D
1252.6284	1251.6211	1251.6135	0.0076	121 - 130	0		K.VQPYLDDFQK.K
1283.5580	1282.5508	1282.5652	-0.0144	132 - 140	0		K.WQEEMELYR.Q
1299.5558	1298.5485	1298.5601	-0.0116	132 - 140	0		K.WQEEMELYR.Q + Oxidation (M)
1301.6318	1300.6245	1300.6411	-0.0166	185 - 195	0		R.THLAPYSDEL.R
1307.6958	1306.6885	1306.6187	0.0698	102 - 112	1		K.ETEGLRQEMSK.D
1318.6086	1317.6013	1317.6347	-0.0334	165 - 175	1		K.LSPLGEEMRDR.A + Oxidation (M)
1323.6033	1322.5960	1322.6136	-0.0176	102 - 112	1		K.ETEGLRQEMSK.D + Oxidation (M)
1380.6922	1379.6849	1379.7085	-0.0236	121 - 131	1		K.VQPYLDDFQK.W
1386.6862	1385.6789	1385.7078	-0.0289	251 - 262	0		K.VSFLSALEEYTK.K
1400.6222	1399.6149	1399.6619	-0.0470	52 - 64	0		R.DYVSQFEGSALGK.Q
1462.8200	1461.8127	1461.8442	-0.0315	35 - 47	1		R.VKDLATVYVDVLK.D
1467.7784	1466.7712	1466.7841	-0.0129	143 - 155	1		K.VEPLRAELQEGAR.Q
1612.7497	1611.7424	1611.7780	-0.0356	70 - 83	0		K.LLDNWDSVTSTFSK.L
1815.8328	1814.8255	1814.8434	-0.0179	48 - 64	1		K.DSGRDYVSQFEGSALGK.Q
2202.0786	2201.0713	2201.1116	-0.0403	84 - 101	1		K.LREQLGPTQEFWDNLEK.E

No match to: 832.3686, 852.4759, 855.0295, 861.0514, 877.0207, 893.0028, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1308.6351, 1316.5630, 1317.6197, 1408.7039, 1475.7529, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1993.9556, 2383.9341

5. [AAA35545](#) Mass: 30745 Score: **204** Expect: 1.3e-14 Queries matched: 21

HUMAPOAIP NID: - Homo sapiens

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4409	780.4336	780.4242	0.0094	178	- 184	0	R.AHVDALR.T
831.3855	830.3783	830.4286	-0.0503	213	- 219	0	R.LAEYHAK.A
873.4259	872.4186	872.4352	-0.0165	148	- 155	0	R.AELQEGAR.Q
1012.5758	1011.5686	1011.5713	-0.0027	231	- 239	0	K.AKPALEDLR.Q
1157.6034	1156.5962	1156.6200	-0.0238	202	- 212	1	R.LEALKENGGAR.L
1230.6543	1229.6470	1229.7019	-0.0549	240	- 250	0	R.QGLLPVLESFK.V
1235.5913	1234.5840	1234.6809	-0.0969	37	- 47	0	K.DLATVYVDVLK.D
1252.6284	1251.6211	1251.6135	0.0076	121	- 130	0	K.VQPYLDDFQK.K
1283.5580	1282.5508	1282.5652	-0.0144	132	- 140	0	K.WQEEMELYSR.Q
1299.5558	1298.5485	1298.5601	-0.0116	132	- 140	0	K.WQEEMELYSR.Q + Oxidation (M)
1301.6318	1300.6245	1300.6411	-0.0166	185	- 195	0	R.THLAPYSDEL.R.Q
1307.6958	1306.6885	1306.6187	0.0698	102	- 112	1	K.ETEGLRQEMSK.D
1318.6086	1317.6013	1317.6347	-0.0334	165	- 175	1	K.LSPLGEEMRDR.A + Oxidation (M)
1323.6033	1322.5960	1322.6136	-0.0176	102	- 112	1	K.ETEGLRQEMSK.D + Oxidation (M)
1380.6922	1379.6849	1379.7085	-0.0236	121	- 131	1	K.VQPYLDDFQKK.W
1386.6862	1385.6789	1385.7078	-0.0289	251	- 262	0	K.VSFLSALEEYTK.K
1400.6222	1399.6149	1399.6619	-0.0470	52	- 64	0	R.DYVSQFEGSALGK.Q
1462.8200	1461.8127	1461.8442	-0.0315	35	- 47	1	R.VKDLATVYVDVLK.D
1612.7497	1611.7424	1611.7780	-0.0356	70	- 83	0	K.LLDNWDSTSTFSK.L
1815.8328	1814.8255	1814.8434	-0.0179	48	- 64	1	K.DSGRDYVSQFEGSALGK.Q
2202.0786	2201.0713	2201.1116	-0.0403	84	- 101	1	K.LREQLGPTQEFWDNLEK.E

No match to: 832.3686, 852.4759, 855.0295, 861.0514, 877.0207, 893.0028, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1308.6351, 1316.5630, 1317.6197, 1408.7039, 1467.7784, 1475.7529, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1993.9556, 2383.9341

6. [CAA03490](#) Mass: 23205 Score: **169** Expect: 4.1e-11 Queries matched: 18

SEQUENCE 10 FROM PATENT W09637608.- unidentified.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4409	780.4336	780.4242	0.0094	111	- 117	0	R.AHVDALR.T
831.3855	830.3783	830.4286	-0.0503	146	- 152	0	R.LAEYHAK.A
873.4259	872.4186	872.4352	-0.0165	81	- 88	0	R.AELQEGAR.Q
1012.5758	1011.5686	1011.5713	-0.0027	164	- 172	0	K.AKPALEDLR.Q
1157.6034	1156.5962	1156.6200	-0.0238	135	- 145	1	R.LEALKENGGAR.L
1226.5318	1225.5245	1225.5986	-0.0740	107	- 117	1	R.DCARAHVDALR.T
1230.6543	1229.6470	1229.7019	-0.0549	173	- 183	0	R.QGLLPVLESFK.V
1252.6284	1251.6211	1251.6135	0.0076	54	- 63	0	K.VQPYLDDFQK.K
1283.5580	1282.5508	1282.5652	-0.0144	65	- 73	0	K.WQEEMELYSR.Q
1299.5558	1298.5485	1298.5601	-0.0116	65	- 73	0	K.WQEEMELYSR.Q + Oxidation (M)
1301.6318	1300.6245	1300.6411	-0.0166	118	- 128	0	R.THLAPYSDEL.R.Q
1307.6958	1306.6885	1306.6187	0.0698	35	- 45	1	K.ETEGLRQEMSK.D
1323.6033	1322.5960	1322.6136	-0.0176	35	- 45	1	K.ETEGLRQEMSK.D + Oxidation (M)
1380.6922	1379.6849	1379.7085	-0.0236	54	- 64	1	K.VQPYLDDFQKK.W
1386.6862	1385.6789	1385.7078	-0.0289	184	- 195	0	K.VSFLSALEEYTK.K
1467.7784	1466.7712	1466.7841	-0.0129	76	- 88	1	K.VEPLRAELQEGAR.Q
1612.7497	1611.7424	1611.7780	-0.0356	3	- 16	0	K.LLDNWDSTSTFSK.L
2202.0786	2201.0713	2201.1116	-0.0403	17	- 34	1	K.LREQLGPTQEFWDNLEK.E

No match to: 832.3686, 852.4759, 855.0295, 861.0514, 877.0207, 893.0028, 1158.5981, 1179.5649, 1213.6598, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1400.6222, 1408.7039, 1462.8200, 1475.7529, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2383.9341

7. [1AV1A](#) Mass: 23389 Score: **168** Expect: 5.1e-11 Queries matched: 18

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
781.4409	780.4336	780.4242	0.0094	112	- 118	0	R.AHVDALR.T
831.3855	830.3783	830.4286	-0.0503	147	- 153	0	R.LAEYHAK.A
873.4259	872.4186	872.4352	-0.0165	82	- 89	0	R.AELQEGAR.Q
1012.5758	1011.5686	1011.5713	-0.0027	165	- 173	0	K.AKPALEDLR.Q
1157.6034	1156.5962	1156.6200	-0.0238	136	- 146	1	R.LEALKENGGAR.L
1230.6543	1229.6470	1229.7019	-0.0549	174	- 184	0	R.QGLLPVLESFK.V
1252.6284	1251.6211	1251.6135	0.0076	55	- 64	0	K.VQPYLDDFQK.K
1283.5580	1282.5508	1282.5652	-0.0144	66	- 74	0	K.WQEEMELYR.Q
1299.5558	1298.5485	1298.5601	-0.0116	66	- 74	0	K.WQEEMELYR.Q + Oxidation (M)
1301.6318	1300.6245	1300.6411	-0.0166	119	- 129	0	R.THLAPYSDEL.R.Q
1307.6958	1306.6885	1306.6187	0.0698	36	- 46	1	K.ETEGRLQEMSK.D
1318.6086	1317.6013	1317.6347	-0.0334	99	- 109	1	K.LSPLGEEMRDR.A + Oxidation (M)
1323.6033	1322.5960	1322.6136	-0.0176	36	- 46	1	K.ETEGRLQEMSK.D + Oxidation (M)
1380.6922	1379.6849	1379.7085	-0.0236	55	- 65	1	K.VQPYLDDFQKK.W
1386.6862	1385.6789	1385.7078	-0.0289	185	- 196	0	K.VSFLSAL EEYTK.K
1467.7784	1466.7712	1466.7841	-0.0129	77	- 89	1	K.VEPLRAELQEGAR.Q
1612.7497	1611.7424	1611.7780	-0.0356	4	- 17	0	K.LLDNWDSVTSTFSK.L
2202.0786	2201.0713	2201.1116	-0.0403	18	- 35	1	K.LREQLG PVTQEFWDNLEK.E

No match to: 832.3686, 852.4759, 855.0295, 861.0514, 877.0207, 893.0028, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1308.6351, 1316.5630, 1317.6197, 1400.6222, 1408.7039, 1462.8200, 1475.7529, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2383.9341

8. [Q8HZ97_PANTR](#) Mass: 22075 Score: **137** Expect: 6.5e-08 Queries matched: 15

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

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4409	780.4336	780.4242	0.0094	141	- 147	0	R.AHVDALR.T
831.3855	830.3783	830.4286	-0.0503	176	- 182	0	R.LAEYHAK.A
873.4259	872.4186	872.4352	-0.0165	111	- 118	0	R.AELQEGAR.Q
1157.6034	1156.5962	1156.6200	-0.0238	165	- 175	1	R.LEALKENGGAR.L
1252.6284	1251.6211	1251.6135	0.0076	84	- 93	0	K.VQPYLDDFQK.K
1283.5580	1282.5508	1282.5652	-0.0144	95	- 103	0	K.WQEEMELYR.Q
1299.5558	1298.5485	1298.5601	-0.0116	95	- 103	0	K.WQEEMELYR.Q + Oxidation (M)
1301.6318	1300.6245	1300.6411	-0.0166	148	- 158	0	R.THLAPYSDEL.R.Q
1307.6958	1306.6885	1306.6187	0.0698	65	- 75	1	K.ETEGRLQEMSK.D
1323.6033	1322.5960	1322.6136	-0.0176	65	- 75	1	K.ETEGRLQEMSK.D + Oxidation (M)
1380.6922	1379.6849	1379.7085	-0.0236	84	- 94	1	K.VQPYLDDFQKK.W
1400.6222	1399.6149	1399.6619	-0.0470	15	- 27	0	R.DYVSQFEGSALGK.Q
1612.7497	1611.7424	1611.7780	-0.0356	33	- 46	0	K.LLDNWDSVTSTFSK.L
1815.8328	1814.8255	1814.8434	-0.0179	11	- 27	1	K.DSGRDYVSQFEGSALGK.Q
2202.0786	2201.0713	2201.1116	-0.0403	47	- 64	1	K.LREQLG PVTQEFWDNLEK.E

No match to: 832.3686, 852.4759, 855.0295, 861.0514, 877.0207, 893.0028, 1012.5758, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1386.6862, 1408.7039, 1462.8200, 1467.7784, 1475.7529, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1993.9556, 2383.9341

9. [A26529](#) Mass: 30700 Score: **115** Expect: 1e-05 Queries matched: 15

apolipoprotein A-I precursor - crab-eating macaque

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4409	780.4336	780.4242	0.0094	178	- 184	0	R.AHVDALR.T
831.3855	830.3783	830.4286	-0.0503	213	- 219	0	R.LAEYHAK.A
1012.5758	1011.5686	1011.5713	-0.0027	231	- 239	0	K.AKPALEDLR.Q
1157.6034	1156.5962	1156.6200	-0.0238	202	- 212	1	R.LEALKENGGAR.L
1230.6543	1229.6470	1229.7019	-0.0549	240	- 250	0	R.QGLLPVLESFK.V

1252.6284	1251.6211	1251.6135	0.0076	121 - 130	0	K.VQPYLDDFQK.K
1283.5580	1282.5508	1282.5652	-0.0144	132 - 140	0	K.WQEEMELYR.Q
1299.5558	1298.5485	1298.5601	-0.0116	132 - 140	0	K.WQEEMELYR.Q + Oxidation (M)
1301.6318	1300.6245	1300.6411	-0.0166	185 - 195	0	R.THLAPYSDEL.R.Q
1307.6958	1306.6885	1306.6187	0.0698	102 - 112	1	K.ETEGLRQEMSK.D
1323.6033	1322.5960	1322.6136	-0.0176	102 - 112	1	K.ETEGLRQEMSK.D + Oxidation (M)
1380.6922	1379.6849	1379.7085	-0.0236	121 - 131	1	K.VQPYLDDFQKK.W
1386.6862	1385.6789	1385.7078	-0.0289	251 - 262	0	K.VSFLSALEEYTK.K
1400.6222	1399.6149	1399.6619	-0.0470	52 - 64	0	K.DYVSQFEGSALGK.Q
2202.0786	2201.0713	2201.1116	-0.0403	84 - 101	1	K.LREQLGPTQEFWDNLEK.E

No match to: 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1408.7039, 1462.8200, 1467.7784, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2383.9341

10. JS0079 Mass: 30716 Score: **115** Expect: 1e-05 Queries matched: 15

apolipoprotein A-I precursor - baboon

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4409	780.4336	780.4242	0.0094	178 - 184	0	0	R.AHVDALR.T
831.3855	830.3783	830.4286	-0.0503	213 - 219	0	0	R.LAEYHAK.A
1012.5758	1011.5686	1011.5713	-0.0027	231 - 239	0	0	K.AKPALEDLR.Q
1157.6034	1156.5962	1156.6200	-0.0238	202 - 212	1	1	R.LEALKENGGA.R.L
1230.6543	1229.6470	1229.7019	-0.0549	240 - 250	0	0	R.QGLLPVLESF.K.V
1252.6284	1251.6211	1251.6135	0.0076	121 - 130	0	0	K.VQPYLDDFQK.K
1283.5580	1282.5508	1282.5652	-0.0144	132 - 140	0	0	K.WQEEMELYR.Q
1299.5558	1298.5485	1298.5601	-0.0116	132 - 140	0	0	K.WQEEMELYR.Q + Oxidation (M)
1301.6318	1300.6245	1300.6411	-0.0166	185 - 195	0	0	R.THLAPYSDEL.R.Q
1307.6958	1306.6885	1306.6187	0.0698	102 - 112	1	1	K.ETEGLRQEMSK.D
1323.6033	1322.5960	1322.6136	-0.0176	102 - 112	1	1	K.ETEGLRQEMSK.D + Oxidation (M)
1380.6922	1379.6849	1379.7085	-0.0236	121 - 131	1	1	K.VQPYLDDFQKK.W
1386.6862	1385.6789	1385.7078	-0.0289	251 - 262	0	0	K.VSFLSALEEYTK.K
1400.6222	1399.6149	1399.6619	-0.0470	52 - 64	0	0	K.DYVSQFEGSALGK.Q
2202.0786	2201.0713	2201.1116	-0.0403	84 - 101	1	1	K.LREQLGPTQEFWDNLEK.E

No match to: 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1408.7039, 1462.8200, 1467.7784, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2383.9341

11. Q8HZ95_PONPY Mass: 22116 Score: **105** Expect: 0.0001 Queries matched: 13

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

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4409	780.4336	780.4242	0.0094	141 - 147	0	0	R.AHVDALR.T
831.3855	830.3783	830.4286	-0.0503	176 - 182	0	0	R.LAEYHAK.A
873.4259	872.4186	872.4352	-0.0165	111 - 118	0	0	R.AELQEGAR.Q
1157.6034	1156.5962	1156.6200	-0.0238	165 - 175	1	1	R.LEALKENGGA.R.L
1252.6284	1251.6211	1251.6135	0.0076	84 - 93	0	0	K.VQPYLDDFQK.K
1283.5580	1282.5508	1282.5652	-0.0144	95 - 103	0	0	K.WQEEMELYR.Q
1299.5558	1298.5485	1298.5601	-0.0116	95 - 103	0	0	K.WQEEMELYR.Q + Oxidation (M)
1307.6958	1306.6885	1306.6187	0.0698	65 - 75	1	1	K.ETEGLRQEMSK.D
1323.6033	1322.5960	1322.6136	-0.0176	65 - 75	1	1	K.ETEGLRQEMSK.D + Oxidation (M)
1380.6922	1379.6849	1379.7085	-0.0236	84 - 94	1	1	K.VQPYLDDFQKK.W
1400.6222	1399.6149	1399.6619	-0.0470	15 - 27	0	0	R.DYVSQFEGSALGK.Q
1815.8328	1814.8255	1814.8434	-0.0179	11 - 27	1	1	K.DSGRDYVSQFEGSALGK.Q
2202.0786	2201.0713	2201.1116	-0.0403	47 - 64	1	1	K.LREQLGPTQEFWDNLEK.E

No match to: 832.3686, 852.4759, 855.0295, 861.0514, 877.0207, 893.0028, 1012.5758, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1301.6318, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1386.6862, 1408.7039, 1462.8200, 1467.7784, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1993.9556, 2383.9341

12. [CAD61352](#) Mass: 18392 Score: 77 Expect: 0.062 Queries matched: 10

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

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1235.5913	1234.5840	1234.6809	-0.0969	37 - 47	0	0	K.DLATVYVDVLK.D
1252.6284	1251.6211	1251.6135	0.0076	121 - 130	0	0	K.VQPYLDDFQK.K
1283.5580	1282.5508	1282.5652	-0.0144	132 - 140	0	0	K.WQEEMELYSR.Q
1299.5558	1298.5485	1298.5601	-0.0116	132 - 140	0	0	K.WQEEMELYSR.Q + Oxidation (M)
1307.6958	1306.6885	1306.6187	0.0698	102 - 112	1	1	K.ETEGLRQEMSK.D
1323.6033	1322.5960	1322.6136	-0.0176	102 - 112	1	1	K.ETEGLRQEMSK.D + Oxidation (M)
1380.6922	1379.6849	1379.7085	-0.0236	121 - 131	1	1	K.VQPYLDDFQKK.W
1400.6222	1399.6149	1399.6619	-0.0470	52 - 64	0	0	R.DYVSQFEGSALGK.Q
1462.8200	1461.8127	1461.8442	-0.0315	35 - 47	1	1	R.VKDLATVYVDVLK.D
1815.8328	1814.8255	1814.8434	-0.0179	48 - 64	1	1	K.DSGRDYVSQFEGSALGK.Q

No match to: 781.4409, 831.3855, 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1157.6034, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1301.6318, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1386.6862, 1408.7039, 1467.7784, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1993.9556, 2202.0786, 2383.9341

13. [T47237](#) Mass: 87729 Score: 64 Expect: 1.3 Queries matched: 15

myosin II heavy chain [imported] - Naegleria fowleri (fragment)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
831.3855	830.3783	830.4497	-0.0715	488 - 494	1	1	R.VDVENKK.R
832.3686	831.3613	831.3835	-0.0221	271 - 277	1	1	K.KNDADNR.V
873.4259	872.4186	872.4715	-0.0529	597 - 604	1	1	R.AKLDEAAR.R
1226.5318	1225.5245	1225.4955	0.0291	524 - 533	0	0	K.SVEMECDEL.R.E + Oxidation (M)
1230.6543	1229.6470	1229.6251	0.0219	312 - 322	0	0	R.QLDESNNLVAK.L
1238.6094	1237.6021	1237.6224	-0.0202	111 - 121	1	1	K.KSTEMELSSVK.D
1252.6284	1251.6211	1251.6169	0.0042	468 - 477	0	0	R.EYEMQLAQLK.A
1283.5580	1282.5508	1282.5169	0.0338	524 - 533	0	0	K.SVEMECDEL.R.E + Carbamidomethyl (C); Oxidation (M)
1301.6318	1300.6245	1300.6120	0.0126	569 - 580	1	1	R.HSRASAEESATR.Q
1386.6862	1385.6789	1385.7262	-0.0473	311 - 322	1	1	K.RQLDESNNLVAK.L
1408.7039	1407.6966	1407.7180	-0.0214	467 - 477	1	1	R.REYEMQLAQLK.A
1462.8200	1461.8127	1461.6987	0.1140	733 - 746	0	0	K.ASPFSAGELIDDLQ.-
1638.8350	1637.8278	1637.7744	0.0534	200 - 214	1	1	R.SLSDKQNESTSLDSK.V
1722.8620	1721.8548	1721.7526	0.1022	406 - 419	1	1	K.QEMERVQSESENEK.S
1723.9219	1722.9146	1722.8094	0.1052	112 - 126	1	1	K.STEMELSSVKDDLNR.T

No match to: 781.4409, 852.4759, 855.0295, 861.0514, 877.0207, 893.0028, 1012.5758, 1157.6034, 1158.5981, 1179.5649, 1213.6598, 1235.5913, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1299.5558, 1307.6958, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1380.6922, 1400.6222, 1467.7784, 1475.7529, 1612.7497, 1706.8966, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

14. [Q676V0 HPV62](#) Mass: 73294 Score: 64 Expect: 1.4 Queries matched: 14

Putative replication protein E1.- Human papillomavirus type 62.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
873.4259	872.4186	872.3624	0.0563	171 - 179	0	0	R.GGGDGEPEP.S
1157.6034	1156.5962	1156.6200	-0.0238	80 - 90	1	1	R.DDAAAVQALKR.K
1158.5981	1157.5908	1157.5863	0.0046	643 - 652	1	1	R.CVPGETNRLL.- + Carbamidomethyl (C)
1213.6598	1212.6525	1212.5750	0.0776	313 - 322	0	0	R.SAPCALYWFR.T
1230.6543	1229.6470	1229.5797	0.0673	419 - 428	0	0	R.MSMAQWIAHR.S
1235.5913	1234.5840	1234.5726	0.0114	403 - 412	1	1	K.DAITMCKYYK.R
1242.5535	1241.5462	1241.6148	-0.0686	400 - 409	1	1	K.YIKDAITMCK.Y + Carbamidomethyl (C)

1258.5465 1257.5392 1257.6097 -0.0705 400 - 409 1 K.YIKDAITMCK.Y + Carbamidomethyl (C); Oxidation (M)
 1301.6318 1300.6245 1300.6737 -0.0491 450 - 460 0 K.IEFVTFMSALK.M + Oxidation (M)
 1308.6351 1307.6279 1307.5890 0.0389 403 - 412 1 K.DAITMCKYYK.R + Carbamidomethyl (C); Oxidation (M)
 1316.5630 1315.5558 1315.6732 -0.1174 537 - 548 0 R.SVL DGNQISIDR.K
 1380.6922 1379.6849 1379.7269 -0.0420 113 - 124 1 R.LNAISLDRGHER.A
 1386.6862 1385.6789 1385.6808 -0.0019 418 - 428 1 K.RMSMAQWIAHR.S
 1467.7784 1466.7712 1466.7439 0.0273 469 - 482 1 K.KSCIVIYGPSDTGK.S

No match to: 781.4409, 831.3855, 832.3686, 852.4759, 855.0295, 861.0514, 877.0207, 893.0028, 1012.5758, 1179.5649, 1226.5318, 1238.6094, 1240.5125, 1252.6284, 1277.6779, 1283.5580, 1299.5558, 1307.6958, 1317.6197, 1318.6086, 1323.6033, 1400.6222, 1408.7039, 1462.8200, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

15. [Q8TV91_METKA](#) Mass: 29481 Score: 63 Expect: 1.8 Queries matched: 9

Predicted transcriptional regulator containing a DNA-binding HTH domain.- *Methanopyrus kandleri*.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
831.3855	830.3783	830.3956	-0.0173	1	7	0	- .MEEGPIR.V
1213.6598	1212.6525	1212.7264	-0.0738	240	250	0	K.ALVVITTPMLR.R
1301.6318	1300.6245	1300.6735	-0.0489	136	148	1	K.TGARAIQAADAEK.G
1307.6958	1306.6885	1306.6954	-0.0070	224	236	0	K.FGVVDGAIMAALK.G + Oxidation (M)
1323.6033	1322.5960	1322.6717	-0.0757	69	80	1	R.AEYVLTDKGAEK.A
1380.6922	1379.6849	1379.7408	-0.0559	2	13	1	M.EEGPIRVPNELK.D
1400.6222	1399.6149	1399.7381	-0.1231	211	223	0	R.AALNMLGIEPDLK.F + Oxidation (M)
1475.7529	1474.7456	1474.7602	-0.0146	103	115	1	R.MTWAAIAEDIRK.G
1993.9556	1992.9483	1992.9390	0.0093	116	132	0	K.GEEIYLYMEDGLLYASK.S

No match to: 781.4409, 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1157.6034, 1158.5981, 1179.5649, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1252.6284, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1386.6862, 1408.7039, 1462.8200, 1467.7784, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 2202.0786, 2383.9341

16. [Q02568_9BILA](#) Mass: 17537 Score: 62 Expect: 1.8 Queries matched: 7

Enolase (Fragment).- *Cerebratulus cf. lacteus*.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4409	780.4336	780.3766	0.0570	11	16	0	R.QIYDSR.G
1012.5758	1011.5686	1011.5825	-0.0140	2	10	1	M.STITKVHAR.Q
1308.6351	1307.6279	1307.6391	-0.0112	93	104	1	K.MLTLDGSDNKS.F
1462.8200	1461.8127	1461.8013	0.0114	105	119	0	K.FGANAILGVSLAVCK.A
1723.9219	1722.9146	1722.9627	-0.0481	62	79	0	K.GVNTAVANVINSLGPAVK.G
1791.7119	1790.7047	1790.8798	-0.1752	17	33	0	R.GNPTVEVEVTTGQGTFR.A
1993.9556	1992.9483	1992.9310	0.0174	85	102	1	K.EQTAVDEKMLTLDGSDNK.S

No match to: 831.3855, 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1157.6034, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1252.6284, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1301.6318, 1307.6958, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1380.6922, 1386.6862, 1400.6222, 1408.7039, 1467.7784, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1815.8328, 2202.0786, 2383.9341

17. [H87687](#) Mass: 130186 Score: 62 Expect: 2 Queries matched: 15

helicase, UvrD/Rep family [imported] - *Caulobacter crescentus*

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
832.3686	831.3613	831.4086	-0.0473	905	911	0	K.ESQEALR.L
852.4759	851.4686	851.4977	-0.0291	1038	1044	1	R.RGELIHK.L
1157.6034	1156.5962	1156.6200	-0.0238	1123	1132	1	R.VDRLVDDAR.V
1179.5649	1178.5577	1178.5931	-0.0354	961	971	0	R.TIGDGETAFLR.Y
1230.6543	1229.6470	1229.6186	0.0284	840	850	1	R.EVRVMTAHGSK.G + Oxidation (M)
1301.6318	1300.6245	1300.6160	0.0086	739	749	0	R.SEERPEWAAAR.A
1307.6958	1306.6885	1306.6517	0.0368	135	146	1	K.LVGEADARYDAK.S
1308.6351	1307.6279	1307.6258	0.0021	936	947	1	K.DDKVGGWYAAAR.A

1386.6862 1385.6789 1385.7190 -0.0401 1174 - 1186 0 R.TVEAALVWTDGPK.L
 1400.6222 1399.6149 1399.7419 -0.1270 310 - 323 1 K.QDAKSAEALAAVAR.D
 1475.7529 1474.7456 1474.7099 0.0357 258 - 271 1 R.CGGLAGAVSDAWRR.C + Carbamidomethyl (C)
 1612.7497 1611.7424 1611.8416 -0.0991 43 - 56 1 R.LPHGGRIVMHDPQR.I
 1638.8350 1637.8278 1637.9360 -0.1082 1187 - 1201 1 K.LMPVPEKVMALALAR.L
 1815.8328 1814.8255 1815.0029 -0.1774 815 - 831 0 R.DLEALVADFAALDIIVK.R
 2383.9341 2382.9268 2383.0927 -0.1659 587 - 606 1 R.ELPGEDREAWKPLDEEGER.S

No match to: 781.4409, 831.3855, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1158.5981, 1213.6598, 1226.5318, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1252.6284, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1380.6922, 1408.7039, 1462.8200, 1467.7784, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1993.9556, 2202.0786

18. [Q6DU55_PRUPE](#) Mass: 67223 Score: 60 Expect: 3.2 Queries matched: 12

S-locus-like receptor protein kinase (Fragment).- *Prunus persica* (Peach).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1012.5758	1011.5686	1011.5284	0.0402	357	-	364	0 K.INHMNLVR.T + Oxidation (M)
1158.5981	1157.5908	1157.6154	-0.0246	296	-	304	1 R.MYLYAELKK.A
1235.5913	1234.5840	1234.6557	-0.0717	194	-	204	0 R.SPTIEGSLYLR.L
1238.6094	1237.6021	1237.5873	0.0148	126	-	135	0 K.FKPTCSQSQR.V + Carbamidomethyl (C)
1299.5558	1298.5485	1298.5812	-0.0327	232	-	243	0 K.IGTSSMYDNPSK.T
1307.6958	1306.6885	1306.5876	0.1008	365	-	375	1 R.TWGFCEGKHR.L
1318.6086	1317.6013	1317.6789	-0.0776	546	-	557	1 R.LEGQFGRNQAAK.M
1323.6033	1322.5960	1322.6579	-0.0618	53	-	63	1 R.RLTDDYDGNLR.L
1408.7039	1407.6966	1407.7292	-0.0326	126	-	137	1 K.FKPTCSQSQRVK.F
1467.7784	1466.7712	1466.7187	0.0524	276	-	288	1 R.SQGMSAPLVDKYR.L + Oxidation (M)
1723.9219	1722.9146	1722.7916	0.1230	558	-	572	1 K.MVEVGISCVEEDRNK.R + Oxidation (M)
1993.9556	1992.9483	1992.9244	0.0239	553	-	570	1 R.NQAAKMVEVGISCVEEDR.N + Oxidation (M)

No match to: 781.4409, 831.3855, 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1157.6034, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1240.5125, 1242.5535, 1252.6284, 1258.5465, 1277.6779, 1283.5580, 1301.6318, 1308.6351, 1316.5630, 1317.6197, 1380.6922, 1386.6862, 1400.6222, 1462.8200, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1791.7119, 1815.8328, 2202.0786, 2383.9341

19. [Q7MS71_WOLSU](#) Mass: 44173 Score: 59 Expect: 4.2 Queries matched: 9

Hypothetical protein hydC.- *Wolinella succinogenes*.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
852.4759	851.4686	851.4388	0.0298	275	-	281	1 K.DAKEYVK.H
1012.5758	1011.5686	1011.5283	0.0402	1	-	9	1 -.MGRGEPLPR.I
1158.5981	1157.5908	1157.6022	-0.0113	83	-	90	0 R.YYFLHLFR.D
1213.6598	1212.6525	1212.6978	-0.0453	321	-	330	1 R.ISFIRELHAK.I
1301.6318	1300.6245	1300.6855	-0.0610	139	-	148	0 K.ILYFWGDFLK.K
1386.6862	1385.6789	1385.7489	-0.0700	263	-	274	1 K.IIMQDLKGHFGK.D
1612.7497	1611.7424	1611.7582	-0.0158	71	-	82	1 R.FSHFDFSWRDLR.Y
1815.8328	1814.8255	1814.9831	-0.1576	4	-	18	1 R.GEPLPRIYVWSPFVR.V
1993.9556	1992.9483	1993.0091	-0.0608	178	-	194	1 R.TRIIDSMVHGYKPYEGK.D

No match to: 781.4409, 831.3855, 832.3686, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1157.6034, 1179.5649, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1252.6284, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1307.6958, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1380.6922, 1400.6222, 1408.7039, 1462.8200, 1467.7784, 1475.7529, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 2202.0786, 2383.9341

20. [Q4IBZ3_GIBZE](#) Mass: 31681 Score: 58 Expect: 4.9 Queries matched: 8

Hypothetical protein.- *Gibberella zeae* (*Fusarium graminearum*).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1230.6543	1229.6470	1229.6669	-0.0199	67	-	75	1 K.ISWQWNKLR.T
1258.5465	1257.5392	1257.5964	-0.0572	209	-	217	1 K.YCHEFKLYR.V
1308.6351	1307.6279	1307.6730	-0.0451	258	-	268	0 R.WSLMVMSALR.M + Oxidation (M)

1408.7039	1407.6966	1407.6856	0.0110	223 - 234	0	K.VPNEYLAMASWK.E
1467.7784	1466.7712	1466.6976	0.0736	87 - 99	0	K.MFAVTEHSGLFGR.T + Oxidation (M)
1612.7497	1611.7424	1611.7740	-0.0315	275 - 289	0	R.SGQASLETNTSVQYK.-
1993.9556	1992.9483	1992.9767	-0.0284	223 - 239	1	K.VPNEYLAMASWKEAAWK.T
2383.9341	2382.9268	2383.1590	-0.2322	269 - 289	1	R.MWQLGRSGQASLETNTSVQYK.-

No match to: 781.4409, 831.3855, 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1157.6034, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1252.6284, 1277.6779, 1283.5580, 1299.5558, 1301.6318, 1307.6958, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1380.6922, 1386.6862, 1400.6222, 1462.8200, 1475.7529, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 2202.0786

21. [E96933](#) Mass: 18193 Score: 57 Expect: 5.9 Queries matched: 8

hypothetical protein CAC0275 [imported] - Clostridium acetobutylicum

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1012.5758	1011.5686	1011.5349	0.0337	144 - 152	0		K.ANHISTIEK.T
1157.6034	1156.5962	1156.6492	-0.0530	50 - 58	1		R.TIQYYKTLK.E
1242.5535	1241.5462	1241.6114	-0.0652	77 - 86	0		K.MSFLIDQFNK.K
1258.5465	1257.5392	1257.6063	-0.0671	77 - 86	0		K.MSFLIDQFNK.K + Oxidation (M)
1277.6779	1276.6706	1276.6411	0.0295	121 - 131	1		R.FVKNTSDTHK.T
1283.5580	1282.5508	1282.5928	-0.0421	21 - 30	1		K.SEYEKIEEEK.H
1317.6197	1316.6124	1316.7122	-0.0997	38 - 49	1		R.VMSAVLVKEADR.T
1386.6862	1385.6789	1385.7013	-0.0224	77 - 87	1		K.MSFLIDQFNKK.T + Oxidation (M)

No match to: 781.4409, 831.3855, 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1252.6284, 1299.5558, 1301.6318, 1307.6958, 1308.6351, 1316.5630, 1318.6086, 1323.6033, 1380.6922, 1400.6222, 1408.7039, 1462.8200, 1467.7784, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

22. [Q3KQC8_XENLA](#) Mass: 28985 Score: 57 Expect: 6.8 Queries matched: 9

Hypothetical protein.- Xenopus laevis (African clawed frog).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
852.4759	851.4686	851.4211	0.0475	12 - 19	0		K.CGDLVFAK.M
1179.5649	1178.5577	1178.4687	0.0890	150 - 161	0		K.GNAEGSSDEEGK.L
1242.5535	1241.5462	1241.6127	-0.0665	20 - 29	1		K.MKGYPHWPAR.V
1258.5465	1257.5392	1257.6077	-0.0685	20 - 29	1		K.MKGYPHWPAR.V + Oxidation (M)
1307.6958	1306.6885	1306.5636	0.1248	149 - 161	1		K.KGNAEGSSDEEGK.L
1317.6197	1316.6124	1316.6096	0.0029	192 - 202	1		K.TKVEDDQEPEK.N
1386.6862	1385.6789	1385.7401	-0.0612	240 - 251	1		K.VEEKPVAEKETK.E
1612.7497	1611.7424	1611.7852	-0.0428	30 - 44	1		R.VDEVPEPNAKSSANR.Y
2202.0786	2201.0713	2200.9430	0.1283	203 - 221	1		K.NEKEDPQPEESVQMPDSK.E

No match to: 781.4409, 831.3855, 832.3686, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1157.6034, 1158.5981, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1252.6284, 1277.6779, 1283.5580, 1299.5558, 1301.6318, 1308.6351, 1316.5630, 1318.6086, 1323.6033, 1380.6922, 1400.6222, 1408.7039, 1462.8200, 1467.7784, 1475.7529, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2383.9341

23. [Q9N0V7_RABIT](#) Mass: 60174 Score: 56 Expect: 7.6 Queries matched: 10

Cystathionine beta-synthase (EC 4.2.1.22).- Oryctolagus cuniculus (Rabbit).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1157.6034	1156.5962	1156.6274	-0.0312	370 - 379	0		R.CVVILPDSVR.N + Carbamidomethyl (C)
1158.5981	1157.5908	1157.5175	0.0733	109 - 119	0		K.CEFFNAGGSVK.D
1235.5913	1234.5840	1234.6743	-0.0903	98 - 108	1		K.NFGLKCELLAK.C
1242.5535	1241.5462	1241.6040	-0.0578	326 - 336	1		K.STDKEAFAR.M
1308.6351	1307.6279	1307.6729	-0.0451	162 - 172	1		K.GYRCIIVPEK.M
1323.6033	1322.5960	1322.6805	-0.0845	385 - 394	1		K.FLSDRWMLQK.G
1612.7497	1611.7424	1611.8005	-0.0580	212 - 224	0		K.QEIPNSHILDQYR.N
1723.9219	1722.9146	1722.8796	0.0350	370 - 384	1		R.CVVILPDSVRNYMSK.F

1815.8328 1814.8255 1814.8694 -0.0439 103 - 119 1 K.CELLAKCEFFNAGGSVK.D
 2202.0786 2201.0713 2201.1547 -0.0834 337 - 359 0 R.MLIAQEGLLCGGSAGSAVAVK.A + Carbamidomethyl (C)
No match to: 781.4409, 831.3855, 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1238.6094, 1240.5125, 1252.6284, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1301.6318, 1307.6958, 1316.5630, 1317.6197, 1318.6086, 1380.6922, 1386.6862, 1400.6222, 1408.7039, 1462.8200, 1467.7784, 1475.7529, 1638.8350, 1706.8966, 1722.8620, 1791.7119, 1993.9556, 2383.9341

24. [Q5NCF0_MOUSE](#) Mass: 19181 Score: 56 Expect: 8.1 Queries matched: 8

Novel Sybindin-like family domain-containing protein.- Mus musculus (Mouse).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1157.6034	1156.5962	1156.5513	0.0449	59	- 68	0	K.DGFLSFQTSR.Y
1230.6543	1229.6470	1229.6300	0.0170	37	- 46	0	K.LMYGMLFSIR.S
1277.6779	1276.6706	1276.6564	0.0142	2	- 11	0	M.TVHNLYLFDR.N
1323.6033	1322.5960	1322.7241	-0.1281	142	- 152	0	R.RPTTHCLQVIR.M
1380.6922	1379.6849	1379.7456	-0.0607	142	- 152	0	R.RPTTHCLQVIR.M + Carbamidomethyl (C)
1386.6862	1385.6789	1385.7336	-0.0547	82	- 94	0	K.VVMNTDLGVGPIR.D + Oxidation (M)
1408.7039	1407.6966	1407.6969	-0.0002	1	- 11	0	-.MTVHNLYLFDR.N
1612.7497	1611.7424	1611.8297	-0.0872	69	- 81	1	R.YKLHYYETPTGIK.V

No match to: 781.4409, 831.3855, 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1252.6284, 1258.5465, 1283.5580, 1299.5558, 1301.6318, 1307.6958, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1400.6222, 1462.8200, 1467.7784, 1475.7529, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

25. [AAL97589](#) Mass: 22480 Score: 56 Expect: 8.7 Queries matched: 8

AE010023 NID: - Streptococcus pyogenes MGAS8232

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1157.6034	1156.5962	1156.5434	0.0528	101	- 109	0	K.MIEEYLTSLR.D + Oxidation (M)
1158.5981	1157.5908	1157.6516	-0.0608	54	- 64	1	K.NLARTSSKPGK.T
1235.5913	1234.5840	1234.7033	-0.1193	43	- 53	1	K.SSFINTILGRK.N
1301.6318	1300.6245	1300.6009	0.0236	128	- 137	0	K.EDIQMYDFLK.Y
1317.6197	1316.6124	1316.5958	0.0166	128	- 137	0	K.EDIQMYDFLK.Y + Oxidation (M)
1380.6922	1379.6849	1379.7700	-0.0851	138	- 149	0	K.YYDIPVIVVATK.A
1386.6862	1385.6789	1385.6826	-0.0037	174	- 185	0	K.SDTFIVFSSVER.I
1467.7784	1466.7712	1466.7405	0.0306	65	- 76	0	K.TQLLNFFNIDDK.L

No match to: 781.4409, 831.3855, 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1238.6094, 1240.5125, 1242.5535, 1252.6284, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1307.6958, 1308.6351, 1316.5630, 1318.6086, 1323.6033, 1400.6222, 1408.7039, 1462.8200, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

26. [CAA40001](#) Mass: 3140 Score: 55 Expect: 10 Queries matched: 4

BSDCIA NID: - Bacillus subtilis

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1179.5649	1178.5577	1178.6183	-0.0606	15	- 24	0	K.YELLTEQVGK.Q
1252.6284	1251.6211	1251.5771	0.0440	1	- 10	0	-.PDVFDEVFER.T
1307.6958	1306.6885	1306.7132	-0.0247	14	- 24	1	R.KYELLTEQVGK.Q
1408.7039	1407.6966	1407.7245	-0.0279	15	- 26	1	K.YELLTEQVGKQT.-

No match to: 781.4409, 831.3855, 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1157.6034, 1158.5981, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1301.6318, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1380.6922, 1386.6862, 1400.6222, 1462.8200, 1467.7784, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

27. [Q219J6_RHOPB](#) Mass: 54585 Score: 55 Expect: 10 Queries matched: 10

Transcriptional regulator, XRE family.- Rhodopseudomonas palustris (strain BisB18).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
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1213.6598	1212.6525	1212.6251	0.0275	117 - 126	1	R.LYAAYTEARR.G
1230.6543	1229.6470	1229.6516	-0.0046	143 - 152	1	R.FEANPIERVR.D
1238.6094	1237.6021	1237.6891	-0.0870	191 - 200	1	R.LREQHSIVTR.I
1299.5558	1298.5485	1298.6255	-0.0770	469 - 480	1	R.ASSFAFSNAREL.-
1307.6958	1306.6885	1306.5876	0.1008	304 - 314	0	R.FNAGFEQVCHR.L
1317.6197	1316.6124	1316.5714	0.0411	442 - 451	1	R.LCEREHCSQR.A + Carbamidomethyl (C)
1318.6086	1317.6013	1317.6459	-0.0446	126 - 137	1	R.RGETLAAQMADR.E
1408.7039	1407.6966	1407.8310	-0.1344	46 - 57	0	R.NQRPVTAQILLR.L
1467.7784	1466.7712	1466.8456	-0.0745	372 - 384	1	R.LLKQVIELPDGSR.Y
1638.8350	1637.8278	1637.8195	0.0083	102 - 116	0	R.DLAELCPGVTHSLQR.L

No match to: 781.4409, 831.3855, 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1157.6034, 1158.5981, 1179.5649, 1226.5318, 1235.5913, 1240.5125, 1242.5535, 1252.6284, 1258.5465, 1277.6779, 1283.5580, 1301.6318, 1308.6351, 1316.5630, 1323.6033, 1380.6922, 1386.6862, 1400.6222, 1462.8200, 1475.7529, 1612.7497, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

28. [Q4LAF2_STAHI](#) Mass: 57597 Score: 55 Expect: 11 Queries matched: 10

Type I restriction-modification system DNA methylase.- *Staphylococcus haemolyticus* (strain JCSC1435).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
831.3855	830.3783	830.4286	-0.0504	10 - 16	0		K.LWQAADK.L
1213.6598	1212.6525	1212.6713	-0.0188	104 - 114	1		K.ENESLKGVLPE.E
1240.5125	1239.5052	1239.5917	-0.0865	17 - 27	1		K.LRGSMDDAEYK.N
1252.6284	1251.6211	1251.6346	-0.0136	475 - 485	0		R.ITSELSEQFAK.S
1408.7039	1407.6966	1407.7357	-0.0391	474 - 485	1		K.RITSELSEQFAK.S
1467.7784	1466.7712	1466.7616	0.0095	475 - 487	1		R.ITSELSEQFAKSK.E
1475.7529	1474.7456	1474.7701	-0.0245	97 - 109	1		K.AMIAIEKENESLK.G
1706.8966	1705.8893	1705.8675	0.0218	2 - 16	1		M.ATIGFEEKLWQAADK.L
1722.8620	1721.8548	1721.8664	-0.0116	151 - 165	1		R.VYEFYIAKFASAEGK.N
1723.9219	1722.9146	1722.7559	0.1587	422 - 436	1		R.GTNDKYYEDIAGFCK.V

No match to: 781.4409, 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1157.6034, 1158.5981, 1179.5649, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1242.5535, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1301.6318, 1307.6958, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1380.6922, 1386.6862, 1400.6222, 1462.8200, 1612.7497, 1638.8350, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

29. [AAM79212](#) Mass: 22460 Score: 55 Expect: 11 Queries matched: 8

AE014074 NID: - *Streptococcus pyogenes* MGAS315

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1157.6034	1156.5962	1156.5434	0.0528	101 - 109	0		K.MIEEYLTSR.D + Oxidation (M)
1158.5981	1157.5908	1157.6516	-0.0608	54 - 64	1		K.NLARTSSKPGK.T
1235.5913	1234.5840	1234.7033	-0.1193	43 - 53	1		K.SSFINTILGRK.N
1301.6318	1300.6245	1300.6009	0.0236	128 - 137	0		K.EDIQMYDFLK.Y
1317.6197	1316.6124	1316.5958	0.0166	128 - 137	0		K.EDIQMYDFLK.Y + Oxidation (M)
1380.6922	1379.6849	1379.7700	-0.0851	138 - 149	0		K.YYDIPVIVVATK.A
1386.6862	1385.6789	1385.6826	-0.0037	174 - 185	0		K.SDTFIVFSSVER.I
1467.7784	1466.7712	1466.7405	0.0306	65 - 76	0		K.TQLLNFFNIDDK.L

No match to: 781.4409, 831.3855, 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1238.6094, 1240.5125, 1242.5535, 1252.6284, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1307.6958, 1308.6351, 1316.5630, 1318.6086, 1323.6033, 1400.6222, 1408.7039, 1462.8200, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

30. [AAK33806](#) Mass: 22479 Score: 54 Expect: 12 Queries matched: 8

AE006538 NID: - *Streptococcus pyogenes* M1 GAS

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1157.6034	1156.5962	1156.5434	0.0528	101 - 109	0		K.MIEEYLTSR.D + Oxidation (M)
1158.5981	1157.5908	1157.6516	-0.0608	54 - 64	1		K.NLARTSSKPGK.T

1235.5913	1234.5840	1234.7033	-0.1193	43	-	53	1	K.SSFINTILGRK.N
1301.6318	1300.6245	1300.6009	0.0236	128	-	137	0	K.EDIQMYDFLK.Y
1317.6197	1316.6124	1316.5958	0.0166	128	-	137	0	K.EDIQMYDFLK.Y + Oxidation (M)
1380.6922	1379.6849	1379.7700	-0.0851	138	-	149	0	K.YYDIPVIVVATK.A
1386.6862	1385.6789	1385.6826	-0.0037	174	-	185	0	K.SDTFIVFSSVER.I
1467.7784	1466.7712	1466.7405	0.0306	65	-	76	0	K.TQLLNFFNIDDK.L

No match to: 781.4409, 831.3855, 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1238.6094, 1240.5125, 1242.5535, 1252.6284, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1307.6958, 1308.6351, 1316.5630, 1318.6086, 1323.6033, 1400.6222, 1408.7039, 1462.8200, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

31. [Q4WN94_ASPFU](#) Mass: 42187 Score: 54 Expect: 14 Queries matched: 9

Actin binding protein, putative.- *Aspergillus fumigatus* (Sartorya fumigata).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
832.3686	831.3613	831.4166	-0.0553	283	-	288	0	R.VYFFEK.E
1226.5318	1225.5245	1225.5840	-0.0594	37	-	46	1	K.RTDPYQFGSR.Y
1242.5535	1241.5462	1241.5789	-0.0326	107	-	116	1	K.NNTSNFFKDR.K
1252.6284	1251.6211	1251.5230	0.0981	269	-	277	0	R.YMDENFYVR.G + Oxidation (M)
1307.6958	1306.6885	1306.6153	0.0732	82	-	92	1	R.ESPVSDFDKQR.F
1317.6197	1316.6124	1316.6095	0.0029	354	-	366	1	R.ETPAAVEAEKADS.-
1318.6086	1317.6013	1317.6353	-0.0340	278	-	288	1	R.GDGTRVYFFEK.E
1467.7784	1466.7712	1466.7346	0.0365	96	-	106	1	K.DPAKWNNLFYK.N
1722.8620	1721.8548	1721.7467	0.1081	269	-	282	1	R.YMDENFYVRGDGTR.V

No match to: 781.4409, 831.3855, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1157.6034, 1158.5981, 1179.5649, 1213.6598, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1301.6318, 1308.6351, 1316.5630, 1323.6033, 1380.6922, 1386.6862, 1400.6222, 1408.7039, 1462.8200, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

32. [Q2RK76_M00TA](#) Mass: 45037 Score: 54 Expect: 14 Queries matched: 10

UDP-N-acetylglucosamine 1-carboxyvinyltransferase.- *Moorella thermoacetica* (strain ATCC 39073).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
832.3686	831.3613	831.4385	-0.0771	266	-	272	1	K.LREMGAR.I
852.4759	851.4686	851.4725	-0.0039	333	-	339	1	K.HAAELRR.L
1012.5758	1011.5686	1011.4695	0.0991	220	-	227	1	R.ELKGCYK.I + Carbamidomethyl (C)
1179.5649	1178.5577	1178.5754	-0.0177	223	-	232	1	K.GCDYKIIPDR.I
1213.6598	1212.6525	1212.6574	-0.0049	404	-	414	1	K.RLGD LGADIQR.L
1252.6284	1251.6211	1251.5838	0.0372	129	-	140	0	K.GLMAMGAEVTEK.L + Oxidation (M)
1301.6318	1300.6245	1300.7173	-0.0927	47	-	58	0	R.LQDVSVMAAVIR.S
1317.6197	1316.6124	1316.7122	-0.0997	47	-	58	0	R.LQDVSVMAAVIR.S + Oxidation (M)
1815.8328	1814.8255	1814.9382	-0.1127	23	-	40	0	K.NAALPIMAAATLLATGECR.L
2202.0786	2201.0713	2201.1262	-0.0549	188	-	206	1	R.EPEIVDLQNFLNMGARIR.G + Oxidation (M)

No match to: 781.4409, 831.3855, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1157.6034, 1158.5981, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1307.6958, 1308.6351, 1316.5630, 1318.6086, 1323.6033, 1380.6922, 1386.6862, 1400.6222, 1408.7039, 1462.8200, 1467.7784, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1993.9556, 2383.9341

33. [Q8GC31_LEUCI](#) Mass: 47411 Score: 53 Expect: 16 Queries matched: 9

Putative mobilization protein.- *Leuconostoc citreum*.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
852.4759	851.4686	851.3886	0.0800	23	-	29	0	K.TDHHTNK.E
1157.6034	1156.5962	1156.5369	0.0593	57	-	65	1	R.LNDVYCMKR.D + Oxidation (M)
1226.5318	1225.5245	1225.6302	-0.1057	349	-	358	1	K.LDHEELTKNK.K
1240.5125	1239.5052	1239.6247	-0.1195	191	-	200	1	K.KYNDQFNALK.N
1252.6284	1251.6211	1251.6723	-0.0512	10	-	21	0	R.GAVPGLAVHFER.K

1258.5465 1257.5392 1257.6201 -0.0809 373 - 383 1 R.EDPTDKISPTR.L
 1299.5558 1298.5485 1298.5383 0.0102 314 - 323 0 R.EQQQMDYAMR.D
 1301.6318 1300.6245 1300.6259 -0.0013 201 - 211 0 K.NELADVEENIR.A
 1380.6922 1379.6849 1379.7673 -0.0824 10 - 22 1 R.GAVPGLAVHFERK.T

No match to: 781.4409, 831.3855, 832.3686, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1158.5981, 1179.5649, 1213.6598, 1230.6543, 1235.5913, 1238.6094, 1242.5535, 1277.6779, 1283.5580, 1307.6958, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1386.6862, 1400.6222, 1408.7039, 1462.8200, 1467.7784, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

34. [Q16V40_AEDAE](#) Mass: 22771 Score: 53 Expect: 16 Queries matched: 8

Hypothetical protein.- Aedes aegypti (Yellowfever mosquito).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
852.4759	851.4686	851.5229	-0.0542	83	-	90	0 R.ALTLIHGK.K
1158.5981	1157.5908	1157.5387	0.0522	27	-	35	1 R.TDMYRESIK.H + Oxidation (M)
1230.6543	1229.6470	1229.6186	0.0284	2	-	13	1 M.STTPPCNVGRGAK.R
1283.5580	1282.5508	1282.6669	-0.1162	15	-	25	1 R.NVKSSYFSVPR.R
1307.6958	1306.6885	1306.6485	0.0399	41	-	52	1 R.NLCATRNIAMGK.A + Oxidation (M)
1612.7497	1611.7424	1611.7650	-0.0225	53	-	65	1 K.ACWNLNCRFTLSK.E + Carbamidomethyl (C)
1723.9219	1722.9146	1722.7752	0.1394	47	-	60	1 R.NIAMGKACWNLNCR.F + 2 Carbamidomethyl (C); Oxidation (M)
2383.9341	2382.9268	2383.1492	-0.2224	113	-	132	1 K.FAVVYKIFPGVNFCTCESFR.Y + Carbamidomethyl (C)

No match to: 781.4409, 831.3855, 832.3686, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1157.6034, 1179.5649, 1213.6598, 1226.5318, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1252.6284, 1258.5465, 1277.6779, 1299.5558, 1301.6318, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1380.6922, 1386.6862, 1400.6222, 1408.7039, 1462.8200, 1467.7784, 1475.7529, 1638.8350, 1706.8966, 1722.8620, 1791.7119, 1815.8328, 1993.9556, 2202.0786

35. [Q1EPB8_MUSAC](#) Mass: 14866 Score: 53 Expect: 16 Queries matched: 6

Hypothetical protein.- Musa acuminata (Banana).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
852.4759	851.4686	851.4072	0.0614	17	-	23	1 R.QRFCGNK.S
1012.5758	1011.5686	1011.4906	0.0779	24	-	32	1 K.SEKSMSLSK.T + Oxidation (M)
1283.5580	1282.5508	1282.5538	-0.0030	8	-	18	1 R.EFDGSSDSRQR.F
1475.7529	1474.7456	1474.6841	0.0615	121	-	133	0 R.WHPTEAQSSSFAK.W
1638.8350	1637.8278	1637.8009	0.0269	2	-	16	1 M.ITLGVREFDGSSDSR.Q
1723.9219	1722.9146	1722.9199	-0.0052	93	-	108	1 R.CNRLSQAVAPPELGLR.A

No match to: 781.4409, 831.3855, 832.3686, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1157.6034, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1252.6284, 1258.5465, 1277.6779, 1299.5558, 1301.6318, 1307.6958, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1380.6922, 1386.6862, 1400.6222, 1408.7039, 1462.8200, 1467.7784, 1612.7497, 1706.8966, 1722.8620, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

36. [Q3WCG3_9ACTO](#) Mass: 35265 Score: 53 Expect: 18 Queries matched: 8

Pyruvate dehydrogenase (Lipoamide) (EC 1.2.4.1).- Frankia sp. EAN1pec.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
852.4759	851.4686	851.4865	-0.0179	73	-	80	0 R.GLHDLIGK.G
1157.6034	1156.5962	1156.5872	0.0090	17	-	25	0 R.LYELMTLMK.A + Oxidation (M)
1230.6543	1229.6470	1229.6629	-0.0158	6	-	16	1 R.TAGISGQVWRR.L
1240.5125	1239.5052	1239.6281	-0.1229	263	-	274	0 R.MAAAVEADPIPR.F
1277.6779	1276.6706	1276.5506	0.1200	322	-	332	1 R.DVYADPRNCPA.- + Carbamidomethyl (C)
1462.8200	1461.8127	1461.7068	0.1060	49	-	62	0 R.GQEIAAAMGVCLR.S + Carbamidomethyl (C); Oxidation (M)
1706.8966	1705.8893	1705.8569	0.0324	230	-	245	1 R.ARSGGGPTLVECVTFR.F + Carbamidomethyl (C)
1723.9219	1722.9146	1722.7824	0.1323	248	-	262	0 R.GHYFGDPMAYIPAER.M

No match to: 781.4409, 831.3855, 832.3686, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1235.5913, 1238.6094, 1242.5535, 1252.6284, 1258.5465, 1283.5580, 1299.5558, 1301.6318, 1307.6958, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1380.6922, 1386.6862, 1400.6222, 1408.7039, 1467.7784, 1475.7529, 1612.7497, 1638.8350, 1722.8620, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

37. [Q1RUA7_MEDTR](#) Mass: 7463 Score: 53 Expect: 18 Queries matched: 5

Hypothetical protein.- Medicago truncatula (Barrel medic).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
852.4759	851.4686	851.4211	0.0475	12	- 18	0	K.LPTCQYK.C
873.4259	872.4186	872.4286	-0.0100	19	- 26	0	K.CGSTPRPR.H
1252.6284	1251.6211	1251.6897	-0.0686	1	- 11	0	- .MLDIPPLNVPK.L + Oxidation (M)
1318.6086	1317.6013	1317.6888	-0.0875	47	- 58	0	R.QTVSATSELLNR.C
1706.8966	1705.8893	1705.8392	0.0501	12	- 26	1	K.LPTCQYKCGSTPRPR.H

No match to: 781.4409, 831.3855, 832.3686, 855.0295, 861.0514, 877.0207, 893.0028, 1012.5758, 1157.6034, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1301.6318, 1307.6958, 1308.6351, 1316.5630, 1317.6197, 1323.6033, 1380.6922, 1386.6862, 1400.6222, 1408.7039, 1462.8200, 1467.7784, 1475.7529, 1612.7497, 1638.8350, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

38. [Q9C902_ARATH](#) Mass: 86001 Score: 52 Expect: 18 Queries matched: 12

Protein kinase, putative; 19229-23534 (Hypothetical protein At3g06620).- Arabidopsis thaliana (Mouse-ear cress).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
852.4759	851.4686	851.4905	-0.0219	354	- 360	0	K.FVSKPFK.D
873.4259	872.4186	872.4545	-0.0358	388	- 394	0	K.GLSWPWK.G
1157.6034	1156.5962	1156.5699	0.0263	753	- 761	0	K.YMIQFQATR.A
1230.6543	1229.6470	1229.6377	0.0093	40	- 50	0	R.SHSVSPHRPAR.R
1235.5913	1234.5840	1234.6240	-0.0400	157	- 167	1	R.DAAFAMNIARR.C
1238.6094	1237.6021	1237.6165	-0.0144	125	- 134	0	R.IIFWNAMAEK.V + Oxidation (M)
1242.5535	1241.5462	1241.6265	-0.0802	51	- 61	1	R.RNIGEGAPSWR.K
1301.6318	1300.6245	1300.6598	-0.0352	752	- 761	1	R.KYMIQFQATR.A + Oxidation (M)
1386.6862	1385.6789	1385.7388	-0.0599	40	- 51	1	R.SHSVSPHRPARR.N
1400.6222	1399.6149	1399.6918	-0.0769	654	- 665	0	K.GTPQWMAPEVLR.N + Oxidation (M)
1467.7784	1466.7712	1466.7616	0.0095	13	- 24	0	K.ILELEESQEHLK.Q
1722.8620	1721.8548	1721.7541	0.1006	721	- 734	0	R.WISLMESCWHSCLK.L

No match to: 781.4409, 831.3855, 832.3686, 855.0295, 861.0514, 877.0207, 893.0028, 1012.5758, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1240.5125, 1252.6284, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1307.6958, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1380.6922, 1408.7039, 1462.8200, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

39. [Q9TSS5_BOSIN](#) Mass: 10093 Score: 52 Expect: 19 Queries matched: 5

BoLA-DRB3 protein (Fragment).- Bos indicus (Zebu).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1158.5981	1157.5908	1157.4778	0.1131	32	- 40	0	R.FDSWGFEFR.A
1299.5558	1298.5485	1298.5931	-0.0446	73	- 83	0	R.HNYGVFESFTV.-
1638.8350	1637.8278	1637.7368	0.0910	5	- 17	1	K.SECHFFNGTERVR.Y + Carbamidomethyl (C)
1791.7119	1790.7047	1790.8223	-0.1177	18	- 31	1	R.YLDRYYTNGEENVR.F
2383.9341	2382.9268	2383.0141	-0.0873	22	- 40	1	R.YYTNGEENVRFDSDWGFEFR.A

No match to: 781.4409, 831.3855, 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1157.6034, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1252.6284, 1258.5465, 1277.6779, 1283.5580, 1301.6318, 1307.6958, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1380.6922, 1386.6862, 1400.6222, 1408.7039, 1462.8200, 1467.7784, 1475.7529, 1612.7497, 1706.8966, 1722.8620, 1723.9219, 1815.8328, 1993.9556, 2202.0786

40. [Q5VU61_HUMAN](#) Mass: 26265 Score: 52 Expect: 21 Queries matched: 10

Tropomyosin 3.- Homo sapiens (Human).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
832.3686	831.3613	831.4338	-0.0724	74	- 80	1	R.ALKDEEK.M
1157.6034	1156.5962	1156.6564	-0.0602	43	- 52	1	R.EQRLATALQK.L
1158.5981	1157.5908	1157.6768	-0.0860	2	- 12	1	M.AGITTIEAVKR.K
1179.5649	1178.5577	1178.5172	0.0405	130	- 138	1	R.CREMDEQIR.L

1252.6284	1251.6211	1251.5336	0.0875	130 - 138	1	R.CREMDEQIR.L + Carbamidomethyl (C); Oxidation (M)
1308.6351	1307.6279	1307.6105	0.0173	174 - 184	1	K.EAETRAEFAER.S
1318.6086	1317.6013	1317.6664	-0.0650	189 - 199	1	K.LEKTIDDLK.L
1380.6922	1379.6849	1379.7184	-0.0335	161 - 171	1	K.YEEEEIKILTDK.L
1467.7784	1466.7712	1466.6633	0.1079	213 - 224	0	R.MLDQTLLDLNEM.- + 2 Oxidation (M)
1475.7529	1474.7456	1474.7701	-0.0245	81 - 92	1	K.MELQEIQLKEAK.H + Oxidation (M)

No match to: 781.4409, 831.3855, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1301.6318, 1307.6958, 1316.5630, 1317.6197, 1323.6033, 1386.6862, 1400.6222, 1408.7039, 1462.8200, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

41. [S11390](#) Mass: 29003 Score: 52 Expect: 21 Queries matched: 10

tropomyosin 5 - mouse

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
832.3686	831.3613	831.4338	-0.0724	98 - 104	1	R.ALKDEEK.M	
1179.5649	1178.5577	1178.5172	0.0405	154 - 162	1	R.CREMDEQIR.L	
1252.6284	1251.6211	1251.5336	0.0875	154 - 162	1	R.CREMDEQIR.L + Carbamidomethyl (C); Oxidation (M)	
1277.6779	1276.6706	1276.6809	-0.0103	1 - 12	1	- .MAGTTTIEAVKR.K	
1308.6351	1307.6279	1307.6105	0.0173	198 - 208	1	K.EAETRAEFAER.S	
1316.5630	1315.5558	1315.6367	-0.0810	43 - 54	0	R.EQAEAEVASLNR.R	
1318.6086	1317.6013	1317.6664	-0.0650	213 - 223	1	K.LEKTIDDLK.L	
1380.6922	1379.6849	1379.7184	-0.0335	185 - 195	1	K.YEEEEIKILTDK.L	
1467.7784	1466.7712	1466.6633	0.1079	237 - 248	0	R.MLDQTLLDLNEM.- + 2 Oxidation (M)	
1475.7529	1474.7456	1474.7701	-0.0245	105 - 116	1	K.MELQEIQLKEAK.H + Oxidation (M)	

No match to: 781.4409, 831.3855, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1157.6034, 1158.5981, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1283.5580, 1299.5558, 1301.6318, 1307.6958, 1317.6197, 1323.6033, 1386.6862, 1400.6222, 1408.7039, 1462.8200, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

42. [Q54L29_DICDI](#) Mass: 11417 Score: 52 Expect: 22 Queries matched: 6

Hypothetical protein.- Dictyostelium discoideum AX4.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
832.3686	831.3613	831.3796	-0.0183	2 - 8	0	M.EENCLPK.K	
1157.6034	1156.5962	1156.6968	-0.1006	22 - 31	1	R.LIKFPPSLSR.L	
1277.6779	1276.6706	1276.5506	0.1200	12 - 21	1	K.RFEMSDSYSR.L	
1301.6318	1300.6245	1300.7503	-0.1257	25 - 36	1	K.FPPSLRSLSIGK.E	
1307.6958	1306.6885	1306.6306	0.0579	64 - 74	1	K.HFDGNFKDLSK.S	
1475.7529	1474.7456	1474.7126	0.0330	13 - 24	1	R.FEMSDSYSRLIK.F	

No match to: 781.4409, 831.3855, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1252.6284, 1258.5465, 1283.5580, 1299.5558, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1380.6922, 1386.6862, 1400.6222, 1408.7039, 1462.8200, 1467.7784, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

43. [Q5ZUP2_LEGPH](#) Mass: 50366 Score: 51 Expect: 23 Queries matched: 9

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

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
832.3686	831.3613	831.3909	-0.0295	191 - 197	1	K.DEGKMPR.Y	
1238.6094	1237.6021	1237.6666	-0.0645	251 - 261	0	R.QIEEALTHLGK.F	
1240.5125	1239.5052	1239.5778	-0.0726	322 - 331	1	K.NCNSSLARYR.A + Carbamidomethyl (C)	
1242.5535	1241.5462	1241.6114	-0.0652	262 - 271	1	K.FLPKTCSDFK.T + Carbamidomethyl (C)	
1258.5465	1257.5392	1257.6564	-0.1172	284 - 294	0	K.AQIESNVLQEK.I	
1323.6033	1322.5960	1322.7234	-0.1274	377 - 387	1	R.LLKTYFEANPK.V	
1462.8200	1461.8127	1461.7133	0.0994	182 - 194	1	R.DNMQILIVGKDEGK.M + Oxidation (M)	
1706.8966	1705.8893	1706.0355	-0.1462	94 - 108	1	K.NKQAILFLLGALLHR.Y	

1723.9219 1722.9146 1722.9668 -0.0522 251 - 265 1 R.QIEEALHLGKFLPK.T

No match to: 781.4409, 831.3855, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1157.6034, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1252.6284, 1277.6779, 1283.5580, 1299.5558, 1301.6318, 1307.6958, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1380.6922, 1386.6862, 1400.6222, 1408.7039, 1467.7784, 1475.7529, 1612.7497, 1638.8350, 1722.8620, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

44. [A25530](#) Mass: 29015 Score: 51 Expect: 23 Queries matched: 10

tropomyosin, fibroblast - human

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
832.3686	831.3613	831.4338	-0.0724	98	- 104	1	R.ALKDEEK.M
1158.5981	1157.5908	1157.6768	-0.0860	2	- 12	1	M.AGITTIEAVKR.K
1179.5649	1178.5577	1178.5172	0.0405	154	- 162	1	R.CREMDEQIR.L
1252.6284	1251.6211	1251.5336	0.0875	154	- 162	1	R.CREMDEQIR.L + Carbamidomethyl (C); Oxidation (M)
1308.6351	1307.6279	1307.6105	0.0173	198	- 208	1	K.EAETRAEFAER.S
1316.5630	1315.5558	1315.6367	-0.0810	43	- 54	0	R.EQAEEVASLNR.R
1318.6086	1317.6013	1317.6664	-0.0650	213	- 223	1	K.LEKTIDDLK.L
1380.6922	1379.6849	1379.7184	-0.0335	185	- 195	1	K.YEEEEIKILTDK.L
1467.7784	1466.7712	1466.6633	0.1079	237	- 248	0	R.MLDQTLDLNEM.- + 2 Oxidation (M)
1475.7529	1474.7456	1474.7701	-0.0245	105	- 116	1	K.MELQEIQLKEAK.H + Oxidation (M)

No match to: 781.4409, 831.3855, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1157.6034, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1301.6318, 1307.6958, 1317.6197, 1323.6033, 1386.6862, 1400.6222, 1408.7039, 1462.8200, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

45. [Q4HE11_CAMCO](#) Mass: 31370 Score: 51 Expect: 23 Queries matched: 8

Hypothetical protein.- Campylobacter coli RM2228.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
831.3855	830.3783	830.3956	-0.0173	93	- 99	0	R.EVMHTSK.K
1158.5981	1157.5908	1157.5716	0.0192	84	- 92	1	K.YKEELSSFR.E
1242.5535	1241.5462	1241.6444	-0.0982	212	- 222	0	K.FIFGSNYPVAK.I
1283.5580	1282.5508	1282.6193	-0.0685	104	- 113	1	K.RLFEADFEEK.I
1316.5630	1315.5558	1315.5940	-0.0383	119	- 129	0	K.TFNIPFEACMK.N + Oxidation (M)
1318.6086	1317.6013	1317.6751	-0.0738	17	- 27	1	K.MPISWLKGNK.L + Oxidation (M)
1722.8620	1721.8548	1721.9504	-0.0956	212	- 227	1	K.FIFGSNYPVAKIAPAK.W
1723.9219	1722.9146	1722.9079	0.0067	105	- 118	1	R.LFEADFEEKIEILK.T

No match to: 781.4409, 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1157.6034, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1252.6284, 1258.5465, 1277.6779, 1299.5558, 1301.6318, 1307.6958, 1308.6351, 1317.6197, 1323.6033, 1380.6922, 1386.6862, 1400.6222, 1408.7039, 1462.8200, 1467.7784, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

46. [Q8XVL4_RALSO](#) Mass: 63203 Score: 51 Expect: 23 Queries matched: 10

Probable prolyl-trna synthetase protein (EC 6.1.1.15).- Ralstonia solanacearum (Pseudomonas solanacearum).

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
852.4759	851.4686	851.4435	0.0251	147	- 153	1	R.FGIMRGR.E + Oxidation (M)
873.4259	872.4186	872.3664	0.0522	159	- 165	0	K.DAYSFDR.D
1213.6598	1212.6525	1212.5622	0.0903	391	- 402	0	R.NVVEGDPSPDGK.G
1238.6094	1237.6021	1237.6190	-0.0169	166	- 176	1	R.DAEGLKVSYEK.M
1400.6222	1399.6149	1399.7533	-0.1384	1	- 12	1	- .MKASQFFISTLK.E
1467.7784	1466.7712	1466.6863	0.0848	172	- 183	1	K.VSYEKMYGAYTR.I
1475.7529	1474.7456	1474.7820	-0.0364	330	- 344	0	R.AFGTPPGYLGPIGTK.Q
1638.8350	1637.8278	1637.8963	-0.0685	34	- 48	1	K.KLGAGLYTMPVGLR.V
1706.8966	1705.8893	1705.7296	0.1597	438	- 452	0	K.TQPMMSGCYGIGITR.I + 3 Oxidation (M)
1815.8328	1814.8255	1814.9137	-0.0882	127	- 140	1	K.QMPVNFYQITKFR.D + Oxidation (M)

No match to: 781.4409, 831.3855, 832.3686, 855.0295, 861.0514, 877.0207, 893.0028, 1012.5758, 1157.6034, 1158.5981, 1179.5649, 1226.5318, 1230.6543, 1235.5913, 1240.5125, 1242.5535, 1252.6284, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1301.6318, 1307.6958, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1380.6922, 1386.6862, 1408.7039, 1462.8200, 1612.7497, 1722.8620, 1723.9219, 1791.7119, 1993.9556, 2202.0786, 2383.9341

47. [Q22LV9_TETTH](#) Mass: 52292 Score: 51 Expect: 24 Queries matched: 9

Hypothetical protein.- Tetrahymena thermophila SB210.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1235.5913	1234.5840	1234.5836	0.0003	116	- 125	1	K.RMSQSQNQTR.V
1240.5125	1239.5052	1239.5771	-0.0719	322	- 331	1	R.VFPNKDYDDK.V
1299.5558	1298.5485	1298.6255	-0.0770	185	- 194	1	R.RDVDINYNK.H
1308.6351	1307.6279	1307.6218	0.0061	356	- 366	0	K.NSSQIFNNTQR.E
1408.7039	1407.6966	1407.7510	-0.0544	9	- 20	1	K.QKVPQYLGNSFK.D
1467.7784	1466.7712	1466.7517	0.0194	394	- 406	0	R.LFGAEAQNYSLVR.A
1723.9219	1722.9146	1722.8325	0.0821	308	- 321	0	R.TNPQIEFLNNYSQR.V
1815.8328	1814.8255	1814.9202	-0.0947	419	- 433	1	R.NFNIISYADNKIEFK.K
2202.0786	2201.0713	2201.0065	0.0648	149	- 166	1	R.ESFFFTSVSRFVDDNNYK.M

No match to: 781.4409, 831.3855, 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1157.6034, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1238.6094, 1242.5535, 1252.6284, 1258.5465, 1277.6779, 1283.5580, 1301.6318, 1307.6958, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1380.6922, 1386.6862, 1400.6222, 1462.8200, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1791.7119, 1993.9556, 2383.9341

48. [Q9Y355_HUMAN](#) Mass: 7429 Score: 51 Expect: 26 Queries matched: 5

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

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
781.4409	780.4336	780.4242	0.0094	14	- 20	0	R.AHVDALR.T
831.3855	830.3783	830.4286	-0.0503	49	- 55	0	R.LAEYHAK.A
1157.6034	1156.5962	1156.6200	-0.0238	38	- 48	1	R.LEALKENGGAR.L
1301.6318	1300.6245	1300.6411	-0.0166	21	- 31	0	R.THLAPYSDEL.R.Q
1318.6086	1317.6013	1317.6347	-0.0334	1	- 11	1	-.LSPLGEEMRDR.A + Oxidation (M)

No match to: 832.3686, 852.4759, 855.0295, 861.0514, 873.4259, 877.0207, 893.0028, 1012.5758, 1158.5981, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1252.6284, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1307.6958, 1308.6351, 1316.5630, 1317.6197, 1323.6033, 1380.6922, 1386.6862, 1400.6222, 1408.7039, 1462.8200, 1467.7784, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

49. [T35704](#) Mass: 16760 Score: 51 Expect: 27 Queries matched: 6

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

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
832.3686	831.3613	831.4272	-0.0659	1	- 7	0	-.MAENVLR.G
873.4259	872.4186	872.4716	-0.0529	131	- 138	0	R.VTIAADQR.S
1158.5981	1157.5908	1157.6305	-0.0396	35	- 45	1	R.VPGFVVRGGDR.L
1252.6284	1251.6211	1251.5454	0.0756	23	- 33	0	R.GGFCDGTVFHR.R + Carbamidomethyl (C)
1386.6862	1385.6789	1385.7377	-0.0587	144	- 157	0	R.ALWPGGGTAMVTLI.-
1408.7039	1407.6966	1407.6465	0.0501	23	- 34	1	R.GGFCDGTVFHR.R + Carbamidomethyl (C)

No match to: 781.4409, 831.3855, 852.4759, 855.0295, 861.0514, 877.0207, 893.0028, 1012.5758, 1157.6034, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1301.6318, 1307.6958, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1380.6922, 1400.6222, 1462.8200, 1467.7784, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

50. [Q9KJG9_STRLI](#) Mass: 16717 Score: 51 Expect: 27 Queries matched: 6

Peptidyl-prolyl cis-trans isomerase.- Streptomyces lividans.

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
832.3686	831.3613	831.4272	-0.0659	1	- 7	0	-.MAENVLR.G
873.4259	872.4186	872.4716	-0.0529	131	- 138	0	R.VTIAADQR.S

1158.5981	1157.5908	1157.6305	-0.0396	35	-	45	1	R.VPGFVVRGGDR.L
1252.6284	1251.6211	1251.5454	0.0756	23	-	33	0	R.GGFCDGTVFHR.R + Carbamidomethyl (C)
1386.6862	1385.6789	1385.7377	-0.0587	144	-	157	0	R.ALWPGGGTAMVTLI.-
1408.7039	1407.6966	1407.6465	0.0501	23	-	34	1	R.GGFCDGTVFHRR.V + Carbamidomethyl (C)

No match to: 781.4409, 831.3855, 852.4759, 855.0295, 861.0514, 877.0207, 893.0028, 1012.5758, 1157.6034, 1179.5649, 1213.6598, 1226.5318, 1230.6543, 1235.5913, 1238.6094, 1240.5125, 1242.5535, 1258.5465, 1277.6779, 1283.5580, 1299.5558, 1301.6318, 1307.6958, 1308.6351, 1316.5630, 1317.6197, 1318.6086, 1323.6033, 1380.6922, 1400.6222, 1462.8200, 1467.7784, 1475.7529, 1612.7497, 1638.8350, 1706.8966, 1722.8620, 1723.9219, 1791.7119, 1815.8328, 1993.9556, 2202.0786, 2383.9341

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 : 49

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