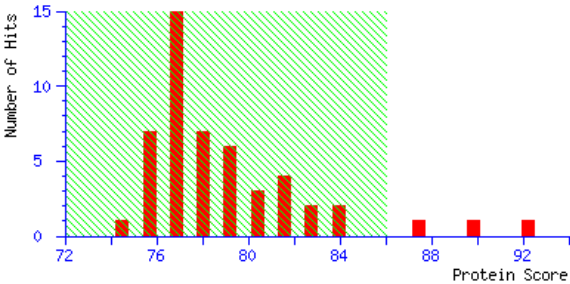


Mascot Search Results

User :
Email :
Search title : SampleSetID: 674, AnalysisID: 5211, MaldiWellID: 59823, SpectrumID: 120880, Path=\\161005\\MSMS\\16-85 combined NCBI euk
Database : NCBInr 160208 (79581714 sequences; 29080698065 residues)
Taxonomy : Eukaryota (eucaryotes) (20445761 sequences)
Timestamp : 24 Oct 2016 at 16:33:12 GMT
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
Top Score : 92 for gi|576695773, Actin [Echinococcus granulosus]

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 86 are significant (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Format As Protein Summary (deprecated) Help

Significance threshold p< 0.05 Max. number of hits 20

Re-Search All Search Unmatched

Index

Accession	Mass	Score	Description
1. gi 576695773	43780	92	Actin [Echinococcus granulosus]
2. gi 302128114	40525	90	actin 1 [Guillardia theta]
3. gi 671759043	34615	88	BLTX569 [Nephila pilipes]
4. gi 668451006	39303	83	actin-4 [Anopheles sinensis]
5. gi 157011451	38465	83	actin [Rhodomonas sp. CCMP768]
6. gi 525328837	42035	83	actin-4 [Bombyx mori]
7. gi 116222091	38633	83	actin, partial [Leucocryptos marina]
8. gi 11138772	40969	82	cryptophyte-like actin [Pyrenomonas helgolandii]
9. gi 907090477	41892	82	actin-A3b, cytoplasmic [Spizellomyces punctatus DAOM BR117]
10. gi 116222121	39739	81	actin, partial [Leucocryptos marina]
11. gi 525328637	42153	81	actin-4 [Bombyx mori]
12. gi 161661023	42236	81	actin 5C [Lycosa singoriensis]
13. gi 924266820	42126	81	beta-actin [Brachionus plicatilis]
14. gi 671758954	32446	80	BLTX520 [Nephila pilipes]
15. gi 728791	41911	80	RecName: Full=Actin-1/2
16. gi 728793	42028	80	RecName: Full=Actin-3
17. gi 525328777	42222	80	actin-4 [Bombyx mori]
18. gi 53829578	34090	79	actin [Chytridiomycetes confervae]
19. gi 167683038	31146	79	actin [Euagrion chisense]
20. gi 198424630	41914	79	PREDICTED: actin, non-muscle 6.2-like [Ciona intestinalis]

Results List

1.	gi 576695773	Mass: 43780	Score: 92	Expect: 0.012	Matches: 9
Actin [Echinococcus granulosus]					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Ions Peptide
1187.5472	1186.5399	1186.5587	-15.84	58 - 68	0 --- R.HQGVMMVGMGQK.D + Oxidation (M)
1515.6952	1514.6879	1514.7419	-35.61	103 - 113	0 --- K.IWHHTFYNELR.V
1614.7885	1613.7812	1613.7798	0.90	378 - 391	1 --- K.QEYDESGPGIVHRK.C
1627.7979	1626.7906	1626.8035	-7.93	1 - 15	0 --- -.MANPLPSIDNLSPSR.L + Oxidation (M)
1790.8569	1789.8496	1789.8846	-19.56	257 - 272	0 --- K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	257 - 272	0 38 K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	114 - 131	0 --- R.VAPEEHPVLLTEAPLNPK.A
2223.0964	2222.0891	2222.0017	39.3	16 - 36	0 --- R.LAMGDEEVQALVVDNGSGMCK.A
3151.7104	3150.7031	3150.6350	21.6	166 - 195	0 --- R.TTGIVLDSGDGVTHSVPIYEGYALPHAILR.L
No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1048.4686, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1212.5769, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1516.6957, 1544.7119, 1578.7366, 1594.7228, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2270.1453, 2289.1655, 2453.2537, 2505.3000					

2. [gi|302128114](#) Mass: 40525 Score: 90 Expect: 0.022 Matches: 9

actin 1 [Guillardia theta]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1048.4686	1047.4613	1047.4253	34.4	169	- 176	0	---	R.DLTDYMMK.I + 2 Oxidation (M)
1187.5472	1186.5399	1186.5587	-15.84	25	- 35	0	---	R.HQGVMMVGMGQK.D + Oxidation (M)
1212.5769	1211.5696	1211.5306	32.2	36	- 46	0	---	K.DSYIGDEAQS.K
1515.6952	1514.6879	1514.7419	-35.61	70	- 80	0	---	K.IWHHTFYNELR.V
1516.6957	1515.6884	1515.6954	-4.59	345	- 357	0	---	K.QEYDESGPSIVHR.K
1790.8569	1789.8496	1789.8846	-19.56	224	- 239	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	224	- 239	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	81	- 98	0	---	R.VAPEEHPVLLTEAPLNPK.A
3151.7104	3150.7031	3150.6350	21.6	133	- 162	0	---	R.TTGIVLDSGDGVSHVTVPIYEGYALPHAILR.L

No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1544.7119, 1578.7366, 1594.7228, 1614.7885, 1627.7979, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2289.1655, 2453.2537, 2505.3000

3. [gi|671759043](#) Mass: 34615 Score: 88 Expect: 0.036 Matches: 8

BLTX569 [Nephila pilipes]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1187.5472	1186.5399	1186.5587	-15.84	41	- 51	0	---	R.HQGVMMVGMGQK.D + Oxidation (M)
1515.6952	1514.6879	1514.7419	-35.61	86	- 96	0	---	K.IWHHTFYNELR.V
1627.7979	1626.7906	1626.8366	-28.24	198	- 211	1	---	R.GYSFVTTAEREIVR.D
1787.8616	1786.8543	1786.8713	-9.48	293	- 307	0	---	K.TCTPTLYSLVYHHVP.-
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	97	- 114	0	---	R.VAPEEHPVLLTEAPLNPK.A
3151.7104	3150.7031	3150.6350	21.6	149	- 178	0	---	R.TTGIVLDSGDGVSHVTVPIYEGYALPHAILR.L

No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1048.4686, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1212.5769, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1544.7119, 1578.7366, 1594.7228, 1614.7885, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2289.1655, 2453.2537, 2505.3000

4. [gi|668451006](#) Mass: 39303 Score: 83 Expect: 0.093 Matches: 8

actin-4 [Anopheles sinensis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1094.5594	1093.5521	1093.5880	-32.79	193	- 201	1	---	K.ILTERGYSR.R
1187.5472	1186.5399	1186.5587	-15.84	41	- 51	0	---	R.HQGVMMVGMGQK.D + Oxidation (M)
1515.6952	1514.6879	1514.7419	-35.61	86	- 96	0	---	K.IWHHTFYNELR.V
1516.6957	1515.6884	1515.6954	-4.59	336	- 348	0	---	K.QEYDESGPSIVHR.K
1790.8569	1789.8496	1789.8846	-19.56	215	- 230	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	215	- 230	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	97	- 114	0	---	R.VAPEEHPVLLTEAPLNPK.A
3151.7104	3150.7031	3150.6350	21.6	149	- 178	0	---	R.TTGIVLDSGDGVSHVTVPIYEGYALPHAILR.L

No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1048.4686, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1212.5769, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1544.7119, 1578.7366, 1594.7228, 1614.7885, 1627.7979, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2289.1655, 2453.2537, 2505.3000

5. [gi|157011451](#) Mass: 38465 Score: 83 Expect: 0.093 Matches: 8

actin [Rhodomonas sp. CCMP768]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1048.4686	1047.4613	1047.4253	34.4	159	- 166	0	---	R.DLTDYMMK.I + 2 Oxidation (M)
1187.5472	1186.5399	1186.5587	-15.84	15	- 25	0	---	R.HQGVMMVGMGQK.D + Oxidation (M)
1212.5769	1211.5696	1211.5306	32.2	26	- 36	0	---	K.DSYIGDEAQS.K
1515.6952	1514.6879	1514.7419	-35.61	60	- 70	0	---	K.IWHHTFYNELR.V
1790.8569	1789.8496	1789.8846	-19.56	214	- 229	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	214	- 229	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	71	- 88	0	---	R.VAPEEHPVLLTEAPLNPK.A
3151.7104	3150.7031	3150.6350	21.6	123	- 152	0	---	R.TTGIVLDSGDGVSHVTVPIYEGYALPHAILR.L

No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1516.6957, 1544.7119, 1578.7366, 1594.7228, 1614.7885, 1627.7979, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2289.1655, 2453.2537, 2505.3000

6. [gi|525328837](#) Mass: 42035 Score: 83 Expect: 0.1 Matches: 8

actin-4 [Bombyx mori]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1187.5472	1186.5399	1186.5587	-15.84	41	- 51	0	---	R.HQGVMMVGMGQK.D + Oxidation (M)
1515.6952	1514.6879	1514.7419	-35.61	86	- 96	0	---	K.IWHHTFYNELR.V
1516.6957	1515.6884	1515.6954	-4.59	361	- 373	0	---	K.QEYDESGPSIVHR.K
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	97	- 114	0	---	R.VAPEEHPVLLTEAPLNPK.A

2453.2537 2452.2464 2452.2961 -20.27 97 - 119 1 --- R.VAPEEHPVLLTEAPLNPKANGEK.M
 3151.7104 3150.7031 3150.6350 21.6 149 - 178 0 --- R.TTGIVLDSGDGVSHTVPIYEGYALPHAILR.L
No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1048.4686, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1212.5769, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1544.7119, 1578.7366, 1594.7228, 1614.7885, 1627.7979, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2289.1655, 2505.3000

7. [gi|116222091](#) Mass: 38633 Score: 83 Expect: 0.1 Matches: 8

actin, partial [Leucocryptos marina]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1048.4686	1047.4613	1047.4253	34.4	162	169	0	---	R.DLTDYMMK.I + 2 Oxidation (M)
1187.5472	1186.5399	1186.5587	-15.84	18	28	0	---	R.HQGVMMGMGQK.D + Oxidation (M)
1515.6952	1514.6879	1514.7419	-35.61	63	73	0	---	K.IWHHTFYNELR.V
1790.8569	1789.8496	1789.8846	-19.56	217	232	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	217	232	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	74	91	0	---	R.VAPEEHPVLLTEAPLNPK.A
2223.0964	2222.0891	2221.9984	40.8	270	290	0	---	K.DLYGSVVMSSGGTTMFNGIADR.M + 2 Oxidation (M)
3151.7104	3150.7031	3150.6350	21.6	126	155	0	---	R.TTGIVLDSGDGVSHTVPIYEGYALPHAILR.L

No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1212.5769, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1516.6957, 1544.7119, 1578.7366, 1594.7228, 1614.7885, 1627.7979, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2270.1453, 2289.1655, 2453.2537, 2505.3000

8. [gi|11138772](#) Mass: 40969 Score: 82 Expect: 0.13 Matches: 8

cryptophyte-like actin [Pyrenomonas helgolandii]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1048.4686	1047.4613	1047.4253	34.4	174	181	0	---	R.DLTDYMMK.I + 2 Oxidation (M)
1187.5472	1186.5399	1186.5587	-15.84	30	40	0	---	R.HQGVMMGMGQK.D + Oxidation (M)
1212.5769	1211.5696	1211.5306	32.2	41	51	0	---	K.DSYIGDEAQS.K
1515.6952	1514.6879	1514.7419	-35.61	75	85	0	---	K.IWHHTFYNELR.V
1790.8569	1789.8496	1789.8846	-19.56	229	244	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	229	244	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	86	103	0	---	R.VAPEEHPVLLTEAPLNPK.A
3151.7104	3150.7031	3150.6350	21.6	138	167	0	---	R.TTGIVLDSGDGVSHTVPIYEGYALPHAILR.L

No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1516.6957, 1544.7119, 1578.7366, 1594.7228, 1614.7885, 1627.7979, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2289.1655, 2453.2537, 2505.3000

9. [gi|907090477](#) Mass: 41892 Score: 82 Expect: 0.14 Matches: 9

actin-A3b, cytoplasmic [Spizellomyces punctatus DAOM BR117]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1187.5472	1186.5399	1186.5587	-15.84	40	50	0	---	R.HQGVMMGMGQK.D + Oxidation (M)
1515.6952	1514.6879	1514.7419	-35.61	85	95	0	---	K.IWHHTFYNELR.V
1516.6957	1515.6884	1515.6954	-4.59	360	372	0	---	K.QEYDESGPSIVHR.K
1578.7366	1577.7293	1577.7905	-38.78	313	326	1	---	R.MQREITALAPSSMK.I + Oxidation (M)
1594.7228	1593.7155	1593.7854	-43.86	313	326	1	---	R.MQREITALAPSSMK.I + 2 Oxidation (M)
1790.8569	1789.8496	1789.8846	-19.56	239	254	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	239	254	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	96	113	0	---	R.VAPEEHPVLLTEAPLNPK.A
3151.7104	3150.7031	3150.6350	21.6	148	177	0	---	R.TTGIVLDSGDGVSHTVPIYEGYALPHAILR.L

No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1048.4686, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1212.5769, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1516.6957, 1544.7119, 1578.7366, 1594.7228, 1614.7885, 1627.7979, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2289.1655, 2453.2537, 2505.3000

10. [gi|116222121](#) Mass: 39739 Score: 81 Expect: 0.15 Matches: 8

actin, partial [Leucocryptos marina]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1011.4347	1010.4274	1010.3829	44.1	348	356	0	---	K.QEYDESGPS.-
1048.4686	1047.4613	1047.4253	34.4	172	179	0	---	R.DLTDYMMK.I + 2 Oxidation (M)
1187.5472	1186.5399	1186.5587	-15.84	28	38	0	---	R.HQGVMMGMGQK.D + Oxidation (M)
1515.6952	1514.6879	1514.7419	-35.61	73	83	0	---	K.IWHHTFYNELR.V
1790.8569	1789.8496	1789.8846	-19.56	227	242	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	227	242	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	84	101	0	---	R.VAPEEHPVLLTEAPLNPK.A
3151.7104	3150.7031	3150.6350	21.6	136	165	0	---	R.TTGIVLDSGDGVSHTVPIYEGYALPHAILR.L

No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1027.4290, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1212.5769, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1516.6957, 1544.7119, 1578.7366, 1594.7228, 1614.7885, 1627.7979, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2289.1655, 2453.2537, 2505.3000

11. [gi|525328637](#) Mass: 42153 Score: 81 Expect: 0.15 Matches: 8

actin-4 [Bombyx mori]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1187.5472	1186.5399	1186.5587	-15.84	41	- 51	0	---	R.HQGVMMVGGMQK.D + Oxidation (M)
1515.6952	1514.6879	1514.7419	-35.61	86	- 96	0	---	K.IWHHTFYNELR.V
1516.6957	1515.6884	1515.6954	-4.59	361	- 373	0	---	K.QEYDESGPSIVHR.K
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	97	- 114	0	---	R.VAPEEHPVLLTEAPLNPK.A
2289.1655	2288.1582	2288.0631	41.6	293	- 313	0	---	K.DLYANTVLSGDTTMYPGIADR.M + Oxidation (M)
3151.7104	3150.7031	3150.6350	21.6	149	- 178	0	---	R.TTGIVLDSGDGVSHTVPIYEGYALPHAILR.L
No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1048.4686, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1212.5769, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1544.7119, 1578.7366, 1594.7228, 1614.7885, 1627.7979, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2453.2537, 2505.3000								

12. [gi|161661023](#) Mass: 42236 Score: 81 Expect: 0.17 Matches: 8

actin 5C [Lycosa singoriensis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1187.5472	1186.5399	1186.5587	-15.84	41	- 51	0	---	R.HQGVMMVGGMQK.D + Oxidation (M)
1515.6952	1514.6879	1514.7419	-35.61	86	- 96	0	---	K.IWHHTFYNELR.V
1516.6957	1515.6884	1515.6954	-4.59	361	- 373	0	---	K.QEYDESGPSIVHR.K
1627.7979	1626.7906	1626.8366	-28.24	198	- 211	1	---	R.GYSFVTTAEREIVR.D
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	97	- 114	0	---	R.VAPEEHPVLLTEAPLNPK.A
3151.7104	3150.7031	3150.6350	21.6	149	- 178	0	---	R.TTGIVLDSGDGVSHTVPIYEGYALPHAILR.L
No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1048.4686, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1212.5769, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1544.7119, 1578.7366, 1594.7228, 1614.7885, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2289.1655, 2453.2537, 2505.3000								

13. [gi|924266820](#) Mass: 42126 Score: 81 Expect: 0.17 Matches: 8

beta-actin [Brachionus plicatilis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1187.5472	1186.5399	1186.5587	-15.84	41	- 51	0	---	R.HQGVMMVGGMQK.D + Oxidation (M)
1515.6952	1514.6879	1514.7419	-35.61	86	- 96	0	---	K.IWHHTFYNELR.V
1516.6957	1515.6884	1515.6954	-4.59	361	- 373	0	---	K.QEYDESGPSIVHR.K
1627.7979	1626.7906	1626.8366	-28.24	198	- 211	1	---	R.GYSFVTTAEREIVR.D
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	97	- 114	0	---	R.VAPEEHPVLLTEAPLNPK.A
3151.7104	3150.7031	3150.6350	21.6	149	- 178	0	---	R.TTGIVLDSGDGVSHTVPIYEGYALPHAILR.L
No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1048.4686, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1212.5769, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1544.7119, 1578.7366, 1594.7228, 1614.7885, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2289.1655, 2453.2537, 2505.3000								

14. [gi|671758954](#) Mass: 32446 Score: 80 Expect: 0.2 Matches: 7

BLTX520 [Nephila pilipes]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1187.5472	1186.5399	1186.5587	-15.84	41	- 51	0	---	R.HQGVMMVGGMQK.D + Oxidation (M)
1515.6952	1514.6879	1514.7419	-35.61	86	- 96	0	---	K.IWHHTFYNELR.V
1627.7979	1626.7906	1626.8366	-28.24	198	- 211	1	---	R.GYSFVTTAEREIVR.D
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	97	- 114	0	---	R.VAPEEHPVLLTEAPLNPK.A
3151.7104	3150.7031	3150.6350	21.6	149	- 178	0	---	R.TTGIVLDSGDGVSHTVPIYEGYALPHAILR.L
No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1048.4686, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1212.5769, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1516.6957, 1544.7119, 1578.7366, 1594.7228, 1614.7885, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2289.1655, 2453.2537, 2505.3000								

15. [gi|728791](#) Mass: 41911 Score: 80 Expect: 0.21 Matches: 8

RecName: Full=Actin-1/2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1048.4686	1047.4613	1047.4253	34.4	185	- 192	0	---	R.DLTDYMMK.I + 2 Oxidation (M)
1187.5472	1186.5399	1186.5587	-15.84	41	- 51	0	---	R.HQGVMMVGGMQK.D + Oxidation (M)
1515.6952	1514.6879	1514.7419	-35.61	86	- 96	0	---	K.IWHHTFYNELR.V
1516.6957	1515.6884	1515.6954	-4.59	361	- 373	0	---	K.QEYDESGPSIVHR.K
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	97	- 114	0	---	R.VAPEEHPVLLTEAPLNPK.A
3151.7104	3150.7031	3150.6350	21.6	149	- 178	0	---	R.TTGIVLDSGDGVSHTVPIYEGYALPHAIIR.L
No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1066.4897, 1079.4001,								

1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1212.5769, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1544.7119, 1578.7366, 1594.7228, 1614.7885, 1627.7979, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2289.1655, 2453.2537, 2505.3000

16. [gi|728793](#) Mass: 42028 Score: 80 Expect: 0.21 Matches: 8

RecName: Full=Actin-3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1048.4686	1047.4613	1047.4253	34.4	185	- 192	0	---	R.DLTDYMMK.I + 2 Oxidation (M)
1187.5472	1186.5399	1186.5587	-15.84	41	- 51	0	---	R.HQGVMMVGMGQK.D + Oxidation (M)
1515.6952	1514.6879	1514.7419	-35.61	86	- 96	0	---	K.IWHHTFYNELR.V
1516.6957	1515.6884	1515.6954	-4.59	361	- 373	0	---	K.QEYDESGPSIVHR.K
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	97	- 114	0	---	R.VAPEEHPVLLTEAPLNPK.A
3151.7104	3150.7031	3150.6350	21.6	149	- 178	0	---	R.TTGIVLDSGDGVSHTVPIYEGYALPHAIIR.L
No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1212.5769, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1544.7119, 1578.7366, 1594.7228, 1614.7885, 1627.7979, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2289.1655, 2453.2537, 2505.3000								

17. [gi|525328777](#) Mass: 42222 Score: 80 Expect: 0.22 Matches: 8

actin-4 [Bombyx mori]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1187.5472	1186.5399	1186.5587	-15.84	41	- 51	0	---	R.HQGVMMVGMGQK.D + Oxidation (M)
1515.6952	1514.6879	1514.7419	-35.61	86	- 96	0	---	K.IWHHTFYNELR.V
1516.6957	1515.6884	1515.7317	-28.58	362	- 374	1	---	R.EYDESGPSIVHRK.C
1544.7119	1543.7046	1543.7379	-21.56	361	- 373	1	---	K.REYDESGPSIVHR.K
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	240	- 255	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	97	- 114	0	---	R.VAPEEHPVLLTEAPLNPK.A
3151.7104	3150.7031	3150.6350	21.6	149	- 178	0	---	R.TTGIVLDSGDGVSHTVPIYEGYALPHAILR.L
No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1048.4686, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1212.5769, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1578.7366, 1594.7228, 1614.7885, 1627.7979, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2289.1655, 2453.2537, 2505.3000								

18. [gi|53829578](#) Mass: 34090 Score: 79 Expect: 0.25 Matches: 8

actin [Chytridiomycetes confervae]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1515.6952	1514.6879	1514.7419	-35.61	11	- 21	0	---	K.IWHHTFYNELR.V
1516.6957	1515.6884	1515.6954	-4.59	286	- 298	0	---	K.QEYDESGPSIVHR.K
1578.7366	1577.7293	1577.7905	-38.78	239	- 252	1	---	R.MQREITALAPSSMK.I + Oxidation (M)
1594.7228	1593.7155	1593.7854	-43.86	239	- 252	1	---	R.MQREITALAPSSMK.I + 2 Oxidation (M)
1790.8569	1789.8496	1789.8846	-19.56	165	- 180	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	165	- 180	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	22	- 39	0	---	R.VAPEEHPVLLTEAPLNPK.A
3151.7104	3150.7031	3150.6350	21.6	74	- 103	0	---	R.TTGIVLDSGDGVSHTVPIYEGYALPHAILR.L
No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1048.4686, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1187.5472, 1198.6349, 1212.5769, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1544.7119, 1614.7885, 1627.7979, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2289.1655, 2453.2537, 2505.3000								

19. [gi|167683038](#) Mass: 31146 Score: 79 Expect: 0.25 Matches: 8

actin [Euagrus chiosseus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1187.5472	1186.5399	1186.5587	-15.84	3	- 13	0	---	R.HQGVMMVGMGQK.D + Oxidation (M)
1440.7216	1439.7143	1439.7126	1.21	1	- 13	1	---	-.PRHQGVMMVGMGQK.D + Oxidation (M)
1440.7216	1439.7143	1439.7126	1.21	1	- 13	1	---	-.PRHQGVMMVGMGQK.D + Oxidation (M)
1515.6952	1514.6879	1514.7419	-35.61	48	- 58	0	---	K.IWHHTFYNELR.V
1627.7979	1626.7906	1626.8366	-28.24	160	- 173	1	---	R.GYSFVTTAEREIVR.D
1790.8569	1789.8496	1789.8846	-19.56	202	- 217	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	202	- 217	0	38	K.SYELPDGQVITIGNER.F
3151.7104	3150.7031	3150.6350	21.6	111	- 140	0	---	R.TTGIVLDSGDGVSHTVPIYEGYALPHAILR.L
No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1048.4686, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1212.5769, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1441.7207, 1492.6938, 1516.6957, 1544.7119, 1578.7366, 1594.7228, 1614.7885, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1954.0328, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2289.1655, 2453.2537, 2505.3000								

20. [gi|198424630](#) Mass: 41914 Score: 79 Expect: 0.26 Matches: 8

PREDICTED: actin, non-muscle 6.2-like [Ciona intestinalis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1187.5472	1186.5399	1186.5587	-15.84	40	- 50	0	---	R.HQGVMMVGMGQK.D + Oxidation (M)
1212.5769	1211.5696	1211.5306	32.2	51	- 61	0	---	K.DTYVGDEAQS.K

1515.6952	1514.6879	1514.7419	-35.61	85	-	95	0	---	K.IWHHTFYNELR.V
1516.6957	1515.6884	1515.6954	-4.59	360	-	372	0	---	K.QEYDESGPSIVHR.K
1790.8569	1789.8496	1789.8846	-19.56	239	-	254	0	---	K.SYELPDGQVITIGNER.F
1790.8569	1789.8496	1789.8846	-19.56	239	-	254	0	38	K.SYELPDGQVITIGNER.F
1954.0328	1953.0255	1953.0571	-16.17	96	-	113	0	---	R.VAPEEHPVLLTEAPLNPK.A
3151.7104	3150.7031	3150.6350	21.6	148	-	177	0	---	R.TTGIVLDSGDVSHTVPIYEGYALPHAIR.L

No match to: 854.2010, 854.9677, 917.1951, 938.4907, 965.4046, 976.3974, 982.4263, 1011.4347, 1027.4290, 1048.4686, 1066.4897, 1079.4001, 1090.5597, 1093.5967, 1094.5594, 1102.5715, 1132.4640, 1134.5709, 1198.6349, 1213.5813, 1229.5739, 1239.5970, 1290.6926, 1296.6246, 1299.6790, 1299.6790, 1327.7103, 1365.5906, 1389.5822, 1432.6368, 1439.7170, 1440.7216, 1440.7216, 1441.7207, 1492.6938, 1544.7119, 1578.7366, 1594.7228, 1614.7885, 1627.7979, 1656.9398, 1739.8674, 1763.8535, 1771.8756, 1782.8629, 1787.8616, 1818.8699, 1819.8746, 1846.9039, 1871.9236, 1888.9052, 1905.9562, 1933.9780, 1980.0444, 1982.0553, 2223.0964, 2270.1453, 2289.1655, 2453.2537, 2505.3000

Search Parameters

Type of search : Sequence Query
 Enzyme : Trypsin
 Fixed modifications : [Carbamidomethyl \(C\)](#)
 Variable modifications : [Oxidation \(M\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 50 ppm
 Fragment Mass Tolerance: ± 0.3 Da
 Max Missed Cleavages : 1
 Instrument type : MALDI-TOF-TOF

Query1 (854.2010,1+) : <no title>
 Query2 (854.9677,1+) : <no title>
 Query3 (917.1951,1+) : <no title>
 Query4 (938.4907,1+) : <no title>
 Query5 (965.4046,1+) : <no title>
 Query6 (976.3974,1+) : <no title>
 Query7 (982.4263,1+) : <no title>
 Query8 (1011.4347,1+) : <no title>
 Query9 (1027.4290,1+) : <no title>
 Query10 (1048.4686,1+) : <no title>
 Query11 (1066.4897,1+) : <no title>
 Query12 (1079.4001,1+) : <no title>
 Query13 (1090.5597,1+) : <no title>
 Query14 (1093.5967,1+) : <no title>
 Query15 (1094.5594,1+) : <no title>
 Query16 (1102.5715,1+) : <no title>
 Query17 (1132.4640,1+) : <no title>
 Query18 (1134.5709,1+) : <no title>
 Query19 (1187.5472,1+) : <no title>
 Query20 (1198.6349,1+) : <no title>
 Query21 (1212.5769,1+) : <no title>
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 Query25 (1290.6926,1+) : <no title>
 Query26 (1296.6246,1+) : <no title>
 Query27 (1299.6790,1+) : <no title>
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 Query29 (1327.7103,1+) : <no title>
 Query30 (1365.5906,1+) : <no title>
 Query31 (1389.5822,1+) : <no title>
 Query32 (1432.6368,1+) : <no title>
 Query33 (1439.7170,1+) : <no title>
 Query34 (1440.7216,1+) : <no title>
 Query35 (1440.7216,1+) : MaldiWellID: 59823, SpectrumID: 120883,
 Query36 (1441.7207,1+) : <no title>
 Query37 (1492.6938,1+) : <no title>
 Query38 (1515.6952,1+) : <no title>
 Query39 (1516.6957,1+) : <no title>
 Query40 (1544.7119,1+) : <no title>
 Query41 (1578.7366,1+) : <no title>
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 Query47 (1763.8535,1+) : <no title>
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 Query49 (1782.8629,1+) : <no title>
 Query50 (1787.8616,1+) : <no title>
 Query51 (1790.8569,1+) : <no title>
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 Query62 (1982.0553,1+) : <no title>
 Query63 (2223.0964,1+) : <no title>
 Query64 (2270.1453,1+) : <no title>
 Query65 (2289.1655,1+) : <no title>
 Query66 (2453.2537,1+) : <no title>

Query67 (2505.3000,1+) : <no title>

Query68 (3151.7104,1+) : <no title>

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