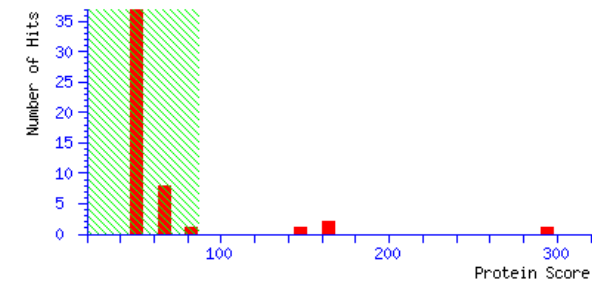


**Mascot Search Results**

User :  
Email :  
Search title : SampleSetID: 674, AnalysisID: 5211, MaldiWellID: 59830, SpectrumID: 120913, Path=\\161005\\MSMS\\16-85 combined NCBI euk  
Database : NCBI nr 160208 (79581714 sequences; 29080698065 residues)  
Taxonomy : Eukaryota (eucaryotes) (20445761 sequences)  
Timestamp : 24 Oct 2016 at 21:31:17 GMT  
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.  
Top Score : 294 for gi|157111905, AAEL005997-PA [Aedes aegypti]

**Mascot Score Histogram**

Protein score is  $-10 \times \log(P)$ , 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 ion 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. <a href="#">gi 157111905</a>	14908	294	AAEL005997-PA [Aedes aegypti]
2. <a href="#">gi 58585202</a>	15140	158	fatty acid binding protein [Apis mellifera]
3. <a href="#">gi 380010943</a>	15327	158	PREDICTED: probable fatty acid-binding protein isoform X1 [Apis florea]
4. <a href="#">gi 861650258</a>	15607	155	myelin p2 [Lasius niger]
5. <a href="#">gi 729356040</a>	21358	75	PREDICTED: methyl-CpG-binding domain-containing protein 4 [Tarenaya hassleriana]
6. <a href="#">gi 938080859</a>	13259	71	myelin P2 protein-like, partial [Scleropages formosus]
7. <a href="#">gi 719799249</a>	18163	64	PREDICTED: synaptosomal-associated protein 47-like, partial [Tinamus guttatus]
8. <a href="#">gi 907633116</a>	14909	64	PREDICTED: probable fatty acid-binding protein [Stomoxys calcitrans]
9. <a href="#">gi 557755593</a>	14807	63	PREDICTED: probable fatty acid-binding protein [Musca domestica]
10. <a href="#">gi 557772282</a>	14880	63	PREDICTED: probable fatty acid-binding protein [Musca domestica]
11. <a href="#">gi 119497547</a>	25229	62	hypothetical protein NFIA_023460 [Neosartorya fischeri NRRL 181]
12. <a href="#">gi 119626132</a>	20834	61	ring finger and CHY zinc finger domain containing 1, isoform CRA_d [Homo sapiens]
13. <a href="#">gi 543344810</a>	56087	59	PREDICTED: zinc finger with UFM1-specific peptidase domain protein [Pseudopodoces humilis]
14. <a href="#">gi 426344676</a>	22017	57	PREDICTED: RING finger and CHY zinc finger domain-containing protein 1 [Gorilla gorilla gorilla]
15. <a href="#">gi 62275766</a>	22993	56	ring finger and CHY zinc finger domain containing 1 variant 2 [Homo sapiens]
16. <a href="#">gi 529001618</a>	78269	56	PREDICTED: 5-aminolevulinate synthase, nonspecific, mitochondrial isoform X1 [Bos taurus]
17. <a href="#">gi 966643494</a>	9069	56	hypothetical protein cypCar_00048158, partial [Cyprinus carpio]
18. <a href="#">gi 195111990</a>	14622	55	uncharacterized protein Dmoj_GI22452 [Drosophila mojavensis]
19. <a href="#">gi 195396232</a>	14555	55	uncharacterized protein Dvir_GJ10051 [Drosophila virilis]
20. <a href="#">gi 449497787</a>	55807	54	PREDICTED: zinc finger with UFM1-specific peptidase domain protein [Taeniopygia guttata]

**Results List**

1.	<a href="#">gi 157111905</a>	Mass: 14908	Score: 294	Expect: 8.1e-023	Matches: 19
AAEL005997-PA [Aedes aegypti]					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Ions Peptide
	915.5168	914.5095	914.5372	-30.21	23 - 31 0 --- K.ALGVGMVLR.K
	931.5215	930.5142	930.5321	-19.18	23 - 31 0 --- K.ALGVGMVLR.K + Oxidation (M)
	931.5215	930.5142	930.5321	-19.18	23 - 31 0 15 K.ALGVGMVLR.K + Oxidation (M)
	1014.5773	1013.5700	1013.5869	-16.68	99 - 107 0 --- K.GEKPTTIIR.E
	1091.4143	1090.4070	1090.4277	-18.98	14 - 22 0 --- K.SEGFDDYMK.A
	1107.4049	1106.3976	1106.4226	-22.61	14 - 22 0 --- K.SEGFDDYMK.A + Oxidation (M)
	1349.6675	1348.6602	1348.6657	-4.03	81 - 92 1 --- K.VKSVCTLEGDNK.L
	1484.8214	1483.8141	1483.8610	-31.58	32 - 45 1 --- R.KLGNSISPTVELVK.E
	1509.6316	1508.6243	1508.6631	-25.68	67 - 79 0 --- K.LGEEFEETVDGR.K
	1509.6316	1508.6243	1508.6631	-25.68	67 - 79 0 98 K.LGEEFEETVDGR.K
	1637.7262	1636.7189	1636.7580	-23.89	67 - 80 1 --- K.LGEEFEETVDGRK.V
	1639.6735	1638.6662	1638.7050	-23.64	46 - 59 0 --- K.EGDEYTFNTTSTFK.N
	1762.9647	1761.9574	1762.0101	-29.89	93 - 107 1 --- K.LIHEQKGEKPTTIIR.E
	1784.8005	1783.7932	1783.8264	-18.62	65 - 79 1 --- K.FKLGEFEETVDGR.K

1784.8005 1783.7932 1783.8264 -18.62 65 - 79 1 34 K.FKLGEFEFEETVDGR.K  
 2003.9338 2002.9265 2002.9492 -11.34 14 - 31 1 --- K.SEGFDDYMKALGVGMVLR.K + Oxidation (M)  
 2019.9290 2018.9217 2018.9442 -11.11 14 - 31 1 --- K.SEGFDDYMKALGVGMVLR.K + 2 Oxidation (M)  
 2810.5203 2809.5130 2809.4168 34.3 99 - 124 1 --- K.GEKPTTIREFDTDLIATMTAGNAK.C + Oxidation (M)  
 2977.5911 2976.5838 2976.4604 41.5 33 - 59 1 --- K.LGNSISPTVELVKEGDEYFTNTSTFK.N  
**No match to:** 855.0471, 861.0775, 900.4517, 901.4653, 944.5119, 945.4998, 957.5150, 973.5156, 1011.4759, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1318.6571, 1465.7028, 1507.7032, 1535.6725, 1537.6628, 1553.6627, 1563.6956, 1565.6914, 1565.6914, 1593.7247, 1621.6700, 1665.7517, 1686.7816, 1693.7960, 1721.8564, 1742.8522, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1790.8728, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1860.9581, 1891.9137, 1912.9138, 1938.9232, 1940.9351, 1971.9380, 2047.9374, 2198.0242, 2226.1143, 2370.2100, 3105.7104

2. [gi|58585202](#) Mass: 15140 Score: 158 Expect: 3.2e-009 Matches: 6

fatty acid binding protein [Apis mellifera]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1509.6316	1508.6243	1508.6631	-25.68	67	79	0	---	K.LGEFEFEETVDGR.K
1509.6316	1508.6243	1508.6631	-25.68	67	79	0	98	K.LGEFEFEETVDGR.K
1637.7262	1636.7189	1636.7580	-23.89	67	80	1	---	K.LGEFEFEETVDGRK.V
1686.7816	1685.7743	1685.7930	-11.10	101	114	1	---	K.QTTIEREFSSTEMK.A
1784.8005	1783.7932	1783.8264	-18.62	65	79	1	---	K.FKLGEFEFEETVDGR.K
1784.8005	1783.7932	1783.8264	-18.62	65	79	1	34	K.FKLGEFEFEETVDGR.K

**No match to:** 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 931.5215, 931.5215, 944.5119, 945.4998, 957.5150, 973.5156, 1011.4759, 1014.5773, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1465.7028, 1484.8214, 1507.7032, 1535.6725, 1537.6628, 1537.6628, 1553.6627, 1563.6956, 1565.6914, 1565.6914, 1593.7247, 1621.6700, 1639.6735, 1665.7517, 1693.7960, 1721.8564, 1742.8522, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1790.8728, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1860.9581, 1891.9137, 1912.9138, 1938.9232, 1940.9351, 1971.9380, 2003.9338, 2019.9290, 2047.9374, 2198.0242, 2226.1143, 2370.2100, 2810.5203, 2977.5911, 3105.7104

3. [gi|380010943](#) Mass: 15327 Score: 158 Expect: 3.2e-009 Matches: 6

PREDICTED: probable fatty acid-binding protein isoform X1 [Apis florea]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1509.6316	1508.6243	1508.6631	-25.68	68	80	0	---	K.LGEFEFEETVDGR.K
1509.6316	1508.6243	1508.6631	-25.68	68	80	0	98	K.LGEFEFEETVDGR.K
1637.7262	1636.7189	1636.7580	-23.89	68	81	1	---	K.LGEFEFEETVDGRK.V
1686.7816	1685.7743	1685.7930	-11.10	102	115	1	---	K.QTTIEREFSSTEMK.A
1784.8005	1783.7932	1783.8264	-18.62	66	80	1	---	K.FKLGEFEFEETVDGR.K
1784.8005	1783.7932	1783.8264	-18.62	66	80	1	34	K.FKLGEFEFEETVDGR.K

**No match to:** 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 931.5215, 931.5215, 944.5119, 945.4998, 957.5150, 973.5156, 1011.4759, 1014.5773, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1465.7028, 1484.8214, 1507.7032, 1535.6725, 1537.6628, 1537.6628, 1553.6627, 1563.6956, 1565.6914, 1565.6914, 1593.7247, 1621.6700, 1639.6735, 1665.7517, 1693.7960, 1721.8564, 1742.8522, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1790.8728, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1860.9581, 1891.9137, 1912.9138, 1938.9232, 1940.9351, 1971.9380, 2003.9338, 2019.9290, 2047.9374, 2198.0242, 2226.1143, 2370.2100, 2810.5203, 2977.5911, 3105.7104

4. [gi|861650258](#) Mass: 15607 Score: 155 Expect: 6.5e-009 Matches: 6

myelin p2 [Lasius niger]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1014.5773	1013.5700	1013.5869	-16.69	97	105	1	---	K.LVQVQKGD.K.N
1509.6316	1508.6243	1508.6631	-25.68	72	84	0	---	K.LGEFEFEETVDGR.K
1509.6316	1508.6243	1508.6631	-25.68	72	84	0	98	K.LGEFEFEETVDGR.K
1637.7262	1636.7189	1636.7580	-23.89	72	85	1	---	K.LGEFEFEETVDGRK.V
1784.8005	1783.7932	1783.8264	-18.62	70	84	1	---	K.FKLGEFEFEETVDGR.K
1784.8005	1783.7932	1783.8264	-18.62	70	84	1	34	K.FKLGEFEFEETVDGR.K

**No match to:** 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 931.5215, 931.5215, 944.5119, 945.4998, 957.5150, 973.5156, 1011.4759, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1465.7028, 1484.8214, 1507.7032, 1535.6725, 1537.6628, 1537.6628, 1553.6627, 1563.6956, 1565.6914, 1565.6914, 1593.7247, 1621.6700, 1639.6735, 1665.7517, 1686.7816, 1693.7960, 1721.8564, 1742.8522, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1790.8728, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1860.9581, 1891.9137, 1912.9138, 1938.9232, 1940.9351, 1971.9380, 2003.9338, 2019.9290, 2047.9374, 2198.0242, 2226.1143, 2370.2100, 2810.5203, 2977.5911, 3105.7104

5. [gi|729356040](#) Mass: 21358 Score: 75 Expect: 0.6 Matches: 9

PREDICTED: methyl-CpG-binding domain-containing protein 4 [Tarenaya hassleriana]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
945.4998	944.4925	944.4927	-0.18	163	172	1	---	K.AGTPAEKGSQ.K
1349.6675	1348.6602	1348.6333	20.0	53	63	1	---	R.IPEDPFSCSEK.K
1553.6627	1552.6554	1552.6893	-21.79	39	50	0	---	R.EIDTQEEYEEIR.S
1686.7816	1685.7743	1685.7753	-0.56	23	36	1	---	R.SIDTYAAQCEKCLK.W
1784.8005	1783.7932	1783.8338	-22.76	105	119	1	---	K.DYSKMDAYITLTGK.K + Oxidation (M)
1784.8005	1783.7932	1783.7319	34.4	65	80	0	---	K.GVSCQDPADLDYDSSR.T
1796.8127	1795.8054	1795.8224	-9.45	39	52	1	---	R.EIDTQEEYEEIR.S.I
1840.8684	1839.8611	1839.8785	-9.43	17	33	1	---	K.ASALGRSIDTYAAQCEK.C
1912.9138	1911.9065	1911.8269	41.7	64	80	1	---	K.KGVSCQDPADLDYDSSR.T

**No match to:** 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 931.5215, 931.5215, 944.5119, 957.5150, 973.5156, 1011.4759, 1014.5773, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1465.7028, 1484.8214, 1507.7032, 1509.6316, 1509.6316, 1535.6725, 1537.6628, 1537.6628, 1553.6627, 1563.6956, 1565.6914, 1565.6914, 1593.7247, 1621.6700, 1637.7262, 1639.6735, 1665.7517, 1693.7960, 1721.8564, 1742.8522, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1790.8728, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1860.9581, 1891.9137, 1938.9232, 1940.9351, 1971.9380, 2003.9338, 2019.9290, 2047.9374, 2198.0242, 2226.1143, 2370.2100, 2810.5203, 2977.5911, 3105.7104

6. [gi|938080859](#) Mass: 13259 Score: 71 Expect: 1.6 Matches: 5

myelin P2 protein-like, partial [Scleropages formosus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1509.6316	1508.6243	1508.6631	-25.68	68	80	0	---	K.LGEFEFEETVADDR.K
1509.6316	1508.6243	1508.6631	-25.68	68	80	0	42	K.LGEFEFEETVADDR.K

1637.7262 1636.7189 1636.7580 -23.89 68 - 81 1 --- K.LGEEFEVTTADDRK.T  
 1784.8005 1783.7932 1783.8264 -18.62 66 - 80 1 --- K.FKLGEFEVTTADDRK.K  
 1784.8005 1783.7932 1783.8264 -18.62 66 - 80 1 12 K.FKLGEFEVTTADDRK.K  
 No match to: 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 931.5215, 931.5215, 944.5119, 945.4998, 957.5150, 973.5156, 1011.4759, 1014.5773, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1465.7028, 1484.8214, 1507.7032, 1535.6725, 1537.6628, 1537.6627, 1553.6627, 1563.6956, 1565.6914, 1593.7247, 1621.6700, 1639.6735, 1665.7517, 1686.7816, 1693.7960, 1721.8564, 1742.8522, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1790.8728, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1860.9581, 1891.9137, 1912.9138, 1938.9232, 1940.9351, 1971.9380, 2003.9338, 2019.9290, 2047.9374, 2198.0242, 2226.1143, 2370.2100, 2810.5203, 2977.5911, 3105.7104

7. [gi|719799249](#) Mass: 18163 Score: 64 Expect: 8.5 Matches: 7

PREDICTED: synaptosomal-associated protein 47-like, partial [Tinamus guttatus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
945.4998	944.4925	944.4927	-0.19	53	61	0	---	R.TDSNVKPGK.L
1484.8214	1483.8141	1483.7896	16.6	92	103	1	---	R.VHTPYEISVRQR.F
1665.7517	1664.7444	1664.8153	-42.60	119	132	0	---	K.MPEAIPILEMQFSK.K + 2 Oxidation (M)
1761.9404	1760.9331	1760.9205	7.19	119	133	1	---	K.MPEAIPILEMQFSK.K
1771.9172	1770.9099	1770.9363	-14.90	20	36	1	---	K.APLEAKPKETATVSDSK.N
1860.9581	1859.9508	1859.9588	-4.31	28	44	1	---	K.ETATVSDSKNQEGIIIR.I
2226.1143	2225.1070	2225.1474	-18.15	62	81	0	---	K.LTLLASGLIEISDCNSQVIHR.F

No match to: 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 931.5215, 931.5215, 944.5119, 957.5150, 973.5156, 1011.4759, 1014.5773, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1465.7028, 1507.7032, 1509.6316, 1509.6316, 1535.6725, 1537.6628, 1537.6627, 1553.6627, 1563.6956, 1565.6914, 1593.7247, 1621.6700, 1639.6735, 1665.7517, 1686.7816, 1693.7960, 1721.8564, 1742.8522, 1762.9647, 1763.9694, 1784.8005, 1784.8005, 1790.8728, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1891.9137, 1912.9138, 1938.9232, 1940.9351, 1971.9380, 2003.9338, 2019.9290, 2047.9374, 2198.0242, 2370.2100, 2810.5203, 2977.5911, 3105.7104

8. [gi|907633116](#) Mass: 14909 Score: 64 Expect: 9.1 Matches: 6

PREDICTED: probable fatty acid-binding protein [Stomoxys calcitrans]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
973.5156	972.5083	972.5426	-35.28	23	31	0	---	K.ELGVGMVLR.K
1509.6316	1508.6243	1508.6631	-25.68	67	79	0	---	K.LGEEFDEETLDGR.K
1509.6316	1508.6243	1508.6631	-25.68	67	79	0	38	K.LGEEFDEETLDGR.K
1637.7262	1636.7189	1636.7580	-23.89	67	80	1	---	K.LGEEFDEETLDGRK.V
1784.8005	1783.7932	1783.7610	18.0	9	22	1	---	K.YKLDSENDFEYMK.E + Oxidation (M)
1784.8005	1783.7932	1783.7610	18.0	9	22	1	---	K.YKLDSENDFEYMK.E + Oxidation (M)

No match to: 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 931.5215, 931.5215, 944.5119, 945.4998, 957.5150, 1011.4759, 1014.5773, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1465.7028, 1484.8214, 1507.7032, 1535.6725, 1537.6628, 1537.6627, 1553.6627, 1563.6956, 1565.6914, 1593.7247, 1621.6700, 1639.6735, 1665.7517, 1686.7816, 1693.7960, 1721.8564, 1742.8522, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1790.8728, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1860.9581, 1891.9137, 1912.9138, 1938.9232, 1940.9351, 1971.9380, 2003.9338, 2019.9290, 2047.9374, 2198.0242, 2226.1143, 2370.2100, 2810.5203, 2977.5911, 3105.7104

9. [gi|557755593](#) Mass: 14807 Score: 63 Expect: 9.6 Matches: 5

PREDICTED: probable fatty acid-binding protein [Musca domestica]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
973.5156	972.5083	972.5426	-35.28	23	31	0	---	K.ELGVGMVLR.K
1509.6316	1508.6243	1508.6631	-25.68	67	79	0	---	K.LGEEFDEETLDGR.K
1509.6316	1508.6243	1508.6631	-25.68	67	79	0	38	K.LGEEFDEETLDGR.K
1637.7262	1636.7189	1636.7580	-23.89	67	80	1	---	K.LGEEFDEETLDGRK.V
1938.9232	1937.9159	1937.9187	-1.42	81	97	1	---	K.VKSVCTMDGNTLTQEQK.G

No match to: 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 931.5215, 931.5215, 944.5119, 945.4998, 957.5150, 1011.4759, 1014.5773, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1465.7028, 1484.8214, 1507.7032, 1535.6725, 1537.6628, 1537.6627, 1553.6627, 1563.6956, 1565.6914, 1593.7247, 1621.6700, 1639.6735, 1665.7517, 1686.7816, 1693.7960, 1721.8564, 1742.8522, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1784.8005, 1784.8005, 1790.8728, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1860.9581, 1891.9137, 1912.9138, 1940.9351, 1971.9380, 2003.9338, 2019.9290, 2047.9374, 2198.0242, 2226.1143, 2370.2100, 2810.5203, 2977.5911, 3105.7104

10. [gi|557722282](#) Mass: 14880 Score: 63 Expect: 9.6 Matches: 5

PREDICTED: probable fatty acid-binding protein [Musca domestica]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
973.5156	972.5083	972.5426	-35.28	23	31	0	---	K.ELGVGMVLR.K
1509.6316	1508.6243	1508.6631	-25.68	67	79	0	---	K.LGEEFDEETLDGR.K
1509.6316	1508.6243	1508.6631	-25.68	67	79	0	38	K.LGEEFDEETLDGR.K
1637.7262	1636.7189	1636.7580	-23.89	67	80	1	---	K.LGEEFDEETLDGRK.V
1938.9232	1937.9159	1937.9187	-1.42	81	97	1	---	K.VKSVCTMDGNTLTQEQK.G

No match to: 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 931.5215, 931.5215, 944.5119, 945.4998, 957.5150, 1011.4759, 1014.5773, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1465.7028, 1484.8214, 1507.7032, 1535.6725, 1537.6628, 1537.6627, 1553.6627, 1563.6956, 1565.6914, 1593.7247, 1621.6700, 1639.6735, 1665.7517, 1686.7816, 1693.7960, 1721.8564, 1742.8522, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1784.8005, 1784.8005, 1790.8728, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1860.9581, 1891.9137, 1912.9138, 1940.9351, 1971.9380, 2003.9338, 2019.9290, 2047.9374, 2198.0242, 2226.1143, 2370.2100, 2810.5203, 2977.5911, 3105.7104

11. [gi|119497547](#) Mass: 25229 Score: 62 Expect: 11 Matches: 8

hypothetical protein NFIA\_023460 [Neosartorya fischeri NRRL 181]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
957.5150	956.5077	956.4756	33.6	71	77	0	---	R.EFVPYFR.T
973.5156	972.5083	972.4988	9.78	63	70	1	---	R.EAREEALR.E
1032.5603	1031.5530	1031.5546	-1.52	28	35	1	---	R.VIRITCDR.G
1742.8522	1741.8449	1741.8457	-0.47	78	92	0	---	R.TEVSPHACIYLAPER.D
1763.9694	1762.9621	1763.0206	-33.17	16	30	1	---	R.LHIWLSLPPSSRVIR.I
1840.8684	1839.8611	1839.9003	-21.28	159	173	1	---	R.DTVEVIRDAFEYVR.N
1891.9137	1890.9064	1890.8909	8.19	1	15	0	---	-.MSHFHFPPMLPAEIR.L + 2 Oxidation (M)

3105.7104 3104.7031 3104.6171 27.7 2 - 27 1 --- M.SHFHFFPMLPAEIRLHIWSLSLPSSR.V

No match to: 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 931.5215, 931.5215, 944.5119, 945.4998, 1011.4759, 1014.5773, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1465.7028, 1484.8214, 1507.7032, 1509.6316, 1509.6316, 1535.6725, 1537.6628, 1537.6628, 1553.6627, 1563.6956, 1565.6914, 1565.6914, 1593.7247, 1621.6700, 1637.7262, 1639.6735, 1665.7517, 1686.7816, 1693.7960, 1721.8564, 1761.9404, 1762.9647, 1771.9172, 1784.8005, 1784.8005, 1790.8728, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1860.9581, 1912.9138, 1938.9232, 1940.9351, 1971.9380, 2003.9338, 2019.9290, 2047.9374, 2198.0242, 2226.1143, 2370.2100, 2810.5203, 2977.5911

12. [gi|119626132](#) Mass: 20834 Score: 61 Expect: 17 Matches: 8

ring finger and CHY zinc finger domain containing 1, isoform CRA\_d [Homo sapiens]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1465.7028	1464.6955	1464.6636	21.8	122	-	133	0	K.CNLCLAMNLQGR.H + Oxidation (M)
1507.7032	1506.6959	1506.6708	16.7	19	-	30	1	R.GCEHYDRGCLLK.A
1565.6914	1564.6841	1564.6900	-3.73	1	-	15	1	-.MAATAREDGASGQER.G + Oxidation (M)
1565.6914	1564.6841	1564.6900	-3.73	1	-	15	1	-.MAATAREDGASGQER.G + Oxidation (M)
1665.7517	1664.7444	1664.6961	29.0	42	-	54	0	R.LCHDNNEHQDLDR.F
1742.8522	1741.8449	1741.7876	32.9	143	-	156	0	R.QNCPICLEDIHTSR.V
1891.9137	1890.9064	1890.8287	41.1	99	-	113	1	K.QYHCENCGICRIGPK.E
1940.9351	1939.9278	1939.8595	35.2	42	-	56	1	R.LCHDNNEHQDLDRFK.V

No match to: 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 931.5215, 931.5215, 944.5119, 945.4998, 957.5150, 973.5156, 1011.4759, 1014.5773, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1484.8214, 1509.6316, 1509.6316, 1535.6725, 1537.6628, 1537.6628, 1553.6627, 1563.6956, 1593.7247, 1621.6700, 1637.7262, 1639.6735, 1686.7816, 1693.7960, 1721.8564, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1784.8005, 1784.8005, 1790.8728, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1860.9581, 1912.9138, 1938.9232, 1971.9380, 2003.9338, 2019.9290, 2047.9374, 2198.0242, 2226.1143, 2370.2100, 2810.5203, 2977.5911, 3105.7104

13. [gi|543344810](#) Mass: 56087 Score: 59 Expect: 26 Matches: 10

PREDICTED: zinc finger with UFM1-specific peptidase domain protein [Pseudopodoces humilis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
944.5119	943.5046	943.5134	-9.28	23	-	29	1	R.RPSLCRR.Q
1537.6628	1536.6555	1536.6977	-27.47	212	-	226	0	K.ADMLESASGIDDGK.T + Oxidation (M)
1537.6628	1536.6555	1536.6977	-27.47	212	-	226	0	K.ADMLESASGIDDGK.T + Oxidation (M)
1565.6914	1564.6841	1564.7594	-48.10	48	-	62	0	R.QTETARPDPGPPGSR.S
1565.6914	1564.6841	1564.7594	-48.10	48	-	62	0	R.QTETARPDPGPPGSR.S
1665.7517	1664.7444	1664.7927	-28.99	211	-	226	1	R.KADMLESASGIDDGK.T + Oxidation (M)
1721.8564	1720.8491	1720.8605	-6.60	47	-	62	1	R.RQTETARPDPGPPGSR.S
1790.8728	1789.8655	1789.9462	-45.05	457	-	472	0	K.QYQIVAVDGVLSLEEK.A
2019.9290	2018.9217	2018.9711	-24.47	249	-	266	0	R.HVNLASAGVDHFHSLGDR.G
2370.2100	2369.2027	2369.1178	35.9	414	-	433	1	K.NKSLCLLLFDPGCSQQMQK.L + Oxidation (M)

No match to: 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 931.5215, 931.5215, 945.4998, 957.5150, 973.5156, 1011.4759, 1014.5773, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1465.7028, 1484.8214, 1507.7032, 1509.6316, 1509.6316, 1535.6725, 1537.6628, 1537.6628, 1553.6627, 1563.6956, 1593.7247, 1621.6700, 1637.7262, 1639.6735, 1686.7816, 1693.7960, 1742.8522, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1784.8005, 1784.8005, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1860.9581, 1891.9137, 1912.9138, 1938.9232, 1940.9351, 1971.9380, 2003.9338, 2047.9374, 2198.0242, 2226.1143, 2810.5203, 2977.5911, 3105.7104

14. [gi|426344676](#) Mass: 22017 Score: 57 Expect: 39 Matches: 8

PREDICTED: RING finger and CHY zinc finger domain-containing protein 1 [Gorilla gorilla gorilla]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1465.7028	1464.6955	1464.6636	21.8	122	-	133	0	K.CNLCLAMNLQGR.H + Oxidation (M)
1507.7032	1506.6959	1506.6708	16.7	19	-	30	1	R.GCEHYDRGCLLK.A
1565.6914	1564.6841	1564.6900	-3.73	1	-	15	1	-.MAATAREDGASGQER.G + Oxidation (M)
1565.6914	1564.6841	1564.6900	-3.73	1	-	15	1	-.MAATAREDGASGQER.G + Oxidation (M)
1665.7517	1664.7444	1664.6961	29.0	42	-	54	0	R.LCHDNNEHQDLDR.F
1742.8522	1741.8449	1741.7876	32.9	143	-	156	0	R.QNCPICLEDIHTSR.V
1891.9137	1890.9064	1890.8287	41.1	99	-	113	1	K.QYHCENCGICRIGPK.E
1940.9351	1939.9278	1939.8595	35.2	42	-	56	1	R.LCHDNNEHQDLDRFK.V

No match to: 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 931.5215, 931.5215, 944.5119, 945.4998, 957.5150, 973.5156, 1011.4759, 1014.5773, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1484.8214, 1509.6316, 1509.6316, 1535.6725, 1537.6628, 1537.6628, 1553.6627, 1563.6956, 1593.7247, 1621.6700, 1637.7262, 1639.6735, 1686.7816, 1693.7960, 1721.8564, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1784.8005, 1784.8005, 1790.8728, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1860.9581, 1912.9138, 1938.9232, 1971.9380, 2003.9338, 2019.9290, 2047.9374, 2198.0242, 2226.1143, 2370.2100, 2810.5203, 2977.5911, 3105.7104

15. [gi|62275766](#) Mass: 22993 Score: 56 Expect: 48 Matches: 8

ring finger and CHY zinc finger domain containing 1 variant 2 [Homo sapiens]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1465.7028	1464.6955	1464.6636	21.8	122	-	133	0	K.CNLCLAMNLQGR.H + Oxidation (M)
1507.7032	1506.6959	1506.6708	16.7	19	-	30	1	R.GCEHYDRGCLLK.A
1565.6914	1564.6841	1564.6900	-3.73	1	-	15	1	-.MAATAREDGASGQER.G + Oxidation (M)
1565.6914	1564.6841	1564.6900	-3.73	1	-	15	1	-.MAATAREDGASGQER.G + Oxidation (M)
1665.7517	1664.7444	1664.6961	29.0	42	-	54	0	R.LCHDNNEHQDLDR.F
1742.8522	1741.8449	1741.7876	32.9	143	-	156	0	R.QNCPICLEDIHTSR.V
1891.9137	1890.9064	1890.8287	41.1	99	-	113	1	K.QYHCENCGICRIGPK.E
1940.9351	1939.9278	1939.8595	35.2	42	-	56	1	R.LCHDNNEHQDLDRFK.V

No match to: 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 931.5215, 931.5215, 944.5119, 945.4998, 957.5150, 973.5156, 1011.4759, 1014.5773, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1484.8214, 1509.6316, 1509.6316, 1535.6725, 1537.6628, 1537.6628, 1553.6627, 1563.6956, 1593.7247, 1621.6700, 1637.7262, 1639.6735, 1686.7816, 1693.7960, 1721.8564, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1784.8005, 1784.8005, 1790.8728, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1860.9581, 1912.9138, 1938.9232, 1971.9380, 2003.9338, 2019.9290, 2047.9374, 2198.0242, 2226.1143, 2370.2100, 2810.5203, 2977.5911, 3105.7104

16. [gi|529001618](#) Mass: 78269 Score: 56 Expect: 49 Matches: 14

PREDICTED: 5-aminolevulinatase synthase, nonspecific, mitochondrial isoform X1 [Bos taurus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
931.5215	930.5142	930.5247	-11.21	552	- 559	1	---	R.ILRSTEGR.T
931.5215	930.5142	930.5247	-11.21	552	- 559	1	3	R.ILRSTEGR.T
973.5156	972.5083	972.4737	35.6	13	- 21	0	---	R.QGSRPEGS.R
1465.7028	1464.6955	1464.6636	21.8	1	- 12	1	---	-MRSCPSECILGR.Q
1693.7960	1692.7887	1692.8427	-31.86	491	- 506	1	---	R.DGVMPKMDIISGTLGK.A + 2 Oxidation (M)
1721.8564	1720.8491	1720.8025	27.1	675	- 687	1	---	R.RPLHFEMMSEREK.S + 2 Oxidation (M)
1796.8127	1795.8054	1795.8887	-46.35	187	- 202	0	---	K.ASLALQEDVQEMHAVR.E
1812.8328	1811.8255	1811.8836	-32.04	187	- 202	0	---	K.ASLALQEDVQEMHAVR.E + Oxidation (M)
1812.8328	1811.8255	1811.8836	-32.04	187	- 202	0	---	K.ASLALQEDVQEMHAVR.E + Oxidation (M)
1938.9232	1937.9159	1937.8823	17.4	595	- 611	1	---	R.VADAAKNTVECDLMTR.H + Oxidation (M)
1940.9351	1939.9278	1939.9785	-26.14	186	- 202	1	---	R.KASLALQEDVQEMHAVR.E + Oxidation (M)
1971.9380	1970.9307	1970.9343	-1.79	169	- 186	1	---	K.CPFLAAEMSQGGSSVFRK.A
2003.9338	2002.9265	2002.9353	-4.38	658	- 674	0	---	R.VGLELKPSSAECNFCR.R
2370.2100	2369.2027	2369.2170	-6.04	574	- 594	0	---	R.QMLMDAGLPVHVCPSHIIPVR.V
No match to: 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 944.5119, 945.4998, 957.5150, 1011.4759, 1014.5773, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1484.8214, 1507.7032, 1509.6316, 1509.6316, 1535.6725, 1537.6628, 1537.6628, 1553.6627, 1563.6956, 1565.6914, 1565.6914, 1593.7247, 1621.6700, 1637.7262, 1639.6735, 1665.7517, 1686.7816, 1742.8522, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1784.8005, 1784.8005, 1790.8728, 1799.8158, 1806.7749, 1839.8523, 1840.8684, 1860.9581, 1891.9137, 1912.9138, 2019.9290, 2047.9374, 2198.0242, 2226.1143, 2810.5203, 2977.5911, 3105.7104								

17. [gi|966643494](#) Mass: 9069 Score: 56 Expect: 58 Matches: 6

hypothetical protein cypCar\_00048158, partial [Cyprinus carpio]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
931.5215	930.5142	930.5134	0.86	65	- 72	1	---	R.GTLDEKLR.C
931.5215	930.5142	930.5134	0.86	65	- 72	1	---	R.GTLDEKLR.C
1563.6956	1562.6883	1562.7406	-33.42	34	- 46	0	---	K.FASFVFNVDENK.D
1891.9137	1890.9064	1890.8901	8.65	34	- 49	1	---	K.FASFVFNVDENKDGRI
1938.9232	1937.9159	1937.9306	-7.55	3	- 20	1	---	K.GFIKDCPSGQLDAAGFQK.I
2370.2100	2369.2027	2369.2114	-3.68	50	- 70	1	---	R.IEFSEFIQALSVTSRGTLDEK.L
No match to: 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 944.5119, 945.4998, 957.5150, 973.5156, 1011.4759, 1014.5773, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1465.7028, 1484.8214, 1507.7032, 1509.6316, 1509.6316, 1535.6725, 1537.6628, 1537.6628, 1553.6627, 1563.6956, 1565.6914, 1565.6914, 1593.7247, 1621.6700, 1637.7262, 1639.6735, 1665.7517, 1686.7816, 1693.7960, 1721.8564, 1742.8522, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1784.8005, 1784.8005, 1790.8728, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1860.9581, 1912.9138, 1940.9351, 1971.9380, 2003.9338, 2019.9290, 2047.9374, 2198.0242, 2226.1143, 2810.5203, 2977.5911, 3105.7104								

18. [gi|195111990](#) Mass: 14622 Score: 55 Expect: 66 Matches: 4

uncharacterized protein Dmoj\_GI22452 [Drosophila mojavensis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
973.5156	972.5083	972.5426	-35.28	23	- 31	0	---	K.ELGVGMVLR.K
1509.6316	1508.6243	1508.6631	-25.68	67	- 79	0	---	K.LGEEDDEETLDGR.K
1509.6316	1508.6243	1508.6631	-25.68	67	- 79	0	38	K.LGEEDDEETLDGR.K
1637.7262	1636.7189	1636.7580	-23.89	67	- 80	1	---	K.LGEEDDEETLDGRK.V
No match to: 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 931.5215, 931.5215, 944.5119, 945.4998, 957.5150, 1011.4759, 1014.5773, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1465.7028, 1484.8214, 1507.7032, 1535.6725, 1537.6628, 1537.6628, 1553.6627, 1563.6956, 1565.6914, 1565.6914, 1593.7247, 1621.6700, 1639.6735, 1665.7517, 1686.7816, 1693.7960, 1721.8564, 1742.8522, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1784.8005, 1784.8005, 1790.8728, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1860.9581, 1891.9137, 1912.9138, 1938.9232, 1940.9351, 1971.9380, 2003.9338, 2019.9290, 2047.9374, 2198.0242, 2226.1143, 2370.2100, 2810.5203, 2977.5911, 3105.7104								

19. [gi|195396232](#) Mass: 14555 Score: 55 Expect: 66 Matches: 4

uncharacterized protein Dvir\_GJ10051 [Drosophila virilis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
973.5156	972.5083	972.5426	-35.28	23	- 31	0	---	K.ELGVGMVLR.K
1509.6316	1508.6243	1508.6631	-25.68	67	- 79	0	---	K.LGEEDDEETLDGR.K
1509.6316	1508.6243	1508.6631	-25.68	67	- 79	0	38	K.LGEEDDEETLDGR.K
1637.7262	1636.7189	1636.7580	-23.89	67	- 80	1	---	K.LGEEDDEETLDGRK.V
No match to: 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 931.5215, 931.5215, 944.5119, 945.4998, 957.5150, 1011.4759, 1014.5773, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1465.7028, 1484.8214, 1507.7032, 1535.6725, 1537.6628, 1537.6628, 1553.6627, 1563.6956, 1565.6914, 1565.6914, 1593.7247, 1621.6700, 1639.6735, 1665.7517, 1686.7816, 1693.7960, 1721.8564, 1742.8522, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1784.8005, 1784.8005, 1790.8728, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1860.9581, 1891.9137, 1912.9138, 1938.9232, 1940.9351, 1971.9380, 2003.9338, 2019.9290, 2047.9374, 2198.0242, 2226.1143, 2370.2100, 2810.5203, 2977.5911, 3105.7104								

20. [gi|449497787](#) Mass: 55807 Score: 54 Expect: 73 Matches: 10

PREDICTED: zinc finger with UFM1-specific peptidase domain protein [Taeniopygia guttata]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
931.5215	930.5142	930.4770	40.0	151	- 157	1	---	R.QRLEEEK.R
931.5215	930.5142	930.4770	40.0	151	- 157	1	3	R.QRLEEEK.R
944.5119	943.5046	943.5134	-9.28	16	- 22	1	---	R.RPSLCRR.Q
1553.6627	1552.6554	1552.6749	-12.53	205	- 219	0	---	K.AEMMESLASGIDGK.T
1621.6700	1620.6627	1620.7058	-26.59	26	- 39	0	---	R.CPLCAASLGCDLR.R
1771.9172	1770.9099	1770.8220	49.7	40	- 55	1	---	R.RHMETAHPEPGPPGSR.R + Oxidation (M)
1790.8728	1789.8655	1789.9462	-45.05	451	- 466	0	---	K.QYQIVAVDGVLSLEEK.A
1796.8127	1795.8054	1795.8644	-32.85	1	- 15	1	---	-MVLCDVCGRALPHPR.R + Oxidation (M)
2019.9290	2018.9217	2018.9711	-24.47	242	- 259	0	---	R.HVNLSAGVDHFFHSLGDR.G
2370.2100	2369.2027	2369.1178	35.9	407	- 426	1	---	K.NKSLCLLLFDPGCSQQMQK.L + Oxidation (M)
No match to: 855.0471, 861.0775, 900.4517, 901.4653, 915.5168, 945.4998, 957.5150, 973.5156, 1011.4759, 1014.5773, 1032.5603, 1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1465.7028, 1484.8214, 1507.7032, 1535.6725, 1537.6628, 1537.6628, 1553.6627, 1563.6956, 1565.6914, 1565.6914, 1593.7247, 1621.6700, 1639.6735, 1665.7517, 1686.7816, 1693.7960, 1721.8564, 1742.8522, 1761.9404, 1762.9647, 1763.9694, 1771.9172, 1784.8005, 1784.8005, 1790.8728, 1796.8127, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1860.9581, 1891.9137, 1912.9138, 1938.9232, 1940.9351, 1971.9380, 2003.9338, 2019.9290, 2047.9374, 2198.0242, 2226.1143, 2370.2100, 2810.5203, 2977.5911, 3105.7104								



1034.1128, 1036.1082, 1050.0876, 1091.4143, 1107.4049, 1318.6571, 1349.6675, 1465.7028, 1484.8214, 1507.7032, 1509.6316, 1509.6316, 1535.6725, 1537.6628, 1537.6628, 1563.6956, 1565.6914, 1565.6914, 1593.7247, 1637.7262, 1639.6735, 1665.7517, 1686.7816, 1693.7960, 1721.8564, 1742.8522, 1761.9404, 1762.9647, 1763.9694, 1784.8005, 1784.8005, 1799.8158, 1806.7749, 1812.8328, 1812.8328, 1839.8523, 1840.8684, 1860.9581, 1891.9137, 1912.9138, 1938.9232, 1940.9351, 1971.9380, 2003.9338, 2047.9374, 2198.0242, 2226.1143, 2810.5203, 2977.5911, 3105.7104

## 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 :  $\pm 50$  ppm  
Fragment Mass Tolerance:  $\pm 0.3$  Da  
Max Missed Cleavages : 1  
Instrument type : MALDI-TOF-TOF  
Query1 (855.0471,1+) : <no title>  
Query2 (861.0775,1+) : <no title>  
Query3 (900.4517,1+) : <no title>  
Query4 (901.4653,1+) : <no title>  
Query5 (915.5168,1+) : <no title>  
Query6 (931.5215,1+) : <no title>  
Query7 (931.5215,1+) : MalDIWellID: 59830, SpectrumID: 120914,  
Query8 (944.5119,1+) : <no title>  
Query9 (945.4998,1+) : <no title>  
Query10 (957.5150,1+) : <no title>  
Query11 (973.5156,1+) : <no title>  
Query12 (1011.4759,1+) : <no title>  
Query13 (1014.5773,1+) : <no title>  
Query14 (1032.5603,1+) : <no title>  
Query15 (1034.1128,1+) : <no title>  
Query16 (1036.1082,1+) : <no title>  
Query17 (1050.0876,1+) : <no title>  
Query18 (1091.4143,1+) : <no title>  
Query19 (1107.4049,1+) : <no title>  
Query20 (1318.6571,1+) : <no title>  
Query21 (1349.6675,1+) : <no title>  
Query22 (1465.7028,1+) : <no title>  
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Query24 (1507.7032,1+) : <no title>  
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Query27 (1535.6725,1+) : <no title>  
Query28 (1537.6628,1+) : <no title>  
Query29 (1537.6628,1+) : MalDIWellID: 59830, SpectrumID: 120916,  
Query30 (1553.6627,1+) : <no title>  
Query31 (1563.6956,1+) : <no title>  
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Query34 (1593.7247,1+) : <no title>  
Query35 (1621.6700,1+) : <no title>  
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Query37 (1639.6735,1+) : <no title>  
Query38 (1665.7517,1+) : <no title>  
Query39 (1686.7816,1+) : <no title>  
Query40 (1693.7960,1+) : <no title>  
Query41 (1721.8564,1+) : <no title>  
Query42 (1742.8522,1+) : <no title>  
Query43 (1761.9404,1+) : <no title>  
Query44 (1762.9647,1+) : <no title>  
Query45 (1763.9694,1+) : <no title>  
Query46 (1771.9172,1+) : <no title>  
Query47 (1784.8005,1+) : <no title>  
Query48 (1784.8005,1+) : MalDIWellID: 59830, SpectrumID: 120918,  
Query49 (1790.8728,1+) : <no title>  
Query50 (1796.8127,1+) : <no title>  
Query51 (1799.8158,1+) : <no title>  
Query52 (1806.7749,1+) : <no title>  
Query53 (1812.8328,1+) : <no title>  
Query54 (1812.8328,1+) : MalDIWellID: 59830, SpectrumID: 120919,  
Query55 (1839.8523,1+) : <no title>  
Query56 (1840.8684,1+) : <no title>  
Query57 (1860.9581,1+) : <no title>  
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Query59 (1912.9138,1+) : <no title>  
Query60 (1938.9232,1+) : <no title>  
Query61 (1940.9351,1+) : <no title>  
Query62 (1971.9380,1+) : <no title>  
Query63 (2003.9338,1+) : <no title>  
Query64 (2019.9290,1+) : <no title>  
Query65 (2047.9374,1+) : <no title>  
Query66 (2198.0242,1+) : <no title>  
Query67 (2226.1143,1+) : <no title>  
Query68 (2370.2100,1+) : <no title>  
Query69 (2810.5203,1+) : <no title>  
Query70 (2977.5911,1+) : <no title>  
Query71 (3105.7104,1+) : <no title>

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