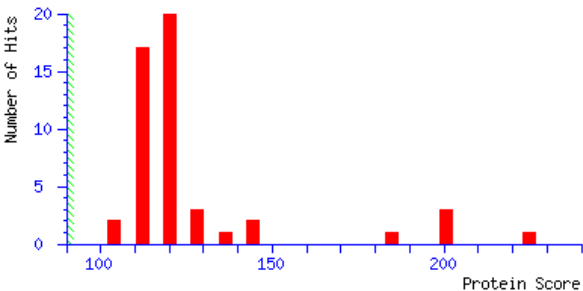


Mascot Search Results

User :
Email :
Search title : SampleSetID: 692, AnalysisID: 5361, MaldiWellID: 60693, SpectrumID: 127292, Path=\\161031\\MSMS\\run 65 NCBI all ok 1
Database : NCBI nr 160208 (79581714 sequences; 29080698065 residues)
Timestamp : 28 Nov 2016 at 11:47:36 GMT
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
Top Score : 225 for gi|157119815, AAEL008787-PA [Aedes aegypti]

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 92 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 157119815	68528	225	AAEL008787-PA [Aedes aegypti]
2. gi 568251241	68474	203	ATP synthase alpha subunit vacuolar [Anopheles darlingi]
3. gi 668451472	68457	198	hypothetical protein ZHAS_00008066 [Anopheles sinensis]
4. gi 2454488	68898	198	V-ATPase A-subunit [Aedes aegypti]
5. gi 31207753	68507	188	AGAP003153-PA [Anopheles gambiae str. PEST]
6. gi 900887300	68219	144	LOW QUALITY PROTEIN: uncharacterized protein Dsimw501_GD23860 [Drosophila simulans]
7. gi 170043178	68430	141	ATP synthase alpha subunit vacuolar [Culex quinquefasciatus]
8. gi 827665724	68453	134	V-ATPase subunit A [Pectinophora gossypiella]
9. gi 755940378	68754	125	PREDICTED: V-type proton ATPase catalytic subunit A [Fopius arisanus]
10. gi 970919090	68747	125	PREDICTED: V-type proton ATPase catalytic subunit A [Diachasma alloeum]
11. gi 194761296	68442	125	uncharacterized protein Dana_GF14214 [Drosophila ananassae]
12. gi 907623080	68603	124	PREDICTED: V-type proton ATPase catalytic subunit A isoform 2 [Stomoxys calcitrans]
13. gi 826135855	68267	124	vATPase_A [Diabrotica virgifera virgifera]
14. gi 939658367	68394	123	PREDICTED: V-type proton ATPase catalytic subunit A [Microplitis demolitor]
15. gi 195578837	57844	120	GD23860 [Drosophila simulans]
16. gi 498996523	68562	118	PREDICTED: V-type proton ATPase catalytic subunit A isoform 2 [Ceratitis capitata]
17. gi 24583984	68544	118	vacuolar H[+] ATPase 68 kDa subunit 2, isoform A [Drosophila melanogaster]
18. gi 195034208	68614	118	GH11385 [Drosophila grimshawi]
19. gi 195118495	68563	118	uncharacterized protein Dmoj_GI18088 [Drosophila mojavensis]
20. gi 195434356	68483	118	uncharacterized protein Dwil_GK15307 [Drosophila willistoni]

Results List

1.	gi 157119815	Mass: 68528	Score: 225	Expect: 2.5e-015	Matches: 17
AAEL008787-PA [Aedes aegypti]					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Ions Peptide
	1149.5933	1148.5860	1148.5978	-10.29	465 - 473 0 --- K.NFQEFVPLR.T
	1249.5691	1248.5618	1248.5267	28.1	540 - 549 0 --- R.NMIGFYDMAR.H + 2 Oxidation (M)
	1301.6184	1300.6111	1300.6750	-49.15	200 - 209 0 --- K.WSMLQVWPVR.Q
	1317.6819	1316.6746	1316.6700	3.54	200 - 209 0 --- K.WSMLQVWPVR.Q + Oxidation (M)
	1410.7363	1409.7290	1409.7554	-18.74	43 - 54 0 --- R.VGYVELVGEIIR.L
	1410.7363	1409.7290	1409.7554	-18.74	43 - 54 0 36 R.VGYVELVGEIIR.L
	1515.7159	1514.7086	1514.7875	-52.06	306 - 320 0 --- R.TALVANTSNNPVAAR.E
	1698.8561	1697.8488	1697.8777	-17.03	16 - 31 0 --- K.FGYVFAVSGPVVTAER.M
	1698.8561	1697.8488	1697.8777	-17.03	16 - 31 0 65 K.FGYVFAVSGPVVTAER.M
	1731.8138	1730.8065	1730.7934	7.59	263 - 277 0 --- K.YNSDVIIVGCGER.G
	1749.8416	1748.8343	1748.8621	-15.88	321 - 335 0 --- R.EASIYTGITLSEYFR.D
	1749.8416	1748.8343	1748.8621	-15.88	321 - 335 0 46 R.EASIYTGITLSEYFR.D
	1797.8328	1796.8255	1796.8403	-8.22	362 - 378 0 --- R.LAEMPADSGYPAYLGAR.L + Oxidation (M)

2100.0376 2099.0303 2099.0323 -0.96 594 - 610 1 --- K.IKADFDQLYEDLQQAFR.N
 2117.0234 2116.0161 2116.0266 -4.93 457 - 473 1 --- R.ALDDFYDKNFQEFVPLR.T
 2181.0813 2180.0740 2180.0671 3.18 287 - 305 1 --- R.DFPELSVEIDGVTEIMKR.T + Oxidation (M)
 2209.1272 2208.1199 2208.1539 -15.39 140 - 160 0 --- K.VGSHITGGDLYGLVHENTLVK.H

No match to: 1150.5878, 1150.5878, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1712.8463, 1726.8776, 1733.8228, 1737.8322, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1894.9434, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2101.0217, 2115.0562, 2118.0183, 2118.0183, 2146.0603, 2154.0588, 2167.0801, 2220.1287, 2225.1433

2. [gi|568251241](#) Mass: 68474 Score: 203 Expect: 4e-013 Matches: 14

ATP synthase alpha subunit vacuolar [Anopheles darlingi]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1149.5933	1148.5860	1148.5978	-10.29	465	- 473	0	---	K.NFQEFVPLR.T
1249.5691	1248.5618	1248.5267	28.1	540	- 549	0	---	K.NMIGFYDMAR.H + 2 Oxidation (M)
1410.7363	1409.7290	1409.7554	-18.74	43	- 54	0	---	R.VGYVELVGEIIR.L
1410.7363	1409.7290	1409.7554	-18.74	43	- 54	0	36	R.VGYVELVGEIIR.L
1515.7159	1514.7086	1514.7875	-52.06	306	- 320	0	---	R.TALVANTSMPVAAR.E
1698.8561	1697.8488	1697.8777	-17.03	16	- 31	0	---	K.FGYVFAVSGPVVTAER.M
1698.8561	1697.8488	1697.8777	-17.03	16	- 31	0	65	K.FGYVFAVSGPVVTAER.M
1749.8416	1748.8343	1748.8621	-15.88	321	- 335	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	321	- 335	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	362	- 378	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
1894.9434	1893.9361	1893.8787	30.3	534	- 549	1	---	K.TVGMLKNMIGFYDMAR.H + 3 Oxidation (M)
2117.0234	2116.0161	2116.0266	-4.93	457	- 473	1	---	R.ALDDFYDKNFQEFVPLR.T
2181.0813	2180.0740	2180.0671	3.18	287	- 305	1	---	R.DFPELSVEIDGVTEIMKR.T + Oxidation (M)
2209.1272	2208.1199	2208.1539	-15.39	140	- 160	0	---	K.VGSHITGGDLYGLVHENTLVK.H

No match to: 1150.5878, 1150.5878, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1301.6184, 1317.6819, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1712.8463, 1726.8776, 1731.8138, 1733.8228, 1737.8322, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2100.0376, 2101.0217, 2115.0562, 2118.0183, 2118.0183, 2146.0603, 2154.0588, 2167.0801, 2220.1287, 2225.1433

3. [gi|668451472](#) Mass: 68457 Score: 198 Expect: 1.3e-012 Matches: 14

hypothetical protein ZHAS_0008066 [Anopheles sinensis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1249.5691	1248.5618	1248.5267	28.1	540	- 549	0	---	K.NMIGFYDMAR.H + 2 Oxidation (M)
1410.7363	1409.7290	1409.7554	-18.74	43	- 54	0	---	R.VGYVELVGEIIR.L
1410.7363	1409.7290	1409.7554	-18.74	43	- 54	0	36	R.VGYVELVGEIIR.L
1515.7159	1514.7086	1514.7875	-52.06	306	- 320	0	---	R.TALVANTSMPVAAR.E
1698.8561	1697.8488	1697.8777	-17.03	16	- 31	0	---	K.FGYVFAVSGPVVTAER.M
1698.8561	1697.8488	1697.8777	-17.03	16	- 31	0	65	K.FGYVFAVSGPVVTAER.M
1749.8416	1748.8343	1748.8621	-15.88	321	- 335	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	321	- 335	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	362	- 378	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
1894.9434	1893.9361	1893.8787	30.3	534	- 549	1	---	K.TVGMLKNMIGFYDMAR.H + 3 Oxidation (M)
2118.0183	2117.0110	2116.9888	10.5	594	- 610	1	---	K.IKADFDQLYEDMQQAFR.N
2118.0183	2117.0110	2116.9888	10.5	594	- 610	1	---	K.IKADFDQLYEDMQQAFR.N
2181.0813	2180.0740	2180.0671	3.18	287	- 305	1	---	R.DFPELSVEIDGVTEIMKR.T + Oxidation (M)
2209.1272	2208.1199	2208.1539	-15.39	140	- 160	0	---	K.VGSHITGGDLYGLVHENTLVK.H

No match to: 1149.5933, 1150.5878, 1150.5878, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1301.6184, 1317.6819, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1712.8463, 1726.8776, 1731.8138, 1733.8228, 1737.8322, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2100.0376, 2101.0217, 2115.0562, 2117.0234, 2146.0603, 2154.0588, 2167.0801, 2220.1287, 2225.1433

4. [gi|2454488](#) Mass: 68898 Score: 198 Expect: 1.3e-012 Matches: 14

V-ATPase A-subunit [Aedes aegypti]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1249.5691	1248.5618	1248.5267	28.1	542	- 551	0	---	R.NMIGFYDMAR.H + 2 Oxidation (M)
1301.6184	1300.6111	1300.6750	-49.15	201	- 210	0	---	K.WSMLQWVPVR.Q
1317.6819	1316.6746	1316.6700	3.54	201	- 210	0	---	K.WSMLQWVPVR.Q + Oxidation (M)
1410.7363	1409.7290	1409.7554	-18.74	43	- 54	0	---	R.VGYVELVGEIIR.L
1410.7363	1409.7290	1409.7554	-18.74	43	- 54	0	36	R.VGYVELVGEIIR.L
1515.7159	1514.7086	1514.7875	-52.06	307	- 321	0	---	R.TALVANTSMPVAAR.E
1698.8561	1697.8488	1697.8777	-17.03	16	- 31	0	---	K.FGYVFAVSGPVVTAER.M
1698.8561	1697.8488	1697.8777	-17.03	16	- 31	0	65	K.FGYVFAVSGPVVTAER.M
1731.8138	1730.8065	1730.7934	7.59	264	- 278	0	---	K.YNSNDVIVVGGER.G
1749.8416	1748.8343	1748.8621	-15.88	322	- 336	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	322	- 336	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	363	- 379	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
2100.0376	2099.0303	2099.0323	-0.96	595	- 611	1	---	K.IKADFDQLYEDLQQAFR.N
2181.0813	2180.0740	2180.0671	3.18	288	- 306	1	---	R.DFPELSVEIDGVTEIMKR.T + Oxidation (M)

No match to: 1149.5933, 1150.5878, 1150.5878, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1712.8463, 1726.8776, 1733.8228, 1737.8322, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1894.9434, 1926.9658, 1931.9445,

1968.9597, 2029.9998, 2077.0229, 2101.0217, 2115.0562, 2117.0234, 2118.0183, 2118.0183, 2146.0603, 2154.0588, 2167.0801, 2209.1272, 2220.1287, 2225.1433

5. [gi|31207753](#) Mass: 68507 Score: 188 Expect: 1.3e-011 Matches: 13

AGAP003153-PA [Anopheles gambiae str. PEST]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1249.5691	1248.5618	1248.5267	28.1	540	549	0	---	K.NMIGFYDMAR.H + 2 Oxidation (M)
1410.7363	1409.7290	1409.7554	-18.74	43	54	0	---	R.VGYELVGEIIR.L
1410.7363	1409.7290	1409.7554	-18.74	43	54	0	36	R.VGYELVGEIIR.L
1515.7159	1514.7086	1514.7875	-52.06	306	320	0	---	R.TALVANTSMPVAAR.E
1698.8561	1697.8488	1697.8777	-17.03	16	31	0	---	K.FGYVFAVSGPVVTAER.M
1698.8561	1697.8488	1697.8777	-17.03	16	31	0	65	K.FGYVFAVSGPVVTAER.M
1749.8416	1748.8343	1748.8621	-15.88	321	335	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	321	335	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	362	378	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
1894.9434	1893.9361	1893.8787	30.3	534	549	1	---	K.TVGMLKNMIGFYDMAR.H + 3 Oxidation (M)
2118.0183	2117.0110	2116.9928	8.61	457	473	1	---	R.ALEDFYDKNFPEFVPMR.T
2118.0183	2117.0110	2116.9928	8.61	457	473	1	---	R.ALEDFYDKNFPEFVPMR.T
2181.0813	2180.0740	2180.0671	3.18	287	305	1	---	R.DFPELSVEIDGVTESIMKR.T + Oxidation (M)

No match to: 1149.5933, 1150.5878, 1150.5878, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1301.6184, 1317.6819, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1712.8463, 1726.8776, 1731.8138, 1733.8228, 1737.8322, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2100.0376, 2101.0217, 2115.0562, 2117.0234, 2146.0603, 2154.0588, 2167.0801, 2209.1272, 2220.1287, 2225.1433

6. [gi|900887300](#) Mass: 68219 Score: 144 Expect: 3.2e-007 Matches: 11

LOW QUALITY PROTEIN: uncharacterized protein Dsimw501_GD23860 [Drosophila simulans]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1410.7363	1409.7290	1409.7554	-18.74	43	54	0	---	R.VGYELVGEIIR.L
1410.7363	1409.7290	1409.7554	-18.74	43	54	0	36	R.VGYELVGEIIR.L
1515.7159	1514.7086	1514.7875	-52.06	306	320	0	---	R.TALVANTSMPVAAR.E
1731.8138	1730.8065	1730.7934	7.59	263	277	0	---	K.YNSDVIIVGCGER.G
1737.8322	1736.8249	1736.7278	55.9	511	524	0	---	K.DDFLQNSYSSYDR.F
1749.8416	1748.8343	1748.8621	-15.88	321	335	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	321	335	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	362	378	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
2118.0183	2117.0110	2117.0986	-41.36	454	470	1	18	R.YGLIFYDKNFPEFVPLR.T
2181.0813	2180.0740	2180.0671	3.18	287	305	1	---	R.DFPELSVEIDGVTESIMKR.T + Oxidation (M)
2209.1272	2208.1199	2208.1539	-15.39	140	160	0	---	K.VGSHITGGDLYGLVHENTLVK.H

No match to: 1149.5933, 1150.5878, 1150.5878, 1249.5691, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1301.6184, 1317.6819, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1698.8561, 1698.8561, 1712.8463, 1726.8776, 1733.8228, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1894.9434, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2100.0376, 2101.0217, 2115.0562, 2117.0234, 2118.0183, 2146.0603, 2154.0588, 2167.0801, 2220.1287, 2225.1433

7. [gi|170043178](#) Mass: 68430 Score: 141 Expect: 6.3e-007 Matches: 13

ATP synthase alpha subunit vacuolar [Culex quinquefasciatus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1149.5933	1148.5860	1148.5978	-10.29	465	473	0	---	K.NFQEFVPLR.T
1410.7363	1409.7290	1409.7554	-18.74	43	54	0	---	R.VGYELVGEIIR.L
1410.7363	1409.7290	1409.7554	-18.74	43	54	0	36	R.VGYELVGEIIR.L
1515.7159	1514.7086	1514.7875	-52.06	306	320	0	---	R.TALVANTSMPVAAR.E
1670.8300	1669.8227	1669.8716	-29.26	16	31	0	---	K.FGYVFAVSGPVVTAER.M
1749.8416	1748.8343	1748.8621	-15.88	321	335	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	321	335	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	362	378	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
1859.8604	1858.8531	1858.9321	-42.48	569	584	1	---	R.EAMGNILYQLSSMKFK.D
2100.0376	2099.0303	2099.0323	-0.96	594	610	1	---	K.IKADFDQLYEDLQQAER.N
2117.0234	2116.0161	2116.0266	-4.93	457	473	1	---	R.ALDDFYDKNFQEFVPLR.T
2181.0813	2180.0740	2180.0671	3.18	287	305	1	---	R.DFPELSVEIDGVTESIMKR.T + Oxidation (M)
2209.1272	2208.1199	2208.1539	-15.39	140	160	0	---	K.VGSHITGGDLYGLVHENTLVK.H

No match to: 1150.5878, 1150.5878, 1249.5691, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1301.6184, 1317.6819, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1672.8260, 1676.8251, 1697.8495, 1698.8561, 1698.8561, 1712.8463, 1726.8776, 1731.8138, 1733.8228, 1737.8322, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1894.9434, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2101.0217, 2115.0562, 2118.0183, 2118.0183, 2146.0603, 2154.0588, 2167.0801, 2220.1287, 2225.1433

8. [gi|827665724](#) Mass: 68453 Score: 134 Expect: 3.2e-006 Matches: 8

V-ATPase subunit A [Pectinophora gossypiella]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1515.7159	1514.7086	1514.7875	-52.06	310	324	0	---	R.TALVANTSMPVAAR.E
1698.8561	1697.8488	1697.8777	-17.03	20	35	0	---	K.FGYVFAVSGPVVTAER.M
1698.8561	1697.8488	1697.8777	-17.03	20	35	0	65	K.FGYVFAVSGPVVTAER.M
1749.8416	1748.8343	1748.8621	-15.88	325	339	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	325	339	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	366	382	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
2154.0588	2153.0515	2153.0344	7.96	1	19	1	---	-.MTTTRPLKTIAMSDSSEK.F

2209.1272 2208.1199 2208.0984 9.75 291 - 309 1 --- R.DFPELTVEIEGVTESIMKR.T + Oxidation (M)

No match to: 1149.5933, 1150.5878, 1150.5878, 1249.5691, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1301.6184, 1317.6819, 1410.7363, 1410.7363, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1712.8463, 1726.8776, 1731.8138, 1733.8228, 1737.8322, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1894.9434, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2100.0376, 2101.0217, 2115.0562, 2117.0234, 2118.0183, 2118.0183, 2146.0603, 2167.0801, 2181.0813, 2220.1287, 2225.1433

9. [gi|755940378](#) Mass: 68754 Score: 125 Expect: 2.5e-005 Matches: 12

PREDICTED: V-type proton ATPase catalytic subunit A [Fopius arisanus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1149.5933	1148.5860	1148.5978	-10.29	467	- 475	0	---	K.NFQEFVPLR.T
1410.7363	1409.7290	1409.7554	-18.74	45	- 56	0	---	R.VGYELVGEIIR.L
1410.7363	1409.7290	1409.7554	-18.74	45	- 56	0	36	R.VGYELVGEIIR.L
1515.7159	1514.7086	1514.7875	-52.06	308	- 322	0	---	R.TALVANTSMPVAAR.E
1731.8138	1730.8065	1730.7934	7.59	265	- 279	0	---	K.YNSDVIIVGCGER.G
1749.8416	1748.8343	1748.8621	-15.88	323	- 337	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	323	- 337	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	364	- 380	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
2117.0234	2116.0161	2116.0266	-4.93	459	- 475	1	---	R.ALDDFYDKNFQEFVPLR.T
2118.0183	2117.0110	2117.0290	-8.49	596	- 612	1	---	K.IRSDFDQLHEDIQQAFR.N
2118.0183	2117.0110	2117.0290	-8.49	596	- 612	1	---	K.IRSDFDQLHEDIQQAFR.N
2209.1272	2208.1199	2208.0984	9.75	289	- 307	1	---	R.DFPELTVEIEGVTESIMKR.T + Oxidation (M)
No match to: 1150.5878, 1150.5878, 1249.5691, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1301.6184, 1317.6819, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1698.8561, 1698.8561, 1712.8463, 1726.8776, 1733.8228, 1737.8322, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1894.9434, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2100.0376, 2101.0217, 2115.0562, 2146.0603, 2154.0588, 2167.0801, 2181.0813, 2220.1287, 2225.1433								

10. [gi|970919090](#) Mass: 68747 Score: 125 Expect: 2.5e-005 Matches: 12

PREDICTED: V-type proton ATPase catalytic subunit A [Diachasma alloeum]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1149.5933	1148.5860	1148.5978	-10.29	467	- 475	0	---	K.NFQEFVPLR.T
1410.7363	1409.7290	1409.7554	-18.74	45	- 56	0	---	R.VGYELVGEIIR.L
1410.7363	1409.7290	1409.7554	-18.74	45	- 56	0	36	R.VGYELVGEIIR.L
1515.7159	1514.7086	1514.7875	-52.06	308	- 322	0	---	R.TALVANTSMPVAAR.E
1731.8138	1730.8065	1730.7934	7.59	265	- 279	0	---	K.YNSDVIIVGCGER.G
1749.8416	1748.8343	1748.8621	-15.88	323	- 337	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	323	- 337	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	364	- 380	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
2117.0234	2116.0161	2116.0266	-4.93	459	- 475	1	---	R.ALDDFYDKNFQEFVPLR.T
2118.0183	2117.0110	2117.0290	-8.49	596	- 612	1	---	K.IRSDFDQLHEDIQQAFR.N
2118.0183	2117.0110	2117.0290	-8.49	596	- 612	1	---	K.IRSDFDQLHEDIQQAFR.N
2209.1272	2208.1199	2208.0984	9.75	289	- 307	1	---	R.DFPELTVEIEGVTESIMKR.T + Oxidation (M)
No match to: 1150.5878, 1150.5878, 1249.5691, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1301.6184, 1317.6819, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1698.8561, 1698.8561, 1712.8463, 1726.8776, 1733.8228, 1737.8322, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1894.9434, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2100.0376, 2101.0217, 2115.0562, 2146.0603, 2154.0588, 2167.0801, 2181.0813, 2220.1287, 2225.1433								

11. [gi|194761296](#) Mass: 68442 Score: 125 Expect: 2.5e-005 Matches: 11

uncharacterized protein Dana_GF14214 [Drosophila ananassae]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1268.6672	1267.6599	1267.6496	8.17	200	- 209	0	---	K.HSMLQVWPVR.Q + Oxidation (M)
1410.7363	1409.7290	1409.7554	-18.74	43	- 54	0	---	R.VGYELVGEIIR.L
1410.7363	1409.7290	1409.7554	-18.74	43	- 54	0	36	R.VGYELVGEIIR.L
1515.7159	1514.7086	1514.7875	-52.06	306	- 320	0	---	R.TALVANTSMPVAAR.E
1731.8138	1730.8065	1730.7934	7.59	263	- 277	0	---	K.YNSDVIIVGCGER.G
1737.8322	1736.8249	1736.7278	55.9	514	- 527	0	---	K.DDFLQQNSYSSYDR.F
1749.8416	1748.8343	1748.8621	-15.88	321	- 335	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	321	- 335	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	362	- 378	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
2181.0813	2180.0740	2180.0671	3.18	287	- 305	1	---	R.DFPELSVEIDGVTESIMKR.T + Oxidation (M)
2209.1272	2208.1199	2208.1539	-15.39	140	- 160	0	---	K.VGSHITGGDLYGLVHENTLVK.H
No match to: 1149.5933, 1150.5878, 1150.5878, 1249.5691, 1264.5995, 1281.6362, 1300.6208, 1300.6208, 1301.6184, 1317.6819, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1698.8561, 1698.8561, 1712.8463, 1726.8776, 1733.8228, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1894.9434, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2100.0376, 2101.0217, 2115.0562, 2117.0234, 2118.0183, 2118.0183, 2146.0603, 2154.0588, 2167.0801, 2220.1287, 2225.1433								

12. [gi|907623080](#) Mass: 68603 Score: 124 Expect: 3.2e-005 Matches: 11

PREDICTED: V-type proton ATPase catalytic subunit A isoform 2 [Stomoxys calcitrans]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1149.5933	1148.5860	1148.5978	-10.29	466	- 474	0	---	K.NFQEFVPLR.T
1410.7363	1409.7290	1409.7554	-18.74	43	- 54	0	---	R.VGYELVGEIIR.L
1410.7363	1409.7290	1409.7554	-18.74	43	- 54	0	36	R.VGYELVGEIIR.L
1515.7159	1514.7086	1514.7875	-52.06	307	- 321	0	---	R.TALVANTSMPVAAR.E
1731.8138	1730.8065	1730.7934	7.59	264	- 278	0	---	K.YNSDVIIVGCGER.G


```

1737.8322 1736.8249 1736.7278 55.9 515 - 528 0 --- K.DDFLQQNSYSSYDR.F
1749.8416 1748.8343 1748.8621 -15.88 322 - 336 0 --- R.EASIYTGITLSEYFR.D
1749.8416 1748.8343 1748.8621 -15.88 322 - 336 0 46 R.EASIYTGITLSEYFR.D
1797.8328 1796.8255 1796.8403 -8.22 363 - 379 0 --- R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
2117.0234 2116.0161 2116.0266 -4.93 458 - 474 1 --- R.ALDDFYDKNFQEFVPLR.T
2209.1272 2208.1199 2208.1539 -15.39 141 - 161 0 --- K.VGSHITGGDLYGLVHENTLVK.H
No match to: 1150.5878, 1150.5878, 1249.5691, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1301.6184, 1317.6819,
1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617,
1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1698.8561,
1698.8561, 1712.8463, 1726.8776, 1733.8228, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604,
1894.9434, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2100.0376, 2101.0217, 2115.0562, 2118.0183, 2118.0183,
2146.0603, 2154.0588, 2167.0801, 2181.0813, 2220.1287, 2225.1433

```

13. [gi|826135855](#) Mass: 68267 Score: 124 Expect: 3.2e-005 Matches: 12

vATPase_A [Diabrotica virgifera virgifera]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1300.6208	1299.6135	1299.6055	6.19	549	560	0	---	R.HAVESTAQSENK.I
1300.6208	1299.6135	1299.6055	6.19	549	560	0	---	R.HAVESTAQSENK.I
1410.7363	1409.7290	1409.7554	-18.74	42	53	0	---	R.VGYELVGEIIR.L
1410.7363	1409.7290	1409.7554	-18.74	42	53	0	36	R.VGYELVGEIIR.L
1515.7159	1514.7086	1514.7875	-52.06	305	319	0	---	R.TALVANTSMPVAAR.E
1575.7825	1574.7752	1574.7320	27.4	568	581	0	---	R.DSMGILYQLSSMK.F + Oxidation (M)
1731.8138	1730.8065	1730.7934	7.59	262	276	0	---	K.YSNSDVIIYVGCGER.G
1749.8416	1748.8343	1748.8621	-15.88	320	334	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	320	334	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	361	377	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
2077.0229	2076.0156	2075.9721	20.9	286	303	0	---	R.DFPELTVEIDGHTESIMK.R + Oxidation (M)
2100.0376	2099.0303	2099.0323	-0.96	593	609	1	---	K.IKADFDQLYEDIQQAFR.N

No match to: 1149.5933, 1150.5878, 1150.5878, 1249.5691, 1264.5995, 1268.6672, 1281.6362, 1301.6184, 1317.6819, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1698.8561, 1698.8561, 1712.8463, 1726.8776, 1733.8228, 1737.8322, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1894.9434, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2101.0217, 2115.0562, 2117.0234, 2118.0183, 2118.0183, 2146.0603, 2154.0588, 2167.0801, 2181.0813, 2209.1272, 2220.1287, 2225.1433

14. [gi|939658367](#) Mass: 68394 Score: 123 Expect: 4e-005 Matches: 12

PREDICTED: V-type proton ATPase catalytic subunit A [Microplitis demolitor]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1149.5933	1148.5860	1148.5978	-10.29	465	473	0	---	K.NFQEFVPLR.T
1410.7363	1409.7290	1409.7554	-18.74	43	54	0	---	R.VGYELVGEIIR.L
1410.7363	1409.7290	1409.7554	-18.74	43	54	0	36	R.VGYELVGEIIR.L
1515.7159	1514.7086	1514.7875	-52.06	306	320	0	---	R.TALVANTSMPVAAR.E
1731.8138	1730.8065	1730.7934	7.59	263	277	0	---	K.YSNSDVIIYVGCGER.G
1737.8322	1736.8249	1736.7278	55.9	514	527	0	---	K.DDFLQQNSYSSYDR.F
1749.8416	1748.8343	1748.8621	-15.88	321	335	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	321	335	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	362	378	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
2117.0234	2116.0161	2116.0266	-4.93	457	473	1	---	R.ALDDFYDKNFQEFVPLR.T
2118.0183	2117.0110	2117.0290	-8.49	594	610	1	---	K.IRSDFDQLHEDIQQAFR.N
2118.0183	2117.0110	2117.0290	-8.49	594	610	1	---	K.IRSDFDQLHEDIQQAFR.N

No match to: 1150.5878, 1150.5878, 1249.5691, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1301.6184, 1317.6819, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1698.8561, 1698.8561, 1712.8463, 1726.8776, 1733.8228, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1894.9434, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2100.0376, 2101.0217, 2115.0562, 2146.0603, 2154.0588, 2167.0801, 2181.0813, 2209.1272, 2220.1287, 2225.1433

15. [gi|195578837](#) Mass: 57844 Score: 120 Expect: 8e-005 Matches: 10

GD23860 [Drosophila simulans]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1410.7363	1409.7290	1409.7554	-18.74	33	44	0	---	R.VGYELVGEIIR.L
1410.7363	1409.7290	1409.7554	-18.74	33	44	0	36	R.VGYELVGEIIR.L
1515.7159	1514.7086	1514.7875	-52.06	296	310	0	---	R.TALVANTSMPVAAR.E
1731.8138	1730.8065	1730.7934	7.59	253	267	0	---	K.YSNSDVIIYVGCGER.G
1737.8322	1736.8249	1736.7278	55.9	417	430	0	---	K.DDFLQQNSYSSYDR.F
1749.8416	1748.8343	1748.8621	-15.88	311	325	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	311	325	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	352	368	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
2181.0813	2180.0740	2180.0671	3.18	277	295	1	---	R.DFPELSVEIDGVTESIMKR.T + Oxidation (M)
2209.1272	2208.1199	2208.1539	-15.39	130	150	0	---	K.VGSHITGGDLYGLVHENTLVK.H

No match to: 1149.5933, 1150.5878, 1150.5878, 1249.5691, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1301.6184, 1317.6819, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1698.8561, 1698.8561, 1712.8463, 1726.8776, 1733.8228, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1894.9434, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2100.0376, 2101.0217, 2115.0562, 2117.0234, 2118.0183, 2118.0183, 2146.0603, 2154.0588, 2167.0801, 2220.1287, 2225.1433

16. [gi|498996523](#) Mass: 68562 Score: 118 Expect: 0.00013 Matches: 10

PREDICTED: V-type proton ATPase catalytic subunit A isoform 2 [Ceratitis capitata]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1410.7363	1409.7290	1409.7554	-18.74	43	54	0	---	R.VGYELVGEIIR.L

1410.7363	1409.7290	1409.7554	-18.74	43	-	54	0	36	R.VGYELVGEIIR.L
1515.7159	1514.7086	1514.7875	-52.06	306	-	320	0	---	R.TALVANTSMPVAAR.E
1731.8138	1730.8065	1730.7934	7.59	263	-	277	0	---	K.YNSDVIIYVGCGER.G
1737.8322	1736.8249	1736.7278	55.9	514	-	527	0	---	K.DDFLQQNSYSSYDR.F
1749.8416	1748.8343	1748.8621	-15.88	321	-	335	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	321	-	335	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	362	-	378	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
2181.0813	2180.0740	2180.0671	3.18	287	-	305	1	---	R.DFPELSVEIDGVTESIMKR.T + Oxidation (M)
2209.1272	2208.1199	2208.1539	-15.39	140	-	160	0	---	K.VGSHITGGDLYGLVHENTLVK.H

No match to: 1149.5933, 1150.5878, 1150.5878, 1249.5691, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1301.6184, 1317.6819, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1698.8561, 1698.8561, 1712.8463, 1726.8776, 1733.8228, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1894.9434, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2100.0376, 2101.0217, 2115.0562, 2117.0234, 2118.0183, 2118.0183, 2146.0603, 2154.0588, 2167.0801, 2220.1287, 2225.1433

17. [gi|24583984](#) Mass: 68544 Score: 118 Expect: 0.00013 Matches: 10vacuolar H⁺ ATPase 68 kDa subunit 2, isoform A [Drosophila melanogaster]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
1410.7363	1409.7290	1409.7554	-18.74	43	-	54	0	---	R.VGYELVGEIIR.L
1410.7363	1409.7290	1409.7554	-18.74	43	-	54	0	36	R.VGYELVGEIIR.L
1515.7159	1514.7086	1514.7875	-52.06	306	-	320	0	---	R.TALVANTSMPVAAR.E
1731.8138	1730.8065	1730.7934	7.59	263	-	277	0	---	K.YNSDVIIYVGCGER.G
1737.8322	1736.8249	1736.7278	55.9	514	-	527	0	---	K.DDFLQQNSYSSYDR.F
1749.8416	1748.8343	1748.8621	-15.88	321	-	335	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	321	-	335	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	362	-	378	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
2181.0813	2180.0740	2180.0671	3.18	287	-	305	1	---	R.DFPELSVEIDGVTESIMKR.T + Oxidation (M)
2209.1272	2208.1199	2208.1539	-15.39	140	-	160	0	---	K.VGSHITGGDLYGLVHENTLVK.H

No match to: 1149.5933, 1150.5878, 1150.5878, 1249.5691, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1301.6184, 1317.6819, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1698.8561, 1698.8561, 1712.8463, 1726.8776, 1733.8228, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1894.9434, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2100.0376, 2101.0217, 2115.0562, 2117.0234, 2118.0183, 2118.0183, 2146.0603, 2154.0588, 2167.0801, 2220.1287, 2225.1433

18. [gi|195034208](#) Mass: 68614 Score: 118 Expect: 0.00013 Matches: 10

GH11385 [Drosophila grimshawi]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
1410.7363	1409.7290	1409.7554	-18.74	43	-	54	0	---	R.VGYELVGEIIR.L
1410.7363	1409.7290	1409.7554	-18.74	43	-	54	0	36	R.VGYELVGEIIR.L
1515.7159	1514.7086	1514.7875	-52.06	306	-	320	0	---	R.TALVANTSMPVAAR.E
1731.8138	1730.8065	1730.7934	7.59	263	-	277	0	---	K.YNSDVIIYVGCGER.G
1737.8322	1736.8249	1736.7278	55.9	514	-	527	0	---	K.DDFLQQNSYSSYDR.F
1749.8416	1748.8343	1748.8621	-15.88	321	-	335	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	321	-	335	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	362	-	378	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
2181.0813	2180.0740	2180.0671	3.18	287	-	305	1	---	R.DFPELSVEIDGVTESIMKR.T + Oxidation (M)
2209.1272	2208.1199	2208.1539	-15.39	140	-	160	0	---	K.VGSHITGGDLYGLVHENTLVK.H

No match to: 1149.5933, 1150.5878, 1150.5878, 1249.5691, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1301.6184, 1317.6819, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1698.8561, 1698.8561, 1712.8463, 1726.8776, 1733.8228, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1894.9434, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2100.0376, 2101.0217, 2115.0562, 2117.0234, 2118.0183, 2118.0183, 2146.0603, 2154.0588, 2167.0801, 2220.1287, 2225.1433

19. [gi|195118495](#) Mass: 68563 Score: 118 Expect: 0.00013 Matches: 10

uncharacterized protein Dmoj_GI18088 [Drosophila mojavensis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
1410.7363	1409.7290	1409.7554	-18.74	43	-	54	0	---	R.VGYELVGEIIR.L
1410.7363	1409.7290	1409.7554	-18.74	43	-	54	0	36	R.VGYELVGEIIR.L
1515.7159	1514.7086	1514.7875	-52.06	306	-	320	0	---	R.TALVANTSMPVAAR.E
1731.8138	1730.8065	1730.7934	7.59	263	-	277	0	---	K.YNSDVIIYVGCGER.G
1737.8322	1736.8249	1736.7278	55.9	514	-	527	0	---	K.DDFLQQNSYSSYDR.F
1749.8416	1748.8343	1748.8621	-15.88	321	-	335	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	321	-	335	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	362	-	378	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
2181.0813	2180.0740	2180.0671	3.18	287	-	305	1	---	R.DFPELSVEIDGVTESIMKR.T + Oxidation (M)
2209.1272	2208.1199	2208.1539	-15.39	140	-	160	0	---	K.VGSHITGGDLYGLVHENTLVK.H

No match to: 1149.5933, 1150.5878, 1150.5878, 1249.5691, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1301.6184, 1317.6819, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1698.8561, 1698.8561, 1712.8463, 1726.8776, 1733.8228, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1894.9434, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2100.0376, 2101.0217, 2115.0562, 2117.0234, 2118.0183, 2118.0183, 2146.0603, 2154.0588, 2167.0801, 2220.1287, 2225.1433

20. [gi|195434356](#) Mass: 68483 Score: 118 Expect: 0.00013 Matches: 10

uncharacterized protein Dwil_GK15307 [Drosophila willistoni]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
1410.7363	1409.7290	1409.7554	-18.74	43	-	54	0	---	R.VGYELVGEIIR.L
1410.7363	1409.7290	1409.7554	-18.74	43	-	54	0	36	R.VGYELVGEIIR.L

1515.7159	1514.7086	1514.7875	-52.06	306	-	320	0	---	R.TALVANTSNNMPVAAR.E
1731.8138	1730.8065	1730.7934	7.59	263	-	277	0	---	K.YNSDVIIYVGCGER.G
1737.8322	1736.8249	1736.7278	55.9	514	-	527	0	---	K.DDFLQQNSYSSYDR.F
1749.8416	1748.8343	1748.8621	-15.88	321	-	335	0	---	R.EASIYTGITLSEYFR.D
1749.8416	1748.8343	1748.8621	-15.88	321	-	335	0	46	R.EASIYTGITLSEYFR.D
1797.8328	1796.8255	1796.8403	-8.22	362	-	378	0	---	R.LAEMPADSGYPAYLGAR.L + Oxidation (M)
2181.0813	2180.0740	2180.0671	3.18	287	-	305	1	---	R.DFPELSVEIDGVTEIMKR.T + Oxidation (M)
2209.1272	2208.1199	2208.1539	-15.39	140	-	160	0	---	K.VGSHITGGDLYGLVHENTLVK.H

No match to: 1149.5933, 1150.5878, 1150.5878, 1249.5691, 1264.5995, 1268.6672, 1281.6362, 1300.6208, 1300.6208, 1301.6184, 1317.6819, 1438.7572, 1440.7452, 1467.7462, 1480.7366, 1487.7006, 1509.7490, 1530.7404, 1540.7133, 1573.7457, 1575.7825, 1585.7617, 1598.7848, 1621.7739, 1642.8068, 1645.8134, 1653.7876, 1655.8257, 1670.8300, 1672.8260, 1676.8251, 1697.8495, 1698.8561, 1698.8561, 1712.8463, 1726.8776, 1733.8228, 1746.8339, 1755.8691, 1790.8733, 1806.8781, 1809.8772, 1818.8867, 1859.8604, 1894.9434, 1926.9658, 1931.9445, 1968.9597, 2029.9998, 2077.0229, 2100.0376, 2101.0217, 2115.0562, 2117.0234, 2118.0183, 2118.0183, 2146.0603, 2154.0588, 2167.0801, 2220.1287, 2225.1433

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 : ± 80 ppm
 Fragment Mass Tolerance: ± 0.3 Da
 Max Missed Cleavages : 1
 Instrument type : MALDI-TOF-TOF

Query1 (1149.5933,1+) : <no title>
 Query2 (1150.5878,1+) : <no title>
 Query3 (1150.5878,1+) : MaldiWellID: 60693, SpectrumID: 127297,
 Query4 (1249.5691,1+) : <no title>
 Query5 (1264.5995,1+) : <no title>
 Query6 (1268.6672,1+) : <no title>
 Query7 (1281.6362,1+) : <no title>
 Query8 (1300.6208,1+) : <no title>
 Query9 (1300.6208,1+) : MaldiWellID: 60693, SpectrumID: 127296,
 Query10 (1301.6184,1+) : <no title>
 Query11 (1317.6819,1+) : <no title>
 Query12 (1410.7363,1+) : <no title>
 Query13 (1410.7363,1+) : MaldiWellID: 60693, SpectrumID: 127293,
 Query14 (1438.7572,1+) : <no title>
 Query15 (1440.7452,1+) : <no title>
 Query16 (1467.7462,1+) : <no title>
 Query17 (1480.7366,1+) : <no title>
 Query18 (1487.7006,1+) : <no title>
 Query19 (1509.7490,1+) : <no title>
 Query20 (1515.7159,1+) : <no title>
 Query21 (1530.7404,1+) : <no title>
 Query22 (1540.7133,1+) : <no title>
 Query23 (1573.7457,1+) : <no title>
 Query24 (1575.7825,1+) : <no title>
 Query25 (1585.7617,1+) : <no title>
 Query26 (1598.7848,1+) : <no title>
 Query27 (1621.7739,1+) : <no title>
 Query28 (1642.8068,1+) : <no title>
 Query29 (1645.8134,1+) : <no title>
 Query30 (1653.7876,1+) : <no title>
 Query31 (1655.8257,1+) : <no title>
 Query32 (1670.8300,1+) : <no title>
 Query33 (1672.8260,1+) : <no title>
 Query34 (1676.8251,1+) : <no title>
 Query35 (1697.8495,1+) : <no title>
 Query36 (1698.8561,1+) : <no title>
 Query37 (1698.8561,1+) : MaldiWellID: 60693, SpectrumID: 127294,
 Query38 (1712.8463,1+) : <no title>
 Query39 (1726.8776,1+) : <no title>
 Query40 (1731.8138,1+) : <no title>
 Query41 (1733.8228,1+) : <no title>
 Query42 (1737.8322,1+) : <no title>
 Query43 (1746.8339,1+) : <no title>
 Query44 (1749.8416,1+) : <no title>
 Query45 (1749.8416,1+) : MaldiWellID: 60693, SpectrumID: 127295,
 Query46 (1755.8691,1+) : <no title>
 Query47 (1790.8733,1+) : <no title>
 Query48 (1797.8328,1+) : <no title>
 Query49 (1806.8781,1+) : <no title>
 Query50 (1809.8772,1+) : <no title>
 Query51 (1818.8867,1+) : <no title>
 Query52 (1859.8604,1+) : <no title>
 Query53 (1894.9434,1+) : <no title>
 Query54 (1926.9658,1+) : <no title>
 Query55 (1931.9445,1+) : <no title>
 Query56 (1968.9597,1+) : <no title>
 Query57 (2029.9998,1+) : <no title>
 Query58 (2077.0229,1+) : <no title>
 Query59 (2100.0376,1+) : <no title>
 Query60 (2101.0217,1+) : <no title>
 Query61 (2115.0562,1+) : <no title>

Query62 (2117.0234,1+) : <no title>
Query63 (2118.0183,1+) : <no title>
Query64 (2118.0183,1+) : MaldiWellID: 60693, SpectrumID: 127298,
Query65 (2146.0603,1+) : <no title>
Query66 (2154.0588,1+) : <no title>
Query67 (2167.0801,1+) : <no title>
Query68 (2181.0813,1+) : <no title>
Query69 (2209.1272,1+) : <no title>
Query70 (2220.1287,1+) : <no title>
Query71 (2225.1433,1+) : <no title>

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