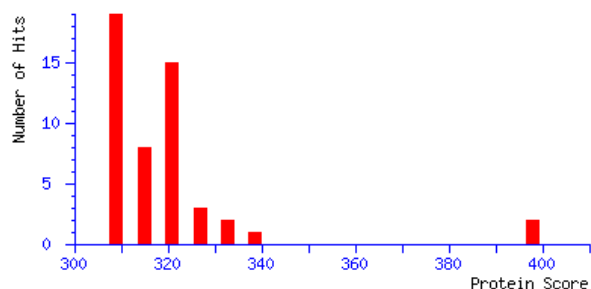


Mascot Search Results

User :
 Email :
 Search title : SampleSetID: 692, AnalysisID: 5361, MaldiWellID: 60696, SpectrumID: 127311, Path=\\161031\\MSMS\\run 65 NCBI all ok 1
 Database : NCBI nr 160208 (79581714 sequences; 29080698065 residues)
 Timestamp : 28 Nov 2016 at 12:51:59 GMT
 Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
 Top Score : 398 for gi|195402199, ATPsyn-beta [Drosophila virilis]

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 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 [Help](#)

Significance threshold $p < 0.05$ Max. number of hits

Index

Accession	Mass	Score	Description
1. gi 195402199	54241	398	ATPsyn-beta [Drosophila virilis]
2. gi 263359637	56564	397	hypothetical protein DVIR88_6g0010 [Drosophila virilis]
3. gi 909569540	40760	337	PREDICTED: ATP synthase subunit beta, mitochondrial, partial [Papilio polytes]
4. gi 157136033	53940	333	AAEL003393-PA [Aedes aegypti]
5. gi 817067126	55316	330	PREDICTED: ATP synthase subunit beta, mitochondrial [Athalia rosae]
6. gi 260800391	56311	325	hypothetical protein BRAFLDRAFT_113766 [Branchiostoma floridae]
7. gi 256387195	35746	324	ATP synthase beta subunit [Crinoidea sp. MR-2009]
8. gi 46909255	46163	324	ATP synthase beta subunit, partial [Stylochus sp. KJP-2004]
9. gi 759037183	55084	322	PREDICTED: ATP synthase subunit beta, mitochondrial [Cerapachys biroi]
10. gi 94468834	53937	322	F0F1-type ATP synthase beta subunit [Aedes aegypti]
11. gi 157132308	53878	322	AAEL002827-PA [Aedes aegypti]
12. gi 568252760	53734	321	ATP synthase beta subunit [Anopheles darlingi]
13. gi 427379097	55170	321	ecto-ATPase [Spodoptera litura]
14. gi 501291835	55635	320	ATP synthase-beta [Riptortus pedestris]
15. gi 939665174	55265	320	PREDICTED: ATP synthase subunit beta, mitochondrial [Halyomorpha halys]
16. gi 383854658	55022	320	PREDICTED: ATP synthase subunit beta, mitochondrial [Megachile rotundata]
17. gi 954551532	55087	320	PREDICTED: ATP synthase subunit beta, mitochondrial [Polistes canadensis]
18. gi 970892555	55494	319	PREDICTED: ATP synthase subunit beta, mitochondrial [Diachasma alloeum]
19. gi 340724488	54997	319	PREDICTED: ATP synthase subunit beta, mitochondrial [Bombus terrestris]
20. gi 815790072	55419	319	PREDICTED: ATP synthase subunit beta, mitochondrial [Linepithema humile]

Results List

1.	gi 195402199	Mass: 54241	Score: 398	Expect: 1.3e-032	Matches: 18
ATPsyn-beta [Drosophila virilis]					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Ions Peptide
975.5482	974.5409	974.5549	-14.37	180 - 190	0 --- K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	88 - 99	0 --- R.TIAMDGTEGLVR.G + Oxidation (M)
1406.6683	1405.6610	1405.6739	-9.14	204 - 217	0 --- K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	204 - 217	0 89 K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	289 - 302	0 --- R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	260 - 272	0 --- R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	260 - 272	0 75 R.VALTGLTVAEYFR.D
1457.7886	1456.7813	1456.8323	-35.00	191 - 203	0 --- K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	191 - 203	0 --- K.TVLIMELINNVAK.A + Oxidation (M)
1601.7986	1600.7913	1600.8031	-7.39	243 - 257	0 --- K.VALVYQGMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	243 - 257	0 --- K.VALVYQGMNEPPGAR.A + Oxidation (M)
1677.8896	1676.8823	1676.9210	-23.04	73 - 87	0 --- R.LVLEVAQHLGENTVR.T
1917.9587	1916.9514	1916.9778	-13.77	240 - 257	1 --- K.TSKVALVYQGMNEPPGAR.A

1922.9504 1921.9431 1921.9422 0.50 273 - 288 0 --- R.DEEGQDVLLFIDNIFR.F
 1922.9504 1921.9431 1921.9422 0.50 273 - 288 0 97 R.DEEGQDVLLFIDNIFR.F
 1951.0226 1950.0153 1950.0898 -38.21 103 - 121 1 --- K.VLDTGSPIRIPVGAETLGR.I
 1988.0200 1987.0127 1987.0262 -6.78 366 - 384 0 --- R.AIAELGIYPAVDPLDSTSR.I
 1988.0200 1987.0127 1987.0262 -6.78 366 - 384 0 59 R.AIAELGIYPAVDPLDSTSR.I
 No match to: 1189.5919, 1300.6198, 1301.6213, 1367.7294, 1376.7365, 1395.7634, 1396.7566, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1463.7360, 1467.7928, 1492.7432, 1496.7778, 1515.7438, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1842.9082, 1921.9567, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2225.1423, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

2. [gi|263359637](#) Mass: 56564 Score: 397 Expect: 1.6e-032 Matches: 18

hypothetical protein DVIR88_6g0010 [Drosophila virilis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
975.5482	974.5409	974.5549	-14.37	200	210	0	---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	108	119	0	---	R.TIAMDGTGLVR.G + Oxidation (M)
1406.6683	1405.6610	1405.6739	-9.14	224	237	0	---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	224	237	0	89	K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	309	322	0	---	R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	280	292	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	280	292	0	75	R.VALTGLTVAEYFR.D
1457.7886	1456.7813	1456.8323	-35.00	211	223	0	---	K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	211	223	0	---	K.TVLIMELINNVAK.A + Oxidation (M)
1601.7986	1600.7913	1600.8031	-7.39	263	277	0	---	K.VALVYQMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	263	277	0	---	K.VALVYQMNEPPGAR.A + Oxidation (M)
1677.8896	1676.8823	1676.9210	-23.04	93	107	0	---	R.LVLEVAQHLGENTVR.T
1917.9587	1916.9514	1916.9778	-13.77	260	277	1	---	K.TSKVALVYQMNEPPGAR.A
1922.9504	1921.9431	1921.9422	0.50	293	308	0	---	R.DEEGQDVLLFIDNIFR.F
1922.9504	1921.9431	1921.9422	0.50	293	308	0	97	R.DEEGQDVLLFIDNIFR.F
1951.0226	1950.0153	1950.0898	-38.21	123	141	1	---	K.VLDTGSPIRIPVGAETLGR.I
1988.0200	1987.0127	1987.0262	-6.78	386	404	0	---	R.AIAELGIYPAVDPLDSTSR.I
1988.0200	1987.0127	1987.0262	-6.78	386	404	0	59	R.AIAELGIYPAVDPLDSTSR.I

No match to: 1189.5919, 1300.6198, 1301.6213, 1367.7294, 1376.7365, 1395.7634, 1396.7566, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1463.7360, 1467.7928, 1492.7432, 1496.7778, 1515.7438, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1842.9082, 1921.9567, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2225.1423, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

3. [gi|909569540](#) Mass: 40760 Score: 337 Expect: 1.6e-026 Matches: 19

PREDICTED: ATP synthase subunit beta, mitochondrial, partial [Papilio polytes]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
975.5482	974.5409	974.5549	-14.37	126	136	0	---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	34	45	0	---	R.TIAMDGTGLVR.G + Oxidation (M)
1367.7294	1366.7221	1366.7456	-17.18	68	79	0	---	R.IINVIGEPIDER.G
1406.6683	1405.6610	1405.6739	-9.14	150	163	0	---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	150	163	0	89	K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	235	248	0	---	R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	206	218	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	206	218	0	75	R.VALTGLTVAEYFR.D
1457.7886	1456.7813	1456.8323	-35.00	137	149	0	---	K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	137	149	0	---	K.TVLIMELINNVAK.A + Oxidation (M)
1601.7986	1600.7913	1600.8031	-7.39	189	203	0	---	K.VALVYQMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	189	203	0	---	K.VALVYQMNEPPGAR.A + Oxidation (M)
1677.8896	1676.8823	1676.9210	-23.04	19	33	0	---	R.LVLEVAQHLGENTVR.T
1705.9220	1704.9147	1704.9158	-0.66	1	15	0	---	-DNLPPILNALEVQNR.S
1917.9587	1916.9514	1916.9778	-13.77	186	203	1	---	K.TSKVALVYQMNEPPGAR.A
1921.9567	1920.9494	1920.9581	-4.54	219	234	0	---	R.DQEGQDVLLFIDNIFR.F
1988.0200	1987.0127	1987.0262	-6.78	312	330	0	---	R.AIAELGIYPAVDPLDSTSR.I
1988.0200	1987.0127	1987.0262	-6.78	312	330	0	59	R.AIAELGIYPAVDPLDSTSR.I
2225.1423	2224.1350	2224.1422	-3.25	331	350	1	---	R.IMDPNIIGAETHYVARGVQK.I

No match to: 1189.5919, 1300.6198, 1301.6213, 1376.7365, 1395.7634, 1396.7566, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1463.7360, 1467.7928, 1492.7432, 1496.7778, 1515.7438, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1842.9082, 1922.9504, 1922.9504, 1951.0226, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

4. [gi|157136033](#) Mass: 53940 Score: 333 Expect: 4e-026 Matches: 20

AAEL003393-PA [Aedes aegypti]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
975.5482	974.5409	974.5549	-14.37	178	188	0	---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	86	97	0	---	R.TIAMDGTGLVR.G + Oxidation (M)
1367.7294	1366.7221	1366.7456	-17.18	120	131	0	---	R.IINVIGEPIDER.G
1406.6683	1405.6610	1405.6739	-9.14	202	215	0	---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	202	215	0	89	K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	287	300	0	---	R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	258	270	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	258	270	0	75	R.VALTGLTVAEYFR.D
1457.7886	1456.7813	1456.8323	-35.00	189	201	0	---	K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	189	201	0	---	K.TVLIMELINNVAK.A + Oxidation (M)

1520.7416 1519.7343 1519.8140 -52.45 1 - 14 1 --- -.MLSSLRNVLSTGSR.V
 1601.7986 1600.7913 1600.8031 -7.39 241 - 255 0 --- K.VALVYQGMNEPPGAR.A
 1617.7932 1616.7859 1616.7981 -7.51 241 - 255 0 --- K.VALVYQGMNEPPGAR.A + Oxidation (M)
 1677.8896 1676.8823 1676.9210 -23.04 71 - 85 0 --- R.LVLEVAQHLGENTVR.T
 1842.9082 1841.9009 1841.9094 -4.59 383 - 398 0 --- R.IMDPNIIGAEHYNIAR.G + Oxidation (M)
 1917.9587 1916.9514 1916.9778 -13.77 238 - 255 1 --- K.TSKVALVYQGMNEPPGAR.A
 1921.9567 1920.9494 1920.9581 -4.54 271 - 286 0 --- R.DQEGQDVLFLIDNIFR.F
 1951.0226 1950.0153 1950.0898 -38.21 101 - 119 1 --- R.VLDTGSPIRIPVGAETLGR.I
 1988.0200 1987.0127 1987.0262 -6.78 364 - 382 0 --- R.AIAELGIYPAVDPLDSTSR.I
 1988.0200 1987.0127 1987.0262 -6.78 364 - 382 0 59 R.AIAELGIYPAVDPLDSTSR.I

No match to: 1189.5919, 1300.6198, 1301.6213, 1376.7365, 1395.7634, 1396.7566, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1463.7360, 1467.7928, 1492.7432, 1496.7778, 1515.7438, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1922.9504, 1922.9504, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2225.1423, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

5. [gi|817067126](#) Mass: 55316 Score: 330 Expect: 8e-026 Matches: 20

PREDICTED: ATP synthase subunit beta, mitochondrial [Athalia rosae]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
975.5482	974.5409	974.5549	-14.37	195	205	0	---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	103	114	0	---	R.TIAMDGTEGLVR.G + Oxidation (M)
1367.7294	1366.7221	1366.7456	-17.18	137	148	0	---	R.IINVIGEPIDER.G
1395.7634	1394.7561	1394.8497	-67.08	16	28	0	---	R.VVKPVLLQTEAAK.V
1406.6683	1405.6610	1405.6739	-9.14	219	232	0	---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	219	232	0	89	K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	304	317	0	---	R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	275	287	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	275	287	0	75	R.VALTGLTVAEYFR.D
1457.7886	1456.7813	1456.8323	-35.00	206	218	0	---	K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	206	218	0	---	K.TVLIMELINNVAK.A + Oxidation (M)
1492.7432	1491.7359	1491.7901	-36.33	1	15	1	---	-.MMLSAVSKAASGALR.V
1601.7986	1600.7913	1600.8031	-7.39	258	272	0	---	K.VALVYQGMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	258	272	0	---	K.VALVYQGMNEPPGAR.A + Oxidation (M)
1677.8896	1676.8823	1676.9210	-23.04	88	102	0	---	R.LVLEVAQHLGENTVR.T
1842.9082	1841.9009	1841.9094	-4.59	400	415	0	---	R.IMDPNIIGAEHYNIAR.N + Oxidation (M)
1917.9587	1916.9514	1916.9778	-13.77	255	272	1	---	K.TSKVALVYQGMNEPPGAR.A
1921.9567	1920.9494	1920.9581	-4.54	288	303	0	---	R.DQEGQDVLFLIDNIFR.F
1988.0200	1987.0127	1987.0262	-6.78	381	399	0	---	R.AIAELGIYPAVDPLDSTSR.I
1988.0200	1987.0127	1987.0262	-6.78	381	399	0	59	R.AIAELGIYPAVDPLDSTSR.I

No match to: 1189.5919, 1300.6198, 1301.6213, 1376.7365, 1396.7566, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1463.7360, 1467.7928, 1496.7778, 1515.7438, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1922.9504, 1922.9504, 1951.0226, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2225.1423, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

6. [gi|260800391](#) Mass: 56311 Score: 325 Expect: 2.5e-025 Matches: 16

hypothetical protein BRAFLDRAFT_113766 [Branchiostoma floridae]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
975.5482	974.5409	974.5549	-14.37	198	208	0	---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	106	117	0	---	R.TIAMDGTEGLVR.G + Oxidation (M)
1367.7294	1366.7221	1366.7456	-17.18	140	151	0	---	R.IINVIGEPIDER.G
1406.6683	1405.6610	1405.6739	-9.14	222	235	0	---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	222	235	0	89	K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	307	320	0	---	R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	278	290	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	278	290	0	75	R.VALTGLTVAEYFR.D
1457.7886	1456.7813	1456.8323	-35.00	209	221	0	---	K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	209	221	0	---	K.TVLIMELINNVAK.A + Oxidation (M)
1601.7986	1600.7913	1600.8031	-7.39	261	275	0	---	K.VALVYQGMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	261	275	0	---	K.VALVYQGMNEPPGAR.A + Oxidation (M)
1677.8896	1676.8823	1676.9210	-23.04	91	105	0	---	R.LILEVAQHLGDNTVR.T
1922.9504	1921.9431	1921.9422	0.50	291	306	0	---	R.DEEGQDVLFLIDNIFR.F
1922.9504	1921.9431	1921.9422	0.50	291	306	0	97	R.DEEGQDVLFLIDNIFR.F
1951.0226	1950.0153	1950.0422	-13.78	140	157	1	---	R.IINVIGEPIDERGPVDSK.K

No match to: 1189.5919, 1300.6198, 1301.6213, 1376.7365, 1395.7634, 1396.7566, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1463.7360, 1467.7928, 1492.7432, 1496.7778, 1515.7438, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1842.9082, 1917.9587, 1921.9567, 1988.0200, 1988.0200, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2225.1423, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

7. [gi|256387195](#) Mass: 35746 Score: 324 Expect: 3.2e-025 Matches: 14

ATP synthase beta subunit [Crinoidea sp. MR-2009]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
975.5482	974.5409	974.5549	-14.37	81	91	0	---	K.IGLFGGAGVGK.T
1367.7294	1366.7221	1366.7456	-17.18	23	34	0	---	R.IINVIGEPIDER.G
1406.6683	1405.6610	1405.6739	-9.14	105	118	0	---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	105	118	0	89	K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	190	203	0	---	R.FTQAGSEVSALLGR.I

1439.7766	1438.7693	1438.7820	-8.82	161	-	173	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	161	-	173	0	75	R.VALTGLTVAEYFR.D
1601.7986	1600.7913	1600.8031	-7.39	144	-	158	0	---	K.VALVYQGMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	144	-	158	0	---	K.VALVYQGMNEPPGAR.A + Oxidation (M)
1922.9504	1921.9431	1921.9422	0.50	174	-	189	0	---	R.DEEGQDVLLFIDNIFR.F
1922.9504	1921.9431	1921.9422	0.50	174	-	189	0	97	R.DEEGQDVLLFIDNIFR.F
2118.0178	2117.0105	2117.1480	-64.95	23	-	41	1	---	R.IINVIGEPIDERGPITER.R
2118.0178	2117.0105	2117.1480	-64.95	23	-	41	1	---	R.IINVIGEPIDERGPITER.R
2348.1704	2347.1631	2347.1002	26.8	121	-	141	1	---	R.EGNDLYHEMIEGGVIDLKGDK.S + Oxidation (M)

No match to: 1189.5919, 1278.6581, 1300.6198, 1301.6213, 1376.7365, 1395.7634, 1396.7566, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1457.7886, 1463.7360, 1467.7928, 1473.8118, 1492.7432, 1496.7778, 1515.7438, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1677.8896, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1842.9082, 1917.9587, 1921.9567, 1951.0226, 1988.0200, 1988.0200, 2016.0498, 2117.0474, 2147.0840, 2225.1423, 2330.1760, 2366.1665, 2367.1624, 3154.5486, 3211.5518

8. [gi|46909255](#) Mass: 46163 Score: 324 Expect: 3.2e-025 Matches: 15

ATP synthase beta subunit, partial [Stylochus sp. KJP-2004]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
975.5482	974.5409	974.5549	-14.37	125	-	135	0	---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	33	-	44	0	---	R.TIAMDGTEGLVR.G + Oxidation (M)
1367.7294	1366.7221	1366.7456	-17.18	67	-	78	0	---	R.IINVIGEPIDER.G
1406.6683	1405.6610	1405.6739	-9.14	149	-	162	0	---	R.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	149	-	162	0	89	R.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	234	-	247	0	---	R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	205	-	217	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	205	-	217	0	75	R.VALTGLTVAEYFR.D
1515.7438	1514.7365	1514.8490	-74.26	136	-	148	0	---	K.TVLIMELINNIAR.A + Oxidation (M)
1601.7986	1600.7913	1600.8031	-7.39	188	-	202	0	---	K.VALVYQGMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	188	-	202	0	---	K.VALVYQGMNEPPGAR.A + Oxidation (M)
1922.9504	1921.9431	1921.9422	0.50	218	-	233	0	---	R.DEEGQDVLLFIDNIFR.F
1922.9504	1921.9431	1921.9422	0.50	218	-	233	0	97	R.DEEGQDVLLFIDNIFR.F
2118.0178	2117.0105	2117.0324	-10.32	183	-	202	1	---	K.GNNSKVALVYQGMNEPPGAR.A + Oxidation (M)
2118.0178	2117.0105	2117.0324	-10.32	183	-	202	1	---	K.GNNSKVALVYQGMNEPPGAR.A + Oxidation (M)

No match to: 1189.5919, 1300.6198, 1301.6213, 1376.7365, 1395.7634, 1396.7566, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1457.7886, 1463.7360, 1467.7928, 1473.8118, 1492.7432, 1496.7778, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1677.8896, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1842.9082, 1917.9587, 1921.9567, 1951.0226, 1988.0200, 1988.0200, 2016.0498, 2117.0474, 2147.0840, 2225.1423, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

9. [gi|759037183](#) Mass: 55084 Score: 322 Expect: 5e-025 Matches: 19

PREDICTED: ATP synthase subunit beta, mitochondrial [Ceratophyllum demersum]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
975.5482	974.5409	974.5549	-14.37	191	-	201	0	---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	99	-	110	0	---	R.TIAMDGTEGLVR.G + Oxidation (M)
1367.7294	1366.7221	1366.7456	-17.18	133	-	144	0	---	R.IINVIGEPIDER.G
1406.6683	1405.6610	1405.6739	-9.14	215	-	228	0	---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	215	-	228	0	89	K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	300	-	313	0	---	R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	271	-	283	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	271	-	283	0	75	R.VALTGLTVAEYFR.D
1457.7886	1456.7813	1456.8323	-35.00	202	-	214	0	---	K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	202	-	214	0	---	K.TVLIMELINNVAK.A + Oxidation (M)
1601.7986	1600.7913	1600.8031	-7.39	254	-	268	0	---	K.VALVYQGMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	254	-	268	0	---	K.VALVYQGMNEPPGAR.A + Oxidation (M)
1677.8896	1676.8823	1676.9210	-23.04	84	-	98	0	---	R.LVLEVAQHLGENTVR.T
1917.9587	1916.9514	1916.9778	-13.77	251	-	268	1	---	K.TSKVALVYQGMNEPPGAR.A
1921.9567	1920.9494	1920.9581	-4.54	284	-	299	0	---	R.DQEGQDVLLFIDNIFR.F
1988.0200	1987.0127	1987.0262	-6.78	377	-	395	0	---	R.AIAELGIYPAVDPLDSTSR.I
1988.0200	1987.0127	1987.0262	-6.78	377	-	395	0	59	R.AIAELGIYPAVDPLDSTSR.I
2225.1423	2224.1350	2224.1422	-3.25	396	-	415	1	---	R.IMDPNIIGGEHYNIARGVQK.I
2330.1760	2329.1687	2329.2179	-21.11	111	-	132	1	---	R.GQNVFDSGFPRIIPVGAETLGR.I

No match to: 1189.5919, 1300.6198, 1301.6213, 1376.7365, 1395.7634, 1396.7566, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1463.7360, 1467.7928, 1492.7432, 1496.7778, 1515.7438, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1842.9082, 1922.9504, 1922.9504, 1951.0226, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

10. [gi|94468834](#) Mass: 53937 Score: 322 Expect: 5e-025 Matches: 19

F0F1-type ATP synthase beta subunit [Aedes aegypti]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
975.5482	974.5409	974.5549	-14.37	178	-	188	0	---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	86	-	97	0	---	R.TIAMDGTEGLVR.G + Oxidation (M)
1367.7294	1366.7221	1366.7456	-17.18	120	-	131	0	---	R.IINVIGEPIDER.G
1406.6683	1405.6610	1405.6739	-9.14	202	-	215	0	---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	202	-	215	0	89	K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	287	-	300	0	---	R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	258	-	270	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	258	-	270	0	75	R.VALTGLTVAEYFR.D

1457.7886	1456.7813	1456.8323	-35.00	189	-	201	0	---	K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	189	-	201	0	---	K.TVLIMELINNVAK.A + Oxidation (M)
1601.7986	1600.7913	1600.8031	-7.39	241	-	255	0	---	K.VALVYQGMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	241	-	255	0	---	K.VALVYQGMNEPPGAR.A + Oxidation (M)
1677.8896	1676.8823	1676.9210	-23.04	71	-	85	0	---	R.LVLEVAQHLGENTVR.T
1842.9082	1841.9009	1841.9094	-4.59	383	-	398	0	---	R.IMDPNIIGAEHYNIAR.G + Oxidation (M)
1917.9587	1916.9514	1916.9778	-13.77	238	-	255	1	---	K.TSKVALVYQGMNEPPGAR.A
1921.9567	1920.9494	1920.9581	-4.54	271	-	286	0	---	R.DQEGQDVLLFIDNIFR.F
1951.0226	1950.0153	1950.0898	-38.21	101	-	119	1	---	R.VLDTGSPIRIPVGAETLGR.I
1988.0200	1987.0127	1987.0262	-6.78	364	-	382	0	---	R.AIAELGIYPAVDPLDSTSR.I
1988.0200	1987.0127	1987.0262	-6.78	364	-	382	0	59	R.AIAELGIYPAVDPLDSTSR.I

No match to: 1189.5919, 1300.6198, 1301.6213, 1376.7365, 1395.7634, 1396.7566, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1463.7360, 1467.7928, 1492.7432, 1496.7778, 1515.7438, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1922.9504, 1922.9504, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2225.1423, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

11. [gi|157132308](#) Mass: 53878 Score: 322 Expect: 5e-025 Matches: 19

AAEL002827-PA [Aedes aegypti]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
975.5482	974.5409	974.5549	-14.37	178	-	188	0	---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	86	-	97	0	---	R.TIAMDGTEGLVR.G + Oxidation (M)
1367.7294	1366.7221	1366.7456	-17.18	120	-	131	0	---	R.IINVIGEPIDER.G
1406.6683	1405.6610	1405.6739	-9.14	202	-	215	0	---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	202	-	215	0	89	K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	287	-	300	0	---	R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	258	-	270	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	258	-	270	0	75	R.VALTGLTVAEYFR.D
1457.7886	1456.7813	1456.8323	-35.00	189	-	201	0	---	K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	189	-	201	0	---	K.TVLIMELINNVAK.A + Oxidation (M)
1601.7986	1600.7913	1600.8031	-7.39	241	-	255	0	---	K.VALVYQGMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	241	-	255	0	---	K.VALVYQGMNEPPGAR.A + Oxidation (M)
1677.8896	1676.8823	1676.9210	-23.04	71	-	85	0	---	R.LVLEVAQHLGENTVR.T
1842.9082	1841.9009	1841.9094	-4.59	383	-	398	0	---	R.IMDPNIIGAEHYNIAR.G + Oxidation (M)
1917.9587	1916.9514	1916.9778	-13.77	238	-	255	1	---	K.TSKVALVYQGMNEPPGAR.A
1921.9567	1920.9494	1920.9581	-4.54	271	-	286	0	---	R.DQEGQDVLLFIDNIFR.F
1951.0226	1950.0153	1950.0898	-38.21	101	-	119	1	---	R.VLDTGSPIRIPVGAETLGR.I
1988.0200	1987.0127	1987.0262	-6.78	364	-	382	0	---	R.AIAELGIYPAVDPLDSTSR.I
1988.0200	1987.0127	1987.0262	-6.78	364	-	382	0	59	R.AIAELGIYPAVDPLDSTSR.I

No match to: 1189.5919, 1300.6198, 1301.6213, 1376.7365, 1395.7634, 1396.7566, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1463.7360, 1467.7928, 1492.7432, 1496.7778, 1515.7438, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1922.9504, 1922.9504, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2225.1423, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

12. [gi|568252760](#) Mass: 53734 Score: 321 Expect: 6.3e-025 Matches: 19

ATP synthase beta subunit [Anopheles darlingi]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
975.5482	974.5409	974.5549	-14.37	177	-	187	0	---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	85	-	96	0	---	R.TIAMDGTEGLVR.G + Oxidation (M)
1367.7294	1366.7221	1366.7456	-17.18	119	-	130	0	---	R.IINVIGEPIDER.G
1396.7566	1395.7493	1395.7544	-3.64	2	-	14	1	---	M.FSSMKTLVSAAVR.A
1406.6683	1405.6610	1405.6739	-9.14	201	-	214	0	---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	201	-	214	0	89	K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	286	-	299	0	---	R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	257	-	269	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	257	-	269	0	75	R.VALTGLTVAEYFR.D
1457.7886	1456.7813	1456.8323	-35.00	188	-	200	0	---	K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	188	-	200	0	---	K.TVLIMELINNVAK.A + Oxidation (M)
1601.7986	1600.7913	1600.8031	-7.39	240	-	254	0	---	K.VALVYQGMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	240	-	254	0	---	K.VALVYQGMNEPPGAR.A + Oxidation (M)
1677.8896	1676.8823	1676.9210	-23.04	70	-	84	0	---	R.LVLEVAQHLGENTVR.T
1842.9082	1841.9009	1841.9094	-4.59	382	-	397	0	---	R.IMDPNIIGAEHYNIAR.G + Oxidation (M)
1921.9567	1920.9494	1920.9581	-4.54	270	-	285	0	---	R.DQEGQDVLLFIDNIFR.F
1951.0226	1950.0153	1950.0898	-38.21	100	-	118	1	---	R.VLDTGSPIRIPVGAETLGR.I
1988.0200	1987.0127	1987.0262	-6.78	363	-	381	0	---	R.AIAELGIYPAVDPLDSTSR.I
1988.0200	1987.0127	1987.0262	-6.78	363	-	381	0	59	R.AIAELGIYPAVDPLDSTSR.I

No match to: 1189.5919, 1300.6198, 1301.6213, 1376.7365, 1395.7634, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1463.7360, 1467.7928, 1492.7432, 1496.7778, 1515.7438, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1917.9587, 1922.9504, 1922.9504, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2225.1423, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

13. [gi|427379097](#) Mass: 55170 Score: 321 Expect: 6.3e-025 Matches: 19

ecto-ATPase [Spodoptera litura]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
975.5482	974.5409	974.5549	-14.37	192	-	202	0	---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	100	-	111	0	---	R.TIAMDGTEGLVR.G + Oxidation (M)

1367.7294	1366.7221	1366.7456	-17.18	134	-	145	0	---	R.IINVIGEPIDER.G
1406.6683	1405.6610	1405.6739	-9.14	216	-	229	0	---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	216	-	229	0	89	K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	301	-	314	0	---	R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	272	-	284	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	272	-	284	0	75	R.VALTGLTVAEYFR.D
1457.7886	1456.7813	1456.8323	-35.00	203	-	215	0	---	K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	203	-	215	0	---	K.TVLIMELINNVAK.A + Oxidation (M)
1601.7986	1600.7913	1600.8031	-7.39	255	-	269	0	---	K.VALVYQMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	255	-	269	0	---	K.VALVYQMNEPPGAR.A + Oxidation (M)
1677.8896	1676.8823	1676.9210	-23.04	85	-	99	0	---	R.LVLEVAQHLGENTVR.T
1705.9220	1704.9147	1704.9080	3.94	22	-	37	1	---	K.TLTECGKIATVSAINK.R
1917.9587	1916.9514	1916.9778	-13.77	252	-	269	1	---	K.TSKVALVYQMNEPPGAR.A
1921.9567	1920.9494	1920.9581	-4.54	285	-	300	0	---	R.DQEGQDVLFLIDNIFR.F
1988.0200	1987.0127	1987.0262	-6.78	378	-	396	0	---	R.AIAELGIYPAVDPLDSTSR.I
1988.0200	1987.0127	1987.0262	-6.78	378	-	396	0	59	R.AIAELGIYPAVDPLDSTSR.I
2225.1423	2224.1350	2224.1422	-3.25	397	-	416	1	---	R.IMPNIIGAHEHYNVARGVQK.I

No match to: 1189.5919, 1300.6198, 1301.6213, 1376.7365, 1395.7634, 1396.7566, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1463.7360, 1467.7928, 1492.7432, 1496.7778, 1515.7438, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1842.9082, 1922.9504, 1922.9504, 1951.0226, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

14. [gi|501291835](#) Mass: 55635 Score: 320 Expect: 8e-025 Matches: 19

ATP synthase-beta [Riptortus pedestris]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
975.5482	974.5409	974.5549	-14.37	195	-	205	0 ---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	103	-	114	0 ---	R.TIAMDGTGLVLR.G + Oxidation (M)
1367.7294	1366.7221	1366.7456	-17.18	137	-	148	0 ---	R.IINVIGEPIDER.G
1406.6683	1405.6610	1405.6739	-9.14	219	-	232	0 ---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	219	-	232	0 89	K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	304	-	317	0 ---	R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	275	-	287	0 ---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	275	-	287	0 75	R.VALTGLTVAEYFR.D
1457.7886	1456.7813	1456.8323	-35.00	206	-	218	0 ---	K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	206	-	218	0 ---	K.TVLIMELINNVAK.A + Oxidation (M)
1582.8214	1581.8141	1581.7998	9.04	32	-	48	0 ---	R.TAGALSATSYATAAQAK.T
1601.7986	1600.7913	1600.8031	-7.39	258	-	272	0 ---	K.VALVYQMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	258	-	272	0 ---	K.VALVYQMNEPPGAR.A + Oxidation (M)
1677.8896	1676.8823	1676.9210	-23.04	88	-	102	0 ---	R.LVLEVAQHLGENTVR.T
1917.9587	1916.9514	1916.9778	-13.77	255	-	272	1 ---	K.TSKVALVYQMNEPPGAR.A
1921.9567	1920.9494	1920.9581	-4.54	288	-	303	0 ---	R.DQEGQDVLFLFDNIFR.F
1988.0200	1987.0127	1987.0262	-6.78	381	-	399	0 ---	R.AIAELGIYPAVDPLDSTSR.I
1988.0200	1987.0127	1987.0262	-6.78	381	-	399	0 59	R.AIAELGIYPAVDPLDSTSR.I
2225.1423	2224.1350	2224.1422	-3.25	400	-	419	1 ---	R.IMDPNIIGAEGHYNVARGVQK.I

No match to: 1189.5919, 1300.6198, 1301.6213, 1376.7365, 1395.7634, 1396.7566, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1463.7360, 1467.7928, 1492.7432, 1496.7778, 1515.7438, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1842.9082, 1922.9504, 1922.9504, 1951.0226, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

15. [gi|939665174](#) Mass: 55265 Score: 320 Expect: 8e-025 Matches: 19

PREDICTED: ATP synthase subunit beta, mitochondrial [Halyomorpha halys]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
975.5482	974.5409	974.5549	-14.37	191	- 201	0	---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	99	- 110	0	---	R.TIAMDGTGLVR.G + Oxidation (M)
1367.7294	1366.7221	1366.7456	-17.18	133	- 144	0	---	R.IINVIGEPIDER.G
1406.6683	1405.6610	1405.6739	-9.14	215	- 228	0	---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	215	- 228	0	89	K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	300	- 313	0	---	R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	271	- 283	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	271	- 283	0	75	R.VALTGLTVAEYFR.D
1457.7886	1456.7813	1456.8323	-35.00	202	- 214	0	---	K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	202	- 214	0	---	K.TVLIMELINNVAK.A + Oxidation (M)
1582.8214	1581.8141	1581.8474	-21.05	18	- 31	0	---	K.SSLNPQLLQNEALR.C
1601.7986	1600.7913	1600.8031	-7.39	254	- 268	0	---	K.VALVYQMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	254	- 268	0	---	K.VALVYQMNEPPGAR.A + Oxidation (M)
1677.8896	1676.8823	1676.9210	-23.04	84	- 98	0	---	R.LVLEVAQHLGENTVR.T
1917.9587	1916.9514	1916.9778	-13.77	251	- 268	1	---	K.TSKVALVYQMNEPPGAR.A
1921.9567	1920.9494	1920.9581	-4.54	284	- 299	0	---	R.DQEGQDVLFLIDNIFR.F
1988.0200	1987.0127	1987.0262	-6.78	377	- 395	0	---	R.AIAELGIYPAVDPLDSTSR.I
1988.0200	1987.0127	1987.0262	-6.78	377	- 395	0	59	R.AIAELGIYPAVDPLDSTSR.I
2225.1423	2224.1350	2224.1422	-3.25	396	- 415	1	---	R.IMDPNIIGAHEHYNVARGVQK.I

No match to: 1189.5919, 1300.6198, 1301.6213, 1376.7365, 1395.7634, 1396.7566, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1463.7360, 1467.7928, 1492.7432, 1496.7778, 1515.7438, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1842.9082, 1922.9504, 1922.9504, 1951.0226, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

16. [gi|383854658](#) Mass: 55022 Score: 320 Expect: 8e-025 Matches: 19

PREDICTED: ATP synthase subunit beta, mitochondrial [Megachile rotundata]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
975.5482	974.5409	974.5549	-14.37	192	202	0	---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	100	111	0	---	R.TIAMDGTEGLVR.G + Oxidation (M)
1367.7294	1366.7221	1366.7456	-17.18	134	145	0	---	R.IINVIGEPIDER.G
1406.6683	1405.6610	1405.6739	-9.14	216	229	0	---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	216	229	0	89	K.AHGGYSVFAGVGER.T
1410.7430	1409.7357	1409.8242	-62.75	15	27	0	---	R.AVKPTLLQNEVAK.I
1435.7267	1434.7194	1434.7467	-19.00	301	314	0	---	R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	272	284	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	272	284	0	75	R.VALTGLTVAEYFR.D
1457.7886	1456.7813	1456.8323	-35.00	203	215	0	---	K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	203	215	0	---	K.TVLIMELINNVAK.A + Oxidation (M)
1601.7986	1600.7913	1600.8031	-7.39	255	269	0	---	K.VALVYGMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	255	269	0	---	K.VALVYGMNEPPGAR.A + Oxidation (M)
1677.8896	1676.8823	1676.9210	-23.04	85	99	0	---	R.LVLEVAQHLGENTVR.T
1917.9587	1916.9514	1916.9778	-13.77	252	269	1	---	K.TSKVALVYGMNEPPGAR.A
1921.9567	1920.9494	1920.9581	-4.54	285	300	0	---	R.DQEGQDVLFLIDNIFR.F
1988.0200	1987.0127	1987.0262	-6.78	378	396	0	---	R.AIAELGIYPAVDPLDSTSR.I
1988.0200	1987.0127	1987.0262	-6.78	378	396	0	59	R.AIAELGIYPAVDPLDSTSR.I
2225.1423	2224.1350	2224.1422	-3.25	397	416	1	---	R.IMPNIIGAETHYNAVARGVQK.I

No match to: 1189.5919, 1300.6198, 1301.6213, 1376.7365, 1395.7634, 1396.7566, 1404.7286, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1463.7360, 1467.7928, 1492.7432, 1496.7778, 1515.7438, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1842.9082, 1922.9504, 1922.9504, 1951.0226, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

17. [gi|954551532](#) Mass: 55087 Score: 320 Expect: 8e-025 Matches: 19

PREDICTED: ATP synthase subunit beta, mitochondrial [Polistes canadensis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
975.5482	974.5409	974.5549	-14.37	192	202	0	---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	100	111	0	---	R.TIAMDGTEGLVR.G + Oxidation (M)
1367.7294	1366.7221	1366.7456	-17.18	134	145	0	---	R.IINVIGEPIDER.G
1406.6683	1405.6610	1405.6739	-9.14	216	229	0	---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	216	229	0	89	K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	301	314	0	---	R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	272	284	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	272	284	0	75	R.VALTGLTVAEYFR.D
1457.7886	1456.7813	1456.8323	-35.00	203	215	0	---	K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	203	215	0	---	K.TVLIMELINNVAK.A + Oxidation (M)
1520.7416	1519.7343	1519.7963	-40.76	1	15	1	---	-.MMLSAVSRAAAGALR.A + Oxidation (M)
1601.7986	1600.7913	1600.8031	-7.39	255	269	0	---	K.VALVYGMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	255	269	0	---	K.VALVYGMNEPPGAR.A + Oxidation (M)
1677.8896	1676.8823	1676.9210	-23.04	85	99	0	---	R.LVLEVAQHLGENTVR.T
1842.9082	1841.9009	1841.9094	-4.59	397	412	0	---	R.IMPNIIGAETHYNIAR.G + Oxidation (M)
1917.9587	1916.9514	1916.9778	-13.77	252	269	1	---	K.TSKVALVYGMNEPPGAR.A
1921.9567	1920.9494	1920.9581	-4.54	285	300	0	---	R.DQEGQDVLFLIDNIFR.F
1988.0200	1987.0127	1987.0262	-6.78	378	396	0	---	R.AIAELGIYPAVDPLDSTSR.I
1988.0200	1987.0127	1987.0262	-6.78	378	396	0	59	R.AIAELGIYPAVDPLDSTSR.I

No match to: 1189.5919, 1300.6198, 1301.6213, 1376.7365, 1395.7634, 1396.7566, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1463.7360, 1467.7928, 1492.7432, 1496.7778, 1515.7438, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1922.9504, 1922.9504, 1951.0226, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2225.1423, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

18. [gi|970892555](#) Mass: 55494 Score: 319 Expect: 1e-024 Matches: 19

PREDICTED: ATP synthase subunit beta, mitochondrial [Diachasma alloeum]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
975.5482	974.5409	974.5549	-14.37	196	206	0	---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	104	115	0	---	R.TIAMDGTEGLVR.G + Oxidation (M)
1367.7294	1366.7221	1366.7456	-17.18	138	149	0	---	R.IINVIGEPIDER.G
1406.6683	1405.6610	1405.6739	-9.14	220	233	0	---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	220	233	0	89	K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	305	318	0	---	R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	276	288	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	276	288	0	75	R.VALTGLTVAEYFR.D
1457.7886	1456.7813	1456.8323	-35.00	207	219	0	---	K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	207	219	0	---	K.TVLIMELINNVAK.A + Oxidation (M)
1492.7432	1491.7359	1491.7901	-36.33	1	15	1	---	-.MMLSAVSKAAAGALR.A + Oxidation (M)
1601.7986	1600.7913	1600.8031	-7.39	259	273	0	---	K.VALVYGMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	259	273	0	---	K.VALVYGMNEPPGAR.A + Oxidation (M)
1677.8896	1676.8823	1676.9210	-23.04	89	103	0	---	R.LVLEVAQHLGENTVR.T
1842.9082	1841.9009	1841.9094	-4.59	401	416	0	---	R.IMPNIIGAETHYNIAR.G + Oxidation (M)
1917.9587	1916.9514	1916.9778	-13.77	256	273	1	---	K.TSKVALVYGMNEPPGAR.A
1921.9567	1920.9494	1920.9581	-4.54	289	304	0	---	R.DQEGQDVLFLIDNIFR.F
1988.0200	1987.0127	1987.0262	-6.78	382	400	0	---	R.AIAELGIYPAVDPLDSTSR.I
1988.0200	1987.0127	1987.0262	-6.78	382	400	0	59	R.AIAELGIYPAVDPLDSTSR.I

No match to: 1189.5919, 1300.6198, 1301.6213, 1376.7365, 1395.7634, 1396.7566, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1463.7360, 1467.7928, 1496.7778, 1515.7438, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1922.9504, 1922.9504, 1951.0226, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2225.1423, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

19. [gi|340724488](#) Mass: 54997 Score: 319 Expect: 1e-024 Matches: 19

PREDICTED: ATP synthase subunit beta, mitochondrial [Bombus terrestris]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
975.5482	974.5409	974.5549	-14.37	192	- 202	0	---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	100	- 111	0	---	R.TIAMDGTGLVR.G + Oxidation (M)
1367.7294	1366.7221	1366.7456	-17.18	134	- 145	0	---	R.IINVIGEPIDER.G
1406.6683	1405.6610	1405.6739	-9.14	216	- 229	0	---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	216	- 229	0	89	K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	301	- 314	0	---	R.FTQAGSEVSALLGR.I
1438.7720	1437.7647	1437.8303	-45.63	15	- 27	0	---	R.AVKPTLLQNEVAR.I
1439.7766	1438.7693	1438.7820	-8.82	272	- 284	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	272	- 284	0	75	R.VALTGLTVAEYFR.D
1457.7886	1456.7813	1456.8323	-35.00	203	- 215	0	---	K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	203	- 215	0	---	K.TVLIMELINNVAK.A + Oxidation (M)
1496.7778	1495.7705	1495.7630	5.00	28	- 41	1	---	R.ISGSLSVNSRDYAK.A
1601.7986	1600.7913	1600.8031	-7.39	255	- 269	0	---	K.VALVYQMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	255	- 269	0	---	K.VALVYQMNEPPGAR.A + Oxidation (M)
1677.8896	1676.8823	1676.9210	-23.04	85	- 99	0	---	R.LVLEVAQHLGENTVR.T
1917.9587	1916.9514	1916.9778	-13.77	252	- 269	1	---	K.TSKVALVYQMNEPPGAR.A
1921.9567	1920.9494	1920.9581	-4.54	285	- 300	0	---	R.DQEGQDVLLFIDNIFR.F
1988.0200	1987.0127	1987.0262	-6.78	378	- 396	0	---	R.AIAELGIYPAVDPLDSTSR.I
1988.0200	1987.0127	1987.0262	-6.78	378	- 396	0	59	R.AIAELGIYPAVDPLDSTSR.I

No match to: 1189.5919, 1300.6198, 1301.6213, 1376.7365, 1395.7634, 1396.7566, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1456.7876, 1463.7360, 1467.7928, 1492.7432, 1515.7438, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1842.9082, 1922.9504, 1922.9504, 1951.0226, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2225.1423, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

20. [gi|815790072](#) Mass: 55419 Score: 319 Expect: 1e-024 Matches: 19

PREDICTED: ATP synthase subunit beta, mitochondrial [Linepithema humile]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
975.5482	974.5409	974.5549	-14.37	195	- 205	0	---	K.IGLFGGAGVGK.T
1278.6581	1277.6508	1277.6286	17.4	103	- 114	0	---	R.TIAMDGTGLVR.G + Oxidation (M)
1367.7294	1366.7221	1366.7456	-17.18	137	- 148	0	---	R.IINVIGEPIDER.G
1396.7566	1395.7493	1395.8085	-42.42	16	- 28	0	---	R.VAKPSLLQNEVAK.V
1406.6683	1405.6610	1405.6739	-9.14	219	- 232	0	---	K.AHGGYSVFAGVGER.T
1406.6683	1405.6610	1405.6739	-9.14	219	- 232	0	89	K.AHGGYSVFAGVGER.T
1435.7267	1434.7194	1434.7467	-19.00	304	- 317	0	---	R.FTQAGSEVSALLGR.I
1439.7766	1438.7693	1438.7820	-8.82	275	- 287	0	---	R.VALTGLTVAEYFR.D
1439.7766	1438.7693	1438.7820	-8.82	275	- 287	0	75	R.VALTGLTVAEYFR.D
1457.7886	1456.7813	1456.8323	-35.00	206	- 218	0	---	K.TVLIMELINNVAK.A
1473.8118	1472.8045	1472.8272	-15.41	206	- 218	0	---	K.TVLIMELINNVAK.A + Oxidation (M)
1601.7986	1600.7913	1600.8031	-7.39	258	- 272	0	---	K.VALVYQMNEPPGAR.A
1617.7932	1616.7859	1616.7981	-7.51	258	- 272	0	---	K.VALVYQMNEPPGAR.A + Oxidation (M)
1677.8896	1676.8823	1676.9210	-23.04	88	- 102	0	---	R.LVLEVAQHLGENTVR.T
1842.9082	1841.9009	1841.9094	-4.59	400	- 415	0	---	R.IMDPNIIGAEHYNIAR.G + Oxidation (M)
1917.9587	1916.9514	1916.9778	-13.77	255	- 272	1	---	K.TSKVALVYQMNEPPGAR.A
1921.9567	1920.9494	1920.9581	-4.54	288	- 303	0	---	R.DQEGQDVLLFIDNIFR.F
1988.0200	1987.0127	1987.0262	-6.78	381	- 399	0	---	R.AIAELGIYPAVDPLDSTSR.I
1988.0200	1987.0127	1987.0262	-6.78	381	- 399	0	59	R.AIAELGIYPAVDPLDSTSR.I

No match to: 1189.5919, 1300.6198, 1301.6213, 1376.7365, 1395.7634, 1404.7286, 1410.7430, 1424.7126, 1434.7134, 1436.7271, 1438.7720, 1456.7876, 1463.7360, 1467.7928, 1492.7432, 1496.7778, 1515.7438, 1520.7416, 1535.7208, 1553.7272, 1553.7272, 1582.8214, 1610.8411, 1610.8411, 1638.8787, 1642.8344, 1656.8358, 1667.8502, 1670.8577, 1676.8737, 1678.8970, 1698.8724, 1705.9220, 1731.8361, 1733.8561, 1749.8560, 1790.8837, 1797.8563, 1922.9504, 1922.9504, 1951.0226, 2016.0498, 2117.0474, 2118.0178, 2118.0178, 2147.0840, 2225.1423, 2330.1760, 2348.1704, 2366.1665, 2367.1624, 3154.5486, 3211.5518

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 (975.5482,1+) : <no title>
 Query2 (1189.5919,1+) : <no title>
 Query3 (1278.6581,1+) : <no title>
 Query4 (1300.6198,1+) : <no title>
 Query5 (1301.6213,1+) : <no title>
 Query6 (1367.7294,1+) : <no title>
 Query7 (1376.7365,1+) : <no title>

Query8 (1395.7634,1+) : <no title>
Query9 (1396.7566,1+) : <no title>
Query10 (1404.7286,1+) : <no title>
Query11 (1406.6683,1+) : <no title>
Query12 (1406.6683,1+) : MalDIWellID: 60696, SpectrumID: 127312,
Query13 (1410.7430,1+) : <no title>
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Query16 (1435.7267,1+) : <no title>
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Query18 (1438.7720,1+) : <no title>
Query19 (1439.7766,1+) : <no title>
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Query21 (1456.7876,1+) : <no title>
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Query30 (1535.7208,1+) : <no title>
Query31 (1553.7272,1+) : <no title>
Query32 (1553.7272,1+) : MalDIWellID: 60696, SpectrumID: 127314,
Query33 (1582.8214,1+) : <no title>
Query34 (1601.7986,1+) : <no title>
Query35 (1610.8411,1+) : <no title>
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Query37 (1617.7932,1+) : <no title>
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Query46 (1698.8724,1+) : <no title>
Query47 (1705.9220,1+) : <no title>
Query48 (1731.8361,1+) : <no title>
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Query51 (1790.8837,1+) : <no title>
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Query53 (1842.9082,1+) : <no title>
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Query56 (1922.9504,1+) : <no title>
Query57 (1922.9504,1+) : MalDIWellID: 60696, SpectrumID: 127316,
Query58 (1951.0226,1+) : <no title>
Query59 (1988.0200,1+) : <no title>
Query60 (1988.0200,1+) : MalDIWellID: 60696, SpectrumID: 127317,
Query61 (2016.0498,1+) : <no title>
Query62 (2117.0474,1+) : <no title>
Query63 (2118.0178,1+) : <no title>
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Query65 (2147.0840,1+) : <no title>
Query66 (2225.1423,1+) : <no title>
Query67 (2330.1760,1+) : <no title>
Query68 (2348.1704,1+) : <no title>
Query69 (2366.1665,1+) : <no title>
Query70 (2367.1624,1+) : <no title>
Query71 (3154.5486,1+) : <no title>
Query72 (3211.5518,1+) : <no title>

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