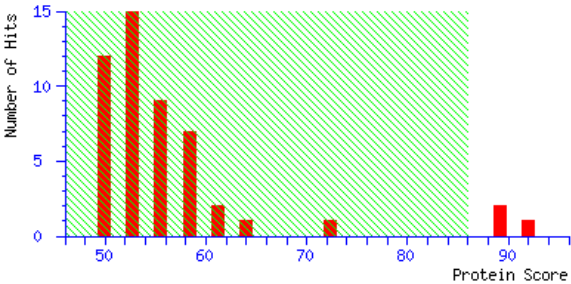


Mascot Search Results

User :  
Email :  
Search title : SampleSetID: 674, AnalysisID: 5211, MaldiWellID: 59829, SpectrumID: 120907, Path=\\161005\\MSMS\\16-85 combined NCBI euk  
Database : NCBInr 160208 (79581714 sequences; 29080698065 residues)  
Taxonomy : Eukaryota (eucaryotes) (20445761 sequences)  
Timestamp : 24 Oct 2016 at 21:22:20 GMT  
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.  
Top Score : 92 for gi|157109281, AAEL005259-PC [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 86 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Format As Protein Summary (deprecated) Help

Significance threshold p< 0.05 Max. number of hits 20

Re-Search All Search Unmatched

Index

Accession	Mass	Score	Description
1. gi 157109281	19268	92	AAEL005259-PC [Aedes aegypti]
2. gi 157109285	21865	90	AAEL005259-PA [Aedes aegypti]
3. gi 157109283	22909	89	AAEL005259-PB [Aedes aegypti]
4. gi 157109510	16327	72	AAEL005293-PA [Aedes aegypti]
5. gi 7715047	10945	65	MHC-DRB, partial [Aotus nancymaeae]
6. gi 94468418	18240	61	cyclophilin [Aedes aegypti]
7. gi 955178734	49776	60	arginine N-methyltransferase type III, putative [Bodo saltans]
8. gi 499050884	146506	59	PREDICTED: plasma membrane calcium-transporting ATPase 3 isoform X1 [Maylandia zebra]
9. gi 157130325	22639	59	AAEL011758-PA [Aedes aegypti]
10. gi 157114975	20486	58	AAEL007039-PA [Aedes aegypti]
11. gi 902162168	41330	58	hypothetical protein SOVF_179060 [Spinacia oleracea]
12. gi 821115488	59326	58	PREDICTED: LOW QUALITY PROTEIN: keratin, type II cytoskeletal 1 [Dasypus novemcinctus]
13. gi 954543243	48924	58	PREDICTED: mitochondrial chaperone BCS1 [Polistes canadensis]
14. gi 499050886	144451	58	PREDICTED: plasma membrane calcium-transporting ATPase 3 isoform X2 [Maylandia zebra]
15. gi 734556601	28224	56	Dehydrogenase/reductase SDR family member 4 [Toxocara canis]
16. gi 17567379	42402	56	Uncharacterized protein CELE_F29G6.2 [Caenorhabditis elegans]
17. gi 821064541	64152	56	putative f-box domain-containing protein [Diplodia seriata]
18. gi 565365442	60359	56	PREDICTED: uncharacterized protein LOC102594226 [Solanum tuberosum]
19. gi 751173750	8500	56	hypothetical protein M378DRAFT_168912 [Amanita muscaria Koide BX008]
20. gi 642102353	25674	55	unnamed protein product [Oncorhynchus mykiss]

Results List

1. [gi|157109281](#) Mass: 19268 Score: 92 Expect: 0.013 Matches: 8

AAEL005259-PC [Aedes aegypti]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.5823	1168.5750	1168.5659	7.81	135	- 145	0	---	R.ALHCGTQTPGK.V
1169.5823	1168.5750	1168.5659	7.81	135	- 145	0	---	R.ALHCGTQTPGK.V
1334.6696	1333.6623	1333.6626	-0.24	50	- 63	0	---	R.AGVDADGSVIFAGR.A
1334.6696	1333.6623	1333.6626	-0.24	50	- 63	0	62	R.AGVDADGSVIFAGR.A
1512.6454	1511.6381	1511.6749	-24.29	121	- 134	0	---	K.MGATVDGEPLYMGR.A + Oxidation (M)
1528.6405	1527.6332	1527.6698	-23.92	121	- 134	0	---	K.MGATVDGEPLYMGR.A + 2 Oxidation (M)
1528.6405	1527.6332	1527.6698	-23.92	121	- 134	0	---	K.MGATVDGEPLYMGR.A + 2 Oxidation (M)
2106.0098	2105.0025	2105.0218	-9.17	101	- 120	0	---	R.QGDFVWEFAANGVVPDGAVK.M
No match to: 876.5241, 889.5440, 904.5552, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1152.5656, 1156.5707, 1170.5707, 1204.6903, 1274.7163, 1302.7775, 1317.6949, 1336.6747, 1345.7133, 1349.7001, 1350.6952, 1381.7509, 1389.7490, 1389.7490, 1393.7178, 1407.7173, 1415.7266, 1427.7552, 1506.7015, 1537.7095, 1539.7147, 1544.6909, 1564.7327, 1572.7570, 1596.7085, 1606.8376, 1625.7717, 1659.8162, 1681.8368, 1682.8351, 1730.7920, 1738.8428, 1739.8273, 1802.8409, 1818.8517, 1844.8796, 1844.8796, 1848.0476, 1866.9254, 1872.9044, 1874.8976, 1881.9272, 1882.9167, 1890.8600, 1918.9139, 2142.0039, 2182.0796, 2198.0232, 2200.0256, 2225.1560, 2365.0332, 2384.1860, 2825.6038								

2. [gi|157109285](#) Mass: 21865 Score: 90 Expect: 0.02 Matches: 8

AAEL005259-PA [Aedes aegypti]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.5823	1168.5750	1168.5659	7.81	159	- 169	0	---	R.ALHCGTQTPGK.V
1169.5823	1168.5750	1168.5659	7.81	159	- 169	0	---	R.ALHCGTQTPGK.V
1334.6696	1333.6623	1333.6626	-0.24	74	- 87	0	---	R.AGVADADGSVIFAGR.A
1334.6696	1333.6623	1333.6626	-0.24	74	- 87	0	62	R.AGVADADGSVIFAGR.A
1512.6454	1511.6381	1511.6749	-24.29	145	- 158	0	---	K.MGATVDGEPLYMGR.A + Oxidation (M)
1528.6405	1527.6332	1527.6698	-23.92	145	- 158	0	---	K.MGATVDGEPLYMGR.A + 2 Oxidation (M)
1528.6405	1527.6332	1527.6698	-23.92	145	- 158	0	---	K.MGATVDGEPLYMGR.A + 2 Oxidation (M)
2106.0098	2105.0025	2105.0218	-9.17	125	- 144	0	---	R.QGDFVWEFAANGVVPDGAVK.M

No match to: 876.5241, 889.5440, 904.5552, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1152.5656, 1156.5707, 1170.5707, 1204.6903, 1274.7163, 1302.7775, 1317.6949, 1336.6747, 1345.7133, 1349.7001, 1350.6952, 1381.7509, 1389.7490, 1389.7490, 1393.7178, 1407.7173, 1415.7266, 1427.7552, 1506.7015, 1537.7095, 1539.7147, 1544.6909, 1564.7327, 1572.7570, 1596.7085, 1606.8376, 1625.7717, 1659.8162, 1681.8368, 1682.8351, 1730.7920, 1738.8428, 1739.8273, 1802.8409, 1818.8517, 1844.8796, 1844.8796, 1848.0476, 1866.9254, 1872.9044, 1874.8976, 1881.9272, 1882.9167, 1890.8600, 1918.9139, 2142.0039, 2182.0796, 2198.0232, 2200.0256, 2225.1560, 2365.0332, 2384.1860, 2825.6038

3. [gi|157109283](#) Mass: 22909 Score: 89 Expect: 0.024 Matches: 8

AAEL005259-PB [Aedes aegypti]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.5823	1168.5750	1168.5659	7.81	169	- 179	0	---	R.ALHCGTQTPGK.V
1169.5823	1168.5750	1168.5659	7.81	169	- 179	0	---	R.ALHCGTQTPGK.V
1334.6696	1333.6623	1333.6626	-0.24	84	- 97	0	---	R.AGVADADGSVIFAGR.A
1334.6696	1333.6623	1333.6626	-0.24	84	- 97	0	62	R.AGVADADGSVIFAGR.A
1512.6454	1511.6381	1511.6749	-24.29	155	- 168	0	---	K.MGATVDGEPLYMGR.A + Oxidation (M)
1528.6405	1527.6332	1527.6698	-23.92	155	- 168	0	---	K.MGATVDGEPLYMGR.A + 2 Oxidation (M)
1528.6405	1527.6332	1527.6698	-23.92	155	- 168	0	---	K.MGATVDGEPLYMGR.A + 2 Oxidation (M)
2106.0098	2105.0025	2105.0218	-9.17	135	- 154	0	---	R.QGDFVWEFAANGVVPDGAVK.M

No match to: 876.5241, 889.5440, 904.5552, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1152.5656, 1156.5707, 1170.5707, 1204.6903, 1274.7163, 1302.7775, 1317.6949, 1336.6747, 1345.7133, 1349.7001, 1350.6952, 1381.7509, 1389.7490, 1389.7490, 1393.7178, 1407.7173, 1415.7266, 1427.7552, 1506.7015, 1537.7095, 1539.7147, 1544.6909, 1564.7327, 1572.7570, 1596.7085, 1606.8376, 1625.7717, 1659.8162, 1681.8368, 1682.8351, 1730.7920, 1738.8428, 1739.8273, 1802.8409, 1818.8517, 1844.8796, 1844.8796, 1848.0476, 1866.9254, 1872.9044, 1874.8976, 1881.9272, 1882.9167, 1890.8600, 1918.9139, 2142.0039, 2182.0796, 2198.0232, 2200.0256, 2225.1560, 2365.0332, 2384.1860, 2825.6038

4. [gi|157109510](#) Mass: 16327 Score: 72 Expect: 1.2 Matches: 6

AAEL005293-PA [Aedes aegypti]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1389.7490	1388.7417	1388.7524	-7.71	52	- 63	0	---	R.DDAPLHISIRPR.D
1389.7490	1388.7417	1388.7524	-7.71	52	- 63	0	40	R.DDAPLHISIRPR.D
1730.7920	1729.7847	1729.8345	-28.79	128	- 143	0	---	R.FVHIGEGAQVDAIVME.- + Oxidation (M)
1739.8273	1738.8200	1738.8209	-0.53	76	- 90	1	---	R.SWGIEERHGGCPVQK.R
2182.0796	2181.0723	2181.0385	15.5	33	- 51	0	---	K.MTHDQFNINLQSGPNVNPR.D
2198.0232	2197.0159	2197.0334	-7.98	33	- 51	0	---	K.MTHDQFNINLQSGPNVNPR.D + Oxidation (M)

No match to: 876.5241, 889.5440, 904.5552, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1152.5656, 1156.5707, 1169.5823, 1169.5823, 1170.5707, 1204.6903, 1274.7163, 1302.7775, 1317.6949, 1334.6696, 1334.6696, 1336.6747, 1345.7133, 1349.7001, 1350.6952, 1381.7509, 1393.7178, 1407.7173, 1415.7266, 1427.7552, 1506.7015, 1512.6454, 1528.6405, 1528.6405, 1537.7095, 1539.7147, 1544.6909, 1564.7327, 1572.7570, 1596.7085, 1606.8376, 1625.7717, 1659.8162, 1681.8368, 1682.8351, 1738.8428, 1802.8409, 1818.8517, 1844.8796, 1844.8796, 1848.0476, 1866.9254, 1872.9044, 1874.8976, 1881.9272, 1882.9167, 1890.8600, 1918.9139, 2106.0098, 2142.0039, 2200.0256, 2225.1560, 2365.0332, 2384.1860, 2825.6038

5. [gi|7715047](#) Mass: 10945 Score: 65 Expect: 6.6 Matches: 7

MHC-DRB, partial [Aotus nancymae]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
904.5552	903.5479	903.5542	-6.91	1	- 7	1	---	-.RFLELVK.S
1334.6696	1333.6623	1333.6415	15.6	25	- 34	0	---	R.YFHNQEELVR.F
1334.6696	1333.6623	1333.6415	15.6	25	- 34	0	---	R.YFHNQEELVR.F
1506.7015	1505.6942	1505.7514	-37.98	55	- 66	0	---	K.YWNGQQDILELK.R
1739.8273	1738.8200	1738.8540	-19.52	76	- 89	1	---	R.HNYGVFESFTVQRR.-
2182.0796	2181.0723	2180.9949	35.5	8	- 24	1	---	K.SECYFFNGTERVQFLER.Y
2225.1560	2224.1487	2224.0760	32.7	35	- 54	1	---	R.FSDVGEYRAVTELGRPDAAK.Y

No match to: 876.5241, 889.5440, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1152.5656, 1156.5707, 1169.5823, 1169.5823, 1170.5707, 1204.6903, 1274.7163, 1302.7775, 1317.6949, 1336.6747, 1345.7133, 1349.7001, 1350.6952, 1381.7509, 1389.7490, 1389.7490, 1393.7178, 1407.7173, 1415.7266, 1427.7552, 1512.6454, 1528.6405, 1528.6405, 1537.7095, 1539.7147, 1544.6909, 1564.7327, 1572.7570, 1596.7085, 1606.8376, 1625.7717, 1659.8162, 1681.8368, 1682.8351, 1730.7920, 1738.8428, 1802.8409, 1818.8517, 1844.8796, 1844.8796, 1848.0476, 1866.9254, 1872.9044, 1874.8976, 1881.9272, 1882.9167, 1890.8600, 1918.9139, 2106.0098, 2142.0039, 2198.0232, 2200.0256, 2365.0332, 2384.1860, 2825.6038

6. [gi|94468418](#) Mass: 18240 Score: 61 Expect: 16 Matches: 4

cyclophylin [Aedes aegypti]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1596.7085	1595.7012	1595.7402	-24.45	6	- 19	0	---	R.CFFDLTADNAPLGR.V
1659.8162	1658.8089	1658.8451	-21.79	126	- 140	0	---	R.HVVFSGVSEGMVDIR.K + Oxidation (M)
1844.8796	1843.8723	1843.9104	-20.67	77	- 91	1	---	K.SIYGKFKFEDENFILR.H
1844.8796	1843.8723	1843.9104	-20.67	77	- 91	1	41	K.SIYGKFKFEDENFILR.H

No match to: 876.5241, 889.5440, 904.5552, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1152.5656, 1156.5707, 1169.5823, 1169.5823, 1170.5707, 1204.6903, 1274.7163, 1302.7775, 1317.6949, 1334.6696, 1334.6696, 1336.6747, 1345.7133, 1349.7001, 1350.6952, 1381.7509, 1389.7490, 1389.7490, 1393.7178, 1407.7173, 1415.7266, 1427.7552, 1506.7015, 1512.6454, 1528.6405, 1528.6405, 1537.7095, 1539.7147, 1544.6909, 1564.7327, 1572.7570, 1606.8376, 1625.7717, 1681.8368, 1682.8351, 1730.7920, 1738.8428, 1739.8273, 1802.8409, 1818.8517, 1848.0476, 1866.9254, 1872.9044, 1874.8976, 1881.9272, 1882.9167, 1890.8600, 1918.9139, 2106.0098, 2142.0039, 2182.0796, 2198.0232, 2200.0256, 2225.1560, 2365.0332, 2384.1860, 2825.6038

7. [gi|955178734](#) Mass: 49776 Score: 60 Expect: 20 Matches: 11

arginine N-methyltransferase type III, putative [Bodo saltans]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1156.5707	1155.5634	1155.5594	3.47	275	- 284	1	---	K.DTASCVFTTK.Y
1274.7163	1273.7090	1273.6522	44.6	1	- 11	1	---	-MPPKQLSSMQK.F
1334.6696	1333.6623	1333.6489	10.1	285	- 295	1	---	K.YGFRMSSVPFK.R + Oxidation (M)
1334.6696	1333.6623	1333.6489	10.1	285	- 295	1	---	K.YGFRMSSVPFK.R + Oxidation (M)
1349.7001	1348.6928	1348.6731	14.7	184	- 195	0	---	K.VMNLSTDLTPK.H
1539.7147	1538.7074	1538.6858	14.1	155	- 167	0	---	K.WVAVEGSTEMCR.L + Oxidation (M)
1606.8376	1605.8303	1605.8470	-10.38	182	- 195	1	---	K.IKVMNLSTDLTPK.H + Oxidation (M)
1625.7717	1624.7644	1624.7958	-19.29	311	- 323	1	---	K.TNQGTQLEREFR.V
1659.8162	1658.8089	1658.8086	0.17	365	- 379	0	---	R.DMQWQALQLVDAGK.E
2200.0256	2199.0183	2199.0273	-4.07	75	- 91	1	---	R.KESFEYQFDEHFLVPER.I
2384.1860	2383.1787	2383.1484	12.7	76	- 94	1	---	K.ESFEYQFDEHFLVPERIAK.A

No match to: 876.5241, 889.5440, 904.5552, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1152.5656, 1169.5823, 1169.5823, 1170.5707, 1204.6903, 1302.7775, 1317.6949, 1336.6747, 1345.7133, 1350.6952, 1381.7509, 1389.7490, 1389.7490, 1393.7178, 1407.7173, 1415.7266, 1427.7552, 1506.7015, 1512.6454, 1528.6405, 1537.7095, 1544.6909, 1564.7327, 1572.7570, 1596.7085, 1681.8368, 1682.8351, 1730.7920, 1738.8428, 1739.8273, 1802.8409, 1818.8517, 1844.8796, 1844.8796, 1848.0476, 1866.9254, 1872.9044, 1874.8976, 1881.9272, 1882.9167, 1890.8600, 1918.9139, 2106.0098, 2142.0039, 2182.0796, 2198.0232, 2225.1560, 2365.0332, 2825.6038

8. [gi|499050884](#) Mass: 146506 Score: 59 Expect: 26 Matches: 17

PREDICTED: plasma membrane calcium-transporting ATPase 3 isoform X1 [Maylandia zebra]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
933.5372	932.5299	932.4940	38.5	654	- 660	1	---	R.SFRPRDR.D
973.6145	972.6072	972.5968	10.7	391	- 399	1	---	K.SVLQGLTK.L
1152.5656	1151.5583	1151.5427	13.6	481	- 489	1	---	K.MMKDNNLVR.H + 2 Oxidation (M)
1204.6903	1203.6830	1203.6281	45.6	47	- 55	1	---	K.ELRELMELR.G + Oxidation (M)
1334.6696	1333.6623	1333.6449	13.1	1237	- 1247	0	---	R.QYSLPVTPCNR.N
1334.6696	1333.6623	1333.6449	13.1	1237	- 1247	0	---	R.QYSLPVTPCNR.N
1389.7490	1388.7417	1388.7452	-2.52	603	- 613	1	---	R.LYKVYTFNSVR.K
1389.7490	1388.7417	1388.7452	-2.52	603	- 613	1	---	R.LYKVYTFNSVR.K
1512.6454	1511.6381	1511.7038	-43.45	641	- 653	1	---	K.KCSYILDANGESR.S
1537.7095	1536.7022	1536.7532	-33.16	1156	- 1168	1	---	R.SSLYEGREKPEER.N
1544.6909	1543.6836	1543.7114	-18.01	253	- 266	0	---	K.IDESSLTGESDHVR.K
1564.7327	1563.7254	1563.7868	-39.24	96	- 108	1	---	R.CQTFGQNFIPPKK.A
1625.7717	1624.7644	1624.8031	-23.83	871	- 884	1	---	K.AVMWGRNVYDSISK.F
1866.9254	1865.9181	1865.9258	-4.13	854	- 870	0	---	K.EASDIILTDDNFSSIVK.A
2198.0232	2197.0159	2196.9957	9.20	56	- 75	1	---	R.GADALQKIEDSYGDTGLCR.R
2365.0332	2364.0259	2364.0726	-19.74	2	- 23	1	---	M.STTATMGEMANSAYFYPKGR.G + Oxidation (M)
2825.6038	2824.5965	2824.4567	49.5	809	- 836	1	---	K.GIIDSVVQQRQVAVTGDGTNDGPALK.K

No match to: 876.5241, 889.5440, 904.5552, 905.5200, 1032.6505, 1034.2173, 1128.5656, 1156.5707, 1169.5823, 1169.5823, 1170.5707, 1274.7163, 1302.7775, 1317.6949, 1336.6747, 1345.7133, 1349.7001, 1350.6952, 1381.7509, 1393.7178, 1407.7173, 1415.7266, 1427.7552, 1506.7015, 1528.6405, 1537.7095, 1544.6909, 1564.7327, 1572.7570, 1596.7085, 1606.8376, 1659.8162, 1681.8368, 1682.8351, 1730.7920, 1738.8428, 1739.8273, 1802.8409, 1818.8517, 1844.8796, 1844.8796, 1848.0476, 1872.9044, 1874.8976, 1881.9272, 1882.9167, 1890.8600, 1918.9139, 2106.0098, 2142.0039, 2182.0796, 2200.0256, 2225.1560, 2365.0332, 2384.1860, 2825.6038

9. [gi|157130325](#) Mass: 22639 Score: 59 Expect: 28 Matches: 4

AAEL011758-PA [Aedes aegypti]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1596.7085	1595.7012	1595.7402	-24.45	48	- 61	0	---	R.CFFDLTADNAPLGR.V
1659.8162	1658.8089	1658.8451	-21.79	168	- 182	0	---	R.HVVFSGSVVEGMDVIR.K + Oxidation (M)
1844.8796	1843.8723	1843.9104	-20.67	119	- 133	1	---	K.SIYGKGFEDENFILR.H
1844.8796	1843.8723	1843.9104	-20.67	119	- 133	1	41	K.SIYGKGFEDENFILR.H

No match to: 876.5241, 889.5440, 904.5552, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1152.5656, 1156.5707, 1169.5823, 1169.5823, 1170.5707, 1204.6903, 1274.7163, 1302.7775, 1317.6949, 1334.6696, 1334.6696, 1336.6747, 1345.7133, 1349.7001, 1350.6952, 1381.7509, 1389.7490, 1389.7490, 1393.7178, 1407.7173, 1415.7266, 1427.7552, 1506.7015, 1512.6454, 1528.6405, 1528.6405, 1537.7095, 1539.7147, 1544.6909, 1564.7327, 1572.7570, 1606.8376, 1625.7717, 1681.8368, 1682.8351, 1730.7920, 1738.8428, 1739.8273, 1802.8409, 1818.8517, 1848.0476, 1866.9254, 1872.9044, 1874.8976, 1881.9272, 1882.9167, 1890.8600, 1918.9139, 2106.0098, 2142.0039, 2182.0796, 2198.0232, 2200.0256, 2225.1560, 2365.0332, 2384.1860, 2825.6038

10. [gi|157114975](#) Mass: 20486 Score: 58 Expect: 30 Matches: 6

AAEL007039-PA [Aedes aegypti]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1128.5656	1127.5583	1127.5512	6.30	180	- 188	1	---	R.TWPRFNPNP.-
1169.5823	1168.5750	1168.5374	32.2	106	- 116	0	---	R.QGAHAPGFNDR.S
1169.5823	1168.5750	1168.5374	32.2	106	- 116	0	21	R.QGAHAPGFNDR.S
1625.7717	1624.7644	1624.7607	2.28	102	- 116	1	---	R.GWGRQGAHAPGFNDR.S
1890.8600	1889.8527	1889.8843	-16.69	163	- 179	0	---	R.QATATACPGNAFFEHIR.T
2142.0039	2140.9966	2141.0068	-4.74	117	- 136	0	---	R.SVGMCMVGTFTNAIPNLAAR.N + 2 Oxidation (M)

No match to: 876.5241, 889.5440, 904.5552, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1156.5707, 1170.5707, 1204.6903, 1274.7163, 1302.7775, 1317.6949, 1334.6696, 1334.6696, 1336.6747, 1345.7133, 1349.7001, 1350.6952, 1381.7509, 1389.7490, 1389.7490, 1393.7178, 1407.7173, 1415.7266, 1427.7552, 1506.7015, 1512.6454, 1528.6405, 1537.7095, 1539.7147, 1544.6909, 1564.7327, 1572.7570, 1596.7085, 1606.8376, 1659.8162, 1681.8368, 1682.8351, 1730.7920, 1738.8428, 1739.8273, 1802.8409, 1818.8517, 1844.8796, 1844.8796, 1848.0476, 1866.9254, 1872.9044, 1874.8976, 1881.9272, 1882.9167, 1918.9139, 2106.0098, 2182.0796, 2198.0232, 2200.0256, 2225.1560, 2365.0332, 2384.1860, 2825.6038

11. [gi|902162168](#) Mass: 41330 Score: 58 Expect: 32 Matches: 10

hypothetical protein SOVF\_179060 [Spinacia oleracea]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.5823	1168.5750	1168.5877	-10.84	322	- 334	0	---	R.YLSGFVGGGGAGK.I
1169.5823	1168.5750	1168.5877	-10.84	322	- 334	0	---	R.YLSGFVGGGGAGK.I

1393.7178 1392.7105 1392.6754 25.2 57 - 67 1 --- K.NTMRSARWPMK.G + Oxidation (M)  
 1415.7266 1414.7193 1414.7867 -47.63 61 - 72 1 --- R.SAWRPMKGLVVR.E + Oxidation (M)  
 1572.7570 1571.7497 1571.8208 -45.25 231 - 243 1 --- K.NNPGFLEVYHVRK.S  
 1596.7085 1595.7012 1595.6570 27.7 283 - 300 0 --- R.GGVGGCGSGGGPGCFTGR.R  
 1659.8162 1658.8089 1658.7729 21.7 203 - 215 0 --- R.EWVNYDGFDFVR.G  
 1730.7920 1729.7847 1729.8595 -43.23 302 - 320 0 --- R.SNGSGGGLLPDTVSGGSLR.R  
 2106.0098 2105.0025 2104.8983 49.5 150 - 167 1 --- K.MGSQYDESDPVGWGKYMR.V  
 2142.0039 2140.9966 2140.9532 20.3 279 - 300 1 --- R.IFERGGVGGCGSGGGPGCFTGR.R  
**No match to:** 876.5241, 889.5440, 904.5552, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1152.5656, 1156.5707, 1170.5707, 1204.6903, 1274.7163, 1302.7775, 1317.6949, 1334.6696, 1334.6696, 1336.6747, 1345.7133, 1349.7001, 1350.6952, 1381.7509, 1389.7490, 1389.7490, 1407.7173, 1427.7552, 1506.7015, 1512.6454, 1528.6405, 1537.7095, 1539.7147, 1544.6909, 1564.7327, 1606.8376, 1625.7717, 1681.8368, 1682.8351, 1738.8428, 1739.8273, 1802.8409, 1818.8517, 1844.8796, 1844.8796, 1848.0476, 1866.9254, 1872.9044, 1874.8976, 1881.9272, 1882.9167, 1890.8600, 1918.9139, 2182.0796, 2198.0232, 2200.0256, 2225.1560, 2365.0332, 2384.1860, 2825.6038

12. [gi|821115488](#) Mass: 59326 Score: 58 Expect: 32 Matches: 11

PREDICTED: LOW QUALITY PROTEIN: keratin, type II cytoskeletal 1 [Dasypus novemcinctus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
905.5200	904.5127	904.4865	28.9	352	359	1	---	R.SEIDSVKK.Q
1170.5707	1169.5634	1169.5281	30.2	64	74	1	---	K.RISMSMSGGR.G + 2 Oxidation (M)
1336.6747	1335.6674	1335.6029	48.3	38	54	1	---	R.RSGGGGGGGGGGFGSR.S
1349.7001	1348.6928	1348.6987	-4.32	166	177	0	---	K.SLNNQFASLIDK.V
1393.7178	1392.7105	1392.7249	-10.30	258	269	1	---	R.TNAENEFVTIKK.D
1539.7147	1538.7074	1538.7762	-44.72	403	414	1	---	R.LLRDYQELMNTK.L + Oxidation (M)
1544.6909	1543.6836	1543.7379	-35.15	238	249	1	---	K.HNQDLVEEYRKN.Y
1572.7570	1571.7497	1571.6821	43.0	15	29	0	---	K.GCFSSGSGVAISCQR.R
1802.8409	1801.8336	1801.8959	-34.54	319	334	1	---	K.YEELQVTAGKHGDSLR.T
1848.0476	1847.0403	1846.9788	33.3	162	177	1	---	R.EQIKSLNNQFASLIDK.V
1872.9044	1871.8971	1871.9701	-38.96	359	374	1	---	K.KQISQIQQSISEAEQR.G

**No match to:** 876.5241, 889.5440, 904.5552, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1152.5656, 1156.5707, 1169.5823, 1169.5823, 1204.6903, 1274.7163, 1302.7775, 1317.6949, 1334.6696, 1334.6696, 1336.6747, 1345.7133, 1350.6952, 1381.7509, 1389.7490, 1389.7490, 1407.7173, 1415.7266, 1427.7552, 1506.7015, 1512.6454, 1528.6405, 1528.6405, 1537.7095, 1564.7327, 1596.7085, 1606.8376, 1625.7717, 1659.8162, 1681.8368, 1682.8351, 1730.7920, 1738.8428, 1739.8273, 1818.8517, 1844.8796, 1844.8796, 1866.9254, 1874.8976, 1881.9272, 1882.9167, 1890.8600, 1918.9139, 2106.0098, 2142.0039, 2182.0796, 2198.0232, 2200.0256, 2225.1560, 2365.0332, 2384.1860, 2825.6038

13. [gi|954543243](#) Mass: 48924 Score: 58 Expect: 33 Matches: 10

PREDICTED: mitochondrial chaperone BCS1 [Polistes canadensis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1170.5707	1169.5634	1169.5863	-19.52	157	166	1	---	R.QMALKEHEGK.T
1317.6949	1316.6876	1316.6369	38.5	34	44	1	---	R.KGMQAGMIFFR.R + 2 Oxidation (M)
1345.7133	1344.7060	1344.6431	46.8	35	45	1	---	K.GMQAGMIFFR.H + 2 Oxidation (M)
1393.7178	1392.7105	1392.7249	-10.30	238	250	0	---	K.SSFITALAGELER.G
1625.7717	1624.7644	1624.8209	-34.74	144	156	1	---	R.DRSLYFNILEEAR.Q
1659.8162	1658.8089	1658.7610	28.9	369	382	1	---	R.FYKSPENVNDMAK.Q + Oxidation (M)
1890.8600	1889.8527	1889.9101	-30.34	96	110	0	---	K.YEFIPSIGTHFFNYR.G
1918.9139	1917.9066	1917.9545	-24.94	71	87	1	---	R.GATRTQHLSVETSFEQK.E
2106.0098	2105.0025	2104.9346	32.2	352	368	0	---	K.EYIGWCSGSQVEQMFLR.F + Oxidation (M)
2384.1860	2383.1787	2383.0784	42.1	372	392	1	---	K.SPENVNDMAKQFANEVMAQK.R + 2 Oxidation (M)

**No match to:** 876.5241, 889.5440, 904.5552, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1152.5656, 1156.5707, 1169.5823, 1169.5823, 1204.6903, 1274.7163, 1302.7775, 1334.6696, 1334.6696, 1336.6747, 1349.7001, 1350.6952, 1381.7509, 1389.7490, 1389.7490, 1407.7173, 1415.7266, 1427.7552, 1506.7015, 1512.6454, 1528.6405, 1528.6405, 1537.7095, 1539.7147, 1544.6909, 1564.7327, 1572.7570, 1596.7085, 1606.8376, 1681.8368, 1682.8351, 1730.7920, 1738.8428, 1739.8273, 1802.8409, 1818.8517, 1844.8796, 1844.8796, 1848.0476, 1866.9254, 1872.9044, 1874.8976, 1881.9272, 1882.9167, 2142.0039, 2182.0796, 2198.0232, 2200.0256, 2225.1560, 2365.0332, 2825.6038

14. [gi|499050886](#) Mass: 144451 Score: 58 Expect: 35 Matches: 17

PREDICTED: plasma membrane calcium-transporting ATPase 3 isoform X2 [Maylandia zebra]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
933.5372	932.5299	932.4940	38.5	635	641	1	---	R.SFRPRDR.D
973.6145	972.6072	972.5968	10.7	372	380	1	---	K.SVLQGLTK.L
1152.5656	1151.5583	1151.5427	13.6	462	470	1	---	K.MMKDNNLVR.H + 2 Oxidation (M)
1204.6903	1203.6830	1203.6281	45.6	47	55	1	---	K.ELRELMELR.G + Oxidation (M)
1334.6696	1333.6623	1333.6449	13.1	1218	1228	0	---	R.QYSLPVTPCNR.N
1334.6696	1333.6623	1333.6449	13.1	1218	1228	0	---	R.QYSLPVTPCNR.N
1389.7490	1388.7417	1388.7452	-2.52	584	594	1	---	R.LYKVYTFNSVR.K
1389.7490	1388.7417	1388.7452	-2.52	584	594	1	---	R.LYKVYTFNSVR.K
1512.6454	1511.6381	1511.7038	-43.45	622	634	1	---	K.KCSYILDANGESR.S
1537.7095	1536.7022	1536.7532	-33.16	1137	1149	1	---	R.SSLVEGREKPEER.N
1544.6909	1543.6836	1543.7114	-18.01	253	266	0	---	K.IDESSLTGESDHVR.K
1564.7327	1563.7254	1563.7868	-39.24	96	108	1	---	R.CQTFGQNFIPPKK.A
1625.7717	1624.7644	1624.8031	-23.83	852	865	1	---	K.AVMWGRNVYDSISK.F
1866.9254	1865.9181	1865.9258	-4.13	835	851	0	---	K.EASDIILTDNFSIVK.A
2198.0232	2197.0159	2196.9957	9.20	56	75	1	---	R.GADALQKIEDSYGDTGLCR.R
2365.0332	2364.0259	2364.0726	-19.74	2	23	1	---	M.STTATMGEMANSVEFYPKGTR.G + Oxidation (M)
2825.6038	2824.5965	2824.4567	49.5	790	817	1	---	K.GIIDSSVVEQRQVVAVTGDGTNDGPALK.K

**No match to:** 876.5241, 889.5440, 904.5552, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1152.5656, 1156.5707, 1169.5823, 1169.5823, 1204.6903, 1274.7163, 1302.7775, 1317.6949, 1336.6747, 1345.7133, 1349.7001, 1350.6952, 1381.7509, 1393.7178, 1407.7173, 1415.7266, 1427.7552, 1506.7015, 1528.6405, 1528.6405, 1539.7147, 1572.7570, 1596.7085, 1606.8376, 1659.8162, 1681.8368, 1682.8351, 1730.7920, 1738.8428, 1739.8273, 1802.8409, 1818.8517, 1844.8796, 1844.8796, 1848.0476, 1872.9044, 1874.8976, 1881.9272, 1882.9167, 1890.8600, 1918.9139, 2106.0098, 2142.0039, 2182.0796, 2200.0256, 2225.1560, 2384.1860



15. [gi|734556601](#) Mass: 28224 Score: 56 Expect: 46 Matches: 8

Dehydrogenase/reductase SDR family member 4 [Toxocara canis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
889.5440	888.5367	888.5280	9.78	18	-	26	0	R.VAIVTASTK.G
1152.5656	1151.5583	1151.5605	-1.85	1	-	12	0	-.MATTATASTAAR.F
1170.5707	1169.5634	1169.5387	21.2	206	-	215	0	K.MLYETPSASR.D + Oxidation (M)
1274.7163	1273.7090	1273.6626	36.4	36	-	48	0	R.LGQDGASVVVSSR.K
1415.7266	1414.7193	1414.7429	-16.68	179	-	190	1	K.SFSQSLAHRNIR.V
1625.7717	1624.7644	1624.7879	-14.44	206	-	219	1	K.MLYETPSASRDTVR.H
1682.8351	1681.8278	1681.9039	-45.23	128	-	142	0	R.SAFLLTQEAVPHLEK.S
1739.8273	1738.8200	1738.8784	-33.59	1	-	17	1	-.MATTATASTAARFLGNR.V

No match to: 876.5241, 904.5552, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1156.5707, 1169.5823, 1169.5823, 1204.6903, 1302.7775, 1317.6949, 1334.6696, 1334.6696, 1336.6747, 1345.7133, 1349.7001, 1350.6952, 1381.7509, 1389.7490, 1389.7490, 1393.7178, 1407.7173, 1427.7552, 1506.7015, 1512.6454, 1528.6405, 1528.6405, 1537.7095, 1539.7147, 1544.6909, 1564.7327, 1572.7570, 1596.7085, 1606.8376, 1659.8162, 1681.8368, 1730.7920, 1738.8428, 1802.8409, 1818.8517, 1844.8796, 1844.8796, 1848.0476, 1866.9254, 1872.9044, 1874.8976, 1881.9272, 1882.9167, 1890.8600, 1918.9139, 2106.0098, 2142.0039, 2182.0796, 2198.0232, 2200.0256, 2225.1560, 2365.0332, 2384.1860, 2825.6038

16. [gi|17567379](#) Mass: 42402 Score: 56 Expect: 51 Matches: 12

Uncharacterized protein CELE\_F29G6.2 [Caenorhabditis elegans]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1156.5707	1155.5634	1155.6023	-33.65	352	-	361	0	R.DEDIELVVPK.A
1349.7001	1348.6928	1348.6358	42.3	225	-	236	0	K.LNTAEESSESIK.M
1389.7490	1388.7417	1388.6783	45.7	33	-	44	1	R.LGQDLEKSENEK.K
1389.7490	1388.7417	1388.6783	45.7	33	-	44	1	R.LGQDLEKSENEK.K
1393.7178	1392.7105	1392.7136	-2.23	84	-	94	1	R.QDLIEDIEKYK.R
1564.7327	1563.7254	1563.8000	-47.69	170	-	182	1	R.SMLGIKEELLMER.D + Oxidation (M)
1606.8376	1605.8303	1605.7603	43.6	244	-	257	0	K.QMAEAVNVQTMVNR.S + Oxidation (M)
1844.8796	1843.8723	1843.9315	-32.12	280	-	295	0	R.ELLASHAIELVESDYR.A
1844.8796	1843.8723	1843.9315	-32.12	280	-	295	0	R.ELLASHAIELVESDYR.A
1881.9272	1880.9199	1880.9237	-1.99	242	-	257	1	K.YKQMAEAVNVQTMVNR.S
1918.9139	1917.9066	1917.9400	-17.43	244	-	260	1	K.QMAEAVNVQTMVNRSPK.A + Oxidation (M)
2384.1860	2383.1787	2383.2352	-23.68	296	-	316	1	R.AITILLDLCLNDKQMAHAHSR.R

No match to: 876.5241, 889.5440, 904.5552, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1152.5656, 1169.5823, 1169.5823, 1170.5707, 1204.6903, 1274.7163, 1302.7775, 1317.6949, 1334.6696, 1334.6696, 1336.6747, 1345.7133, 1350.6952, 1381.7509, 1407.7173, 1415.7266, 1427.7552, 1506.7015, 1512.6454, 1528.6405, 1528.6405, 1537.7095, 1539.7147, 1544.6909, 1572.7570, 1596.7085, 1625.7717, 1659.8162, 1681.8368, 1682.8351, 1730.7920, 1738.8428, 1739.8273, 1802.8409, 1818.8517, 1844.8796, 1866.9254, 1872.9044, 1874.8976, 1882.9167, 1890.8600, 2106.0098, 2142.0039, 2182.0796, 2198.0232, 2200.0256, 2225.1560, 2365.0332, 2825.6038

17. [gi|821064541](#) Mass: 64152 Score: 56 Expect: 51 Matches: 10

putative f-box domain-containing protein [Diplodia seriata]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1128.5656	1127.5583	1127.5611	-2.47	300	-	308	0	R.FTSLNLYDR.R
1336.6747	1335.6674	1335.6936	-19.57	573	-	585	1	R.FVRGLGLSGSTW.-
1407.7173	1406.7100	1406.6765	23.8	434	-	444	1	K.WMERDGFPIR.S
1539.7147	1538.7074	1538.7511	-28.38	2	-	15	0	M.TPHMAELASAVQER.R
1606.8376	1605.8303	1605.8362	-3.67	141	-	156	0	R.TEPGLLAGHAPLSESK.A
1739.8273	1738.8200	1738.7951	14.3	42	-	56	1	R.ERAFASWDSYPGEK.I
1881.9272	1880.9199	1880.8608	31.4	157	-	173	0	K.AIMTETGAVECVSIDNR.Q + Oxidation (M)
2106.0098	2105.0025	2104.9821	9.72	16	-	35	1	R.RSASGVHNADAPNAEMVAHR.L + Oxidation (M)
2225.1560	2224.1487	2224.0464	46.0	157	-	176	1	K.AIMTETGAVECVSIDNRQSK.G + Oxidation (M)
2384.1860	2383.1787	2383.2695	-38.10	316	-	337	1	R.GTVHSGARLSSMALIHHPFIPR.N

No match to: 876.5241, 889.5440, 904.5552, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1156.5707, 1169.5823, 1169.5823, 1170.5707, 1204.6903, 1274.7163, 1302.7775, 1317.6949, 1334.6696, 1334.6696, 1345.7133, 1349.7001, 1350.6952, 1381.7509, 1389.7490, 1389.7490, 1393.7178, 1415.7266, 1427.7552, 1506.7015, 1512.6454, 1528.6405, 1528.6405, 1537.7095, 1544.6909, 1564.7327, 1572.7570, 1596.7085, 1625.7717, 1659.8162, 1681.8368, 1682.8351, 1730.7920, 1738.8428, 1802.8409, 1818.8517, 1844.8796, 1844.8796, 1848.0476, 1866.9254, 1872.9044, 1874.8976, 1882.9167, 1890.8600, 1918.9139, 2142.0039, 2182.0796, 2198.0232, 2200.0256, 2365.0332, 2825.6038

18. [gi|565365442](#) Mass: 60359 Score: 56 Expect: 55 Matches: 10

PREDICTED: uncharacterized protein LOC102594226 [Solanum tuberosum]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1152.5656	1151.5583	1151.5315	23.3	260	-	269	0	R.CLNMAETVAK.G + Oxidation (M)
1204.6903	1203.6830	1203.6281	45.6	287	-	296	1	R.LEELAMKQSR.Q
1336.6747	1335.6674	1335.7220	-40.89	525	-	536	1	K.LSFKTMPGLQSK.F
1407.7173	1406.7100	1406.6824	19.7	132	-	144	1	R.QSPSMTSGRISEK.W
1539.7147	1538.7074	1538.7181	-6.93	256	-	269	1	K.SSGRCLNMAETVAK.G + Oxidation (M)
1866.9254	1865.9181	1865.9166	0.80	270	-	286	0	K.GLPQAQTISQVSQANHR.L
1882.9167	1881.9094	1881.9657	-29.89	354	-	371	1	R.NGVSSIVNSSLSPNKHSR.G
1918.9139	1917.9066	1917.9288	-11.57	155	-	172	1	K.IKLPDNNGLASVCGADK.A + Oxidation (M)
2142.0039	2140.9966	2140.9621	16.1	428	-	447	0	K.SNAHGITQDQDASLSDTPR.V
2384.1860	2383.1787	2383.1127	27.7	121	-	140	1	K.HHWEIFEELRQSPSMTSGR.I

No match to: 876.5241, 889.5440, 904.5552, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1156.5707, 1169.5823, 1169.5823, 1170.5707, 1274.7163, 1302.7775, 1317.6949, 1334.6696, 1334.6696, 1345.7133, 1349.7001, 1350.6952, 1381.7509, 1389.7490, 1389.7490, 1393.7178, 1415.7266, 1427.7552, 1506.7015, 1512.6454, 1528.6405, 1528.6405, 1537.7095, 1544.6909, 1564.7327, 1572.7570, 1596.7085, 1606.8376, 1625.7717, 1659.8162, 1681.8368, 1682.8351, 1730.7920, 1738.8428, 1802.8409, 1818.8517, 1844.8796, 1844.8796, 1848.0476, 1866.9254, 1872.9044, 1874.8976, 1881.9272, 1890.8600, 2106.0098, 2182.0796, 2198.0232, 2200.0256, 2225.1560, 2365.0332, 2825.6038

19. [gi|751173750](#) Mass: 8500 Score: 56 Expect: 58 Matches: 5

hypothetical protein M378DRAFT\_168912 [Amanita muscaria Koide BX008]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1317.6949	1316.6876	1316.6612	20.1	20	- 30	1	---	R.LGDLKWEDVDK.R
1415.7266	1414.7193	1414.7164	2.06	59	- 71	1	---	K.TEARDNAAQQALK.A
1818.8517	1817.8444	1817.9312	-47.73	37	- 52	0	---	R.HLWTSIVEINGTTYGK.G
1872.9044	1871.8971	1871.8584	20.7	1	- 17	0	---	-.MSGPNSPSQELHNYVGR.L
2142.0039	2140.9966	2141.0436	-21.94	1	- 19	1	---	-.MSGPNSPSQELHNYVGRLR.L
No match to: 876.5241, 889.5440, 904.5552, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1152.5656, 1156.5707, 1169.5823, 1169.5823, 1170.5707, 1204.6903, 1274.7163, 1302.7775, 1334.6696, 1334.6696, 1336.6747, 1345.7133, 1349.7001, 1350.6952, 1381.7509, 1389.7490, 1389.7490, 1393.7178, 1407.7173, 1427.7552, 1506.7015, 1512.6454, 1528.6405, 1528.6405, 1537.7095, 1539.7147, 1544.6909, 1564.7327, 1572.7570, 1596.7085, 1606.8376, 1625.7717, 1659.8162, 1681.8368, 1682.8351, 1730.7920, 1738.8428, 1739.8273, 1802.8409, 1844.8796, 1844.8796, 1848.0476, 1866.9254, 1874.8976, 1881.9272, 1882.9167, 1890.8600, 1918.9139, 2106.0098, 2182.0796, 2198.0232, 2200.0256, 2225.1560, 2365.0332, 2384.1860, 2825.6038								

20. [gi|642102353](#) Mass: 25674 Score: 55 Expect: 68 Matches: 9

unnamed protein product [Oncorhynchus mykiss]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1152.5656	1151.5583	1151.5645	-5.35	53	- 61	1	---	K.LEKVMDDFR.A
1537.7095	1536.7022	1536.6991	2.03	56	- 68	1	---	K.VMDDFRASPTDQR.G
1606.8376	1605.8303	1605.8515	-13.18	90	- 103	0	---	K.IVEGYNGIPFTIQR.L
1625.7717	1624.7644	1624.7259	23.7	128	- 141	0	---	K.NVMVSCVCPTSEK.N + Oxidation (M)
1802.8409	1801.8336	1801.8127	11.6	150	- 165	0	---	R.MNGVMFPGNTAIYSER.N + Oxidation (M)
1818.8517	1817.8444	1817.8076	20.2	150	- 165	0	---	R.MNGVMFPGNTAIYSER.N + 2 Oxidation (M)
1872.9044	1871.8971	1871.9022	-2.72	19	- 34	1	---	K.KDACPALDQFLCHVAK.T
1890.8600	1889.8527	1889.8427	5.31	1	- 15	0	---	-.MEIDTLLECFTDFEK.K
2200.0256	2199.0183	2199.0711	-23.98	35	- 52	1	---	K.TGETMISWSQFKSYFLFK.L
No match to: 876.5241, 889.5440, 904.5552, 905.5200, 933.5372, 973.6145, 1032.6505, 1034.2173, 1128.5656, 1156.5707, 1169.5823, 1169.5823, 1170.5707, 1204.6903, 1274.7163, 1302.7775, 1317.6949, 1334.6696, 1334.6696, 1336.6747, 1345.7133, 1349.7001, 1350.6952, 1381.7509, 1389.7490, 1389.7490, 1393.7178, 1407.7173, 1415.7266, 1427.7552, 1506.7015, 1512.6454, 1528.6405, 1528.6405, 1539.7147, 1544.6909, 1564.7327, 1572.7570, 1596.7085, 1659.8162, 1681.8368, 1682.8351, 1730.7920, 1738.8428, 1739.8273, 1844.8796, 1844.8796, 1848.0476, 1866.9254, 1874.8976, 1881.9272, 1882.9167, 1918.9139, 2106.0098, 2142.0039, 2182.0796, 2198.0232, 2225.1560, 2365.0332, 2384.1860, 2825.6038								

## 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 (876.5241,1+) : <no title>  
 Query2 (889.5440,1+) : <no title>  
 Query3 (904.5552,1+) : <no title>  
 Query4 (905.5200,1+) : <no title>  
 Query5 (933.5372,1+) : <no title>  
 Query6 (973.6145,1+) : <no title>  
 Query7 (1032.6505,1+) : <no title>  
 Query8 (1034.2173,1+) : <no title>  
 Query9 (1128.5656,1+) : <no title>  
 Query10 (1152.5656,1+) : <no title>  
 Query11 (1156.5707,1+) : <no title>  
 Query12 (1169.5823,1+) : <no title>  
 Query13 (1169.5823,1+) : MaldiWellID: 59829, SpectrumID: 120911,  
 Query14 (1170.5707,1+) : <no title>  
 Query15 (1204.6903,1+) : <no title>  
 Query16 (1274.7163,1+) : <no title>  
 Query17 (1302.7775,1+) : <no title>  
 Query18 (1317.6949,1+) : <no title>  
 Query19 (1334.6696,1+) : <no title>  
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 Query21 (1336.6747,1+) : <no title>  
 Query22 (1345.7133,1+) : <no title>  
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 Query24 (1350.6952,1+) : <no title>  
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 Query26 (1389.7490,1+) : <no title>  
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 Query28 (1393.7178,1+) : <no title>  
 Query29 (1407.7173,1+) : <no title>  
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 Query36 (1537.7095,1+) : <no title>  
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 Query39 (1564.7327,1+) : <no title>  
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 Query41 (1596.7085,1+) : <no title>  
 Query42 (1606.8376,1+) : <no title>  
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Query45 (1681.8368,1+) : <no title>  
Query46 (1682.8351,1+) : <no title>  
Query47 (1730.7920,1+) : <no title>  
Query48 (1738.8428,1+) : <no title>  
Query49 (1739.8273,1+) : <no title>  
Query50 (1802.8409,1+) : <no title>  
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Query54 (1848.0476,1+) : <no title>  
Query55 (1866.9254,1+) : <no title>  
Query56 (1872.9044,1+) : <no title>  
Query57 (1874.8976,1+) : <no title>  
Query58 (1881.9272,1+) : <no title>  
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Query60 (1890.8600,1+) : <no title>  
Query61 (1918.9139,1+) : <no title>  
Query62 (2106.0098,1+) : <no title>  
Query63 (2142.0039,1+) : <no title>  
Query64 (2182.0796,1+) : <no title>  
Query65 (2198.0232,1+) : <no title>  
Query66 (2200.0256,1+) : <no title>  
Query67 (2225.1560,1+) : <no title>  
Query68 (2365.0332,1+) : <no title>  
Query69 (2384.1860,1+) : <no title>  
Query70 (2825.6038,1+) : <no title>

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