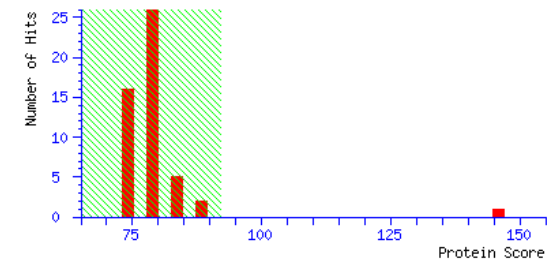


Mascot Search Results

User :  
Email :  
Search title : SampleSetID: 692, AnalysisID: 5361, MaldiWellID: 60694, SpectrumID: 127299, Path=\\161031\\MSMS\\run 65 NCBI all ok 1  
Database : NCBI nr 160208 (79581714 sequences; 29080698065 residues)  
Timestamp : 28 Nov 2016 at 12:28:16 GMT  
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.  
Top Score : 146 for gi|157119583, AAEL008708-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 157119583	53093	146	AAEL008708-PA [Aedes aegypti]
2. gi 515567296	47301	89	hypothetical protein [Staphylococcus lentus]
3. gi 517685802	43305	88	galactonate dehydratase [Rhizobium sp. 42MFCr.1]
4. gi 403295466	133524	86	PREDICTED: protein FAM184A isoform X1 [Saimiri boliviensis boliviensis]
5. gi 516242151	283896	85	hypothetical protein [Streptococcus agalactiae]
6. gi 307186672	88853	84	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase, partial [Camponotus floridanus]
7. gi 851188668	68812	83	ATPase AAA [Candidatus Acidianus copahuensis]
8. gi 725593996	127771	82	PREDICTED: protein FAM184A isoform X2 [Saimiri boliviensis boliviensis]
9. gi 573949653	15625	81	PREDICTED: bifunctional monodehydroascorbate reductase and carbonic anhydrase nectarin-3-like [Oryza brachyantha]
10. gi 915505193	39921	81	S-adenosylmethionine:tRNA ribosyltransferase-isomerase [Helicobacter pylori]
11. gi 4098878	22582	80	heat shock protein 70B/SSB1 [Pneumocystis wakefieldiae]
12. gi 446541073	57246	80	OMA87-like protein, partial [Leptospira interrogans]
13. gi 541049004	53961	79	putative v-type proton atpase subunit h 2 [Ascaris suum]
14. gi 771612100	63606	79	hypothetical protein [Desulfonatronum thioautotrophicum]
15. gi 799250295	93952	78	hypothetical protein HIM_01726 [Hirsutella minnesotensis 3608]
16. gi 456972883	60186	77	outer membrane protein, OMP85 family [Leptospira interrogans serovar Grippotyphosa str. LT2186]
17. gi 736810611	35344	77	hypothetical protein [[Eubacterium] sulci]
18. gi 815697785	36358	77	lytic enzyme [Stenotrophomonas maltophilia]
19. gi 218191195	28374	77	hypothetical protein OsI_08122 [Oryza sativa Indica Group]
20. gi 966498831	22294	77	TetR family transcriptional regulator [Legionella santicrucis]

Results List

1.	gi 157119583	Mass: 53093	Score: 146	Expect: 2e-007	Matches: 5
AAEL008708-PA [Aedes aegypti]					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Ions Peptide
1264.5852	1263.5779	1263.5707	5.75	198 - 208	0 --- R.GCYGTIFSGRF.V
1585.7638	1584.7565	1584.7685	-7.54	363 - 375	0 --- R.HAFGDWINEDLIR.A
1585.7638	1584.7565	1584.7685	-7.54	363 - 375	0 82 R.HAFGDWINEDLIR.A
1655.8876	1654.8803	1654.9043	-14.47	55 - 70	0 --- K.GPIFVIVGNGPIETR.Y
1655.8876	1654.8803	1654.9043	-14.47	55 - 70	0 55 K.GPIFVIVGNGPIETR.Y
No match to: 983.5101, 983.5101, 1020.5240, 1111.5724, 1128.5876, 1128.5876, 1237.6635, 1237.6635, 1238.6617, 1240.6185, 1267.6644, 1268.6685, 1296.6947, 1321.6318, 1359.7007, 1526.7316, 1535.7430, 1553.7305, 1581.7991, 1601.8033, 1613.7943, 1617.7871, 1622.8406, 1623.8719, 1638.8364, 1642.7878, 1646.7791, 1656.8875, 1669.8287, 1675.8157, 1683.8801, 1688.8220, 1698.8710, 1712.8909, 1776.8607, 1780.8707, 1790.8802, 1794.8982, 1818.9015, 1822.9069, 1851.9087, 1852.9109, 1879.9312, 1987.9928, 1993.9722, 2044.0343, 2045.0272, 2101.0442, 2107.0676, 2132.0586, 2175.0510, 2179.0537, 2183.0798, 2188.0881, 2220.0830, 2225.1509, 2229.1431, 2242.1299, 2282.1685, 2330.1729, 2386.1428, 2612.2639, 3153.6074, 3163.6431, 3210.6301					
2.	gi 515567296	Mass: 47301	Score: 89	Expect: 0.11	Matches: 13
hypothetical protein [Staphylococcus lentus]					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Ions Peptide
1267.6644	1266.6571	1266.6819	-19.58	61 - 71	1 --- K.YSSLTALKEQK.Q
1296.6947	1295.6874	1295.6873	0.06	157 - 166	1 --- K.YIFKEEAQIR.I
1601.8033	1600.7960	1600.8824	-53.97	167 - 179	1 --- R.IYERDEIPVNIK.G
1638.8364	1637.8291	1637.9213	-56.27	320 - 334	0 --- K.VQNSINIVVIGRPTK.G
1655.8876	1654.8803	1654.8429	22.6	1 - 13	0 --- -.MLPYVSIFYEYIHK.Q + Oxidation (M)
1655.8876	1654.8803	1654.8429	22.6	1 - 13	0 --- -.MLPYVSIFYEYIHK.Q + Oxidation (M)
1852.9109	1851.9036	1851.9267	-12.48	381 - 395	1 --- R.HALYDYDIKFAINNR.C
1987.9928	1986.9855	1986.9033	41.4	364 - 379	0 --- K.NYDSMVYPNELIEWSK.R

2044.0343 2043.0270 2043.0273 -0.11 14 - 30 0 --- K.QVEHNINTQESILEVYK.E  
 2101.0442 2100.0369 2099.9834 25.5 96 - 114 0 --- R.FVVGDEITALSGDGIYCR.K  
 2132.0586 2131.0513 2130.9932 27.3 363 - 379 1 --- R.KNYDSMVYPNELIEWSK.R + Oxidation (M)  
 2229.1431 2228.1358 2228.0783 25.8 96 - 115 1 --- R.FVVGDEITALSGDGIYCRK.R  
 2612.2639 2611.2566 2611.3057 -18.81 298 - 319 1 --- R.FEDITIIIDKDTETAAEWVQK.V  
 No match to: 983.5101, 983.5101, 1020.5240, 1111.5724, 1128.5876, 1128.5876, 1237.6635, 1237.6635, 1238.6617, 1240.6185, 1264.5852, 1268.6685, 1321.6318, 1359.7007, 1526.7316, 1535.7430, 1553.7305, 1581.7991, 1585.7638, 1585.7638, 1613.7943, 1617.7871, 1622.8406, 1623.8719, 1642.7791, 1646.7791, 1656.8875, 1669.8287, 1675.8157, 1683.8801, 1688.8220, 1698.8710, 1712.8909, 1776.8607, 1780.8707, 1790.8802, 1794.8982, 1818.9015, 1822.9069, 1851.9087, 1879.9312, 1993.9722, 2045.0272, 2107.0676, 2175.0510, 2179.0537, 2183.0798, 2188.0881, 2220.0830, 2225.1509, 2242.1299, 2282.1685, 2330.1729, 2386.1428, 3153.6074, 3163.6431, 3210.6301

3. [gi|517685802](#) Mass: 43305 Score: 88 Expect: 0.13 Matches: 13

galactonate dehydratase [Rhizobium sp. 42MFCr.1]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1296.6947	1295.6874	1295.6180	53.6	198	209	0	---	R.LSVAEASFCNK.L
1359.7007	1358.6934	1358.6942	-0.59	45	56	1	---	R.EKAVSGAIEHYR.E
1613.7943	1612.7870	1612.8937	-66.13	210	223	1	---	K.LGRGVLDLFLEPIR.D
1617.7871	1616.7798	1616.8099	-18.62	366	378	1	---	K.AESFRFEAPHLK.R
1622.8406	1621.8333	1621.8246	5.38	198	212	1	---	R.LSVAEASFCNKLGR.G
1638.8364	1637.8291	1637.7838	27.7	328	341	0	---	K.LGFDNSDFFPVQPR.L
1655.8876	1654.8803	1654.7912	53.8	236	250	0	---	R.MTDIPFAIGEEFASK.W
1655.8876	1654.8803	1654.7912	53.8	236	250	0	---	R.MTDIPFAIGEEFASK.W
1780.8707	1779.8634	1779.8944	-17.42	153	167	1	---	R.FFPVGQNSKDIFEP.R
1790.8802	1789.8729	1789.8934	-11.42	63	76	1	---	R.DPMQIGRIWQEVYR.S
1822.9069	1821.8996	1821.9010	-0.73	182	197	0	---	R.EALGDEVVLGIDYHHR.L
2179.0537	2178.0464	2178.2201	-79.74	2	20	1	---	M.TTTFKITAIPYVWVGTR.N
2330.1729	2329.1656	2329.2980	-56.85	7	26	1	---	K.ITAIPYVWVGTRNQMLVK.V + Oxidation (M)

No match to: 983.5101, 983.5101, 1020.5240, 1111.5724, 1128.5876, 1128.5876, 1237.6635, 1237.6635, 1238.6617, 1240.6185, 1264.5852, 1267.6644, 1268.6685, 1321.6318, 1526.7316, 1535.7430, 1553.7305, 1581.7991, 1585.7638, 1585.7638, 1601.8033, 1623.8719, 1642.7878, 1646.7791, 1656.8875, 1669.8287, 1675.8157, 1683.8801, 1688.8220, 1698.8710, 1712.8909, 1776.8607, 1794.8982, 1818.9015, 1851.9087, 1852.9109, 1879.9312, 1987.9928, 1993.9722, 2044.0343, 2045.0272, 2101.0442, 2107.0676, 2132.0586, 2175.0510, 2183.0798, 2188.0881, 2220.0830, 2225.1509, 2229.1431, 2242.1299, 2282.1685, 2386.1428, 2612.2639, 3153.6074, 3163.6431, 3210.6301

4. [gi|403295466](#) Mass: 133524 Score: 86 Expect: 0.22 Matches: 25

PREDICTED: protein FAM184A isoform X1 [Saimiri boliviensis boliviensis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1128.5876	1127.5803	1127.6550	-66.21	440	448	1	---	K.QQIIELEKK.V
1128.5876	1127.5803	1127.6550	-66.21	440	448	1	---	K.QQIIELEKK.V
1264.5852	1263.5779	1263.5990	-16.64	917	926	1	---	R.IRSESNQMR.L + Oxidation (M)
1321.6318	1320.6245	1320.6925	-51.46	247	257	1	---	K.LIEDYEGKLNK.A
1359.7007	1358.6934	1358.6790	10.6	363	374	1	---	K.EVESELAARER.L
1526.7316	1525.7243	1525.7558	-20.65	510	521	1	---	K.KLQMLEEQHNK.E
1553.7305	1552.7232	1552.7886	-42.08	174	186	1	---	R.SFGQLQVQFEKDK.R
1585.7638	1584.7565	1584.7943	-23.83	493	506	0	---	K.HHMAIEAVHNSAIR.D
1585.7638	1584.7565	1584.7943	-23.83	493	506	0	---	K.HHMAIEAVHNSAIR.D
1601.8033	1600.7960	1600.7892	4.25	493	506	0	---	K.HHMAIEAVHNSAIR.D + Oxidation (M)
1613.7943	1612.7870	1612.8056	-11.54	602	615	0	---	K.DALLNVEGELQQR.Q
1622.8406	1621.8333	1621.9039	-43.51	110	123	1	---	R.KIQVLASLEDHIK.M
1642.7878	1641.7805	1641.7707	6.01	207	221	1	---	K.SQDHSASVNGQKE.T
1646.7791	1645.7718	1645.8233	-31.25	987	1000	0	---	R.ESKPEDIQMITDLK.A
1655.8876	1654.8803	1654.7984	49.5	511	523	1	---	K.LQMLEEQHNKE.L
1655.8876	1654.8803	1654.7984	49.5	511	523	1	---	K.LQMLEEQHNKE.L
1656.8875	1655.8802	1655.7824	59.1	471	484	0	---	R.LEEEVMQLNEAHSK.T
1669.8287	1668.8214	1668.8505	-17.41	936	949	1	---	R.LEKELDMVTADHLR.E
1698.8710	1697.8637	1697.8406	13.6	222	235	1	---	K.TEELHRMEVEALNK.T
1776.8607	1775.8534	1775.8611	-4.33	310	325	0	---	K.TELQMVQDEAGSLDK.C
1818.9015	1817.8942	1817.9193	-13.78	986	1000	1	---	K.RESKPEDIQMITDLK.A + Oxidation (M)
2107.0676	2106.0603	2105.9847	35.9	137	153	1	---	K.HRVEDMLCAEAQHVQR.I
2175.0510	2174.0437	2174.0451	-0.63	565	585	0	---	K.SEQGLGSAEGVIASLQESQER.L
2242.1299	2241.1226	2241.0405	36.6	793	810	1	---	R.ESMEGFRIEMQELQTLR.F + Oxidation (M)
2282.1685	2281.1612	2281.1120	21.6	466	484	1	---	K.NLQNRLEEEVMQLNEAHSK.T

No match to: 983.5101, 983.5101, 1020.5240, 1111.5724, 1237.6635, 1237.6635, 1238.6617, 1240.6185, 1267.6644, 1268.6685, 1296.6947, 1535.7430, 1581.7991, 1617.7871, 1623.8719, 1638.8364, 1675.8157, 1683.8801, 1688.8220, 1712.8909, 1780.8707, 1790.8802, 1794.8982, 1822.9069, 1851.9087, 1852.9109, 1879.9312, 1987.9928, 1993.9722, 2044.0343, 2045.0272, 2101.0442, 2132.0586, 2179.0537, 2183.0798, 2188.0881, 2220.0830, 2225.1509, 2229.1431, 2330.1729, 2386.1428, 2612.2639, 3153.6074, 3163.6431, 3210.6301

5. [gi|516242151](#) Mass: 283896 Score: 85 Expect: 0.24 Matches: 28

hypothetical protein [Streptococcus agalactiae]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
983.5101	982.5028	982.4607	42.8	314	322	0	---	R.SDETGSLFK.Q
983.5101	982.5028	982.4607	42.8	314	322	0	8	R.SDETGSLFK.Q
1111.5724	1110.5651	1110.5570	7.30	276	284	1	---	R.IFRNGEYGR.D
1267.6644	1266.6571	1266.6204	29.0	314	324	1	---	R.SDETGSLFQKR.G
1268.6685	1267.6612	1267.6118	39.0	2022	2031	1	---	K.IPMSKEYQEK.H + Oxidation (M)
1321.6318	1320.6245	1320.6561	-23.92	406	417	1	---	R.EADKASFSLPEK.N
1535.7430	1534.7357	1534.7200	10.3	2211	2222	0	---	K.FYNLPMLSMFK.E + Oxidation (M)
1581.7991	1580.7918	1580.7869	3.15	1022	1035	1	---	R.FDDMGNLKTIVTK.D
1613.7943	1612.7870	1612.7767	6.41	1305	1320	0	---	R.NGGVIAFITSSGTMCK.K + Oxidation (M)
1622.8406	1621.8333	1621.7406	57.2	503	516	0	---	R.EDMTQILSWSDAAR.R
1638.8364	1637.8291	1637.7355	57.2	503	516	0	---	R.EDMTQILSWSDAAR.R + Oxidation (M)
1642.7878	1641.7805	1641.7998	-11.74	1706	1719	1	---	R.ELPHLGVEENGKEK.E
1646.7791	1645.7718	1645.7485	14.2	469	482	1	---	K.DTFRGGNGFYIDER.E
1655.8876	1654.8803	1654.7587	73.5	2340	2353	1	---	K.GDGEFNIYDDIRNK.L
1655.8876	1654.8803	1654.7587	73.5	2340	2353	1	---	K.GDGEFNIYDDIRNK.L
1656.8875	1655.8802	1655.8770	1.92	87	100	1	---	K.KVDYIFDITQTVSK.N
1712.8909	1711.8836	1711.7584	73.2	1800	1814	1	---	K.DRGNDLAEMTFGTNR.V + Oxidation (M)

1776.8607	1775.8534	1775.9669	-63.88	15	-	29	1	---	K.QDVLQSEAEYLKLLK.V
1794.8982	1793.8909	1793.8366	30.3	503	-	517	1	---	R.EDMTQILSWSDAARR.I + Oxidation (M)
1818.9015	1817.8942	1817.8254	37.9	1016	-	1030	1	---	K.DYTITRFDDMGNNLK.T + Oxidation (M)
1852.9109	1851.9036	1851.9513	-25.74	1303	-	1320	1	---	K.VRNGGVIAFIATSSGTMDK.K
2044.0343	2043.0270	2042.9691	28.4	2264	-	2281	1	---	R.ADAVRNQNQVEPTEDNMLK.I
2101.0442	2100.0369	2099.9834	25.5	1036	-	1054	0	---	K.DNTEYLGGMITGSDVIPYR.K
2132.0586	2131.0513	2131.1637	-52.72	2289	-	2307	1	---	K.LALDQRLINPLLPDDPNK.V
2175.0510	2174.0437	2174.0749	-14.35	1105	-	1123	1	---	R.LNNNLEAISMLNRVESGER.E + Oxidation (M)
2229.1431	2228.1358	2228.0783	25.8	1036	-	1055	1	---	K.DNTEYLGGMITGSDVIPYR.K
2330.1729	2329.1656	2329.1914	-11.07	646	-	667	1	---	K.VHGFITEDEVLATISRGSGVDK.G
2386.1428	2385.1355	2385.1886	-22.25	2354	-	2374	1	---	K.LVNMGIPKEEIAFIHEADTDK.Q + Oxidation (M)
No match to: 1020.5240, 1128.5876, 1128.5876, 1237.6635, 1237.6635, 1238.6617, 1240.6185, 1264.5852, 1296.6947, 1359.7007, 1526.7316, 1553.7305, 1585.7638, 1585.7638, 1601.8033, 1617.7871, 1623.8719, 1669.8287, 1675.8157, 1683.8801, 1688.8220, 1698.8710, 1780.8707, 1790.8802, 1822.9069, 1851.9087, 1879.9312, 1987.9928, 1993.9722, 2045.0272, 2107.0676, 2179.0537, 2183.0798, 2188.0881, 2220.0830, 2225.1509, 2242.1299, 2282.1685, 2612.2639, 3153.6074, 3163.6431, 3210.6301									

6. [gil307186672](#) Mass: 88853 Score: 84 Expect: 0.3 Matches: 18  
Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase, partial [Camponotus floridanus]

observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1237.6635	1236.6562	1236.6074	39.5	429	- 437	0	---	K.FIQCWTNLR.L
1237.6635	1236.6562	1236.6074	39.5	429	- 437	0	---	K.FIQCWTNLR.L
1264.5852	1263.5779	1263.5666	8.96	714	- 723	1	---	K.GRQYPPMEDR.S + Oxidation (M)
1267.6644	1266.6571	1266.6932	-28.46	438	- 449	0	---	R.LSSAPPLQLGER.Y
1268.6685	1267.6612	1267.6884	-21.45	85	- 96	0	---	K.DAQLNAASPILR.L
1585.7638	1584.7565	1584.7831	-16.75	631	- 643	1	---	R.CLNPGKYAQHLER.W
1585.7638	1584.7565	1584.7831	-16.75	631	- 643	1	---	R.CLNPGKYAQHLER.W
1601.8033	1600.7960	1600.7304	41.0	695	- 707	1	---	K.GFFCQVTNEDRTK.C
1622.8406	1621.8333	1621.8273	3.70	193	- 206	0	---	R.MILVDIDDFVGEK.G + Oxidation (M)
1638.8364	1637.8291	1637.9213	-56.25	85	- 99	1	---	K.DAQLNAASPILRLR.TA
1655.8876	1654.8803	1654.8427	22.7	335	- 348	0	---	K.VTSTEEYPHLRPAR.L
1655.8876	1654.8803	1654.8427	22.7	335	- 348	0	---	K.VTSTEEYPHLRPAR.L
1712.8909	1711.8836	1711.9720	-51.62	3	- 18	1	---	K.VEVTKGKSLPVLTLNDK.G
1818.9015	1817.8942	1818.0152	-66.52	727	- 741	1	---	K.LLQRYYLSHNTALVK.L
1822.9069	1821.8996	1822.0141	-62.85	225	- 241	1	---	R.IQALVPGFKFNLGFSKG.Y
1851.9087	1850.9014	1851.0003	-53.40	663	- 677	1	---	R.QNPVETLHELQRFK.I
2188.0881	2187.0808	2187.1623	-37.25	360	- 377	1	---	K.VLPRQTCGLFTHTIFIER.Y
2330.1729	2329.1656	2329.2464	-34.68	213	- 233	1	---	K.DDVMALLATQQRQALVPGFK.F + Oxidation (M)
No match to: 983.5101, 983.5101, 1020.5240, 1111.5724, 1128.5876, 1128.5876, 1238.6617, 1240.6185, 1296.6947, 1321.6318, 1359.7007, 1526.7316, 1535.7430, 1553.7305, 1581.7991, 1613.7943, 1617.7871, 1623.8719, 1642.7878, 1646.7791, 1656.8875, 1669.8287, 1675.8157, 1683.8801, 1688.8220, 1698.8710, 1776.8607, 1780.8707, 1790.8802, 1794.8982, 1852.9109, 1879.9312, 1987.9928, 1993.9722, 2044.0343, 2045.0272, 2101.0442, 2107.0676, 2132.0586, 2175.0510, 2179.0537, 2183.0798, 2220.0830, 2225.1509, 2229.1431, 2242.1299, 2282.1685, 2386.1428, 2612.2639, 3153.6074, 3163.6431, 3210.6301								

7. [gil851188668](#) Mass: 68812 Score: 83 Expect: 0.43 Matches: 15  
ATPase AAA [Candidatus Acidianus copahuensis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1128.5876	1127.5803	1127.6550	-66.26	19	- 30	0	---	R.ALGVTGLGDVVGK.V
1128.5876	1127.5803	1127.6550	-66.26	19	- 30	0	---	R.ALGVTGLGDVVGK.V
1296.6947	1295.6874	1295.6609	20.5	169	- 180	0	---	K.LGYLESSETGIK.V
1526.7316	1525.7243	1525.7446	-13.30	1	- 13	1	---	-.MTADELYTGIKER.I
1622.8406	1621.8333	1621.8861	-32.56	397	- 410	1	---	K.STVDNIMRGLYLLK.E
1638.8364	1637.8291	1637.8811	-31.71	397	- 410	1	---	K.STVDNIMRGLYLLK.E + Oxidation (M)
1656.8875	1655.8802	1655.8406	23.9	245	- 259	1	---	K.SVIEGTDAFEKLYGK.M
1794.8982	1793.8909	1793.8941	-1.79	548	- 564	1	---	R.ITSSVAESMGISRTAR.I
1993.9722	1992.9649	1993.0707	-53.05	586	- 603	1	---	K.MKISVPVPPPIGHYDLSK.A + Oxidation (M)
2044.0343	2043.0270	2043.0201	3.41	434	- 450	0	---	K.ILIFDIYNGELDDFTQK.I
2045.0272	2044.0199	2043.9650	26.9	487	- 503	1	---	R.FFPSLQGSSEEDTNYVRR.V
2101.0442	2100.0369	2100.1772	-66.77	565	- 582	1	---	R.ILSWEKNGVAFIISPLWK.Q
2229.1431	2228.1358	2228.1365	-0.30	432	- 450	1	---	K.GKILIFDIYNGELDDFTQK.I
2330.1729	2329.1656	2329.1940	-12.20	203	- 222	1	---	K.TSFIKDIISLYLIEDEESK.V
3163.6431	3162.6358	3162.6866	-16.06	520	- 547	1	---	R.IGFIFATHNPDLNIIIVQLASTKVFVR.I
No match to: 983.5101, 983.5101, 1020.5240, 1111.5724, 1237.6635, 1237.6635, 1238.6617, 1240.6185, 1264.5852, 1267.6644, 1268.6685, 1321.6318, 1359.7007, 1535.7430, 1553.7305, 1581.7991, 1585.7638, 1585.7638, 1601.8033, 1613.7943, 1617.7871, 1623.8719, 1642.7878, 1646.7791, 1655.8876, 1655.8876, 1669.8287, 1675.8157, 1683.8801, 1688.8220, 1698.8710, 1712.8909, 1776.8607, 1780.8707, 1790.8802, 1818.9015, 1822.9069, 1851.9087, 1852.9109, 1879.9312, 1987.9928, 2107.0676, 2132.0586, 2175.0510, 2179.0537, 2183.0798, 2188.0881, 2220.0830, 2225.1509, 2242.1299, 2282.1685, 2386.1428, 2612.2639, 3153.6074, 3210.6301								

8. [gil725593996](#) Mass: 127771 Score: 82 Expect: 0.55 Matches: 24  
PREDICTED: protein FAM184A isoform X2 [Saimiri boliviensis boliviensis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1128.5876	1127.5803	1127.6550	-66.21	440	- 448	1	---	K.QQIIELEKK.V
1128.5876	1127.5803	1127.6550	-66.21	440	- 448	1	---	K.QQIIELEKK.V
1264.5852	1263.5779	1263.5990	-16.64	917	- 926	1	---	R.IRSESNNQMR.L + Oxidation (M)
1321.6318	1320.6245	1320.6925	-51.46	247	- 257	1	---	K.LIEDYEGKLNK.A
1359.7007	1358.6934	1358.6790	10.6	363	- 374	1	---	K.EVESELAARER.L
1526.7316	1525.7243	1525.7558	-20.65	510	- 521	1	---	K.KLQMELEEQHNK.E
1553.7305	1552.7232	1552.7886	-42.08	174	- 186	1	---	R.SFGQLQVQFEKDK.R
1585.7638	1584.7565	1584.7943	-23.83	493	- 506	0	---	K.HHMAIEAVHSNAIR.D
1585.7638	1584.7565	1584.7943	-23.83	493	- 506	0	---	K.HHMAIEAVHSNAIR.D
1601.8033	1600.7960	1600.7892	4.25	493	- 506	0	---	K.HHMAIEAVHSNAIR.D + Oxidation (M)
1613.7943	1612.7870	1612.8056	-11.54	602	- 615	0	---	K.DALLNVEGELQQR.Q
1622.8406	1621.8333	1621.9039	-43.51	110	- 123	1	---	R.KIQVLEASLEDHIK.M
1642.7878	1641.7805	1641.7707	6.01	207	- 221	1	---	K.SQQDHSASVNGQGEK.T
1646.7791	1645.7718	1645.8233	-31.25	938	- 951	0	---	R.ESKPEDIQMITDLK.A
1655.8876	1654.8803	1654.7984	49.5	511	- 523	1	---	K.LQMELEEQHNKEK.L
1655.8876	1654.8803	1654.7984	49.5	511	- 523	1	---	K.LQMELEEQHNKEK.L
1656.8875	1655.8802	1655.7824	59.1	471	- 484	0	---	R.LEEEVMQLNEAHSK.T

1698.8710 1697.8637 1697.8406 13.6 222 - 235 1 --- K.TEELHRMEVEALNK.T  
 1776.8607 1775.8534 1775.8611 -4.33 310 - 325 0 --- K.TELQMVQDEAGSLDK.C  
 1818.9015 1817.8942 1817.9193 -13.78 937 - 951 1 --- K.RESKPEDIQMITDLK.A + Oxidation (M)  
 2107.0676 2106.0603 2105.9847 35.9 137 - 153 1 --- K.HRVEDMQLCAEAQHVQR.I  
 2175.0510 2174.0437 2174.0451 -0.63 565 - 585 0 --- K.SEQGLGSAEGVIAQLQESQER.L  
 2242.1299 2241.1226 2241.0405 36.6 793 - 810 1 --- R.ESMEGFRIEMEQLQTLR.F + Oxidation (M)  
 2282.1685 2281.1612 2281.1120 21.6 466 - 484 1 --- K.NLQNLREEVQMQLNEAHSK.T

No match to: 983.5101, 983.5101, 1020.5240, 1111.5724, 1237.6635, 1237.6635, 1238.6617, 1240.6185, 1267.6644, 1268.6685, 1296.6947, 1535.7430, 1581.7991, 1617.7871, 1623.8719, 1638.8364, 1669.8287, 1675.8157, 1683.8801, 1688.8220, 1712.8909, 1780.8707, 1790.8802, 1794.8982, 1822.9069, 1851.9087, 1852.9109, 1879.9312, 1987.9928, 1993.9722, 2044.0343, 2045.0272, 2101.0442, 2132.0586, 2179.0537, 2183.0798, 2188.0881, 2220.0830, 2225.1509, 2229.1431, 2330.1729, 2386.1428, 2612.2639, 3153.6074, 3163.6431, 3210.6301

9. [gi|573949653](#) Mass: 15625 Score: 81 Expect: 0.65 Matches: 9

PREDICTED: bifunctional monodehydroascorbate reductase and carbonic anhydrase nectarin-3-like [Oryza brachyantha]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1128.5876	1127.5803	1127.5651	13.5	126	135	0	---	R.AVGVVYSWLA.-
1128.5876	1127.5803	1127.5651	13.5	126	135	0	---	R.AVGVVYSWLA.-
1240.6185	1239.6112	1239.6360	-20.00	79	89	0	---	R.RPVSGSGVYYR.Y
1581.7991	1580.7918	1580.7392	33.3	47	59	0	---	R.DATLDMLEPYIER.V + Oxidation (M)
1655.8876	1654.8803	1654.7621	71.5	65	78	1	---	R.KMHEVEVDGEVDPR.R + Oxidation (M)
1655.8876	1654.8803	1654.7621	71.5	65	78	1	24	R.KMHEVEVDGEVDPR.R + Oxidation (M)
1675.8157	1674.8084	1674.7321	45.6	1	14	0	---	-M.HMHSPEHAIDGR.R + Oxidation (M)
1879.9312	1878.9239	1878.9397	-8.39	47	62	1	---	R.DATLDMLEPYIERVAK.K + Oxidation (M)
2044.0343	2043.0270	2042.9592	33.2	15	31	1	---	R.RYDLELHMLHQSDSSGR.Y

No match to: 983.5101, 983.5101, 1020.5240, 1111.5724, 1237.6635, 1237.6635, 1238.6617, 1264.5852, 1267.6644, 1268.6685, 1296.6947, 1321.6318, 1359.7007, 1526.7316, 1535.7430, 1553.7305, 1585.7638, 1585.7638, 1601.8033, 1613.7943, 1617.7871, 1622.8406, 1623.8719, 1638.8364, 1642.7878, 1646.7791, 1656.8875, 1669.8287, 1683.8801, 1688.8220, 1698.8710, 1712.8909, 1776.8607, 1780.8707, 1790.8802, 1794.8982, 1818.9015, 1822.9069, 1851.9087, 1852.9109, 1987.9928, 1993.9722, 2045.0272, 2101.0442, 2107.0676, 2132.0586, 2175.0510, 2179.0537, 2183.0798, 2188.0881, 2220.0830, 2225.1509, 2229.1431, 2242.1299, 2282.1685, 2330.1729, 2386.1428, 2612.2639, 3153.6074, 3163.6431, 3210.6301

10. [gi|915505193](#) Mass: 39921 Score: 81 Expect: 0.65 Matches: 13

S-adenosylmethionine:tRNA ribosyltransferase-isomerase [Helicobacter pylori]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
983.5101	982.5028	982.5124	-9.71	131	138	0	---	R.LIAFYDNK.T
983.5101	982.5028	982.5124	-9.71	131	138	0	---	R.LIAFYDNK.T
1111.5724	1110.5651	1110.6397	-67.13	139	148	0	---	K.TPLNQANILK.L
1321.6318	1320.6245	1320.7190	-71.54	71	82	1	---	R.LFGSKHAFSSK.T
1613.7943	1612.7870	1612.7596	17.0	333	345	1	---	K.YRFYSYDGMIL.L + Oxidation (M)
1622.8406	1621.8333	1621.9515	-72.86	139	152	1	---	K.TPLNQANILKLLER.Y
1623.8719	1622.8646	1622.8623	1.44	306	320	0	---	K.SSLLMLVSAMIGLEK.T + 2 Oxidation (M)
1655.8876	1654.8803	1654.7515	77.9	3	15	0	---	K.EFDLESYDYLHPK.E
1655.8876	1654.8803	1654.7515	77.9	3	15	0	---	K.EFDLESYDYLHPK.E
1852.9109	1851.9036	1852.0049	-54.70	306	322	1	---	K.SSLLMLVSAMIGLEKTK.E + 2 Oxidation (M)
2175.0510	2174.0437	2174.1161	-33.27	38	55	1	---	R.SQKITHTTFEHVLDFFPK.N
2330.1729	2329.1656	2329.2583	-39.79	205	226	1	---	K.GFKHAFLLHVGAGTFLGVETK.D
2386.1428	2385.1355	2385.1866	-21.39	111	130	0	---	K.IFFDANYHAEVLELLHNGQR.L

No match to: 1020.5240, 1128.5876, 1128.5876, 1237.6635, 1237.6635, 1238.6617, 1240.6185, 1264.5852, 1267.6644, 1268.6685, 1296.6947, 1359.7007, 1526.7316, 1535.7430, 1553.7305, 1581.7991, 1585.7638, 1585.7638, 1601.8033, 1617.7871, 1638.8364, 1642.7878, 1646.7791, 1656.8875, 1669.8287, 1675.8157, 1683.8801, 1688.8220, 1698.8710, 1712.8909, 1776.8607, 1780.8707, 1790.8802, 1794.8982, 1818.9015, 1822.9069, 1851.9087, 1879.9312, 1987.9928, 1993.9722, 2044.0343, 2045.0272, 2101.0442, 2107.0676, 2132.0586, 2179.0537, 2183.0798, 2188.0881, 2220.0830, 2225.1509, 2229.1431, 2242.1299, 2282.1685, 2612.2639, 3153.6074, 3163.6431, 3210.6301

11. [gi|4098878](#) Mass: 22582 Score: 80 Expect: 0.76 Matches: 9

heat shock protein 70B/SSB1 [Pneumocystis wakefieldiae]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1526.7316	1525.7243	1525.7413	-11.10	8	20	0	---	R.TTPSYVAFLENER.L
1535.7430	1534.7357	1534.8065	-46.12	84	97	0	---	K.IFSPQEISAMVLGK.M + Oxidation (M)
1553.7305	1552.7232	1552.7886	-42.08	113	126	0	---	K.AVITVPAYFSDSQR.L
1581.7991	1580.7918	1580.8886	-61.19	21	35	1	---	R.LIGESAKNQAVINPK.N
1613.7943	1612.7870	1612.9148	-79.23	127	142	1	---	R.LATKDAGTIAGLDVLR.I
1675.8157	1674.8084	1674.7234	50.8	192	207	0	---	R.ATAGDTHLGGEDFDNR.-
1794.8982	1793.8909	1793.9419	-28.44	84	99	1	---	K.IFSPQEISAMVLGKMK.E + Oxidation (M)
2225.1509	2224.1436	2224.1375	2.74	8	27	1	---	R.TTPSYVAFLENERLIGESAK.N
2282.1685	2281.1612	2281.0723	39.0	1	20	1	---	-ANDQSNRTTPSYVAFLENER.L

No match to: 983.5101, 983.5101, 1020.5240, 1111.5724, 1128.5876, 1128.5876, 1237.6635, 1237.6635, 1238.6617, 1240.6185, 1264.5852, 1267.6644, 1268.6685, 1296.6947, 1321.6318, 1359.7007, 1585.7638, 1585.7638, 1601.8033, 1617.7871, 1622.8406, 1623.8719, 1638.8364, 1642.7878, 1646.7791, 1655.8876, 1656.8875, 1669.8287, 1683.8801, 1688.8220, 1698.8710, 1712.8909, 1776.8607, 1780.8707, 1790.8802, 1818.9015, 1822.9069, 1851.9087, 1852.9109, 1879.9312, 1987.9928, 1993.9722, 2044.0343, 2045.0272, 2101.0442, 2107.0676, 2132.0586, 2175.0510, 2179.0537, 2183.0798, 2188.0881, 2220.0830, 2229.1431, 2242.1299, 2330.1729, 2386.1428, 2612.2639, 3153.6074, 3163.6431, 3210.6301

12. [gi|446541073](#) Mass: 57246 Score: 80 Expect: 0.89 Matches: 13

OMA87-like protein, partial [Leptospira interrogans]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1535.7430	1534.7357	1534.7932	-37.48	102	113	1	---	R.LRFFAQYFNTTK.N
1553.7305	1552.7232	1552.8184	-61.31	414	427	1	---	R.FVGRAMGFGTLELR.W
1581.7991	1580.7918	1580.7623	18.6	492	504	1	---	R.EDKQLFVNFSHAF.-
1655.8876	1654.8803	1654.7951	51.5	202	217	0	---	R.LYSGVSSGPGFNVTD.R.M
1655.8876	1654.8803	1654.7951	51.5	202	217	0	---	R.LYSGVSSGPGFNVTD.R.M
1675.8157	1674.8084	1674.8002	4.93	453	466	1	---	R.VWNDEHKAGLTDYK.Y
1683.8801	1682.8728	1682.9104	-22.33	250	264	1	---	R.LSNIVHVDGKFKVK.S
1822.9069	1821.8996	1821.8315	37.4	20	35	0	---	K.ISAQENFTGCDKPEAR.K
1852.9109	1851.9036	1851.8468	30.7	373	388	0	---	R.FGFGISDGDVPFFFYR.N
2044.0343	2043.0270	2043.0861	-28.93	389	407	1	---	R.NLWGTEVTSGLGGLRTL.R.G
2220.0830	2219.0757	2219.0430	14.8	202	221	1	---	R.LYSGVSSGPGFNVTD.R.M.Y
2330.1729	2329.1656	2329.0750	38.9	318	338	1	---	R.DFEPDPNSGVFLGTYEKASK.T
2386.1428	2385.1355	2385.2176	-34.41	265	287	1	---	K.SVDPIFEGTPLNSGQVPNAKTK.L

No match to: 983.5101, 983.5101, 1020.5240, 1111.5724, 1128.5876, 1128.5876, 1237.6635, 1237.6635, 1238.6617, 1240.6185, 1264.5852, 1267.6644, 1268.6685, 1296.6947, 1321.6318, 1359.7007, 1526.7316, 1585.7638, 1585.7638, 1601.8033, 1613.7943, 1617.7871, 1622.8406, 1623.8719, 1638.8364, 1642.7878, 1646.7791, 1656.8875, 1669.8287, 1688.8220, 1698.8710, 1712.8909, 1776.8607, 1780.8707, 1790.8802, 1794.8982, 1818.9087, 1851.9087, 1879.9312, 1987.9928, 1993.9722, 2045.0272, 2101.0442, 2107.0676, 2132.0586, 2175.0510, 2179.0537, 2183.0798, 2188.0881, 2225.1509, 2229.1431, 2242.1299, 2282.1685, 2612.2639, 3153.6074, 3163.6431, 3210.6301

13. [gi|541049004](#) Mass: 53961 Score: 79 Expect: 0.94 Matches: 13

putative v-type proton atpase subunit h 2 [Ascaris suum]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
983.5101	982.5028	982.4398	64.1	190	- 196	0	---	R.CLQMMLR.I + 2 Oxidation (M)
983.5101	982.5028	982.4398	64.1	190	- 196	0	---	R.CLQMMLR.I + 2 Oxidation (M)
1238.6617	1237.6544	1237.6740	-15.85	80	- 90	0	---	R.TMINFITTVAK.D
1268.6685	1267.6612	1267.6448	12.9	369	- 378	1	---	R.FNEKDFELVK.I
1296.6947	1295.6874	1295.6106	59.3	178	- 189	0	---	K.ASGNEYINTTAR.C
1535.7430	1534.7357	1534.7847	-31.92	290	- 302	1	---	R.EAALQMVQCKTLK.T + Oxidation (M)
1656.8875	1655.8802	1655.8665	8.31	421	- 435	1	---	K.QAVMKLLAADDPNVR.Y + Oxidation (M)
1675.8157	1674.8084	1674.9358	-76.06	124	- 136	1	---	K.RTIWSWFLGILQR.Q
1794.8982	1793.8909	1793.8907	0.10	174	- 189	1	---	K.EQLKASGNEYINTTAR.C
2107.0676	2106.0603	2106.1585	-46.63	426	- 444	1	---	K.LLAADDPNVRVYHALLAVQK.L
2229.1431	2228.1358	2228.0500	38.5	178	- 196	1	---	K.ASGNEYINTTARCLQMMLR.I
2386.1428	2385.1355	2385.1821	-19.52	137	- 157	1	---	R.QDNFIVNQMSVIAKLACFGK.T + Oxidation (M)
3210.6301	3209.6228	3209.6696	-14.56	125	- 151	1	---	R.TIWSWFLGILQRQDNFIVNQMSVIAK.L + Oxidation (M)

No match to: 1020.5240, 1111.5724, 1128.5876, 1237.6635, 1237.6635, 1240.6185, 1264.5852, 1267.6644, 1321.6318, 1359.7007, 1526.7316, 1553.7305, 1581.7991, 1585.7638, 1585.7638, 1601.8033, 1613.7943, 1617.7871, 1622.8406, 1623.8719, 1638.8364, 1642.7878, 1646.7791, 1655.8876, 1655.8876, 1669.8287, 1683.8801, 1688.8220, 1698.8710, 1712.8909, 1776.8607, 1780.8707, 1790.8802, 1818.9015, 1822.9069, 1851.9087, 1852.9109, 1879.9312, 1987.9928, 1993.9722, 2044.0343, 2045.0272, 2101.0442, 2132.0586, 2175.0510, 2179.0537, 2183.0798, 2188.0881, 2220.0830, 2225.1509, 2242.1299, 2282.1685, 2330.1729, 2612.2639, 3153.6074, 3163.6431

14. [gi|771612100](#) Mass: 63606 Score: 79 Expect: 0.96 Matches: 14

hypothetical protein [Desulfonatronum thioautotrophicum]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
983.5101	982.5028	982.4832	20.0	372	- 380	0	---	R.LTDVAHGDR.E
983.5101	982.5028	982.4832	20.0	372	- 380	0	---	R.LTDVAHGDR.E
1264.5852	1263.5779	1263.6129	-27.67	71	- 82	0	---	K.SELVMAAVDASR.A + Oxidation (M)
1268.6685	1267.6612	1267.6269	27.1	372	- 382	1	---	R.LTDVAHGDRER.Q
1613.7943	1612.7870	1612.8784	-56.67	414	- 428	0	---	R.TDQALAVVQTALER.H
1642.7878	1641.7805	1641.7569	14.4	433	- 446	1	---	R.FNDQGVRMQADFSK.D
1688.8220	1687.8147	1687.7658	29.0	105	- 119	1	---	R.EAMSTSYVGRAVMDR.F + Oxidation (M)
1698.8710	1697.8637	1697.9212	-33.88	381	- 394	1	---	R.ERQYASIIAELHR.L
2044.0343	2043.0270	2042.9592	33.2	2	- 20	0	---	M.PSPAQPSPHNLPQNPAAMDR.K + Oxidation (M)
2132.0586	2131.0513	2131.1498	-46.21	414	- 432	1	---	R.TDQALAVVQTALERHQPR.F
2175.0510	2174.0437	2173.9997	20.3	1	- 20	0	---	-MPSPAQPSPHNLPQNPAAMDR.K + Oxidation (M)
2183.0798	2182.0725	2182.1429	-32.26	350	- 370	1	---	R.MTANITHAIRNPLTAAGGFAR.R
2225.1509	2224.1436	2224.1712	-12.41	311	- 328	1	---	R.QQLQQWNLALETEVRVR.L
2229.1431	2228.1358	2228.0571	35.3	138	- 155	1	---	R.NPKYEANPTLNMIEYFR.Q

No match to: 1020.5240, 1111.5724, 1128.5876, 1237.6635, 1237.6635, 1238.6617, 1240.6185, 1267.6644, 1296.6947, 1321.6318, 1359.7007, 1526.7316, 1553.7305, 1581.7991, 1585.7638, 1585.7638, 1601.8033, 1617.7871, 1622.8406, 1623.8719, 1638.8364, 1646.7791, 1655.8876, 1655.8876, 1656.8875, 1669.8287, 1675.8157, 1683.8801, 1712.8909, 1776.8607, 1780.8707, 1790.8802, 1794.8982, 1818.9015, 1822.9069, 1851.9087, 1852.9109, 1879.9312, 1987.9928, 1993.9722, 2045.0272, 2101.0442, 2107.0676, 2179.0537, 2188.0881, 2220.0830, 2242.1299, 2282.1685, 2330.1729, 2386.1428, 2612.2639, 3153.6074, 3163.6431, 3210.6301

15. [gi|799250295](#) Mass: 93952 Score: 78 Expect: 1.3 Matches: 18

hypothetical protein HIM\_01726 [Hirsutella minnesotensis 3608]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1111.5724	1110.5651	1110.5240	37.0	609	- 617	0	---	K.QMDLAHQPR.K + Oxidation (M)
1128.5876	1127.5803	1127.5320	42.9	475	- 485	0	---	R.HPNGSSSSVTR.Q
1128.5876	1127.5803	1127.5320	42.9	475	- 485	0	---	R.HPNGSSSSVTR.Q
1237.6635	1236.6562	1236.6211	28.4	486	- 496	0	---	R.QPQPQAQTPSR.L
1237.6635	1236.6562	1236.6211	28.4	486	- 496	0	---	R.QPQPQAQTPSR.L
1264.5852	1263.5779	1263.6572	-62.70	571	- 583	0	---	K.IGQGASGSVYVAR.I
1321.6318	1320.6245	1320.7190	-71.54	635	- 645	0	---	R.NIVNFLDAFLR.N
1535.7430	1534.7357	1534.7046	20.3	71	- 85	0	---	R.QQTNTDGMGGVAVK.K + Oxidation (M)
1553.7305	1552.7232	1552.6125	71.3	152	- 167	0	---	R.TDGSSSSPGDDGQTK.T
1585.7638	1584.7565	1584.8260	-43.82	822	- 835	1	---	R.ASADELLAHDFLKR.G
1585.7638	1584.7565	1584.8260	-43.82	822	- 835	1	0	R.ASADELLAHDFLKR.G
1638.8364	1637.8291	1637.8260	1.90	227	- 240	1	---	K.LLNSSAITKEDYER.N
1646.7791	1645.7718	1645.7361	21.7	540	- 553	1	---	R.MSTMSENEVMAKLE.E + 3 Oxidation (M)
1794.8982	1793.8909	1793.9420	-28.45	805	- 819	1	---	K.ELKAFLSVCLCDVIK.S
1987.9928	1986.9855	1987.0738	-44.44	132	- 149	1	---	R.DVLNVGRVEAQATIFEIK.R
2179.0537	2178.0464	2178.1294	-38.08	403	- 424	1	---	R.FNPARAAPSAPKPSGSPSNGLR.A
2188.0881	2187.0808	2187.0556	11.5	382	- 402	0	---	K.VPLAQEIGGGYSPSTNQADR.F
3153.6074	3152.6001	3152.4438	49.6	320	- 346	1	---	R.RPGPGEQPQPMQTMSSSTVVSQDMLR.E + 3 Oxidation (M)

No match to: 983.5101, 983.5101, 1020.5240, 1238.6617, 1240.6185, 1267.6644, 1268.6685, 1296.6947, 1359.7007, 1526.7316, 1581.7991, 1601.8033, 1613.7943, 1617.7871, 1622.8406, 1623.8719, 1642.7878, 1655.8876, 1655.8876, 1656.8875, 1669.8287, 1675.8157, 1683.8801, 1688.8220, 1698.8710, 1712.8909, 1776.8607, 1780.8707, 1790.8802, 1818.9015, 1822.9069, 1851.9087, 1852.9109, 1879.9312, 1993.9722, 2044.0343, 2045.0272, 2101.0442, 2107.0676, 2132.0586, 2175.0510, 2183.0798, 2220.0830, 2225.1509, 2229.1431, 2242.1299, 2282.1685, 2330.1729, 2386.1428, 2612.2639, 3163.6431, 3210.6301

16. [gi|456972883](#) Mass: 60186 Score: 77 Expect: 1.4 Matches: 13

outer membrane protein, OMP85 family [Leptospira interrogans serovar Grippotyphosa str. LT2186]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1535.7430	1534.7357	1534.7932	-37.48	125	- 136	1	---	R.LRFFAQYFNTTK.N
1553.7305	1552.7232	1552.8184	-61.31	437	- 450	1	---	R.FVGRAMGFGTLELR.W
1581.7991	1580.7918	1580.7623	18.6	515	- 527	1	---	R.EDKQLFVNFSHAF.-
1655.8876	1654.8803	1654.7951	51.5	225	- 240	0	---	R.LYSGVSSGPGFNVTD.R.M
1655.8876	1654.8803	1654.7951	51.5	225	- 240	0	---	R.LYSGVSSGPGFNVTD.R.M
1675.8157	1674.8084	1674.8002	4.93	476	- 489	1	---	R.VWNDEHKAGLTDYK.Y
1683.8801	1682.8728	1682.9104	-22.33	273	- 287	1	---	R.LSNNVHVNDGKFKV.K



1822.9069 1821.8996 1821.8315 37.4 43 - 58 0 --- K.ISAQENFTGCDKPEAR.K  
 1851.9087 1850.9014 1850.8628 20.9 396 - 411 0 --- R.FGFGISDGNVPFFEYR.N  
 2044.0343 2043.0270 2043.0861 -28.93 412 - 430 1 --- R.NLWGTENTVSGLGGLRTL.R.G  
 2220.0830 2219.0757 2219.0430 14.8 225 - 244 1 --- R.LYSGVSSGPGFNVTRDMYR.Y  
 2330.1729 2329.1656 2329.0750 38.9 341 - 361 1 --- R.DFEPDPNSGVFLGTYEKASK.T  
 2386.1428 2385.1355 2385.2176 -34.41 288 - 310 1 --- K.SVDPIFEGTPLSNSGQVPNAKTK.L  
**No match to:** 983.5101, 983.5101, 1020.5240, 1111.5724, 1128.5876, 1128.5876, 1237.6635, 1237.6635, 1238.6617, 1240.6185, 1264.5852, 1267.6644, 1268.6685, 1296.6947, 1321.6318, 1359.7007, 1526.7316, 1585.7638, 1585.7638, 1601.8033, 1613.7943, 1617.7871, 1622.8406, 1623.8719, 1638.8364, 1642.7878, 1646.7791, 1656.8875, 1669.8287, 1688.8220, 1698.8710, 1712.8909, 1776.8607, 1780.8707, 1790.8802, 1794.8982, 1818.9015, 1852.9109, 1879.9312, 1987.9928, 1993.9722, 2045.0272, 2101.0442, 2107.0676, 2132.0586, 2175.0510, 2179.0537, 2183.0798, 2188.0881, 2225.1509, 2229.1431, 2242.1299, 2282.1685, 2612.2639, 3153.6074, 3163.6431, 3210.6301

17. [gi|736810611](#) Mass: 35344 Score: 77 Expect: 1.5 Matches: 12

hypothetical protein [[Eubacterium] sulci]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1020.5240	1019.5167	1019.4593	56.3	212	-	220	0	R.NMSPEEIGK.M + Oxidation (M)
1111.5724	1110.5651	1110.6397	-67.13	2	-	11	0	M.DGIININKPK.D
1128.5876	1127.5803	1127.5611	17.1	127	-	135	1	K.LYEYAREGK.T
1128.5876	1127.5803	1127.5611	17.1	127	-	135	1	K.LYEYAREGK.T
1264.5852	1263.5779	1263.6459	-53.78	287	-	298	1	K.AGEFLGTAKENK.G
1535.7430	1534.7357	1534.7959	-39.24	181	-	195	1	R.ALGCGAAMSSSLTRIK.S
1553.7305	1552.7232	1552.7079	9.86	196	-	209	0	K.SGCFDIADAIDIEK.I
1794.8982	1793.8909	1793.8869	2.23	194	-	209	1	R.IKSGCFDIADAIDIEK.I
1822.9069	1821.8996	1821.8931	3.59	196	-	211	1	K.SGCFDIADAIDIEKIR.N
2132.0586	2131.0513	2131.1460	-44.42	31	-	51	0	R.VGHLGTLDPMAEGVLPVTIGR.A
2179.0537	2178.0464	2178.1507	-47.87	102	-	121	1	K.AVEAFRGVISQVPPMYSALK.V + Oxidation (M)
2183.0798	2182.0725	2182.0293	19.8	173	-	193	1	R.SICADIGRALGCGAAMSSLTR.I + Oxidation (M)

**No match to:** 983.5101, 983.5101, 1237.6635, 1237.6635, 1238.6617, 1240.6185, 1267.6644, 1268.6685, 1296.6947, 1321.6318, 1359.7007, 1526.7316, 1581.7991, 1585.7638, 1585.7638, 1601.8033, 1613.7943, 1617.7871, 1622.8406, 1623.8719, 1638.8364, 1642.7878, 1646.7791, 1655.8876, 1655.8876, 1656.8875, 1669.8287, 1675.8157, 1683.8801, 1688.8220, 1698.8710, 1712.8909, 1776.8607, 1780.8707, 1790.8802, 1818.9015, 1851.9087, 1852.9109, 1879.9312, 1987.9928, 1993.9722, 2044.0343, 2045.0272, 2101.0442, 2107.0676, 2175.0510, 2188.0881, 2220.0830, 2225.1509, 2229.1431, 2242.1299, 2282.1685, 2330.1729, 2386.1428, 2612.2639, 3153.6074, 3163.6431, 3210.6301

18. [gi|815697785](#) Mass: 36358 Score: 77 Expect: 1.6 Matches: 12

lytic enzyme [Stenotrophomonas maltophilia]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1240.6185	1239.6112	1239.6208	-7.70	199	-	211	0	R.GEVGAPAQPTTGR.D
1359.7007	1358.6934	1358.7459	-38.62	102	-	113	1	K.YHGRGYLPLVGK.E
1585.7638	1584.7565	1584.7968	-25.40	62	-	76	1	R.NGNGALESARQEALR.G
1585.7638	1584.7565	1584.7968	-25.40	62	-	76	1	R.NGNGALESARQEALR.G
1617.7871	1616.7798	1616.7365	26.8	91	-	105	1	R.MGNAPGDSLKYHGR.G
1638.8364	1637.8291	1637.8485	-11.85	196	-	211	1	R.LERGEVGAPAQPTTGR.D
1655.8876	1654.8803	1654.8750	3.20	162	-	177	1	R.EATRALNGALNGIEAR.Q
1655.8876	1654.8803	1654.8750	3.20	162	-	177	1	R.EATRALNGALNGIEAR.Q
1675.8157	1674.8084	1674.8763	-40.54	276	-	291	0	R.TLFAVQGALGDPAMLR.A + Oxidation (M)
1698.8710	1697.8637	1697.8267	21.8	260	-	275	1	K.AGMSRIDHLLAGNDGR.T + Oxidation (M)
2188.0881	2187.0808	2187.1470	-30.26	276	-	296	1	R.TLFAVQGALGDPAMLRASVDR.E
2612.2639	2611.2566	2611.3388	-31.45	234	-	259	1	K.MGPQSGRLRSVQELDAAAGALALSQK.A

**No match to:** 983.5101, 983.5101, 1020.5240, 1111.5724, 1128.5876, 1128.5876, 1237.6635, 1237.6635, 1238.6617, 1240.6185, 1264.5852, 1267.6644, 1268.6685, 1296.6947, 1321.6318, 1359.7007, 1526.7316, 1535.7430, 1553.7305, 1581.7991, 1601.8033, 1613.7943, 1622.8406, 1623.8719, 1642.7878, 1646.7791, 1656.8875, 1669.8287, 1683.8801, 1688.8220, 1712.8909, 1776.8607, 1780.8707, 1790.8802, 1794.8982, 1818.9015, 1822.9069, 1851.9087, 1852.9109, 1879.9312, 1987.9928, 1993.9722, 2044.0343, 2045.0272, 2101.0442, 2107.0676, 2132.0586, 2175.0510, 2179.0537, 2183.0798, 2220.0830, 2225.1509, 2229.1431, 2242.1299, 2282.1685, 2330.1729, 2386.1428, 3153.6074, 3163.6431, 3210.6301

19. [gi|218191195](#) Mass: 28374 Score: 77 Expect: 1.6 Matches: 10

hypothetical protein OsI\_08122 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1240.6185	1239.6112	1239.6322	-16.90	153	-	162	0	R.AMDFLVLEFR.N
1267.6644	1266.6571	1266.6092	37.9	110	-	120	1	R.LENKYSSDPSPK.Y
1296.6947	1295.6874	1295.6431	34.2	209	-	220	0	K.FMEVISGTGDIK.A
1553.7305	1552.7232	1552.7807	-37.01	207	-	220	1	R.EKFMEVISGTGDIK.A
1669.8287	1668.8214	1668.7739	28.5	50	-	64	0	R.EMAETVFTPSLEGMK.H
1822.9069	1821.8996	1821.9546	-30.19	68	-	83	0	K.SESSVILTKPFLDVCK.Q
1851.9087	1850.9014	1850.9138	-6.67	186	-	201	1	K.KWHGWLASSSFTVAMK.L + Oxidation (M)
1852.9109	1851.9036	1851.9288	-13.60	209	-	225	1	K.FMEVISGTGDIKADIEK.F
1879.9312	1878.9239	1878.9226	0.70	221	-	235	1	K.ADIEKFCTTFYPFLK.E
2188.0881	2187.0808	2187.0517	13.3	121	-	138	1	K.YEQLYSVMQEEVQNKTAK.G

**No match to:** 983.5101, 983.5101, 1020.5240, 1111.5724, 1128.5876, 1128.5876, 1237.6635, 1237.6635, 1238.6617, 1240.6185, 1264.5852, 1268.6685, 1296.6947, 1321.6318, 1359.7007, 1526.7316, 1535.7430, 1553.7305, 1581.7991, 1585.7638, 1601.8033, 1613.7943, 1617.7871, 1622.8406, 1623.8719, 1638.8364, 1642.7878, 1646.7791, 1655.8876, 1655.8876, 1656.8875, 1669.8287, 1675.8157, 1683.8801, 1688.8220, 1698.8710, 1712.8909, 1776.8607, 1780.8707, 1790.8802, 1794.8982, 1818.9015, 1822.9069, 1851.9087, 1852.9109, 1879.9312, 1987.9928, 1993.9722, 2044.0343, 2045.0272, 2101.0442, 2107.0676, 2132.0586, 2175.0510, 2179.0537, 2183.0798, 2220.0830, 2225.1509, 2229.1431, 2242.1299, 2282.1685, 2330.1729, 2386.1428, 2612.2639, 3153.6074, 3163.6431, 3210.6301

20. [gi|966498831](#) Mass: 22294 Score: 77 Expect: 1.6 Matches: 9

TetR family transcriptional regulator [Legionella santicrocruis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1359.7007	1358.6934	1358.6507	31.5	39	-	49	0	K.TSSIIHYYPYPTK.E
1656.8875	1655.8802	1655.8519	17.1	50	-	63	0	K.EDLAVAVIDWQLER.M
1818.9015	1817.8942	1817.9267	-17.86	101	-	117	0	K.MCLGILASDVLSLPEK.L + Oxidation (M)
2044.0343	2043.0270	2043.1108	-41.00	101	-	119	1	K.MCLGILASDVLSLPEK.L.N
2107.0676	2106.0603	2106.1064	-21.88	3	-	20	1	K.LTMMQEKILNTAESLIQK.M + Oxidation (M)
2188.0881	2187.0808	2187.2085	-58.38	154	-	172	1	K.NNLPKYLILQLEGLGLMSR.L + Oxidation (M)
2282.1685	2281.1612	2281.2358	-32.69	30	-	49	1	K.DIALIVIGIKTSSIIHYYPYPTK.E
2330.1729	2329.1656	2329.1776	-5.15	10	-	29	1	K.ILNTAESLIQKMGYHAFSYK.D + Oxidation (M)
3210.6301	3209.6228	3209.7370	-35.56	73	-	100	1	K.FNNALSLEKQLQVVDVILSLTLHDEM.K

**No match to:** 983.5101, 983.5101, 1020.5240, 1111.5724, 1128.5876, 1128.5876, 1237.6635, 1237.6635, 1238.6617, 1240.6185, 1264.5852, 1267.6644, 1268.6685, 1296.6947, 1321.6318, 1359.7007, 1526.7316, 1535.7430, 1553.7305, 1581.7991, 1585.7638, 1585.7638, 1601.8033, 1613.7943, 1617.7871, 1622.8406, 1623.8719, 1638.8364, 1642.7878, 1646.7791, 1655.8876, 1655.8876, 1656.8875, 1669.8287, 1675.8157, 1683.8801, 1688.8220, 1698.8710, 1712.8909, 1776.8607, 1780.8707, 1790.8802, 1794.8982, 1818.9015, 1822.9069, 1851.9087, 1852.9109, 1879.9312, 1987.9928, 1993.9722, 2044.0343, 2045.0272, 2101.0442, 2107.0676, 2132.0586, 2175.0510, 2179.0537, 2183.0798, 2220.0830, 2225.1509, 2229.1431, 2242.1299, 2282.1685, 2330.1729, 2386.1428, 2612.2639, 3153.6074, 3163.6431, 3210.6301

1698.8710, 1712.8909, 1776.8607, 1780.8707, 1790.8802, 1794.8982, 1822.9069, 1851.9087, 1852.9109, 1879.9312, 1987.9928, 1993.9722, 2045.0272, 2101.0442, 2132.0586, 2175.0510, 2179.0537, 2183.0798, 2220.0830, 2225.1509, 2229.1431, 2242.1299, 2386.1428, 2612.2639, 3153.6074, 3163.6431

## 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 :  $\pm 80$  ppm  
Fragment Mass Tolerance:  $\pm 0.3$  Da  
Max Missed Cleavages : 1  
Instrument type : MALDI-TOF-TOF  
Query1 (983.5101,1+) : <no title>  
Query2 (983.5101,1+) : MaldiWellID: 60694, SpectrumID: 127302,  
Query3 (1020.5240,1+) : <no title>  
Query4 (1111.5724,1+) : <no title>  
Query5 (1128.5876,1+) : <no title>  
Query6 (1128.5876,1+) : MaldiWellID: 60694, SpectrumID: 127303,  
Query7 (1237.6635,1+) : <no title>  
Query8 (1237.6635,1+) : MaldiWellID: 60694, SpectrumID: 127304,  
Query9 (1238.6617,1+) : <no title>  
Query10 (1240.6185,1+) : <no title>  
Query11 (1264.5852,1+) : <no title>  
Query12 (1267.6644,1+) : <no title>  
Query13 (1268.6685,1+) : <no title>  
Query14 (1296.6947,1+) : <no title>  
Query15 (1321.6318,1+) : <no title>  
Query16 (1359.7007,1+) : <no title>  
Query17 (1526.7316,1+) : <no title>  
Query18 (1535.7430,1+) : <no title>  
Query19 (1553.7305,1+) : <no title>  
Query20 (1581.7991,1+) : <no title>  
Query21 (1585.7638,1+) : <no title>  
Query22 (1585.7638,1+) : MaldiWellID: 60694, SpectrumID: 127300,  
Query23 (1601.8033,1+) : <no title>  
Query24 (1613.7943,1+) : <no title>  
Query25 (1617.7871,1+) : <no title>  
Query26 (1622.8406,1+) : <no title>  
Query27 (1623.8719,1+) : <no title>  
Query28 (1638.8364,1+) : <no title>  
Query29 (1642.7878,1+) : <no title>  
Query30 (1646.7791,1+) : <no title>  
Query31 (1655.8876,1+) : <no title>  
Query32 (1655.8876,1+) : MaldiWellID: 60694, SpectrumID: 127301,  
Query33 (1656.8875,1+) : <no title>  
Query34 (1669.8287,1+) : <no title>  
Query35 (1675.8157,1+) : <no title>  
Query36 (1683.8801,1+) : <no title>  
Query37 (1688.8220,1+) : <no title>  
Query38 (1698.8710,1+) : <no title>  
Query39 (1712.8909,1+) : <no title>  
Query40 (1776.8607,1+) : <no title>  
Query41 (1780.8707,1+) : <no title>  
Query42 (1790.8802,1+) : <no title>  
Query43 (1794.8982,1+) : <no title>  
Query44 (1818.9015,1+) : <no title>  
Query45 (1822.9069,1+) : <no title>  
Query46 (1851.9087,1+) : <no title>  
Query47 (1852.9109,1+) : <no title>  
Query48 (1879.9312,1+) : <no title>  
Query49 (1987.9928,1+) : <no title>  
Query50 (1993.9722,1+) : <no title>  
Query51 (2044.0343,1+) : <no title>  
Query52 (2045.0272,1+) : <no title>  
Query53 (2101.0442,1+) : <no title>  
Query54 (2107.0676,1+) : <no title>  
Query55 (2132.0586,1+) : <no title>  
Query56 (2175.0510,1+) : <no title>  
Query57 (2179.0537,1+) : <no title>  
Query58 (2183.0798,1+) : <no title>  
Query59 (2188.0881,1+) : <no title>  
Query60 (2220.0830,1+) : <no title>  
Query61 (2225.1509,1+) : <no title>  
Query62 (2229.1431,1+) : <no title>  
Query63 (2242.1299,1+) : <no title>  
Query64 (2282.1685,1+) : <no title>  
Query65 (2330.1729,1+) : <no title>  
Query66 (2386.1428,1+) : <no title>  
Query67 (2612.2639,1+) : <no title>  
Query68 (3153.6074,1+) : <no title>  
Query69 (3163.6431,1+) : <no title>  
Query70 (3210.6301,1+) : <no title>

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