

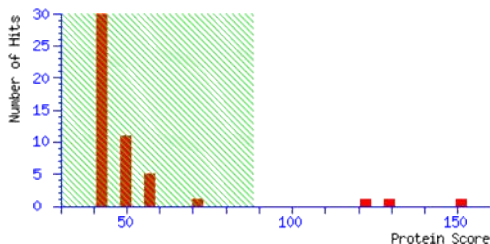
Matrix
SCIENCE

Mascot Search Results

User :
Email :
Search title : BAEDW\2019_10_16\2019_10_16\MSMS 5\C13
Database : NCBIInr 20131104 (33815671 sequences; 11795550776 residues)
Timestamp : 15 Oct 2019 at 09:37:24 GMT
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
Top Score : 151 for gi|7547266, IgG1 heavy chain constant region [Bos taurus]

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 88 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 50

Re-Search All

Search Unmatched

Index

Accession	Mass	Score	Description
1. gi 7547266	36510	151	IgG1 heavy chain constant region [Bos taurus]
2. gi 440891567	11475	129	Ig gamma-1 chain C region, partial [Bos grunniens mutus]
3. gi 108750	51391	121	Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
4. gi 91982959	36562	71	immunoglobulin gamma 1 heavy chain constant region [Bos taurus]
5. gi 498046415	7331	56	hypothetical protein [Neisseria gonorrhoeae]
6. gi 337290484	15574	56	hypothetical protein CULC22_00873 [Corynebacterium ulcerans BR-AD22]
7. gi 546357233	26141	55	putative uncharacterized protein [Blautia hydrogenotrophica CAG:147]
8. gi 489983378	9455	54	hypothetical protein [Mycobacterium phlei]
9. gi 490762382	56174	54	Endoglucanase [Clostridium termitidis]
10. gi 518548361	35653	53	LysR family transcriptional regulator [Ralstonia solanacearum]
11. gi 327305893	11598	52	hypothetical protein TERG_02355 [Trichophyton rubrum CBS 118892]
12. gi 171688784	30526	50	hypothetical protein [Podospira anserina S mat+]
13. gi 495323294	9800	50	hypothetical protein [Reinekea blandensis]
14. gi 255291985	7225	50	hypothetical protein [uncultured bacterium]
15. gi 492883710	4310	50	hypothetical protein [Afipia broomeae]
16. gi 551336008	5799	49	hypothetical protein [Perlucidibaca piscinae]
17. gi 495360281	22699	48	hypothetical protein [Pseudomonas sp. GM80]
18. gi 487598108	4479	48	propanediol utilization ferredoxin, partial [Salmonella enterica]
19. gi 401763462	16967	48	hypothetical protein ECENHK_09860 [Enterobacter cloacae subsp. cloacae ENHKU01]
20. gi 553884411	20219	47	integrase [Gloeobacter sp. JS]
21. gi 497783917	30566	46	Beta-lactamase, partial [Burkholderia ubonensis]
22. gi 150377816	75741	46	mechanosensitive ion channel MscS [Sinorhizobium medicae WSM419]
23. gi 332024455	50459	46	Dual specificity protein phosphatase 22 [Acromyrmex echinatio]
24. gi 489455877	40956	45	thiouridylase [Clostridium botulinum]
25. gi 486622113	3493	45	hypothetical protein [Escherichia coli]
26. gi 546373423	5165	45	hypothetical protein [Prevotella sp. CAG:1058]
27. gi 495396594	25331	45	peptide ABC transporter ATP-binding protein [[Bacteroides] pectinophilus]
28. gi 517950378	44454	44	hypothetical protein [Brevibacillus sp. pH8]
29. gi 493698297	5437	44	hypothetical protein [Haloterrigena thermotolerans]
30. gi 163839610	17902	44	nucleotide-binding protein [Renibacterium salmoninarum ATCC 33209]
31. gi 548180461	10887	44	uncharacterized protein [Bacteroides uniformis CAG:3]
32. gi 339499150	28813	44	short-chain dehydrogenase/reductase SDR [Treponema caldaria DSM 7334]
33. gi 522141702	27885	44	hypothetical protein [Massilia niastensis]
34. gi 497966698	29777	44	peptide ABC transporter ATP-binding protein [Streptomyces sp. SA3_actF]
35. gi 547298347	24974	43	lipoprotein ABC transporter ATP-binding protein Lold [Clostridium hathewayi CAG:224]
36. gi 496545606	25186	43	peptide ABC transporter ATP-binding protein [Lachnospiraceae bacterium 3_1_57FAA_CT1]
37. gi 479202615	25300	43	ABC-type antimicrobial peptide transport system, ATPase component [Roseburia intestinalis M50/1]
38. gi 296132158	47550	43	respiratory-chain NADH dehydrogenase domain 51 kDa subunit [Thermincola potens JR]
39. gi 494243326	26715	43	short-chain dehydrogenase [Methylophaga aminisulfidivorans]
40. gi 491299814	25459	43	hypothetical protein [Amycolatopsis azurea]
41. gi 312112921	46524	43	lytic murein transglycosylase [Rhodocrobium vannielii ATCC 17100]
42. gi 396482791	59448	43	predicted protein [Leptosphaeria maculans JN3]
43. gi 550962788	10224	43	hypothetical protein [Pseudochrobactrum sp. A018b]
44. gi 297182578	12830	43	transposase and inactivated derivatives [uncultured Rhizobiales bacterium HF4000_32B18]
45. gi 341890310	11784	43	hypothetical protein CAEBREN_08480 [Caenorhabditis brenneri]
46. gi 123189376	27775	43	hypothetical protein [Trichomonas vaginalis G3]
47. gi 493826333	24992	42	peptide ABC transporter ATP-binding protein [Clostridium hathewayi]
48. gi 332235189	5332	42	PREDICTED: protein phosphatase 1 regulatory subunit 14D [Nomascus leucogenys]
49. gi 520945468	15697	42	LysR family transcriptional regulator, partial [Pseudomonas syringae]
50. gi 486208296	4883	42	hypothetical protein [Escherichia coli]

Results List

[gi|7547266](#) Mass: 36510 Score: 151 Expect: 2.7e-008 Matches: 10

IgG1 heavy chain constant region [Bos taurus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.5625	56.3	188	197	0	---	R.IQHQQDWTGGK.E
1169.6356	1168.6283	1168.5625	56.3	188	197	0	---	R.IQHQQDWTGGK.E
1301.8031	1300.7958	1300.7252	54.3	203	214	0	---	K.VHNEGLPAPIVR.T
1301.8031	1300.7958	1300.7252	54.3	203	214	0	51	K.VHNEGLPAPIVR.T
2112.1482	2111.1409	2111.0324	51.4	155	172	0	46	K.FSWFVDDVEVNTATTKPR.E
2112.1482	2111.1409	2111.0324	51.4	155	172	0	---	K.FSWFVDDVEVNTATTKPR.E
2151.1111	2150.1038	2149.9957	50.3	273	291	0	13	K.YGTTPPQLDADGSYFLYSR.L
2151.1111	2150.1038	2149.9957	50.3	273	291	0	---	K.YGTTPPQLDADGSYFLYSR.L
2753.4365	2752.4292	2752.2877	51.4	241	263	0	---	K.STVSLTCMVTSFYPDYIAVEWQR.N
2753.4365	2752.4292	2752.2877	51.4	241	263	0	---	K.STVSLTCMVTSFYPDYIAVEWQR.N

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 1874.0144, 2005.0609, 2124.1565, 2124.1565, 2212.2224

2. [gi|440891567](#) Mass: 11475 Score: 129 Expect: 4.3e-006 Matches: 6

Ig gamma-1 chain C region, partial [Bos grunniens mutus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.5625	56.3	71	80	0	---	R.IQHQQDWTGGK.E
1169.6356	1168.6283	1168.5625	56.3	71	80	0	---	R.IQHQQDWTGGK.E
1301.8031	1300.7958	1300.7252	54.3	86	97	0	---	K.VHNEGLPAPIVR.T
1301.8031	1300.7958	1300.7252	54.3	86	97	0	51	K.VHNEGLPAPIVR.T
2112.1482	2111.1409	2111.0324	51.4	38	55	0	46	K.FSWFVDDVEVNTATTKPR.E
2112.1482	2111.1409	2111.0324	51.4	38	55	0	---	K.FSWFVDDVEVNTATTKPR.E

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 1874.0144, 2005.0609, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2212.2224, 2753.4365, 2753.4365

3. [gi|108750](#) Mass: 51391 Score: 121 Expect: 2.7e-005 Matches: 8

Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.5625	56.3	329	338	0	---	R.IQHQQDWTGGK.E
1169.6356	1168.6283	1168.5625	56.3	329	338	0	---	R.IQHQQDWTGGK.E
1301.8031	1300.7958	1300.7252	54.3	344	355	0	---	K.VHNEGLPAPIVR.T
1301.8031	1300.7958	1300.7252	54.3	344	355	0	51	K.VHNEGLPAPIVR.T
2112.1482	2111.1409	2111.0324	51.4	296	313	0	46	K.FSWFVDDVEVNTATTKPR.E
2112.1482	2111.1409	2111.0324	51.4	296	313	0	---	K.FSWFVDDVEVNTATTKPR.E
2753.4365	2752.4292	2752.2877	51.4	382	404	0	---	K.STVSLTCMVTSFYPDYIAVEWQR.N
2753.4365	2752.4292	2752.2877	51.4	382	404	0	---	K.STVSLTCMVTSFYPDYIAVEWQR.N

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 1874.0144, 2005.0609, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2212.2224

4. [gi|91982959](#) Mass: 36562 Score: 71 Expect: 2.9 Matches: 6

immunoglobulin gamma 1 heavy chain constant region [Bos taurus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.5625	56.3	188	197	0	---	R.IQHQQDWTGGK.E
1169.6356	1168.6283	1168.5625	56.3	188	197	0	---	R.IQHQQDWTGGK.E
1301.8031	1300.7958	1300.7252	54.3	203	214	0	---	K.VHNEGLPAPIVR.T
1301.8031	1300.7958	1300.7252	54.3	203	214	0	51	K.VHNEGLPAPIVR.T
2753.4365	2752.4292	2752.2877	51.4	241	263	0	---	K.STVSLTCMVTSFYPDYIAVEWQR.N
2753.4365	2752.4292	2752.2877	51.4	241	263	0	---	K.STVSLTCMVTSFYPDYIAVEWQR.N

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 1874.0144, 2005.0609, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2212.2224

5. [gi|498046415](#) Mass: 7331 Score: 56 Expect: 83 Matches: 5

hypothetical protein [Neisseria gonorrhoeae]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1874.0144	1873.0071	1872.9516	29.6	2	17	1	---	M.PSERLSDGIFPCILNR.V
2005.0609	2004.0536	2003.9921	30.7	1	17	1	---	-M.PSERLSDGIFPCILNR.V
2212.2224	2211.2151	2211.0114	92.2	47	69	0	---	K.GLMPSESGDGIIGESEAVAHAQ.-
2753.4365	2752.4292	2752.1680	94.9	18	42	1	---	R.VYETPDAGGNGVCCAMFGDQRTK.C + Oxidation (M)
2753.4365	2752.4292	2752.1680	94.9	18	42	1	---	R.VYETPDAGGNGVCCAMFGDQRTK.C + Oxidation (M)

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111

6. [gi|337290484](#) Mass: 15574 Score: 56 Expect: 91 Matches: 7

hypothetical protein CULC22_00873 [Corynebacterium ulcerans BR-AD22]

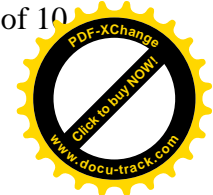
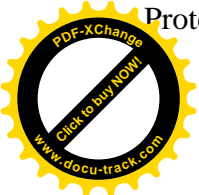
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.6339	-4.81	73	83	0	---	R.LGLPSLDTPEK.G
1169.6356	1168.6283	1168.6339	-4.79	73	83	0	---	R.LGLPSLDTPEK.G
1313.8103	1312.8030	1312.6888	87.0	118	129	1	---	K.VEPASHATFARK.G
1313.8103	1312.8030	1312.6888	87.0	117	128	1	---	R.KVEPASHATFAR.K
1325.8025	1324.7952	1324.7350	45.4	72	83	1	---	K.RLGLPSLDTPEK.G
2753.4365	2752.4292	2752.4535	-8.81	73	98	1	---	R.LGLPSLDTPEKGPELGDNVLLVDGK.G
2753.4365	2752.4292	2752.4535	-8.80	73	98	1	---	R.LGLPSLDTPEKGPELGDNVLLVDGK.G

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1339.7694, 1674.8976, 1874.0144, 2005.0609, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2212.2224

7. [gi|546357233](#) Mass: 26141 Score: 55 Expect: 1.1e+002 Matches: 9

putative uncharacterized protein [Blautia hydrogenotrophica CAG:147]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.6889	-51.86	105	114	0	---	K.NILMPLILDK.R
1169.6356	1168.6283	1168.6889	-51.84	105	114	0	---	K.NILMPLILDK.R
1313.8103	1312.8030	1312.7788	18.4	104	114	1	---	R.KNILMPLILDK.R + Oxidation (M)



1313.8103 1312.8030 1312.7788 18.4 104 - 114 1 --- R.KNILMPLILDK.R + Oxidation (M)
 1325.8025 1324.7952 1324.7900 3.91 105 - 115 1 --- K.NILMPLILDK.R
 2124.1565 2123.1492 2123.2143 -30.65 86 - 103 1 --- R.KVGLVYQFYNLPTLTVR.K
 2124.1565 2123.1492 2123.2143 -30.65 87 - 104 1 --- K.VGLVYQFYNLPTLTVRK.N
 2151.1111 2150.1038 2150.1372 -15.51 211 - 229 1 --- R.IITIEDGKIHDVFHDSAK.W
 2151.1111 2150.1038 2150.1372 -15.50 211 - 229 1 --- R.IITIEDGKIHDVFHDSAK.W

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1339.7694, 1674.8976, 1874.0144, 2005.0609, 2112.1482, 2112.1482, 2212.2224, 2753.4365, 2753.4365

8. [gi|489983378](#) Mass: 9455 Score: 54 Expect: 1.4e+002 Matches: 7

hypothetical protein [Mycobacterium phlei]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1874.0144	1873.0071	1872.9806	14.2	10 - 28	0	---	---	R.ALAAAHTAHDELTAIAAR.L
2112.1482	2111.1409	2110.9702	80.9	67 - 87	1	---	---	R.MAQTAVSAARAATAYDDADGR.V
2112.1482	2111.1409	2110.9702	80.9	67 - 87	1	---	---	R.MAQTAVSAARAATAYDDADGR.V
2124.1565	2123.1492	2123.1375	5.51	29 - 50	0	---	---	R.LSNTPTPAGLGPVGADFAALR.A
2124.1565	2123.1492	2123.1375	5.52	29 - 50	0	---	---	R.LSNTPTPAGLGPVGADFAALR.A
2753.4365	2752.4292	2752.4004	10.5	2 - 28	1	---	---	M.HADTDAIRALAAAHTAHDELTAIAAR.L
2753.4365	2752.4292	2752.4004	10.5	2 - 28	1	---	---	M.HADTDAIRALAAAHTAHDELTAIAAR.L

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 2005.0609, 2151.1111, 2151.1111, 2212.2224

9. [gi|490762382](#) Mass: 56174 Score: 54 Expect: 1.4e+002 Matches: 11

Endoglucanase [Clostridium termitidis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.5462	926.5389	926.5185	22.0	223 - 230	1	---	---	K.AIRDIDPK.H
1301.8031	1300.7958	1300.6809	88.3	49 - 60	1	---	---	K.HMLDTLGSVKGK.M + Oxidation (M)
1301.8031	1300.7958	1300.6809	88.3	49 - 60	1	---	---	K.HMLDTLGSVKGK.M + Oxidation (M)
1313.8103	1312.8030	1312.7827	15.5	11 - 22	1	---	---	K.IINTSGKVVNLR.G
1313.8103	1312.8030	1312.7827	15.5	11 - 22	1	---	---	K.IINTSGKVVNLR.G
1874.0144	1873.0071	1872.9979	4.94	1 - 17	1	---	---	-.MDLLQIENGKIINTSGK.V
2151.1111	2150.1038	2150.0545	22.9	382 - 400	1	---	---	R.NLGAENFVAQYWDSPGRVK.S
2151.1111	2150.1038	2150.0545	22.9	382 - 400	1	---	---	R.NLGAENFVAQYWDSPGRVK.S
2212.2224	2211.2151	2211.0498	74.8	305 - 323	0	---	---	R.QHNVPPIWVGEFGSQYHGEK.E
2753.4365	2752.4292	2752.1785	91.1	332 - 353	0	---	---	K.AMDDQLAVYNECDINWTTWYK.D + Oxidation (M)
2753.4365	2752.4292	2752.1785	91.1	332 - 353	0	---	---	K.AMDDQLAVYNECDINWTTWYK.D + Oxidation (M)

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1325.8025, 1339.7694, 1674.8976, 2005.0609, 2112.1482, 2112.1482, 2124.1565, 2124.1565

10. [gi|518548361](#) Mass: 35653 Score: 53 Expect: 1.9e+002 Matches: 9

LysR family transcriptional regulator [Ralstonia solanacearum]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1339.7694	1338.7621	1338.7846	-16.77	266 - 277	1	---	---	R.ILPAPVAFPKMR.F
1874.0144	1873.0071	1872.8975	58.6	1 - 15	1	---	---	-.MQMHGKDHLDYTLR.V + Oxidation (M)
2005.0609	2004.0536	2003.9986	27.5	298 - 316	0	---	---	R.MIGEVAELPQHPQLETA.-
2124.1565	2123.1492	2123.0444	49.4	194 - 211	0	---	---	K.HYIEMPHLAPAPYAVMQR.S
2124.1565	2123.1492	2123.0444	49.4	194 - 211	0	---	---	K.HYIEMPHLAPAPYAVMQR.S
2151.1111	2150.1038	2150.2074	-48.19	226 - 243	1	---	---	R.RIQVSLPYFGLVPYVLMR.T
2151.1111	2150.1038	2150.2074	-48.18	226 - 243	1	---	---	R.RIQVSLPYFGLVPYVLMR.T
2753.4365	2752.4292	2752.3636	23.8	61 - 85	1	---	---	K.SGMVPTERGHELLALAQSSLEAMER.I
2753.4365	2752.4292	2752.3636	23.9	61 - 85	1	---	---	K.SGMVPTERGHELLALAQSSLEAMER.I

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2212.2224

11. [gi|327305893](#) Mass: 11598 Score: 52 Expect: 2.4e+002 Matches: 5

hypothetical protein TERG_02355 [Trichophyton rubrum CBS 118892]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.6604	-27.47	42 - 51	0	---	---	R.QLPAYVLHTK.E
1169.6356	1168.6283	1168.6604	-27.46	42 - 51	0	18	---	R.QLPAYVLHTK.E
2005.0609	2004.0536	2004.0462	3.68	13 - 29	1	---	---	K.VVDDQTWMLVLRSSSLR.I
2753.4365	2752.4292	2752.3048	45.2	1 - 24	1	---	---	-.MIGSQDEAASEKVVDDQTWMLVLR.S + 2 Oxidation (M)
2753.4365	2752.4292	2752.3048	45.2	1 - 24	1	---	---	-.MIGSQDEAASEKVVDDQTWMLVLR.S + 2 Oxidation (M)

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 1874.0144, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2212.2224

12. [gi|171688784](#) Mass: 30526 Score: 50 Expect: 3.1e+002 Matches: 10

hypothetical protein [Podospira anserina S mat+]

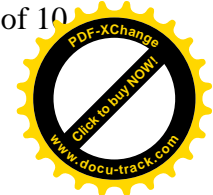
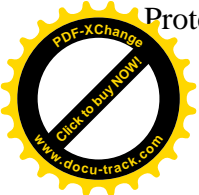
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.6564	-24.03	11 - 21	0	---	---	R.LQGVIANLEGR.V
1169.6356	1168.6283	1168.6564	-24.01	11 - 21	0	---	---	R.LQGVIANLEGR.V
1301.8031	1300.7958	1300.6987	74.7	264 - 276	1	---	---	K.AGSTILSKLTHSS.-
1301.8031	1300.7958	1300.6987	74.7	264 - 276	1	---	---	K.AGSTILSKLTHSS.-
1325.8025	1324.7952	1324.7575	28.5	10 - 21	1	---	---	K.RLQGVIANLEGR.V
2005.0609	2004.0536	2004.0635	-4.94	92 - 110	1	---	---	K.KIMDAGGLVSDIVIGMIK.E + Oxidation (M)
2112.1482	2111.1409	2111.0687	34.2	214 - 230	1	---	---	R.LETYHKQTTPVVNYQK.T
2112.1482	2111.1409	2111.0687	34.2	214 - 230	1	---	---	R.LETYHKQTTPVVNYQK.T
2124.1565	2123.1492	2122.9711	83.9	65 - 82	1	---	---	K.FNCCHLATGDMRLSQVAK.K + Oxidation (M)
2124.1565	2123.1492	2122.9711	83.9	65 - 82	1	---	---	K.FNCCHLATGDMRLSQVAK.K + Oxidation (M)

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1313.8103, 1313.8103, 1339.7694, 1674.8976, 1874.0144, 2151.1111, 2151.1111, 2212.2224, 2753.4365, 2753.4365

13. [gi|495323294](#) Mass: 9800 Score: 50 Expect: 3.1e+002 Matches: 5

hypothetical protein [Reinekea blandensis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
----------	----------	----------	-----	-------	-----	------	------	---------



1301.8031 1300.7958 1300.7350 46.7 27 - 38 1 --- R.AKLSQKPTVDSK.R
 1301.8031 1300.7958 1300.7350 46.7 27 - 38 1 --- R.AKLSQKPTVDSK.R
 1339.7694 1338.7621 1338.6425 89.4 74 - 85 1 --- R.VGFDAVCGKCVK.R
 2753.4365 2752.4292 2752.4258 1.23 41 - 64 1 --- K.VSQTDGIPLVNMENFALFVFLDRK.T
 2753.4365 2752.4292 2752.4258 1.24 40 - 63 1 --- R.KVSQTDGIPLVNMENFALFVFLDRK.K
No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1313.8103, 1313.8103, 1325.8025, 1674.8976, 1874.0144, 2005.0609, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2212.2224

14. [gi|255291985](#) Mass: 7225 Score: 50 Expect: 3.4e+002 Matches: 6

hypothetical protein [uncultured bacterium]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.6022	22.3	3	12	0	---	R.MIAIHAQTER.K
1169.6356	1168.6283	1168.6022	22.3	3	12	0	---	R.MIAIHAQTER.K
1313.8103	1312.8030	1312.6921	84.5	3	13	1	---	R.MIAIHAQTERK.R + Oxidation (M)
1313.8103	1312.8030	1312.6921	84.5	3	13	1	---	R.MIAIHAQTERK.R + Oxidation (M)
1325.8025	1324.7952	1324.7034	69.4	2	12	1	---	M.RMIAIHAQTER.K
2212.2224	2211.2151	2211.1365	35.6	34	54	1	---	R.LRGLIRPDPAVCATASAACGR.K

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1301.8031, 1301.8031, 1339.7694, 1674.8976, 1874.0144, 2005.0609, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2753.4365, 2753.4365

15. [gi|492883710](#) Mass: 4310 Score: 50 Expect: 3.5e+002 Matches: 4

hypothetical protein [Afipia broomeae]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1325.8025	1324.7952	1324.7134	61.7	1	11	0	---	-.MTMLAEIFLLK.L + Oxidation (M)
1339.7694	1338.7621	1338.7983	-27.02	12	23	1	---	K.LEALLRVAADR.R
1874.0144	1873.0071	1873.1110	-55.47	2	17	1	---	M.TMLAEIFLLKLEALLR.V
2005.0609	2004.0536	2004.1515	-48.84	1	17	1	---	-.MTMLAEIFLLKLEALLR.V

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1674.8976, 1874.0144, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2212.2224, 2753.4365, 2753.4365

16. [gi|551336008](#) Mass: 5799 Score: 49 Expect: 4.5e+002 Matches: 4

hypothetical protein [Perlucidibaca piscinae]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1301.8031	1300.7958	1300.6809	88.4	9	21	0	---	K.GIPSPSLVASMRSR.C
1301.8031	1300.7958	1300.6809	88.4	9	21	0	13	K.GIPSPSLVASMRSR.C
1674.8976	1673.8903	1673.8341	33.6	9	24	1	---	K.GIPSPSLVASMRSRCGR.V
2005.0609	2004.0536	2004.0714	-8.87	3	21	1	---	R.VVTPYKGPSPSLVASMRSR.C + Oxidation (M)

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1874.0144, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2212.2224, 2753.4365, 2753.4365

17. [gi|495360281](#) Mass: 22699 Score: 48 Expect: 5.1e+002 Matches: 8

hypothetical protein [Pseudomonas sp. GM80]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.6274	0.77	1	10	0	---	-.MPDLITPQVR.K
1169.6356	1168.6283	1168.6274	0.79	1	10	0	---	-.MPDLITPQVR.K
1313.8103	1312.8030	1312.7173	65.3	1	11	1	---	-.MPDLITPQVRK.L + Oxidation (M)
1313.8103	1312.8030	1312.7173	65.3	1	11	1	---	-.MPDLITPQVRK.L + Oxidation (M)
1674.8976	1673.8903	1673.8559	20.6	40	53	1	---	R.MRAWELADVDSLLR.E
2005.0609	2004.0536	2003.9548	49.3	12	30	0	---	K.LAAIGYGEASTDNNPQEV.R
2112.1482	2111.1409	2110.9411	94.6	70	88	0	---	R.YNQLMAASEAAINADPNMR.S + 2 Oxidation (M)
2112.1482	2111.1409	2110.9411	94.6	70	88	0	---	R.YNQLMAASEAAINADPNMR.S + 2 Oxidation (M)

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1325.8025, 1339.7694, 1874.0144, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2212.2224, 2753.4365, 2753.4365

18. [gi|487598108](#) Mass: 4479 Score: 48 Expect: 5.1e+002 Matches: 3

propanediol utilization ferredoxin, partial [Salmonella enterica]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
2005.0609	2004.0536	2004.0905	-18.41	23	44	1	---	R.AAGVVGAGGAGFPAHVKLQAV.-
2124.1565	2123.1492	2123.0164	62.6	2	20	1	21	M.STAINSEVMSLSADEIRER.V + Oxidation (M)
2124.1565	2123.1492	2123.0164	62.6	2	20	1	---	M.STAINSEVMSLSADEIRER.V + Oxidation (M)

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 1874.0144, 2112.1482, 2112.1482, 2151.1111, 2151.1111, 2212.2224, 2753.4365, 2753.4365

19. [gi|401763462](#) Mass: 16967 Score: 48 Expect: 5.6e+002 Matches: 6

hypothetical protein ECENHK_09860 [Enterobacter cloacae subsp. cloacae ENHKU01]

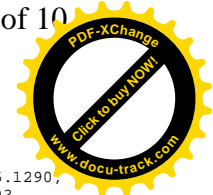
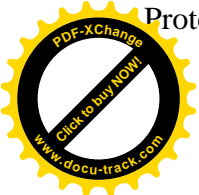
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.5637	841.5564	841.5637	-8.60	77	84	0	---	K.IALATI.IK
1169.6356	1168.6283	1168.6200	7.11	85	95	0	---	K.IGPGNIEINSR.R
1169.6356	1168.6283	1168.6135	12.7	33	42	1	---	K.RLISNHNGMK.K
1325.8025	1324.7952	1324.7211	55.9	85	96	1	---	K.IGPGNIEINSR.R
2753.4365	2752.4292	2752.4125	6.06	110	132	0	---	K.QVQFYNNLTWNHNTAFLAAIK.R
2753.4365	2752.4292	2752.4125	6.07	110	132	0	---	K.QVQFYNNLTWNHNTAFLAAIK.R

No match to: 841.1960, 841.1960, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1339.7694, 1674.8976, 1874.0144, 2005.0609, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2212.2224

20. [gi|553884411](#) Mass: 20219 Score: 47 Expect: 7.1e+002 Matches: 7

integrase [Gloeobacter sp. JS1]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.5764	44.4	138	146	0	---	R.FIEEVYNQK.R
1169.6356	1168.6283	1168.5764	44.4	138	146	0	---	R.FIEEVYNQK.R
1301.8031	1300.7958	1300.6987	74.7	45	56	0	---	R.NIDGELTSLALR.M
1301.8031	1300.7958	1300.6987	74.7	45	56	0	---	R.NIDGELTSLALR.M



2753.4365 2752.4292 2752.1707 93.9 23 - 48 0 --- R.LDGPFSYDAMVSGVPYSGDCIGVSMPL- + 2 Oxidation (M)

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2212.2224

27. [gi|495396594](#) Mass: 25331 Score: 45 Expect: 1.2e+003 Matches: 7

peptide ABC transporter ATP-binding protein [[Bacteroides] pectinophilus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.6889	-51.86	105	-	114	0	K.NILMPLLLDK.R
1169.6356	1168.6283	1168.6889	-51.84	105	-	114	0	K.NILMPLLLDK.R
1313.8103	1312.8030	1312.7788	18.4	104	-	114	1	R.KNILMPLLLDK.R + Oxidation (M)
1313.8103	1312.8030	1312.7788	18.4	104	-	114	1	R.KNILMPLLLDK.R + Oxidation (M)
1325.8025	1324.7952	1324.7900	3.91	105	-	115	1	K.NILMPLLLDKR.K
2124.1565	2123.1492	2123.2143	-30.65	86	-	103	1	R.KVGLVYQFYNIPTLTVR.K
2124.1565	2123.1492	2123.2143	-30.65	87	-	104	1	K.VGLVYQFYNIPTLTVRK.N

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1339.7694, 1674.8976, 1874.0144, 2005.0609, 2112.1482, 2112.1482, 2151.1111, 2151.1111, 2212.2224, 2753.4365, 2753.4365

28. [gi|517950378](#) Mass: 44454 Score: 44 Expect: 1.2e+003 Matches: 9

hypothetical protein [Brevibacillus sp. phR]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.5637	841.5564	841.5273	34.6	399	-	406	0	K.LLDAVLAK.I
1169.6356	1168.6283	1168.6023	22.3	36	-	45	0	R.VHVIMTENAR.K
1169.6356	1168.6283	1168.6023	22.3	36	-	45	0	R.VHVIMTENAR.K
1313.8103	1312.8030	1312.6921	84.5	36	-	46	1	R.VHVIMTENARK.F + Oxidation (M)
1313.8103	1312.8030	1312.6921	84.5	36	-	46	1	R.VHVIMTENARK.F + Oxidation (M)
1339.7694	1338.7621	1338.6350	95.0	226	-	237	1	K.MGYAIAEAARDR.G + Oxidation (M)
2005.0609	2004.0536	2004.1619	-54.03	8	-	28	1	K.TIVLGVGTGGIAAYKAAALTSK.L
2124.1565	2123.1492	2123.1660	-7.92	1	-	21	1	-.MQSLTGKTIIVLGVGTGGIAAYK.A + Oxidation (M)
2124.1565	2123.1492	2123.1660	-7.92	1	-	21	1	-.MQSLTGKTIIVLGVGTGGIAAYK.A + Oxidation (M)

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1325.8025, 1674.8976, 1874.0144, 2112.1482, 2112.1482, 2151.1111, 2151.1111, 2212.2224, 2753.4365, 2753.4365

29. [gi|493698297](#) Mass: 5437 Score: 44 Expect: 1.2e+003 Matches: 4

hypothetical protein [Haloterrigena thermotolerans]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1874.0144	1873.0071	1872.8523	82.7	2	-	17	0	M.TDAAECRPEPLEQETK.E
2005.0609	2004.0536	2003.8928	80.3	1	-	17	0	-.MTDAAECRPEPLEQETK.E
2753.4365	2752.4292	2752.1922	86.1	20	-	43	0	R.DDAHLDDIEGAGCTEWEHLAEK.R
2753.4365	2752.4292	2752.1922	86.1	20	-	43	0	R.DDAHLDDIEGAGCTEWEHLAEK.R

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2212.2224

30. [gi|163839610](#) Mass: 17902 Score: 44 Expect: 1.2e+003 Matches: 7

nucleotide-binding protein [Renibacterium salmoninarum ATCC 33209]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.5462	926.5389	926.5185	22.0	113	-	120	1	K.LIRDEGPK.G
1169.6356	1168.6283	1168.5876	34.8	28	-	36	1	K.EIAQRYDFK.G
1169.6356	1168.6283	1168.5876	34.8	28	-	36	1	K.EIAQRYDFK.G
1313.8103	1312.8030	1312.7099	70.9	121	-	132	1	K.GVKAQIQGDEL.R.V
1313.8103	1312.8030	1312.6735	98.7	16	-	27	0	K.QEVANALNQAQK.E
2753.4365	2752.4292	2752.3742	20.0	139	-	162	1	R.DDLQATMTLLKGFDEADLQFVNLR.-
2753.4365	2752.4292	2752.3742	20.0	139	-	162	1	R.DDLQATMTLLKGFDEADLQFVNLR.-

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1325.8025, 1339.7694, 1674.8976, 1874.0144, 2005.0609, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2212.2224

31. [gi|548180461](#) Mass: 10887 Score: 44 Expect: 1.3e+003 Matches: 7

uncharacterized protein [Bacteroides uniformis CAG:3]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.5585	59.8	2	-	10	1	M.ERHELENSR.E
1169.6356	1168.6283	1168.5585	59.8	2	-	10	1	M.ERHELENSR.E
1874.0144	1873.0071	1872.8754	70.3	17	-	31	1	K.ELEHALNDYGNNEKR.F
2124.1565	2123.1492	2123.1276	10.2	32	-	49	1	R.FASAVTTFHRTLQQTFLFR.S
2124.1565	2123.1492	2123.1276	10.2	32	-	49	1	R.FASAVTTFHRTLQQTFLFR.S
2151.1111	2150.1038	2150.0024	47.2	50	-	68	1	R.SMVEVIKTMGSEGYGYDLR.N + Oxidation (M)
2151.1111	2150.1038	2150.0024	47.2	50	-	68	1	R.SMVEVIKTMGSEGYGYDLR.N + Oxidation (M)

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 2005.0609, 2112.1482, 2112.1482, 2212.2224, 2753.4365, 2753.4365

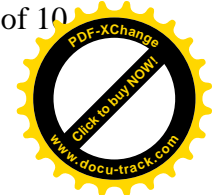
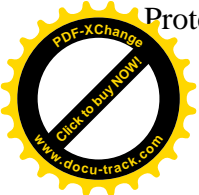
32. [gi|339499150](#) Mass: 28813 Score: 44 Expect: 1.3e+003 Matches: 8

short-chain dehydrogenase/reductase SDR [Treponema caldaria DSM 7334]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
882.6186	881.6113	881.5334	88.3	180	-	187	0	K.SAIHLTK.Y
882.6186	881.6113	881.5334	88.4	180	-	187	0	K.SAIHLTK.Y
1169.6356	1168.6283	1168.7180	-76.71	15	-	27	0	R.IVVVGAGLLGSK.I
1169.6356	1168.6283	1168.7180	-76.69	15	-	27	0	R.IVVVGAGLLGSK.I
1325.8025	1324.7952	1324.8191	-18.00	14	-	27	1	K.RIVVVGAGLLGSK.I
1874.0144	1873.0071	1872.9001	57.1	163	-	179	0	R.IYDGTAMTPVEYAAIK.S
2753.4365	2752.4292	2752.4179	4.11	163	-	187	1	R.IYDGTAMTPVEYAAIKSAIHLTK.Y + Oxidation (M)
2753.4365	2752.4292	2752.4179	4.11	163	-	187	1	R.IYDGTAMTPVEYAAIKSAIHLTK.Y + Oxidation (M)

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1339.7694, 1674.8976, 2005.0609, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2212.2224

33. [gi|522141702](#) Mass: 27885 Score: 44 Expect: 1.4e+003 Matches: 8



hypothetical protein [Massilia niastensis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.5637	841.5564	841.5022	64.5	145	- 152	0	---	R.AVVGLLDR.M
1313.8103	1312.8030	1312.7285	56.7	145	- 156	1	---	R.AVVGLLDRMSPR.H
1313.8103	1312.8030	1312.7285	56.7	145	- 156	1	---	R.AVVGLLDRMSPR.H
1674.8976	1673.8903	1673.9213	-18.50	138	- 152	1	---	R.YQSQLQRAVVGLLDR.M
2124.1565	2123.1492	2123.0912	27.3	3	- 21	1	---	K.HLPPSHGTVIDGQTFRFSK.S
2124.1565	2123.1492	2123.0912	27.3	3	- 21	1	---	K.HLPPSHGTVIDGQTFRFSK.S
2753.4365	2752.4292	2752.4218	2.71	222	- 245	1	---	R.ILAERSTHFPQMSEPELVLEALAR.L + Oxidation (M)
2753.4365	2752.4292	2752.4218	2.72	222	- 245	1	---	R.ILAERSTHFPQMSEPELVLEALAR.L + Oxidation (M)
No match to: 841.1960, 841.1960, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1301.8031, 1301.8031, 1325.8025, 1339.7694, 1874.0144, 2005.0609, 2112.1482, 2112.1482, 2151.1111, 2151.1111, 2212.2224								

34. [gi|497966698](#) Mass: 29777 Score: 44 Expect: 1.5e+003 Matches: 7

peptide ABC transporter ATP-binding protein [Streptomyces sp. SA3_actF]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1301.8031	1300.7958	1300.7537	32.4	155	- 166	1	---	R.VISMVGLLEGR.LK.H
1301.8031	1300.7958	1300.7537	32.4	155	- 166	1	---	R.VISMVGLLEGR.LK.H
1874.0144	1873.0071	1872.9768	16.2	2	- 18	0	---	M.ACVAIVPVSQEFPLVTR.L
2005.0609	2004.0536	2004.0173	18.1	1	- 18	0	---	-MACVAIVPVSQEFPLVTR.L
2151.1111	2150.1038	2150.1888	-39.54	115	- 133	1	---	R.DKIGVFVFQAFNLLPTLTAR.E
2151.1111	2150.1038	2150.1888	-39.53	115	- 133	1	---	R.DKIGVFVFQAFNLLPTLTAR.E
2212.2224	2211.2151	2211.1106	47.3	241	- 260	1	---	R.VVFLADGRIVDEMHHGPTAER.V
No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1301.8031, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2753.4365, 2753.4365								

35. [gi|547298347](#) Mass: 24974 Score: 43 Expect: 1.5e+003 Matches: 6

lipoprotein ABC transporter ATP-binding protein LolD [Clostridium hathewayi CAG:224]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.6889	-51.86	105	- 114	0	---	K.NILMPLLLDK.K
1169.6356	1168.6283	1168.6889	-51.84	105	- 114	0	---	K.NILMPLLLDK.K
1313.8103	1312.8030	1312.7788	18.4	105	- 115	1	---	K.NILMPLLLDK.K + Oxidation (M)
1313.8103	1312.8030	1312.7788	18.4	104	- 114	1	---	R.KNILMPLLLDK.K + Oxidation (M)
2124.1565	2123.1492	2123.2143	-30.65	86	- 103	1	---	R.KVGLVYQFYNIPTLTVR.K
2124.1565	2123.1492	2123.2143	-30.65	87	- 104	1	---	K.VGLVYQFYNIPTLTVRK.N
No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1325.8025, 1339.7694, 1674.8976, 1874.0144, 2005.0609, 2112.1482, 2112.1482, 2151.1111, 2151.1111, 2212.2224, 2753.4365, 2753.4365								

36. [gi|496545606](#) Mass: 25186 Score: 43 Expect: 1.5e+003 Matches: 7

peptide ABC transporter ATP-binding protein [Lachnospiraceae bacterium 3_1_57FAA_CT1]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.6889	-51.86	105	- 114	0	---	K.NILMPLLLDK.R
1169.6356	1168.6283	1168.6889	-51.84	105	- 114	0	---	K.NILMPLLLDK.R
1313.8103	1312.8030	1312.7788	18.4	104	- 114	1	---	R.KNILMPLLLDK.R + Oxidation (M)
1313.8103	1312.8030	1312.7788	18.4	104	- 114	1	---	R.KNILMPLLLDK.R + Oxidation (M)
1325.8025	1324.7952	1324.7900	3.91	105	- 115	1	---	K.NILMPLLLDK.R
2124.1565	2123.1492	2123.2143	-30.65	86	- 103	1	---	R.KVGLVYQFYNIPTLTVR.K
2124.1565	2123.1492	2123.2143	-30.65	87	- 104	1	---	K.VGLVYQFYNIPTLTVRK.N
No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1339.7694, 1674.8976, 1874.0144, 2005.0609, 2112.1482, 2112.1482, 2151.1111, 2151.1111, 2212.2224, 2753.4365, 2753.4365								

37. [gi|479202615](#) Mass: 25300 Score: 43 Expect: 1.5e+003 Matches: 7

ABC-type antimicrobial peptide transport system, ATPase component [Roseburia intestinalis M50/1]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.6889	-51.86	105	- 114	0	---	K.NILMPLLLDK.R
1169.6356	1168.6283	1168.6889	-51.84	105	- 114	0	---	K.NILMPLLLDK.R
1313.8103	1312.8030	1312.7788	18.4	104	- 114	1	---	R.KNILMPLLLDK.R + Oxidation (M)
1313.8103	1312.8030	1312.7788	18.4	104	- 114	1	---	R.KNILMPLLLDK.R + Oxidation (M)
1325.8025	1324.7952	1324.7900	3.91	105	- 115	1	---	K.NILMPLLLDK.R
2124.1565	2123.1492	2123.2143	-30.65	86	- 103	1	---	R.KVGLVYQFYNIPTLTVR.K
2124.1565	2123.1492	2123.2143	-30.65	87	- 104	1	---	K.VGLVYQFYNIPTLTVRK.N
No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1339.7694, 1674.8976, 1874.0144, 2005.0609, 2112.1482, 2112.1482, 2151.1111, 2151.1111, 2212.2224, 2753.4365, 2753.4365								

38. [gi|296132158](#) Mass: 47550 Score: 43 Expect: 1.5e+003 Matches: 8

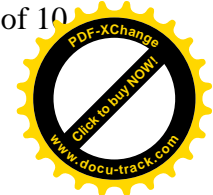
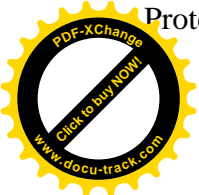
respiratory-chain NADH dehydrogenase domain 51 kDa subunit [Thermincola potens JR]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1313.8103	1312.8030	1312.6921	84.5	237	- 247	1	---	R.KEITMAHTLNR.A
1313.8103	1312.8030	1312.6921	84.5	237	- 247	1	---	R.KEITMAHTLNR.A
1325.8025	1324.7952	1324.6874	81.4	185	- 196	0	---	R.ELVETANVPVEK.Y
1674.8976	1673.8903	1673.8130	46.2	258	- 270	1	---	K.CTEICPRYLGH.R.M
1874.0144	1873.0071	1873.1149	-57.53	220	- 236	1	---	K.ITKGLIVLPENHSLAR.K
2151.1111	2150.1038	2150.2463	-66.25	355	- 373	1	---	R.LIIRLNLESYNLPAPLSPK.S
2151.1111	2150.1038	2150.2463	-66.24	355	- 373	1	---	R.LIIRLNLESYNLPAPLSPK.S
2212.2224	2211.2151	2211.1279	39.4	199	- 219	0	---	K.VIEGGPMGMTVLENPKPVT.K.I
No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1301.8031, 1301.8031, 1339.7694, 2005.0609, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2753.4365, 2753.4365								

39. [gi|494243326](#) Mass: 26715 Score: 43 Expect: 1.6e+003 Matches: 7

short-chain dehydrogenase [Methylophaga aminisulfidivorans]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.5462	926.5389	926.5120	29.1	14	- 21	1	---	R.VGLHMAKR.F + Oxidation (M)
1313.8103	1312.8030	1312.6995	78.8	154	- 165	0	---	K.AGLHNMMVLAK.K + Oxidation (M)
1313.8103	1312.8030	1312.6995	78.8	154	- 165	0	---	K.AGLHNMMVLAK.K + Oxidation (M)



2124.1565 2123.1492 2123.0647 39.8 173 - 192 0 --- K.VNAVAPGPVLFTEHSDEVR.Q
 2124.1565 2123.1492 2123.0647 39.8 173 - 192 0 --- K.VNAVAPGPVLFTEHSDEVR.Q
 2753.4365 2752.4292 2752.4184 3.92 167 - 192 1 --- K.YAPAVKVNAVAPGPVLFTEHSDEVR.Q
 2753.4365 2752.4292 2752.2432 67.6 35 - 58 1 --- R.TETDGVQEMREMGIIHTIQADFNSK.Q + Oxidation (M)
No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1301.8031, 1301.8031, 1325.8025, 1339.7694, 1674.8976, 1874.0144, 2005.0609, 2112.1482, 2112.1482, 2151.1111, 2151.1111, 2212.2224

40. [gi|491299814](#) Mass: 25459 Score: 43 Expect: 1.7e+003 Matches: 7
 hypothetical protein [Amycolatopsis azurea]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.5637	841.5564	841.5134	51.2	206	212	1	---	R.AVVRELR.A
1874.0144	1873.0071	1872.9000	57.2	46	63	1	---	R.RQADACDVIVAEGVGDAK.S
2112.1482	2111.1409	2111.2136	-34.44	1	19	1	---	-.MEIIVSNELGVRVAVLTLR.A
2112.1482	2111.1409	2111.2136	-34.43	1	19	1	---	-.MEIIVSNELGVRVAVLTLR.A
2151.1111	2150.1038	2150.1095	-2.66	29	46	1	---	R.LFPMVHIGTQAYFDTVRR.Q
2151.1111	2150.1038	2150.1095	-2.65	29	46	1	---	R.LFPMVHIGTQAYFDTVRR.Q
2212.2224	2211.2151	2211.1908	11.0	120	139	1	---	R.LMMSLLAPTLGVFLRGFGTR.G + 2 Oxidation (M)

No match to: 841.1960, 841.1960, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 2005.0609, 2124.1565, 2124.1565, 2753.4365, 2753.4365

41. [gi|312112921](#) Mass: 46524 Score: 43 Expect: 1.7e+003 Matches: 9
 lytic murein transglycosylase [Rhodococcus vannielii ATCC 17100]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.5637	841.5564	841.5134	51.2	114	121	1	---	K.ARQLIGGK.Y
1169.6356	1168.6283	1168.5546	63.1	162	171	0	---	R.SLATLAYDCR.R
1169.6356	1168.6283	1168.5546	63.1	162	171	0	---	R.SLATLAYDCR.R
2005.0609	2004.0536	2004.0428	5.38	233	251	1	---	R.SAPDVIGSSANYLKALGWR.R
2151.1111	2150.1038	2150.0103	43.5	90	108	1	---	R.GQSVFSQSFLFSDRMAAK.Y + Oxidation (M)
2151.1111	2150.1038	2150.0103	43.5	90	108	1	---	R.GQSVFSQSFLFSDRMAAK.Y + Oxidation (M)
2212.2224	2211.2151	2211.1899	11.4	395	414	1	---	K.VQKKLGLPVDSPYSPDLVSR.L
2753.4365	2752.4292	2752.2915	50.0	262	284	0	---	R.VPESMDWSQADLTIQHPLSEWQR.M
2753.4365	2752.4292	2752.2915	50.0	262	284	0	---	R.VPESMDWSQADLTIQHPLSEWQR.M

No match to: 841.1960, 841.1960, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 1874.0144, 2112.1482, 2112.1482, 2124.1565, 2124.1565

42. [gi|396482791](#) Mass: 59448 Score: 43 Expect: 1.7e+003 Matches: 5
 predicted protein [Leptospira maculans JN3]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.6313	-2.51	412	423	1	---	R.AAVATGRASHTK.Q
1169.6356	1168.6283	1168.6313	-2.49	412	423	1	18	R.AAVATGRASHTK.Q
2212.2224	2211.2151	2211.1106	47.3	1	20	0	---	-.MTLATNSEAKPLASSVWHR.G + Oxidation (M)
2753.4365	2752.4292	2752.3755	19.5	113	138	1	---	R.ELGTGGVGGVLEPAWGLAPCVWRR.A
2753.4365	2752.4292	2752.3755	19.5	112	137	1	---	R.RELGTGGVGGVLEPAWGLAPCVWR.R

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 1874.0144, 2005.0609, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111

43. [gi|550962788](#) Mass: 10224 Score: 43 Expect: 1.8e+003 Matches: 4
 hypothetical protein [Pseudochrobactrum sp. A018b]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.6676	-33.64	18	28	1	---	R.AQLTPSGLARR.A
1169.6356	1168.6283	1168.6676	-33.62	17	27	1	---	K.RAQLTPSGLAR.R
1674.8976	1673.8903	1673.8413	29.3	2	16	0	---	M.FTHAELWSAIDSVAK.R
2212.2224	2211.2151	2211.1167	44.5	59	78	0	---	K.ILEVMTAMDVMTFAQLLAGEK.S + 2 Oxidation (M)

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1874.0144, 2005.0609, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2753.4365, 2753.4365

44. [gi|297182578](#) Mass: 12830 Score: 43 Expect: 1.8e+003 Matches: 5
 transposase and inactivated derivatives [uncultured Rhizobiales bacterium HF4000_32B18]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1339.7694	1338.7621	1338.7619	0.15	22	35	0	---	K.GIAGLAAAAQEVL.R
1874.0144	1873.0071	1872.9556	27.5	88	103	0	---	R.LTAAQLAMLWEGIDWR.R
2005.0609	2004.0536	2004.0179	17.8	54	69	1	---	R.LKLLTWDGQGFCLYK.V
2151.1111	2150.1038	2150.0435	28.0	1	20	1	---	-.MIGPGTGVRVYLACGPTDMR.K
2151.1111	2150.1038	2150.0435	28.1	1	20	1	---	-.MIGPGTGVRVYLACGPTDMR.K

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 2005.0609, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2212.2224, 2753.4365, 2753.4365

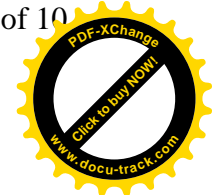
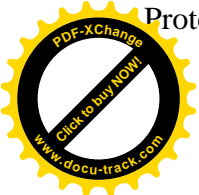
45. [gi|341890310](#) Mass: 11784 Score: 43 Expect: 1.9e+003 Matches: 5
 hypothetical protein CAEBREN_08480 [Caenorhabditis brenneri]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.5637	841.5564	841.5385	21.3	65	71	1	---	K.IAIRIEK.H
1169.6356	1168.6283	1168.5836	38.2	23	32	0	---	K.IELNHSVDSR.R
1169.6356	1168.6283	1168.5836	38.3	23	32	0	---	K.IELNHSVDSR.R
1325.8025	1324.7952	1324.6847	83.4	23	33	1	---	K.IELNHSVDSRR.I
1339.7694	1338.7621	1338.6667	71.3	48	59	1	---	K.KSSDGFTEDLIK.V

No match to: 841.1960, 841.1960, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1674.8976, 1874.0144, 2005.0609, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2212.2224, 2753.4365, 2753.4365

46. [gi|123189376](#) Mass: 27775 Score: 43 Expect: 1.9e+003 Matches: 7
 hypothetical protein [Trichomonas vaginalis G3]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1301.8031	1300.7958	1300.6744	93.4	141	150	1	---	K.DMVMLHLVRR.N + 2 Oxidation (M)
1301.8031	1300.7958	1300.6744	93.4	141	150	1	---	K.DMVMLHLVRR.N + 2 Oxidation (M)



1874.0144 1873.0071 1872.8750 70.5 2 - 17 0 --- M.YQMQSILTACFAPDTK.L
 2005.0609 2004.0536 2003.9155 68.9 1 - 17 0 --- -.MYQMQSILTACFAPDTK.L
 2212.2224 2211.2151 2211.1068 49.0 2 - 20 1 --- M.YQMQSILTACFAPDTKLPK.D
 2753.4365 2752.4292 2752.3564 26.4 186 - 208 1 --- K.QIVQDTLPQTHYDMKGCITLTFK.E + Oxidation (M)
 2753.4365 2752.4292 2752.3564 26.4 186 - 208 1 --- K.QIVQDTLPQTHYDMKGCITLTFK.E + Oxidation (M)
No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111

47. [gi|493826333](#) Mass: 24992 Score: 42 Expect: 1.9e+003 Matches: 6
 peptide ABC transporter ATP-binding protein [Clostridium hathewayi]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.6889	-51.86	105	- 114	0	---	K.NILMPLLLDK.K
1169.6356	1168.6283	1168.6889	-51.84	105	- 114	0	---	K.NILMPLLLDK.K
1313.8103	1312.8030	1312.7788	18.4	105	- 115	1	---	K.NILMPLLLDKK.S + Oxidation (M)
1313.8103	1312.8030	1312.7788	18.4	104	- 114	1	---	R.KNILMPLLLDK.K + Oxidation (M)
2124.1565	2123.1492	2123.2143	-30.65	86	- 103	1	---	R.KVGLVYQFYNIPTLTVR.K
2124.1565	2123.1492	2123.2143	-30.65	87	- 104	1	---	K.VGLVYQFYNIPTLTVR.N

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1325.8025, 1339.7694, 1674.8976, 1874.0144, 2005.0609, 2112.1482, 2112.1482, 2151.1111, 2151.1111, 2212.2224, 2753.4365, 2753.4365

48. [gi|332235189](#) Mass: 5332 Score: 42 Expect: 1.9e+003 Matches: 3
 PREDICTED: protein phosphatase 1 regulatory subunit 14D [Nomascus leucogenys]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1874.0144	1873.0071	1872.9792	14.9	2	- 17	1	---	M.DLSTEEQKTQLEAILR.N
2005.0609	2004.0536	2004.0197	16.9	1	- 17	1	---	-.MDLSTEEQKTQLEAILR.N
2212.2224	2211.2151	2211.1358	35.9	18	- 36	1	---	R.NCPHPTFAFISELLSQLKK.L

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1325.8025, 1339.7694, 1674.8976, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2753.4365, 2753.4365

49. [gi|520945468](#) Mass: 15697 Score: 42 Expect: 1.9e+003 Matches: 7
 LysR family transcriptional regulator, partial [Pseudomonas syringae]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1169.6356	1168.6283	1168.5665	52.9	129	- 138	0	---	R.EYFAVHHAPV.-
1169.6356	1168.6283	1168.5665	52.9	129	- 138	0	---	R.EYFAVHHAPV.-
1313.8103	1312.8030	1312.7616	31.6	75	- 85	1	---	R.GVLLRSLWDVR.T
1313.8103	1312.8030	1312.7616	31.6	75	- 85	1	---	R.GVLLRSLWDVR.T
2112.1482	2111.1409	2111.0548	40.8	35	- 53	0	---	R.DRPFGIWHLNGSQGAETVK.V
2112.1482	2111.1409	2111.0548	40.8	35	- 53	0	---	R.DRPFGIWHLNGSQGAETVK.V
2212.2224	2211.2151	2211.1106	47.3	102	- 121	1	---	R.QDADIWAVHTSPLMSSAKVR.V

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1301.8031, 1301.8031, 1325.8025, 1339.7694, 1674.8976, 1874.0144, 2005.0609, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2753.4365, 2753.4365

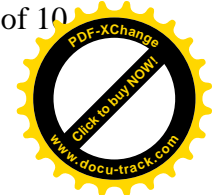
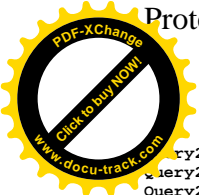
50. [gi|486208296](#) Mass: 4883 Score: 42 Expect: 2e+003 Matches: 4
 hypothetical protein [Escherichia coli]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1325.8025	1324.7952	1324.7714	18.0	5	- 17	0	---	R.NINVITALSVPGK.T
1874.0144	1873.0071	1872.9913	8.42	1	- 17	1	---	-.MNMNRNINVITALSVPGK.T + Oxidation (M)
2753.4365	2752.4292	2752.4218	2.70	18	- 42	1	---	K.TVSDDFIHAVLSNCATRIVLPAPEK.F
2753.4365	2752.4292	2752.4218	2.70	18	- 42	1	---	K.TVSDDFIHAVLSNCATRIVLPAPEK.F

No match to: 841.1960, 841.1960, 842.5637, 855.0995, 871.0715, 882.6186, 882.6186, 893.0596, 909.0323, 915.1290, 915.1290, 927.5462, 947.0018, 1051.7703, 1060.1125, 1060.1126, 1083.1046, 1169.6356, 1169.6356, 1301.8031, 1301.8031, 1313.8103, 1313.8103, 1339.7694, 1674.8976, 2005.0609, 2112.1482, 2112.1482, 2124.1565, 2124.1565, 2151.1111, 2151.1111, 2212.2224

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 : ± 100 ppm
 Fragment Mass Tolerance : ± 0.3 Da
 Max Missed Cleavages : 1
 Instrument type : MALDI-TOF-TOF
 Query1 (841.1960,1+) : Locus:1..5.0.4
 Query2 (841.1960,1+) : <no title>
 Query3 (842.5637,1+) : <no title>
 Query4 (855.0995,1+) : <no title>
 Query5 (871.0715,1+) : <no title>
 Query6 (882.6186,1+) : Locus:1..5.0.7
 Query7 (882.6186,1+) : <no title>
 Query8 (893.0596,1+) : <no title>
 Query9 (909.0323,1+) : <no title>
 Query10 (915.1290,1+) : Locus:1..5.0.12
 Query11 (915.1290,1+) : <no title>
 Query12 (927.5462,1+) : <no title>
 Query13 (947.0018,1+) : <no title>
 Query14 (1051.7703,1+) : <no title>
 Query15 (1060.1125,1+) : <no title>
 Query16 (1060.1126,1+) : Locus:1..5.0.6
 Query17 (1083.1046,1+) : <no title>
 Query18 (1169.6356,1+) : <no title>
 Query19 (1169.6356,1+) : Locus:1..5.0.5
 Query20 (1301.8031,1+) : <no title>
 Query21 (1301.8031,1+) : Locus:1..5.0.1
 Query22 (1313.8103,1+) : <no title>
 Query23 (1313.8103,1+) : Locus:1..5.0.9
 Query24 (1325.8025,1+) : <no title>



Query25 (1339.7694,1+) : <no title>
Query26 (1674.8976,1+) : <no title>
Query27 (1874.0144,1+) : <no title>
Query28 (2005.0609,1+) : <no title>
Query29 (2112.1482,1+) : Locus:1..5.0.2
Query30 (2112.1482,1+) : <no title>
Query31 (2124.1565,1+) : Locus:1..5.0.10
Query32 (2124.1565,1+) : <no title>
Query33 (2151.1111,1+) : Locus:1..5.0.3
Query34 (2151.1111,1+) : <no title>
Query35 (2212.2224,1+) : <no title>
Query36 (2753.4365,1+) : <no title>
Query37 (2753.4365,1+) : Locus:1..5.0.8

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