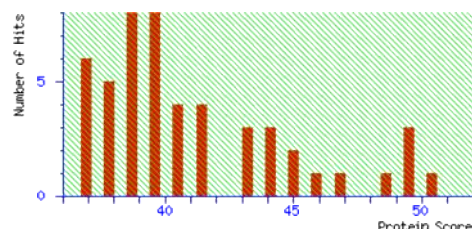


Mascot Search Results

User :
 Email :
 Search title : BAEDW\2019_10_16\2019_10_16\MSMS 5\D1
 Database : NCBIInr 20131104 (33815671 sequences; 11795550776 residues)
 Timestamp : 15 Oct 2019 at 10:55:09 GMT
 Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
 Top Score : 50 for [gi|2232299](#), IgM heavy chain constant region [Bos taurus]

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
 Protein scores greater than 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 [Help](#)

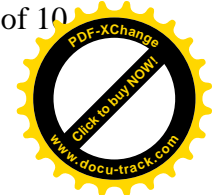
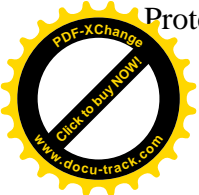
Significance threshold $p <$ Max. number of hits

Index

Accession	Mass	Score	Description
1. gi 2232299	48512	50	IgM heavy chain constant region [Bos taurus]
2. gi 33413902	49848	50	immunoglobulin mu heavy chain constant region [Bos taurus]
3. gi 206597414	28268	50	Major histocompatibility complex class II beta chain BMA2, (similar to HLA class II, D beta chain) pre
4. gi 34538498	50536	50	immunoglobulin heavy chain constant region [Bos taurus]
5. gi 518349625	5336	48	hypothetical protein [Moraxella boeveyi]
6. gi 494742220	17861	47	3-hydroxyacyl-ACP dehydratase [Bartonella melophagi]
7. gi 518846823	5061	46	hypothetical protein [Mycoplasma hominis]
8. gi 488818860	9345	45	hypothetical protein [Phaeosporidium molischianum]
9. gi 446609084	31602	45	prephenate dehydratase [Streptococcus oralis]
10. gi 518026209	30111	44	serine acetyltransferase [Afipia birgiae]
11. gi 24496448	66533	44	immunoglobulin M heavy chain secretory form [Bos taurus]
12. gi 547755423	19340	44	ribosome maturation factor RimM [Clostridium sp. CAG:221]
13. gi 492049521	6980	43	hypothetical protein [Pseudomonas amygdali]
14. gi 488127006	5046	43	hypothetical protein, partial [Helicobacter pylori]
15. gi 68535459	8368	43	hypothetical protein jk0392 [Corynebacterium jeikeium K411]
16. gi 3834667	48810	42	immunoglobulin heavy chain constant region [Bos taurus]
17. gi 547238705	13800	42	ribosomal protein S13 [Firmicutes bacterium CAG:884]
18. gi 345564418	28894	41	hypothetical protein AOL_s00083g474 [Arthrobotrys oligospora ATCC 24927]
19. gi 517947175	20170	41	hypothetical protein [Anaerococcus sp. PH9]
20. gi 522808524	25797	41	hypothetical protein [Mycobacterium marinum]
21. gi 550715204	37257	41	transcriptional activator FtrA [Enterobacter sp. MGH 8]
22. gi 516231730	9834	41	hypothetical protein [Vibrio sp. 71211]
23. gi 517496258	32907	40	hypothetical protein [Bacteroides gallinarum]
24. gi 183984872	25857	40	hypothetical protein MMAR_4904 [Mycobacterium marinum M]
25. gi 443492961	25831	40	putative deacetylase [Mycobacterium liflandii 128FXT]
26. gi 118616343	25912	39	hypothetical protein MUL_0502 [Mycobacterium ulcerans Ag99]
27. gi 491438800	10485	39	acetyltransferase [Corynebacterium jeikeium]
28. gi 491891625	32908	39	hypothetical protein [Bacteroides stercoris]
29. gi 547517138	32936	39	uncharacterized protein [Bacteroides stercoris CAG:120]
30. gi 517368986	14244	39	30S ribosomal protein S13 [Streptomyces sp. LaPPAH-108]
31. gi 516399639	5928	39	integrase [Vibrio vulnificus]
32. gi 479181342	3438	39	Helix-turn-helix domain of resolvase. [Enterococcus sp. 7L76]
33. gi 491349492	31061	39	hypothetical protein [Gordonia sputi]
34. gi 493388713	17048	39	MarR family transcriptional regulator [Streptomyces tsukubaensis]
35. gi 551036884	33460	39	hypothetical protein [Lachnospiraceae bacterium NK4A136]
36. gi 320333797	39533	39	phospho-2-dehydro-3-deoxyheptonate aldolase [Deinococcus maricopensis DSM 21211]
37. gi 409039618	29114	38	hypothetical protein PHACADRAFT_201965 [Phanerochaete carnosae HHB-10118-sp]
38. gi 187251559	20917	38	cross-over junction endonuclease RuvC [Elusimicrobium minutum Pei191]
39. gi 261260695	10351	38	Yclm [Bacillus amyloliquefaciens]
40. gi 517051098	27685	38	transcriptional regulator [Rhizobium sp. BR816]
41. gi 444720581	100358	38	General transcription factor II-I [Tupaia chinensis]
42. gi 71039991	32224	38	conserved ATPase domain protein [Macropis nuda]
43. gi 490661404	4181	38	hypothetical protein [Burkholderia pseudomallei]
44. gi 489236824	65949	37	multidrug ABC transporter ATP-binding protein [Gemella haemolysans]
45. gi 547230974	17853	37	transposase [Bacteroides intestinalis CAG:564]
46. gi 494229523	4528	37	hypothetical protein [Flavobacterium frigidis]
47. gi 28493757	41909	37	pyruvate dehydrogenase E1 component alpha subunit [Tropheryma whippelii str. Twist]
48. gi 517826373	12209	37	hypothetical protein [Hirschia maritima]
49. gi 446609078	29288	37	prephenate dehydratase, partial [Streptococcus sp. GMD1S]
50. gi 551565531	42563	37	hypothetical protein EMIHUADRAFT_210302 [Emiliania huxleyi CCMP1516]

Results List

1.	gi 2232299	Mass: 48512	Score: 50	Expect: 3.1e+002	Matches: 9
IgM heavy chain constant region [Bos taurus]					
Observed	Mr (expt)	Mr (calc)	ppm	Start	End Miss Ions Peptide
1036.6012	1035.5939	1035.5502	42.3	148 - 155	0 --- K.QISLSWFR.D
1036.6012	1035.5939	1035.5502	42.3	148 - 155	0 --- K.QISLSWFR.D



```

1194.6759 1193.6686 1193.6233 37.9 54 - 62 0 --- R.FWTFPEVL.R.D
1194.6759 1193.6686 1193.6233 37.9 54 - 62 0 18 R.FWTFPEVL.R.D
1266.6686 1265.6613 1265.6040 45.3 269 - 278 0 --- K.ALETHTYFER.H
1595.9777 1594.9704 1594.9083 38.9 110 - 124 0 --- K.AEVLSPVSVFVPPR.N
1595.9777 1594.9704 1594.9083 39.0 110 - 124 0 --- K.AEVLSPVSVFVPPR.N
1633.9124 1632.9051 1632.8413 39.1 357 - 370 0 --- K.GFAPADVFVQWLQR.G
1784.0413 1783.0340 1782.9702 35.8 325 - 340 0 --- K.DVAMKPPSVYLLPPTR.E

```

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1618.1177, 1618.1177, 1732.1512, 1902.3138, 1994.0560, 2221.2212, 2284.2476

2. [gi|33413902](#) Mass: 49848 Score: 50 Expect: 3.5e+002 Matches: 9

immunoglobulin mu heavy chain constant region [Bos taurus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1036.6012	1035.5939	1035.5502	42.3	142	-	149	0	K.QISLSWFR.D
1036.6012	1035.5939	1035.5502	42.3	142	-	149	0	K.QISLSWFR.D
1194.6759	1193.6686	1193.6233	37.9	48	-	56	0	R.FWTFPEVL.R.D
1194.6759	1193.6686	1193.6233	37.9	48	-	56	0	R.FWTFPEVL.R.D
1266.6686	1265.6613	1265.6040	45.3	263	-	272	0	K.ALETHTYFER.H
1595.9777	1594.9704	1594.9083	38.9	104	-	118	0	K.AEVLSPVSVFVPPR.N
1595.9777	1594.9704	1594.9083	39.0	104	-	118	0	K.AEVLSPVSVFVPPR.N
1633.9124	1632.9051	1632.8413	39.1	351	-	364	0	K.GFAPADVFVQWLQR.G
1784.0413	1783.0340	1782.9702	35.8	319	-	334	0	K.DVAMKPPSVYLLPPTR.E

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1618.1177, 1618.1177, 1732.1512, 1902.3138, 1994.0560, 2221.2212, 2284.2476

3. [gi|206597414](#) Mass: 28268 Score: 50 Expect: 3.6e+002 Matches: 5

Major histocompatibility complex class II beta chain BMA2, (similar to HLA class II, D beta chain) precursor [Gallus gallus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1165.7815	1164.7742	1164.7958	-18.54	2	-	12	0	M.LVLLGLLLGVR.G
1165.7815	1164.7742	1164.7958	-18.53	2	-	12	0	M.LVLLGLLLGVR.G
1296.7419	1295.7346	1295.8363	-78.45	1	-	12	0	-MLVLLGLLLGVR.G
1448.9645	1447.9572	1447.8147	98.4	115	-	128	0	R.IVPAQTGNPSVIPR.L
1448.9645	1447.9572	1447.8147	98.4	115	-	128	0	R.IVPAQTGNPSVIPR.L

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1334.9314, 1334.9314, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212, 2284.2476

4. [gi|34538498](#) Mass: 50536 Score: 50 Expect: 3.7e+002 Matches: 9

immunoglobulin heavy chain constant region [Bos taurus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1036.6012	1035.5939	1035.5502	42.3	142	-	149	0	K.QISLSWFR.D
1036.6012	1035.5939	1035.5502	42.3	142	-	149	0	K.QISLSWFR.D
1194.6759	1193.6686	1193.6233	37.9	48	-	56	0	R.FWTFPEVL.R.D
1194.6759	1193.6686	1193.6233	37.9	48	-	56	0	R.FWTFPEVL.R.D
1266.6686	1265.6613	1265.6040	45.3	263	-	272	0	K.ALETHTYFER.H
1595.9777	1594.9704	1594.9083	38.9	104	-	118	0	K.AEVLSPVSVFVPPR.N
1595.9777	1594.9704	1594.9083	39.0	104	-	118	0	K.AEVLSPVSVFVPPR.N
1633.9124	1632.9051	1632.8413	39.1	351	-	364	0	K.GFAPADVFVQWLQR.G
1784.0413	1783.0340	1782.9702	35.8	319	-	334	0	K.DVAMKPPSVYLLPPTR.E

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1618.1177, 1618.1177, 1732.1512, 1902.3138, 1994.0560, 2221.2212, 2284.2476

5. [gi|518349625](#) Mass: 5336 Score: 48 Expect: 4.9e+002 Matches: 7

hypothetical protein [Moraxella boeuvrei]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
848.5696	847.5623	847.5068	65.5	23	-	28	1	K.WRFLVK.I
853.5549	852.5476	852.5109	43.1	12	-	18	0	K.IGYFLPK.I
853.5549	852.5477	852.5109	43.1	12	-	18	0	K.IGYFLPK.I
1165.7815	1164.7742	1164.7270	40.5	12	-	21	1	K.IGYFLPKIAK.K
1165.7815	1164.7742	1164.7270	40.5	12	-	21	1	K.IGYFLPKIAK.K
1277.7600	1276.7527	1276.6856	52.6	2	-	11	1	M.FGYLDFDIKK.I
1296.7419	1295.7346	1295.6260	83.8	1	-	10	0	-MFGYLFDFDIK.K + Oxidation (M)

No match to: 842.5546, 850.5803, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1194.6759, 1194.6759, 1266.6686, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212, 2284.2476

6. [gi|494742220](#) Mass: 17861 Score: 47 Expect: 7.1e+002 Matches: 8

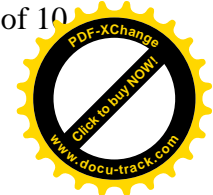
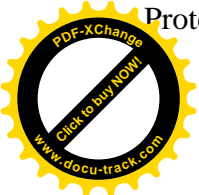
3-hydroxyacyl-ACP dehydratase [Bartonella melophagi]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
850.5803	849.5730	849.5436	34.6	117	-	123	0	K.LHVQLLK.K
1019.5801	1018.5728	1018.5183	53.6	9	-	17	0	K.SLETVDIDK.L
1036.6012	1035.5939	1035.5753	18.0	26	-	33	0	R.YPFLIDR.I
1036.6012	1035.5939	1035.5753	18.0	26	-	33	0	R.YPFLIDR.I
1266.6686	1265.6613	1265.6074	42.6	131	-	141	0	R.FSCVAEVEGIR.V
1595.9777	1594.9704	1594.8752	59.7	91	-	104	1	K.KTSLIYLMTVNNAK.F
1595.9777	1594.9704	1594.8752	59.7	91	-	104	1	K.KTSLIYLMTVNNAK.F
1994.0560	1993.0487	1992.9747	37.1	142	-	159	0	R.VSEAEVSAIMEVEQTMK.-

No match to: 842.5546, 848.5696, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 2221.2212, 2284.2476

7. [gi|518846823](#) Mass: 5061 Score: 46 Expect: 7.9e+002 Matches: 6

hypothetical protein [Mycoplasma hominis]



Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1296.7419	1295.7346	1295.6948	30.8	33	-	42	1	--- K.IFLCNEKLLF.-
1448.9645	1447.9572	1447.9418	10.6	2	-	13	0	--- M.LVYITIIILLIFK.G
1448.9645	1447.9572	1447.9418	10.7	2	-	13	0	--- M.LVYITIIILLIFK.G
1595.9777	1594.9704	1594.9772	-4.27	1	-	13	0	--- -.MLVYITIIILLIFK.G + Oxidation (M)
1595.9777	1594.9704	1594.9772	-4.24	1	-	13	0	--- -.MLVYITIIILLIFK.G + Oxidation (M)
1633.9124	1632.9051	1633.0582	-93.74	2	-	15	1	--- M.LVYITIIILLIFK.GK.K

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1334.9314, 1334.9314, 1475.8114, 1487.8091, 1618.1177, 1618.1177, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212, 2284.2476

8. [gi|488818860](#) Mass: 9345 Score: 45 Expect: 1.1e+003 Matches: 6
hypothetical protein [Phaeosporillum molischianum]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1019.5801	1018.5728	1018.4985	73.0	47	-	54	0	--- R.ENFIHGFR.H
1036.6012	1035.5939	1035.6441	-48.44	4	-	13	0	--- K.LPTVVVGPVR.K
1036.6012	1035.5939	1035.6441	-48.44	4	-	13	0	--- K.LPTVVVGPVR.K
1266.6686	1265.6613	1265.6326	22.7	62	-	72	0	--- K.VLTPTSQSEFK.R
1277.7600	1276.7527	1276.8231	-55.12	2	-	13	1	--- M.IKLPTVVVGPVR.K
1784.0413	1783.0340	1782.8988	75.9	47	-	61	1	--- R.ENFIHGFRHPTMAK.V

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1902.3138, 1994.0560, 2221.2212, 2284.2476

9. [gi|446609084](#) Mass: 31602 Score: 45 Expect: 1.1e+003 Matches: 7
prephenate dehydratase [Streptococcus oralis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.5546	841.5473	841.5021	53.7	223	-	229	0	--- K.IESRPLK.T
1036.6012	1035.5939	1035.5787	14.7	1	-	9	1	--- -.MKIAYLGPK.G + Oxidation (M)
1036.6012	1035.5939	1035.5787	14.7	1	-	9	1	3 --- -.MKIAYLGPK.G + Oxidation (M)
1266.6686	1265.6613	1265.5750	68.2	111	-	120	0	--- K.FIDMHYPEAK.I + Oxidation (M)
1296.7419	1295.7346	1295.6986	27.8	98	-	109	0	--- K.IFSPHQAQGG.K
1784.0413	1783.0340	1782.8941	78.5	133	-	148	0	--- R.FISEHPDQPYAAIAPK.S
2284.2476	2283.2403	2283.2164	10.5	3	-	23	1	--- K.IAYLGPKGSFHHVVTAFPK.E

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1277.7600, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1902.3138, 1994.0560, 2221.2212

10. [gi|518026209](#) Mass: 30111 Score: 44 Expect: 1.3e+003 Matches: 7
serine acetyltransferase [Afipia birgiae]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1036.6012	1035.5939	1035.5362	55.7	116	-	124	0	--- K.GFHAIQHR.L
1036.6012	1035.5939	1035.5362	55.7	116	-	124	0	--- K.GFHAIQHR.L
1266.6686	1265.6613	1265.6418	15.5	125	-	134	0	--- R.LAHWLYHNGR.R
1296.7419	1295.7346	1295.6834	39.6	62	-	73	0	--- R.LDHSALSGDLIR.Q
1994.0560	1993.0487	1992.9177	65.7	74	-	91	0	--- R.QAYNDATIEAEPDLGNAFR.A
2221.2212	2220.2139	2220.2478	-15.26	229	-	251	1	--- R.VASGSVVLKDVNNVTAGVPAK.I
2284.2476	2283.2403	2283.1674	31.9	116	-	134	1	--- K.GFHAIQHR.LAHWLYHNGR.R

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1277.7600, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1902.3138, 1994.0560, 2221.2212

11. [gi|24496448](#) Mass: 66533 Score: 44 Expect: 1.3e+003 Matches: 9
immunoglobulin M heavy chain secretory form [Bos taurus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1036.6012	1035.5939	1035.5502	42.3	292	-	299	0	--- K.QISLSWFR.D
1036.6012	1035.5939	1035.5502	42.3	292	-	299	0	--- K.QISLSWFR.D
1194.6759	1193.6686	1193.6233	37.9	198	-	206	0	--- R.FWTFPEVLR.D
1194.6759	1193.6686	1193.6233	37.9	198	-	206	0	18 --- R.FWTFPEVLR.D
1266.6686	1265.6613	1265.6040	45.3	413	-	422	0	--- K.ALEHTYFER.H
1595.9777	1594.9704	1594.9083	38.9	254	-	268	0	--- K.AEVLSPVVSFVFPVR.N
1595.9777	1594.9704	1594.9083	39.0	254	-	268	0	--- K.AEVLSPVVSFVFPVR.N
1633.9124	1632.9051	1632.8413	39.1	501	-	514	0	--- K.GFAPADVFVQWLQR.G
1784.0413	1783.0340	1782.9702	35.8	469	-	484	0	--- K.DVAMKPPSVYLLPPTRE

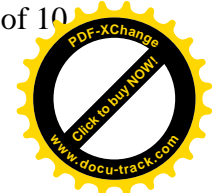
No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1277.7600, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1618.1177, 1618.1177, 1732.1512, 1902.3138, 1994.0560, 2221.2212, 2284.2476

12. [gi|547755423](#) Mass: 19340 Score: 44 Expect: 1.4e+003 Matches: 8
ribosome maturation factor RimM [Clostridium sp. CAG:221]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
853.5549	852.5476	852.4817	77.3	10	-	17	0	--- K.IANTHGLK.G
853.5549	852.5477	852.4817	77.3	10	-	17	0	--- K.IANTHGLK.G
1019.5801	1018.5728	1018.5845	-11.45	1	-	9	1	--- -.MSQLLKVGK.I + Oxidation (M)
1266.6686	1265.6613	1265.7092	-37.80	10	-	21	1	--- K.IANTHGLKGEVK.V
1277.7600	1276.7527	1276.8482	-74.78	130	-	140	1	--- R.KPKELLIPVLK.S
1296.7419	1295.7346	1295.6544	61.9	44	-	54	1	--- K.TISVEGCKFQK.D
1595.9777	1594.9704	1594.8355	84.6	31	-	43	1	--- K.RFNDLEYVIEGK.T
1595.9777	1594.9704	1594.8355	84.6	31	-	43	1	--- K.RFNDLEYVIEGK.T

No match to: 842.5546, 848.5696, 850.5803, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212, 2284.2476

13. [gi|492049521](#) Mass: 6980 Score: 43 Expect: 1.5e+003 Matches: 6
hypothetical protein [Pseudomonas amygdali]



Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1036.6012	1035.5939	1035.5899	3.88	8	16	0	---	R.QVMLHIPAK.A
1036.6012	1035.5939	1035.5899	3.88	8	16	0	---	R.QVMLHIPAK.A
1618.1177	1617.1104	1616.9548	96.2	8	21	1	---	R.QVMLHIPAKALKPR.A + Oxidation (M)
1618.1177	1617.1104	1616.9548	96.2	8	21	1	---	R.QVMLHIPAKALKPR.A + Oxidation (M)
1784.0413	1783.0340	1783.0178	9.08	2	16	1	---	M.TILFTRQVMLHIPAK.A + Oxidation (M)
2221.2212	2220.2139	2220.1069	48.2	25	46	0	---	R.AVNIASVGGEQVMGNAVPAQHR.G + Oxidation (M)

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1633.9124, 1732.1512, 1902.3138, 1994.0560, 2284.2476

14. [gi|488127006](#) Mass: 5046 Score: 43 Expect: 1.6e+003 Matches: 6

hypothetical protein, partial [Helicobacter pylori]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
853.5549	852.5476	852.4779	81.8	34	40	0	---	R.MVIFISK.A + Oxidation (M)
853.5549	852.5477	852.4779	81.8	34	40	0	---	R.MVIFISK.A + Oxidation (M)
864.5864	863.5791	863.5116	78.2	19	25	1	---	K.EALKYLK.T
1165.7815	1164.7742	1164.6689	90.4	31	40	1	---	K.ATRMVIFISK.A
1165.7815	1164.7742	1164.6689	90.4	31	40	1	---	K.ATRMVIFISK.A
1266.6686	1265.6613	1265.6876	-20.75	34	44	1	---	R.MVIFISKACVV.-

No match to: 842.5546, 848.5696, 850.5803, 855.0955, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1194.6759, 1194.6759, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212, 2284.2476

15. [gi|68535459](#) Mass: 8368 Score: 43 Expect: 1.7e+003 Matches: 5

hypothetical protein jk0392 [Corynebacterium jeikeium K411]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1194.6759	1193.6686	1193.6081	50.7	62	71	1	---	K.AFVEKNPDFK.E
1194.6759	1193.6686	1193.6081	50.7	62	71	1	---	K.AFVEKNPDFK.E
1296.7419	1295.7346	1295.6544	62.0	55	66	1	---	K.ASCSAVKAFVEK.N
1475.8114	1474.8041	1474.6841	81.4	19	30	0	---	R.DFNHTVVDPEFR.G
1784.0413	1783.0340	1783.0091	14.0	31	47	0	---	R.QGGLSKPLISEALLETK.E

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1194.6759, 1194.6759, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212, 2284.2476

16. [gi|3834667](#) Mass: 48810 Score: 42 Expect: 2.2e+003 Matches: 7

immunoglobulin heavy chain constant region [Bos taurus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1036.6012	1035.5939	1035.5502	42.3	151	158	0	---	K.QISLSWFR.D
1036.6012	1035.5939	1035.5502	42.3	151	158	0	---	K.QISLSWFR.D
1194.6759	1193.6686	1193.6233	37.9	54	62	0	---	R.FWTFPEVLR.D
1194.6759	1193.6686	1193.6233	37.9	54	62	0	18	R.FWTFPEVLR.D
1266.6686	1265.6613	1265.6040	45.3	272	281	0	---	K.ALEHTYFPER.H
1633.9124	1632.9051	1632.8413	39.1	360	373	0	---	K.GFAPADVFVQWLQR.G
1784.0413	1783.0340	1782.9702	35.8	328	343	0	---	K.DVAMKPPSVYLLPPTR.E

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1732.1512, 1902.3138, 1994.0560, 2221.2212, 2284.2476

17. [gi|547238705](#) Mass: 13800 Score: 42 Expect: 2.4e+003 Matches: 7

ribosomal protein S13 [Firmicutes bacterium CAG:884]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
882.5994	881.5921	881.5195	82.3	94	101	1	---	K.GLPVRGQR.T
882.5994	881.5922	881.5195	82.4	94	101	1	---	K.GLPVRGQR.T
1019.5801	1018.5728	1018.5229	49.0	71	78	1	---	R.REVNMNIK.T + Oxidation (M)
1475.8114	1474.8041	1474.7350	46.8	81	92	1	---	K.MEINSYQGIRHK.K
1595.9777	1594.9704	1594.9195	31.9	14	27	1	---	K.RTVIALTYIYGIGR.S
1595.9777	1594.9704	1594.9195	31.9	14	27	1	---	K.RTVIALTYIYGIGR.S
2284.2476	2283.2403	2283.2661	-11.27	15	35	1	---	R.TVIALTYIYGIGRSLAATICK.D

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212

18. [gi|345564418](#) Mass: 28894 Score: 41 Expect: 2.7e+003 Matches: 4

hypothetical protein AOL_s00083g474 [Arthrotrichy oligospora ATCC 24927]

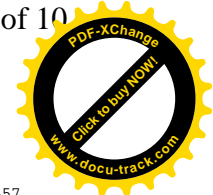
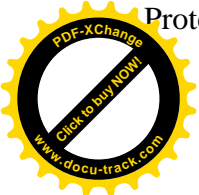
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1194.6759	1193.6686	1193.6445	20.2	176	185	0	---	R.FNVSVQYLKPK.D
1194.6759	1193.6686	1193.6233	38.0	43	51	0	18	R.LPWYLSPLYR.G
1633.9124	1632.9051	1632.7678	84.1	26	38	1	---	K.EITNDRHFSMLR.Y
2221.2212	2220.2139	2220.0805	60.1	4	25	1	---	R.QRPTSSSSPAVASNGGVDTKMK.E + Oxidation (M)

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2284.2476

19. [gi|517947175](#) Mass: 20170 Score: 41 Expect: 2.7e+003 Matches: 7

hypothetical protein [Anaerococcus sp. PH9]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1036.6012	1035.5939	1035.4985	92.1	12	21	0	---	R.DSGNANFALK.L
1036.6012	1035.5939	1035.4985	92.1	12	21	0	---	R.DSGNANFALK.L
1194.6759	1193.6686	1193.6153	44.7	22	31	1	---	K.LVGTQRYSDR.E
1194.6759	1193.6686	1193.6153	44.7	22	31	1	---	K.LVGTQRYSDR.E
1266.6686	1265.6613	1265.6438	13.9	1	11	0	---	-MDLLQAVAYAR.D + Oxidation (M)
1487.8091	1486.8018	1486.6875	76.9	91	103	0	---	R.GCYVISYDAGNLR.Y



2284.2476 2283.2403 2283.1317 47.6 1 - 21 1 --- -.MDLLQAVAYARDSGNANFALK.L + Oxidation (M)

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212

20. [gi|522808524](#) Mass: 25797 Score: 41 Expect: 2.7e+003 Matches: 8

hypothetical protein [Mycobacterium marinum]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
951.6699	950.6626	950.5774	89.7	195	- 202	1	---	R.QLRKPGPR.Q
1151.7755	1150.7682	1150.7074	52.9	31	- 41	0	---	R.SVPLSLLVAPR.L
1151.7755	1150.7682	1150.7074	52.9	31	- 41	0	---	R.SVPLSLLVAPR.L
1266.6686	1265.6613	1265.6153	36.4	51	- 61	0	---	R.DPHTVDWLAGR.R
1595.9777	1594.9704	1594.8613	68.4	97	- 110	1	---	R.VMAADRVLEHLGLR.T + Oxidation (M)
1595.9777	1594.9704	1594.8613	68.4	97	- 110	1	---	R.VMAADRVLEHLGLR.T + Oxidation (M)
1784.0413	1783.0340	1783.0145	11.0	111	- 127	1	---	R.TRLFAAPGWVSPGVVK.A
2284.2476	2283.2403	2283.2124	12.2	128	- 148	1	---	K.ALPGNGFRLLADYHGISDLVR.K

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1902.3138, 1994.0560, 2221.2212

21. [gi|550715204](#) Mass: 37257 Score: 41 Expect: 2.9e+003 Matches: 7

transcriptional activator FtrA [Enterobacter sp. MGH 8]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1165.7815	1164.7742	1164.6880	74.0	273	- 281	1	---	R.WLLTARLHR.A
1165.7815	1164.7742	1164.6880	74.1	273	- 281	1	---	R.WLLTARLHR.A
1194.6759	1193.6686	1193.6339	29.1	251	- 260	1	---	R.VGMSQRTFLR.R
1194.6759	1193.6686	1193.6339	29.1	251	- 260	1	11	R.VGMSQRTFLR.R
1475.8114	1474.8041	1474.7681	24.4	136	- 147	1	---	K.ATTHWRYTQALK.T
1784.0413	1783.0340	1782.9337	56.3	207	- 222	0	---	R.DGSQTQQLSRPVAQLR.E
2284.2476	2283.2403	2283.1680	31.7	207	- 226	1	---	R.DGSQTQQLSRPVAQLRESQR.L

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1902.3138, 1994.0560, 2221.2212

22. [gi|516231730](#) Mass: 9834 Score: 41 Expect: 2.9e+003 Matches: 6

hypothetical protein [Vibrio sp. 71211]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
853.5549	852.5476	852.5109	43.0	5	- 11	0	---	R.LFFIVSK.T
853.5549	852.5477	852.5109	43.1	5	- 11	0	---	R.LFFIVSK.T
1165.7815	1164.7742	1164.7019	62.1	2	- 11	1	---	M.VGRLFFIVSK.T
1165.7815	1164.7742	1164.7019	62.1	2	- 11	1	---	M.VGRLFFIVSK.T
1296.7419	1295.7346	1295.7424	-6.00	1	- 11	1	---	-.MVGRLLFFIVSK.T
1994.0560	1993.0487	1993.0567	-4.01	67	- 83	1	---	R.LNHTMFSAIIEPIAKHR.- + Oxidation (M)

No match to: 842.5546, 848.5696, 850.5803, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 2221.2212, 2284.2476

23. [gi|517496258](#) Mass: 32907 Score: 40 Expect: 3e+003 Matches: 6

hypothetical protein [Bacteroides gallinarum]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.5546	841.5473	841.5749	-32.76	289	- 295	1	---	R.LLLLKSR.-
1194.6759	1193.6686	1193.5533	96.6	52	- 61	0	---	K.GNTKPMMDIR.I + 2 Oxidation (M)
1194.6759	1193.6686	1193.5533	96.6	52	- 61	0	11	K.GNTKPMMDIR.I + 2 Oxidation (M)
1266.6686	1265.6613	1265.6299	24.8	134	- 145	1	---	R.RAGGAGYSCVLR.L
1994.0560	1993.0487	1992.9873	30.8	52	- 68	1	---	K.GNTKPMMDIRIYEGNVR.A
2284.2476	2283.2403	2283.3065	-28.97	4	- 24	1	---	K.IFLLFVMITLALGAFQSKGK.N + Oxidation (M)

No match to: 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 2221.2212

24. [gi|183984872](#) Mass: 25857 Score: 40 Expect: 3.4e+003 Matches: 8

hypothetical protein MMAR_4904 [Mycobacterium marinum M]

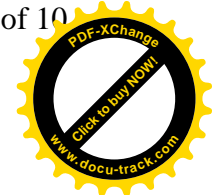
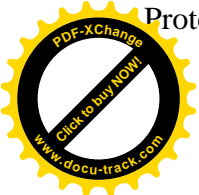
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
951.6699	950.6626	950.5774	89.7	195	- 202	1	---	R.QLRKPGPR.Q
1151.7755	1150.7682	1150.7074	52.9	31	- 41	0	---	R.SVPLSLLVAPR.L
1151.7755	1150.7682	1150.7074	52.9	31	- 41	0	---	R.SVPLSLLVAPR.L
1266.6686	1265.6613	1265.6153	36.4	51	- 61	0	---	R.DPHTVDWLAGR.R
1595.9777	1594.9704	1594.8613	68.4	97	- 110	1	---	R.VMAADRVLEHLGLR.T + Oxidation (M)
1595.9777	1594.9704	1594.8613	68.4	97	- 110	1	---	R.VMAADRVLEHLGLR.T + Oxidation (M)
1784.0413	1783.0340	1783.0145	11.0	111	- 127	1	---	R.TRLFAAPGWVSPGVVK.A
2284.2476	2283.2403	2283.2124	12.2	128	- 148	1	---	K.ALPGNGFRLLADYHGISDLVR.K

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1902.3138, 1994.0560, 2221.2212

25. [gi|443492961](#) Mass: 25831 Score: 40 Expect: 3.4e+003 Matches: 8

putative deacetylase [Mycobacterium liflandii 128FXT]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
951.6699	950.6626	950.5774	89.7	195	- 202	1	---	R.QLRKPGPR.Q
1151.7755	1150.7682	1150.7074	52.9	31	- 41	0	---	R.SVPLSLLVAPR.L
1151.7755	1150.7682	1150.7074	52.9	31	- 41	0	---	R.SVPLSLLVAPR.L
1266.6686	1265.6613	1265.6153	36.4	51	- 61	0	---	R.DPHTVDWLAGR.R
1595.9777	1594.9704	1594.8613	68.4	97	- 110	1	---	R.VMAADRVLEHLGLR.T + Oxidation (M)
1595.9777	1594.9704	1594.8613	68.4	97	- 110	1	---	R.VMAADRVLEHLGLR.T + Oxidation (M)



1784.0413 1783.0340 1783.0145 11.0 111 - 127 1 --- R.TRLFAAPGWVSPGVVK.A
2284.2476 2283.2403 2283.2124 12.2 128 - 148 1 --- K.ALPGNGFRLLADYHGISDLVR.K

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1902.3138, 1994.0560, 2221.2212

26. [gi|118616343](#) Mass: 25912 Score: 39 Expect: 3.9e+003 Matches: 8

hypothetical protein MUL_0502 [Mycobacterium ulcerans Agy99]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
951.6699	950.6626	950.5774	89.7	195	-	202	1	R.QLRKPGPR.Q
1151.7755	1150.7682	1150.7074	52.9	31	-	41	0	R.SVPLSLLVAPR.L
1151.7755	1150.7682	1150.7074	52.9	31	-	41	0	R.SVPLSLLVAPR.L
1266.6686	1265.6613	1265.6153	36.4	51	-	61	0	R.DPHTVDWLGR.R
1595.9777	1594.9704	1594.8613	68.4	97	-	110	1	R.VMAADRVLEHLGLR.T + Oxidation (M)
1595.9777	1594.9704	1594.8613	68.4	97	-	110	1	R.VMAADRVLEHLGLR.T + Oxidation (M)
1784.0413	1783.0340	1783.0145	11.0	111	-	127	1	R.TRLFAAPGWVSPGVVK.A
2284.2476	2283.2403	2283.2124	12.2	128	-	148	1	K.ALPGNGFRLLADYHGISDLVR.K

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1902.3138, 1994.0560, 2221.2212

27. [gi|491438800](#) Mass: 10485 Score: 39 Expect: 3.9e+003 Matches: 5

acetyltransferase [Corynebacterium jeikeium]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1194.6759	1193.6686	1193.6081	50.7	81	-	90	1	K.AFVEKNPDPK.E
1194.6759	1193.6686	1193.6081	50.7	81	-	90	1	K.AFVEKNPDPK.E
1296.7419	1295.7346	1295.6544	62.0	74	-	85	1	K.ASCSAVKAFVEK.N
1475.8114	1474.8041	1474.6841	81.4	38	-	49	0	R.DFNHTVVDPEFR.G
1784.0413	1783.0340	1783.0091	14.0	50	-	66	0	R.GQGLSKPLISEALLET.K

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1266.6686, 1277.7600, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1902.3138, 1994.0560, 2221.2212, 2284.2476

28. [gi|491891625](#) Mass: 32908 Score: 39 Expect: 4e+003 Matches: 6

hypothetical protein [Bacteroides stercoris]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.5546	841.5473	841.5749	-32.76	289	-	295	1	R.LLLLSKR.-
1194.6759	1193.6686	1193.5533	96.6	52	-	61	0	K.GNTKPMMDIR.I + 2 Oxidation (M)
1194.6759	1193.6686	1193.5533	96.6	52	-	61	0	K.GNTKPMMDIR.I + 2 Oxidation (M)
1266.6686	1265.6613	1265.6299	24.8	134	-	145	1	R.RAGGAGYSCVLR.L
1784.0413	1783.0340	1782.8901	80.7	228	-	243	1	K.GDQFQVSLIKYSGGER.Q
1994.0560	1993.0487	1992.9873	30.8	52	-	68	1	K.GNTKPMMDIRIYEGNVR.A

No match to: 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1902.3138, 2221.2212, 2284.2476

29. [gi|547517138](#) Mass: 32936 Score: 39 Expect: 4e+003 Matches: 6

uncharacterized protein [Bacteroides stercoris CAG:120]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.5546	841.5473	841.5749	-32.76	289	-	295	1	R.LLLLSKR.-
1194.6759	1193.6686	1193.5533	96.6	52	-	61	0	K.GNTKPMMDIR.I + 2 Oxidation (M)
1194.6759	1193.6686	1193.5533	96.6	52	-	61	0	K.GNTKPMMDIR.I + 2 Oxidation (M)
1266.6686	1265.6613	1265.6299	24.8	134	-	145	1	R.RAGGAGYSCVLR.L
1784.0413	1783.0340	1782.8901	80.7	228	-	243	1	K.GDQFQVSLIKYSGGER.Q
1994.0560	1993.0487	1992.9873	30.8	52	-	68	1	K.GNTKPMMDIRIYEGNVR.A

No match to: 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1902.3138, 2221.2212, 2284.2476

30. [gi|517368986](#) Mass: 14244 Score: 39 Expect: 4.1e+003 Matches: 7

30S ribosomal protein S13 [Streptomyces sp. LaPpAH-108]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.5546	841.5473	841.4658	96.9	4	-	11	0	R.VSGVDIPR.E
882.5994	881.5921	881.5195	82.3	95	-	102	1	R.GLPVRGQR.T
882.5994	881.5922	881.5195	82.4	95	-	102	1	R.GLPVRGQR.T
1194.6759	1193.6686	1193.5863	69.0	82	-	91	0	K.VEIGCYQGLR.H
1194.6759	1193.6686	1193.5863	69.0	82	-	91	0	K.VEIGCYQGLR.H
1487.8091	1486.8018	1486.7463	37.3	82	-	93	1	K.VEIGCYQGLRHR.R
2221.2212	2220.2139	2220.1274	39.0	47	-	65	1	R.DLSEELVAIREYVDSNIK.T

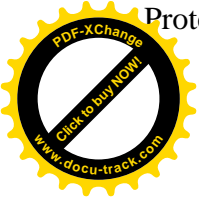
No match to: 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2284.2476

31. [gi|516399639](#) Mass: 5928 Score: 39 Expect: 4.1e+003 Matches: 5

integrase [Vibrio vulnificus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1036.6012	1035.5939	1035.6077	-13.26	6	-	14	1	K.ATLIYARTK.N
1036.6012	1035.5939	1035.6077	-13.26	4	-	12	1	R.TKATLIYAR.T
1277.7600	1276.7527	1276.6663	67.7	34	-	44	0	R.YLGVLELDALR.L
1448.9645	1447.9572	1447.8623	65.5	15	-	27	1	K.NIRAVQILLGHSK.V
1448.9645	1447.9572	1447.8623	65.6	15	-	27	1	K.NIRAVQILLGHSK.V

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2284.2476



1334.9314, 1334.9314, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212, 2284.2476

32. [gi|479181342](#) Mass: 3438 Score: 39 Expect: 4.2e+003 Matches: 3

Helix-turn-helix domain of resolvase. [Enterococcus sp. 7L76]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1266.6686	1265.6613	1265.7707	-86.40	2	13	1	---	M.LKQGIPVAEIAK.E
1277.7600	1276.7527	1276.6775	58.9	14	24	0	---	K.ENGISRPITYK.I
2284.2476	2283.2403	2283.2586	-8.02	4	24	1	---	K.QGIPVAEIAKENGISRPITYK.I

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212

33. [gi|491349492](#) Mass: 31061 Score: 39 Expect: 4.3e+003 Matches: 6

hypothetical protein [Gordonia sputi]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1036.6012	1035.5939	1035.5317	60.1	113	120	1	---	R.MLRVQMAR.T + 2 Oxidation (M)
1036.6012	1035.5939	1035.5317	60.1	113	120	1	---	R.MLRVQMAR.T + 2 Oxidation (M)
1194.6759	1193.6686	1193.6418	22.5	243	251	1	---	R.RIHQLWADR.Q
1194.6759	1193.6686	1193.6227	38.5	107	115	1	11	R.EFDLVRMLR.V + Oxidation (M)
1487.8091	1486.8018	1486.7449	38.3	211	222	1	---	R.EIEEMAELVRLPR.Q + Oxidation (M)
2284.2476	2283.2403	2283.0994	61.7	95	112	1	---	R.TQPYELVSWMDREFDLVR.M

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212

34. [gi|493388713](#) Mass: 17048 Score: 39 Expect: 4.4e+003 Matches: 5

MarR family transcriptional regulator [Streptomyces tsukubaensis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.5546	841.5473	841.5134	40.4	141	148	1	---	K.KALGQVAR.A
848.5696	847.5623	847.4916	83.5	24	30	0	---	R.VLFSVQR.E
1296.7419	1295.7346	1295.6946	30.9	62	73	1	---	R.ASELARLSGQHK.Q
1475.8114	1474.8041	1474.8368	-22.17	48	61	0	---	R.SGAVLAHLRPEGIR.A
1994.0560	1993.0487	1993.0593	-5.29	68	85	1	---	R.LSGQHKQVVGTLVDDLRL

No match to: 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 2221.2212, 2284.2476

35. [gi|551036884](#) Mass: 33460 Score: 39 Expect: 4.5e+003 Matches: 8

hypothetical protein [Lachnospiraceae bacterium NK4A136]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
864.5864	863.5791	863.5116	78.2	64	70	1	---	R.LIKYAEK.M
1036.6012	1035.5939	1035.5197	71.7	54	63	0	---	K.TISVTSSGER.L
1036.6012	1035.5939	1035.5197	71.7	54	63	0	---	K.TISVTSSGER.L
1151.7755	1150.7682	1150.6598	94.2	2	11	0	---	M.TITQLSTFLK.I
1151.7755	1150.7682	1150.6598	94.3	2	11	0	---	M.TITQLSTFLK.I
1266.6686	1265.6613	1265.6842	-18.07	105	114	1	---	R.FPKILMEFNK.D
1296.7419	1295.7346	1295.6543	62.0	67	76	1	---	K.YAEKMLQLER.E + Oxidation (M)
2284.2476	2283.2403	2283.1093	57.4	138	156	1	---	K.GELDMVVTNLPLFEDDRIK.I + Oxidation (M)

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1277.7600, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212

36. [gi|320333797](#) Mass: 39533 Score: 39 Expect: 4.5e+003 Matches: 7

phospho-2-dehydro-3-deoxyheptonate aldolase [Deinococcus maricopensis DSM 21211]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
882.5994	881.5921	881.5586	38.1	302	309	0	---	R.DLLIPLAK.A
882.5994	881.5922	881.5586	38.1	302	309	0	---	R.DLLIPLAK.A
1019.5801	1018.5728	1018.5229	49.0	1	8	1	---	-.MTRIDDLR.R
1194.6759	1193.6686	1193.5937	62.8	346	355	0	---	K.FMAALEPMLR.A + Oxidation (M)
1194.6759	1193.6686	1193.5937	62.8	346	355	0	13	K.FMAALEPMLR.A + Oxidation (M)
1266.6686	1265.6613	1265.7819	-95.29	220	231	1	---	R.EVGGRAGKPVLLK.R
1633.9124	1632.9051	1632.8480	35.0	346	359	1	---	K.FMAALEPMLRAPVR.A + 2 Oxidation (M)

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212, 2284.2476

37. [gi|409039618](#) Mass: 29114 Score: 38 Expect: 4.8e+003 Matches: 7

hypothetical protein PHACADRAFT_201965 [Phanerochaete carnosae HHB-10118-sp]

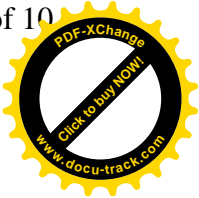
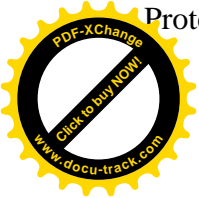
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.5546	841.5473	841.5385	10.5	75	81	1	---	R.LRLELAK.M
848.5696	847.5623	847.4837	92.8	77	83	1	---	R.LELAKMK.S + Oxidation (M)
1036.6012	1035.5939	1035.5138	77.4	195	202	0	---	R.NYFTNHK.E
1036.6012	1035.5939	1035.5138	77.4	195	202	0	---	R.NYFTNHK.E
1487.8091	1486.8018	1486.7416	40.5	203	214	1	---	K.ESLIKYTPDHER.I
1784.0413	1783.0340	1782.9992	19.5	160	175	1	---	R.TKVLVHASELFVEVGR.R
2284.2476	2283.2403	2283.0388	88.3	177	194	0	---	R.SPLFLYMGQHWVTCCTQR.N

No match to: 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1902.3138, 1994.0560, 2221.2212

38. [gi|187251559](#) Mass: 20917 Score: 38 Expect: 4.8e+003 Matches: 6

crossover junction endodeoxyribonuclease RuvC [Elusimicrobium minutum Peil91]

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



848.5696847.5623847.483792.8132 - 1380 ---R.MVQLTLK.L + Oxidation (M)

1036.60121035.59391035.501988.9116 - 1260 ---K.SVICGSGTAGK.A

1036.60121035.59391035.501988.9116 - 1260 ---K.SVICGSGTAGK.A

1784.04131783.03401782.911268.92 - 180 ---M.DNNALTTVLGIDPGLDR.T

1994.05601993.04871993.015616.645 - 611 ---K.DSALPERLEYIFNEIGK.L

2284.24762283.24032283.106758.562 - 800 ---K.LAEAYKPNHVAMEEMFFLK.R + Oxidation (M)

No match to: 842.5546, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1902.3138, 2221.2212

39. [gi|261260695](#) Mass: 10351 Score: 38 Expect: 5e+003 Matches: 5

Yclm [Bacillus amyloliquefaciens]

ObservedMr(expt)Mr(calc)ppmStartEndMissIonsPeptide

853.5549852.5476852.485772.651 - 570 ---K.LIAAYFR.R

853.5549852.5477852.485772.651 - 570 ---K.LIAAYFR.R

1194.67591193.66861193.629233.020 - 300 ---R.SDLFALLNSSK.A

1194.67591193.66861193.629233.020 - 300 11R.SDLFALLNSSK.A

1994.05601993.04871993.0632-7.271 - 171 ---Y.AAIARELNLDFSIIER.I

No match to: 842.5546, 848.5696, 850.5803, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 2221.2212, 2284.2476

40. [gi|517051098](#) Mass: 27685 Score: 38 Expect: 5.4e+003 Matches: 6

transcriptional regulator [Rhizobium sp. BR816]

ObservedMr(expt)Mr(calc)ppmStartEndMissIonsPeptide

1194.67591193.66861193.553996.198 - 1060 ---R.FPECEPLFR.S

1194.67591193.66861193.553996.198 - 1060 13R.FPECEPLFR.S

1487.80911486.80181486.713959.196 - 1061 ---R.HRFPECEPLFR.S

1595.97771594.97041594.894347.781 - 950 ---R.LALGGVRPVEWATAR.H

1595.97771594.97041594.894347.781 - 950 ---R.LALGGVRPVEWATAR.H

1994.05601993.04871993.0632-7.29198 - 2141 ---K.SYWEIATILGISERTV.R

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 2221.2212, 2284.2476

41. [gi|444720581](#) Mass: 100358 Score: 38 Expect: 5.5e+003 Matches: 10

General transcription factor II-I [Tupaia chinensis]

ObservedMr(expt)Mr(calc)ppmStartEndMissIonsPeptide

842.5546841.5473841.538510.5410 - 4161 ---R.ILLAKER.I

848.5696847.5623847.516753.8236 - 2430 ---K.AGISFIIK.S

1036.60121035.59391035.513178.0151 - 1591 ---K.MKSTTQANR.M

1036.60121035.59391035.513178.0151 - 1591 ---K.MKSTTQANR.M

1266.66861265.66131265.6768-12.22358 - 3681 ---R.EFNFQAIIKAK.G

1487.80911486.80181486.8395-25.36185 - 1981 ---K.ALKGSTVVPVPYEK.M

1784.04131783.03401782.912768.0810 - 8251 ---K.FGEAIGMGFPVKVPYR.K + Oxidation (M)

1994.05601993.04871992.956146.5252 - 2700 ---K.TEPTEDSGISLEMAAVTVK.E + Oxidation (M)

2221.22122220.21392220.119542.5250 - 2701 ---K.VKTEPTEDSGISLEMAAVTVK.E + Oxidation (M)

2284.24762283.24032283.199817.7645 - 6641 ---K.VPEIEVTVEEAWNAKITDLK.Q

No match to: 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1902.3138

42. [gi|71039991](#) Mass: 32224 Score: 38 Expect: 6e+003 Matches: 9

conserved ATPase domain protein [Macropis nuda]

ObservedMr(expt)Mr(calc)ppmStartEndMissIonsPeptide

850.5803849.5730849.507277.4143 - 1491 ---K.FLRVSTK.I

1019.58011018.57281018.5771-4.1781 - 901 ---R.LSRSSALASK.A

1151.77551150.76821150.653299.9204 - 2131 ---K.RMFVLAASIK.A + Oxidation (M)

1151.77551150.76821150.653299.9204 - 2131 ---K.RMFVLAASIK.A + Oxidation (M)

1165.78151164.77421164.697965.6253 - 2621 ---K.LSHEVLLRAK.Q

1165.78151164.77421164.697965.6253 - 2621 ---K.LSHEVLLRAK.Q

1194.67591193.66861193.640423.6109 - 1190 ---R.LPDIHNTVTGK.T

1194.67591193.66861193.640423.6109 - 1190 ---R.LPDIHNTVTGK.T

1475.81141474.80411474.8144-6.94263 - 2761 ---K.QIGFSDKQIAAAVK.S

No match to: 842.5546, 848.5696, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212, 2284.2476

43. [gi|490661404](#) Mass: 4181 Score: 38 Expect: 6e+003 Matches: 4

hypothetical protein [Burkholderia pseudomallei]

ObservedMr(expt)Mr(calc)ppmStartEndMissIonsPeptide

1448.96451447.95721447.837282.92 - 151 ---M.RGPLEARPVGLAGR.R

1448.96451447.95721447.837282.93 - 161 ---R.GPLEARPVGLAGRR.D

1595.97771594.97041594.872661.31 - 151 ----.MRGPLEARPVGLAGR.R + Oxidation (M)

1595.97771594.97041594.872661.41 - 151 ----.MRGPLEARPVGLAGR.R + Oxidation (M)

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1475.8114, 1487.8091, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212, 2284.2476

44. [gi|489236824](#) Mass: 65949 Score: 37 Expect: 6.2e+003 Matches: 11

multidrug ABC transporter ATP-binding protein [Gemella haemolysans]

ObservedMr(expt)Mr(calc)ppmStartEndMissIonsPeptide

848.5696847.5623847.491683.5481 - 4870 ---R.QLLTFR.T

882.5994881.5921881.508395.1525 - 5320 ---R.TTIAIAHR.L

882.5994881.5922881.508395.1525 - 5320 ---R.TTIAIAHR.L

1036.6012	1035.5939	1035.4985	92.1	96	-	104	0	---	R.NDSFANLQK.L
1036.6012	1035.5939	1035.4985	92.1	96	-	104	0	---	R.NDSFANLQK.L
1165.7815	1164.7742	1164.6727	87.1	86	-	95	1	---	K.VAHSIVRDLR.N
1165.7815	1164.7742	1164.6727	87.1	86	-	95	1	---	K.VAHSIVRDLR.N
1296.7419	1295.7346	1295.6366	75.7	569	-	579	0	---	K.MYQLQAGMLNK.-
1902.3138	1901.3065	1901.1172	99.6	238	-	254	1	---	K.SLKVDSLLLRPAMALFK.V
1994.0560	1993.0487	1992.9251	62.0	96	-	112	1	---	R.NDSFANLQKLGMSYFDK.T + Oxidation (M)
2221.2212	2220.2139	2220.1208	41.9	201	-	219	1	---	K.LSESEIGMKIIQAFNQEQR.L

No match to: 842.5546, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 2284.2476

45. [gi|547230974](#) Mass: 17853 Score: 37 Expect: 6.4e+003 Matches: 6

transposase [Bacteroides intestinalis CAG:564]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1019.5801	1018.5728	1018.4728	98.2	51	-	58	1	--- K.KGYMAMR.L
1194.6759	1193.6686	1193.5676	84.6	113	-	124	0	--- R.ATNAAESFNAK.I
1194.6759	1193.6686	1193.5676	84.6	113	-	124	0	--- R.ATNAAESFNAK.I
1475.8114	1474.8041	1474.7317	49.1	2	-	14	1	--- M.YHAPVFANGDTRK.Q
1994.0560	1993.0487	1992.9008	74.2	52	-	67	1	--- K.GYMMAMRLGIYHQCK.F + Oxidation (M)
2221.2212	2220.2139	2220.1803	15.1	94	-	111	1	--- R.VARSQTHYLNIIINFERR

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 2284.2476

46. [gi|494229523](#) Mass: 4528 Score: 37 Expect: 6.6e+003 Matches: 6

hypothetical protein [Flavobacterium frigidis]

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Ions	Peptide
1051.7457	1050.7384	1050.6437	90.1	2	-	12	0	--- M.PLPSGLGILGK.Q
1051.7457	1050.7385	1050.6437	90.2	2	-	12	0	--- M.PLPSGLGILGK.Q
1448.9645	1447.9572	1447.8875	48.2	2	-	15	1	--- M.PLPSGLGILGKQLR.F
1448.9645	1447.9572	1447.8875	48.2	2	-	15	1	--- M.PLPSGLGILGKQLR.F
1595.9777	1594.9704	1594.9229	29.8	1	-	15	1	--- -MPLPSGLGILGKQLR.F + Oxidation (M)
1595.9777	1594.9704	1594.9229	29.8	1	-	15	1	--- -MPLPSGLGILGKQLR.F + Oxidation (M)

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1487.8091, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212, 2284.2476

47. [gi|28493757](#) Mass: 41909 Score: 37 Expect: 6.6e+003 Matches: 6

pyruvate dehydrogenase E1 component alpha subunit [Tropheryma whipplei str. Twist]

observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Ions	Peptide
1036.6012	1035.5939	1035.5502	42.3	226	- 235	0	---	R.GYGFIPGIR.I
1036.6012	1035.5939	1035.5502	42.3	226	- 235	0	---	R.GYGFIPGIR.I
1194.6759	1193.6686	1193.6921	-19.63	42	- 50	1	---	R.FYRDIILVR.Q
1194.6759	1193.6686	1193.6921	-19.63	42	- 50	1	18	R.FYRDIILVR.Q
1475.8114	1474.8041	1474.7780	17.7	236	- 249	0	---	R.IDGNVDVIAAYVR.
1487.8091	1486.8018	1486.8620	-40.46	318	- 330	1	---	R.IRADIQLSVIGFR.N

No match to: 842.5546, 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212, 2284.2476

48. [gi|517826373](#) Mass: 12209 Score: 37 Expect: 6.7e+003 Matches: 4

hypothetical protein [Hirschia maritima]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.5546	841.5473	841.5385	10.5	46 -	53	1	---	R.AILQAKAK.T
1194.6759	1193.6686	1193.5652	86.7	26 -	34	0	---	K.ENWICGFIR.S
1194.6759	1193.6686	1193.5652	86.7	26 -	34	0	11	K.ENWICGFIR.S
2284.2476	2283.2403	2283.1980	18.6	82 -	100	1	---	R.LNLFEYIKSFGTGFIFYPK.F

No match to: 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1036.6012, 1036.6012, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212

49. [gi|446609078](#) Mass: 29288 Score: 37 Expect: 6.7e+003 Matches: 6

prephenate dehydratase, partial [Streptococcus sp. GMD1S]

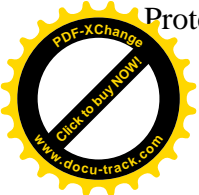
Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Ions	Peptide
842.5546	841.5473	841.5021	53.7	223	-	229	0	--- K.IESRPLK.T
1036.6012	1035.5939	1035.5787	14.7	1	-	9	1	--- -.MKIAYLGPK.G + Oxidation (M
1036.6012	1035.5939	1035.5787	14.7	1	-	9	1	3 -.MKIAYLGPK.G + Oxidation (M
1296.7419	1295.7346	1295.6986	27.8	98	-	109	0	--- K.IFSPHQALAQGK.K
1784.0413	1783.0340	1782.8941	78.5	133	-	148	0	--- R.FISEHPDQPYAAIAPK.S
2284.2476	2283.2403	2283.2164	10.5	3	-	23	1	--- K.IAYLGPKGSFHHVQTAFPK.E

No match to: 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1194.6759, 1194.6759, 1266.6686, 1277.7600, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1475.8114, 1487.8091, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1633.9124, 1732.1512, 1902.3138, 1994.0560, 2221.2212

50. [gi|551565531](#) Mass: 42563 Score: 37 Expect: 6.9e+003 Matches: 8

hypothetical protein EMIHURAFT_210302 [Emiliania huxleyi CCMP1516]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.5546	841.5473	841.4658	96.9	191	-	198	0	--- R.VPLDGVSR.L
1036.6012	1035.5939	1035.5978	-3.74	336	-	343	0	--- K.QVLHVWVR.T
1036.6012	1035.5939	1035.5978	-3.74	336	-	343	0	--- K.QVLHVWVR.T
1194.6759	1193.6686	1193.6115	47.9	181	-	190	0	--- R.FLVGEDMVLRL.V + Oxidation (M)
1194.6759	1193.6686	1193.6115	47.9	181	-	190	0	6 R.FLVGEDMVLRL.V + Oxidation (M)
1475.8114	1474.8041	1474.8507	-31.61	54	-	67	1	--- K.LALGKLGSSIPTYR.L
1487.8091	1486.8018	1486.7715	20.4	179	-	190	1	--- R.HRFLVGEDMVLRL.V + Oxidation (M)



1633.9124 1632.9051 1632.9100 -2.98 156 - 170 0 --- R.WPTQKPAVLPAQAAR.K

No match to: 848.5696, 850.5803, 853.5549, 853.5549, 855.0955, 864.5864, 868.5867, 868.5867, 871.0599, 877.0814, 882.5994, 882.5994, 887.0316, 909.0287, 951.6699, 960.9595, 1017.7114, 1019.5801, 1019.7258, 1033.7395, 1051.7457, 1051.7457, 1060.1041, 1082.0940, 1098.0653, 1151.7755, 1151.7755, 1165.7815, 1165.7815, 1266.6686, 1277.7600, 1296.7419, 1334.9314, 1334.9314, 1448.9645, 1448.9645, 1595.9777, 1595.9777, 1618.1177, 1618.1177, 1732.1512, 1784.0413, 1902.3138, 1994.0560, 2221.2212, 2284.2476

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 (842.5546,1+) : <no title>
 Query2 (848.5696,1+) : <no title>
 Query3 (850.5803,1+) : <no title>
 Query4 (853.5549,1+) : <no title>
 Query5 (853.5549,1+) : Locus:1..5.0.8
 Query6 (855.0955,1+) : <no title>
 Query7 (864.5864,1+) : <no title>
 Query8 (868.5867,1+) : Locus:1..5.0.7
 Query9 (868.5867,1+) : <no title>
 Query10 (871.0599,1+) : <no title>
 Query11 (877.0814,1+) : <no title>
 Query12 (882.5994,1+) : <no title>
 Query13 (882.5994,1+) : Locus:1..5.0.4
 Query14 (887.0316,1+) : <no title>
 Query15 (909.0287,1+) : <no title>
 Query16 (951.6699,1+) : <no title>
 Query17 (960.9595,1+) : <no title>
 Query18 (1017.7114,1+) : <no title>
 Query19 (1019.5801,1+) : <no title>
 Query20 (1019.7258,1+) : <no title>
 Query21 (1033.7395,1+) : <no title>
 Query22 (1036.6012,1+) : <no title>
 Query23 (1036.6012,1+) : Locus:1..5.0.11
 Query24 (1051.7457,1+) : <no title>
 Query25 (1051.7457,1+) : Locus:1..5.0.1
 Query26 (1060.1041,1+) : <no title>
 Query27 (1082.0940,1+) : <no title>
 Query28 (1098.0653,1+) : <no title>
 Query29 (1151.7755,1+) : <no title>
 Query30 (1151.7755,1+) : Locus:1..5.0.12
 Query31 (1165.7815,1+) : Locus:1..5.0.6
 Query32 (1165.7815,1+) : <no title>
 Query33 (1194.6759,1+) : <no title>
 Query34 (1194.6759,1+) : Locus:1..5.0.2
 Query35 (1266.6686,1+) : <no title>
 Query36 (1277.7600,1+) : <no title>
 Query37 (1296.7419,1+) : <no title>
 Query38 (1334.9314,1+) : <no title>
 Query39 (1334.9314,1+) : Locus:1..5.0.3
 Query40 (1448.9645,1+) : Locus:1..5.0.10
 Query41 (1448.9645,1+) : <no title>
 Query42 (1475.8114,1+) : <no title>
 Query43 (1487.8091,1+) : <no title>
 Query44 (1595.9777,1+) : Locus:1..5.0.5
 Query45 (1595.9777,1+) : <no title>
 Query46 (1618.1177,1+) : Locus:1..5.0.9
 Query47 (1618.1177,1+) : <no title>
 Query48 (1633.9124,1+) : <no title>
 Query49 (1732.1512,1+) : <no title>
 Query50 (1784.0413,1+) : <no title>
 Query51 (1902.3138,1+) : <no title>
 Query52 (1994.0560,1+) : <no title>
 Query53 (2221.2212,1+) : <no title>
 Query54 (2284.2476,1+) : <no title>

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