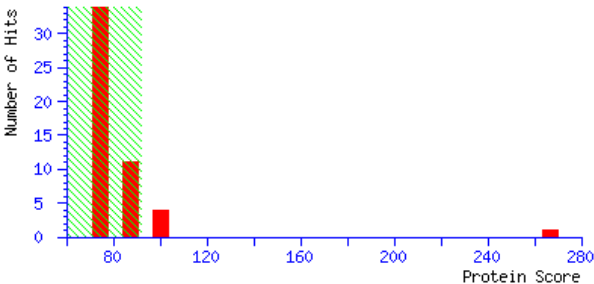


Mascot Search Results

User :
Email :
Search title : SampleSetID: 692, AnalysisID: 5361, MaldiWellID: 60692, SpectrumID: 127285, Path=\\161031\\MSMS\\run 65 NCBI all ok 1
Database : NCBI nr 160208 (79581714 sequences; 29080698065 residues)
Timestamp : 28 Nov 2016 at 11:18:36 GMT
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
Top Score : 267 for gi|157119583, AAEL008708-PA [Aedes aegypti]

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 92 are significant (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Format As

Protein Summary (deprecated) ▼

Help

Significance threshold p< 0.05 Max. number of hits 20

Re-Search All

Search Unmatched

Index

Accession	Mass	Score	Description
1. gi 157119583	53093	267	AAEL008708-PA [Aedes aegypti]
2. gi 973173869	517335	101	PREDICTED: pericentrin isoform X3 [Lepisosteus oculatus]
3. gi 973173019	518326	100	PREDICTED: pericentrin isoform X1 [Lepisosteus oculatus]
4. gi 973173077	517516	100	PREDICTED: pericentrin isoform X2 [Lepisosteus oculatus]
5. gi 973173881	512464	98	PREDICTED: pericentrin isoform X4 [Lepisosteus oculatus]
6. gi 676388977	235879	94	hypothetical protein AURANDRAFT_71752 [Aureococcus anophagefferens]
7. gi 572314937	108011	92	PREDICTED: uncharacterized protein LOC102672997 [Apis dorsata]
8. gi 939160742	18287	87	hypothetical protein [Sulfolobus sp. JCM 16833]
9. gi 973924294	2113274	86	hypothetical protein AQ367_40475 [Streptomyces caeruleatus]
10. gi 746319218	77916	84	hypothetical protein [Pandoraea pnomenusa]
11. gi 170045812	53335	84	lysosomal pro-X carboxypeptidase [Culex quinquefasciatus]
12. gi 740456478	76742	84	B12-binding domain-containing radical SAM protein [[Clostridium] aminophilum]
13. gi 440208481	16760	83	his-tRNA synthetase, partial [Hypobapta xenomorpha]
14. gi 358639159	52503	83	radical SAM family protein [Azoarcus sp. KH32C]
15. gi 239787450	174337	82	Sensor protein [uncultured bacterium]
16. gi 649503612	21793	82	hypothetical protein M082_5993 [Bacteroides fragilis str. 3725 D9 ii]
17. gi 913754691	22021	80	MULTISPECIES: hypothetical protein [Bacteroides]
18. gi 759928248	34237	80	LysR family transcriptional regulator [Ensifer sp. ZNC0028]
19. gi 506413224	307019	80	hypothetical protein [Methylobacterium nodulans]
20. gi 736079929	169685	80	hypothetical protein [Actinoplanes subtropicus]

Results List

1.	gi 157119583	Mass: 53093	Score: 267	Expect: 1.6e-019	Matches: 9
AAEL008708-PA [Aedes aegypti]					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Ions Peptide
	884.4629	883.4556	883.4301	28.9	29 - 35 0 --- K.VDHFNPR.N
	884.4629	883.4556	883.4301	28.9	29 - 35 0 50 K.VDHFNPR.N
	1264.5802	1263.5729	1263.5707	1.79	198 - 208 0 --- R.GCYGTIFSGFR.V
	1264.5802	1263.5729	1263.5707	1.79	198 - 208 0 37 R.GCYGTIFSGFR.V
	1402.6704	1401.6631	1401.5837	56.7	44 - 54 0 --- R.YYSNDEHSYPK.G
	1585.7628	1584.7555	1584.7685	-8.17	363 - 375 0 --- R.HAFGDWINEDLIR.A
	1585.7628	1584.7555	1584.7685	-8.17	363 - 375 0 77 R.HAFGDWINEDLIR.A
	1655.8937	1654.8864	1654.9043	-10.78	55 - 70 0 --- K.GPIFVIVGSGNGPIETR.Y
	1655.8937	1654.8864	1654.9043	-10.78	55 - 70 0 84 K.GPIFVIVGSGNGPIETR.Y
No match to: 983.5128, 983.5128, 1104.5879, 1166.6063, 1173.5913, 1179.6006, 1229.6768, 1237.6604, 1240.5980, 1268.6426, 1276.6123, 1278.6090, 1279.6028, 1359.7040, 1359.7040, 1376.7080, 1404.7360, 1412.7136, 1435.7228, 1444.7155, 1480.7465, 1498.7124, 1526.7263, 1553.7404, 1581.7969, 1583.7972, 1597.7627, 1599.7936, 1601.8167, 1603.8350, 1609.8295, 1613.7913, 1617.7798, 1622.8384, 1623.8735, 1638.8503, 1642.8019, 1645.7986, 1646.7770, 1651.8420, 1653.8228, 1656.8927, 1667.8373,					

1670.8447, 1683.9177, 1689.8406, 1698.8608, 1712.8848, 1749.8521, 1763.8978, 1790.8779, 1791.8766, 1794.9020, 1852.9092, 1888.9403, 2117.0503, 2126.0847, 2208.0913, 2218.0398, 2225.1460, 2330.1763, 3211.5742

2. [gi|973173869](#) Mass: 517335 Score: 101 Expect: 0.0063 Matches: 40

PREDICTED: pericentrin isoform X3 [Lepisosteus oculatus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1104.5879	1103.5806	1103.5822	-1.44	3017	- 3025	1	---	K.KSETEELLR.L
1166.6063	1165.5990	1165.5397	50.9	1141	- 1150	0	---	R.SQESAMLQTR.M + Oxidation (M)
1179.6006	1178.5933	1178.6659	-61.57	661	- 670	0	---	K.HLEILQAEVK.E
1229.6768	1228.6695	1228.6663	2.63	2623	- 2632	1	---	K.KIEQDLLQDK.D
1237.6604	1236.6531	1236.6285	19.9	1151	- 1159	1	---	R.MQFELERLR.E + Oxidation (M)
1264.5802	1263.5729	1263.6129	-31.61	950	- 959	1	---	K.LKESMVEQER.V + Oxidation (M)
1264.5802	1263.5729	1263.6129	-31.61	950	- 959	1	---	K.LKESMVEQER.V + Oxidation (M)
1276.6123	1275.6050	1275.6935	-69.36	2993	- 3005	0	---	R.DAALANLGHLPKG.V
1279.6028	1278.5955	1278.6026	-5.57	998	- 1007	0	---	K.VEEHHQMEIK.E
1359.7040	1358.6967	1358.7154	-13.72	2134	- 2144	1	---	K.DSELETLLQRR.E
1359.7040	1358.6967	1358.7154	-13.72	2134	- 2144	1	10	K.DSELETLLQRR.E
1376.7080	1375.7007	1375.7095	-6.40	1766	- 1776	1	---	K.ENQLREEFALK.Q
1402.6704	1401.6631	1401.6848	-15.45	1677	- 1687	1	---	K.ELQTRREEVNR.L
1444.7155	1443.7082	1443.7205	-8.50	1742	- 1754	0	---	R.ELNAALQEQTAK.L
1480.7465	1479.7392	1479.7681	-19.52	3088	- 3099	1	---	R.EGHLQEIERLK.N
1553.7404	1552.7331	1552.7984	-42.06	4179	- 4192	0	---	R.DQLEPADIVPLSEK.L
1581.7969	1580.7896	1580.7583	19.8	3738	- 3749	0	---	K.IWELQHDLQER.L
1583.7972	1582.7899	1582.7232	42.2	996	- 1007	1	---	K.CKVEEHHQMEIK.E + Oxidation (M)
1585.7628	1584.7555	1584.8008	-28.59	3543	- 3555	1	---	R.DWLRLSELHSISSR.G
1585.7628	1584.7555	1584.8008	-28.59	3543	- 3555	1	6	R.DWLRLSELHSISSR.G
1603.8350	1602.8277	1602.8287	-0.58	679	- 692	1	---	K.ASEELVMRLEVAK.Q
1617.7798	1616.7725	1616.8886	-71.80	4371	- 4385	1	---	R.SLVSVQVSSPKSPFR.L
1642.8019	1641.7946	1641.8573	-38.18	2671	- 2685	1	---	K.EQLEAGQEALIGKEK.Q
1645.7986	1644.7913	1644.8318	-24.64	3687	- 3701	1	---	K.KELSSSSQELHTATK.A
1651.8420	1650.8347	1650.8035	18.9	1624	- 1637	1	---	R.EEGEMVTRQFLGQK.E
1655.8937	1654.8864	1654.7733	68.4	2770	- 2782	0	---	K.NQEIDHLNEQIMR.L + Oxidation (M)
1655.8937	1654.8864	1654.7733	68.4	2770	- 2782	0	---	K.NQEIDHLNEQIMR.L + Oxidation (M)
1667.8373	1666.8300	1666.8097	12.2	3075	- 3087	1	---	K.TELYTECQALRQR.E
1670.8447	1669.8374	1669.8999	-37.40	2973	- 2986	1	---	R.QREAQLVETELQVK.T
1683.9177	1682.9104	1682.8410	41.3	3673	- 3686	1	---	R.AHLRTEQEAIVCEK.K
1689.8406	1688.8333	1688.8581	-14.65	229	- 243	1	---	K.DQSSQLDSLQKEALK.L
1790.8779	1789.8706	1789.8264	24.7	2145	- 2159	1	---	R.ERENEEDNLVAMLR.A + Oxidation (M)
1791.8766	1790.8693	1790.8720	-1.48	2129	- 2143	1	---	K.EMEAKDSELETLLQR.R
1794.9020	1793.8947	1793.8445	28.0	2501	- 2514	1	---	R.HFIDEQAVEREHER.D
1852.9092	1851.9019	1851.9214	-10.50	2823	- 2837	1	---	R.NKEEEVEQLHEVIEK.L
1888.9403	1887.9330	1887.9537	-10.97	449	- 466	1	---	R.EKETALAQLAESSDGALR.L
2117.0503	2116.0430	2116.0648	-10.27	2975	- 2992	1	---	R.EAQLVETELQVKTSEEQR.D
2208.0913	2207.0840	2207.0012	37.5	2415	- 2434	1	---	R.DALTGSMDDNQKGLLEAER.L + Oxidation (M)
2225.1460	2224.1387	2224.1937	-24.72	4034	- 4052	1	---	R.ELTSHRLQQAHTPNLRPAR.D
3211.5742	3210.5669	3210.5966	-9.23	3428	- 3457	0	---	R.GMTLPDDNSISQSAVKPEEDISPQLGLLK.K
No match to: 884.4629, 884.4629, 983.5128, 983.5128, 1173.5913, 1240.5980, 1268.6426, 1278.6090, 1404.7360, 1412.7136, 1435.7228, 1498.7124, 1526.7263, 1597.7627, 1599.7936, 1601.8167, 1609.8295, 1613.7913, 1622.8384, 1623.8735, 1638.8503, 1646.7770, 1653.8228, 1656.8927, 1698.8608, 1712.8848, 1749.8521, 1763.8978, 2126.0847, 2218.0398, 2330.1763								

3. [gi|973173019](#) Mass: 518326 Score: 100 Expect: 0.008 Matches: 40

PREDICTED: pericentrin isoform X1 [Lepisosteus oculatus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1104.5879	1103.5806	1103.5822	-1.44	3017	- 3025	1	---	K.KSETEELLR.L
1166.6063	1165.5990	1165.5397	50.9	1141	- 1150	0	---	R.SQESAMLQTR.M + Oxidation (M)
1179.6006	1178.5933	1178.6659	-61.57	661	- 670	0	---	K.HLEILQAEVK.E
1229.6768	1228.6695	1228.6663	2.63	2623	- 2632	1	---	K.KIEQDLLQDK.D
1237.6604	1236.6531	1236.6285	19.9	1151	- 1159	1	---	R.MQFELERLR.E + Oxidation (M)
1264.5802	1263.5729	1263.6129	-31.61	950	- 959	1	---	K.LKESMVEQER.V + Oxidation (M)
1264.5802	1263.5729	1263.6129	-31.61	950	- 959	1	---	K.LKESMVEQER.V + Oxidation (M)
1276.6123	1275.6050	1275.6935	-69.36	2993	- 3005	0	---	R.DAALANLGHLPKG.V
1279.6028	1278.5955	1278.6026	-5.57	998	- 1007	0	---	K.VEEHHQMEIK.E
1359.7040	1358.6967	1358.7154	-13.72	2134	- 2144	1	---	K.DSELETLLQRR.E
1359.7040	1358.6967	1358.7154	-13.72	2134	- 2144	1	10	K.DSELETLLQRR.E
1376.7080	1375.7007	1375.7095	-6.40	1766	- 1776	1	---	K.ENQLREEFALK.Q
1402.6704	1401.6631	1401.6848	-15.45	1677	- 1687	1	---	K.ELQTRREEVNR.L
1444.7155	1443.7082	1443.7205	-8.50	1742	- 1754	0	---	R.ELNAALQEQTAK.L
1480.7465	1479.7392	1479.7681	-19.52	3088	- 3099	1	---	R.EGHLQEIERLK.N
1553.7404	1552.7331	1552.7984	-42.06	4188	- 4201	0	---	R.DQLEPADIVPLSEK.L
1581.7969	1580.7896	1580.7583	19.8	3747	- 3758	0	---	K.IWELQHDLQER.L
1583.7972	1582.7899	1582.7232	42.2	996	- 1007	1	---	K.CKVEEHHQMEIK.E + Oxidation (M)
1585.7628	1584.7555	1584.8008	-28.59	3552	- 3564	1	---	R.DWLRLSELHSISSR.G
1585.7628	1584.7555	1584.8008	-28.59	3552	- 3564	1	6	R.DWLRLSELHSISSR.G
1603.8350	1602.8277	1602.8287	-0.58	679	- 692	1	---	K.ASEELVMRLEVAK.Q
1617.7798	1616.7725	1616.8886	-71.80	4380	- 4394	1	---	R.SLVSVQVSSPKSPFR.L
1642.8019	1641.7946	1641.8573	-38.18	2671	- 2685	1	---	K.EQLEAGQEALIGKEK.Q
1645.7986	1644.7913	1644.8318	-24.64	3696	- 3710	1	---	K.KELSSSSQELHTATK.A
1651.8420	1650.8347	1650.8035	18.9	1624	- 1637	1	---	R.EEGEMVTRQFLGQK.E

1655.8937	1654.8864	1654.7733	68.4	2770	-	2782	0	---	K.NQEIDHLNEQIMR.L + Oxidation (M)
1655.8937	1654.8864	1654.7733	68.4	2770	-	2782	0	---	K.NQEIDHLNEQIMR.L + Oxidation (M)
1667.8373	1666.8300	1666.8097	12.2	3075	-	3087	1	---	K.TELYTECQALRQR.E
1670.8447	1669.8374	1669.8999	-37.40	2973	-	2986	1	---	R.QREAQLVETELQVK.T
1683.9177	1682.9104	1682.8410	41.3	3682	-	3695	1	---	R.AHLRTEQEAIVCELK.K
1689.8406	1688.8333	1688.8581	-14.65	229	-	243	1	---	K.DQSSQLDSLQKEALK.L
1790.8779	1789.8706	1789.8264	24.7	2145	-	2159	1	---	R.ERENEEDGNLVAMLR.A + Oxidation (M)
1791.8766	1790.8693	1790.8720	-1.48	2129	-	2143	1	---	K.EMEAKDSELETLLQR.R
1794.9020	1793.8947	1793.8445	28.0	2501	-	2514	1	---	R.HFIDEQAVEREHER.D
1852.9092	1851.9019	1851.9214	-10.50	2823	-	2837	1	---	R.NKEEEVEQLHEVIEK.L
1888.9403	1887.9330	1887.9537	-10.97	449	-	466	1	---	R.EKETALAQLAESSDGALR.L
2117.0503	2116.0430	2116.0648	-10.27	2975	-	2992	1	---	R.EAQLVETELQVKTSEEQR.D
2208.0913	2207.0840	2207.0012	37.5	2415	-	2434	1	---	R.DALTGSMDDNQGLLEEAER.L + Oxidation (M)
2225.1460	2224.1387	2224.1937	-24.72	4043	-	4061	1	---	R.ELTSHRLQQAHTPNLRPAR.D
3211.5742	3210.5669	3210.5966	-9.23	3437	-	3466	0	---	R.GMTLPDDNSISQSAVKPEEDISPQLGLLK.K

No match to: 884.4629, 884.4629, 983.5128, 983.5128, 1173.5913, 1240.5980, 1268.6426, 1278.6090, 1404.7360, 1412.7136, 1435.7228, 1498.7124, 1526.7263, 1597.7627, 1599.7936, 1601.8167, 1609.8295, 1613.7913, 1622.8384, 1623.8735, 1638.8503, 1646.7770, 1653.8228, 1656.8927, 1698.8608, 1712.8848, 1749.8521, 1763.8978, 2126.0847, 2218.0398, 2330.1763

4. [gi|973173077](#) Mass: 517516 Score: 100 Expect: 0.0081 Matches: 40

PREDICTED: pericentrin isoform X2 [Lepisosteus oculatus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
1104.5879	1103.5806	1103.5822	-1.44	3010	-	3018	1	---	K.KSETEELLR.L
1166.6063	1165.5990	1165.5397	50.9	1141	-	1150	0	---	R.SQESAMLQTR.M + Oxidation (M)
1179.6006	1178.5933	1178.6659	-61.57	661	-	670	0	---	K.HLEILQAEVK.E
1229.6768	1228.6695	1228.6663	2.63	2616	-	2625	1	---	K.KIEQDLLQDK.D
1237.6604	1236.6531	1236.6285	19.9	1151	-	1159	1	---	R.MQFELERLR.E + Oxidation (M)
1264.5802	1263.5729	1263.6129	-31.61	950	-	959	1	---	K.LKESMVEQER.V + Oxidation (M)
1264.5802	1263.5729	1263.6129	-31.61	950	-	959	1	---	K.LKESMVEQER.V + Oxidation (M)
1276.6123	1275.6050	1275.6935	-69.36	2986	-	2998	0	---	R.DAALANLGHLPKG.V
1279.6028	1278.5955	1278.6026	-5.57	998	-	1007	0	---	K.VEEHHQMEIK.E
1359.7040	1358.6967	1358.7154	-13.72	2134	-	2144	1	---	K.DSELETLLQRR.E
1359.7040	1358.6967	1358.7154	-13.72	2134	-	2144	1	10	K.DSELETLLQRR.E
1376.7080	1375.7007	1375.7095	-6.40	1766	-	1776	1	---	K.ENQLREEFALK.Q
1402.6704	1401.6631	1401.6848	-15.45	1677	-	1687	1	---	K.ELQTRREEVNR.L
1444.7155	1443.7082	1443.7205	-8.50	1742	-	1754	0	---	R.ELNAALQEQTAK.L
1480.7465	1479.7392	1479.7681	-19.52	3081	-	3092	1	---	R.EGHLQEEIERLK.N
1553.7404	1552.7331	1552.7984	-42.06	4181	-	4194	0	---	R.DQLEPADIVPLSEK.L
1581.7969	1580.7896	1580.7583	19.8	3740	-	3751	0	---	K.IWELQHDLQER.L
1583.7972	1582.7899	1582.7232	42.2	996	-	1007	1	---	K.CKVEEHHQMEIK.E + Oxidation (M)
1585.7628	1584.7555	1584.8008	-28.59	3545	-	3557	1	---	R.DWLRSLSHSSSR.G
1585.7628	1584.7555	1584.8008	-28.59	3545	-	3557	1	6	R.DWLRSLSHSSSR.G
1603.8350	1602.8277	1602.8287	-0.58	679	-	692	1	---	K.ASEELVMRLVAK.Q
1617.7798	1616.7725	1616.8886	-71.80	4373	-	4387	1	---	R.SLVSVVSSPKSPFR.L
1642.8019	1641.7946	1641.8573	-38.18	2664	-	2678	1	---	K.EQLEAGQEALIGKEK.Q
1645.7986	1644.7913	1644.8318	-24.64	3689	-	3703	1	---	K.KELSSSSQLHTATK.A
1651.8420	1650.8347	1650.8035	18.9	1624	-	1637	1	---	R.EEGEMVTRQFLGQK.E
1655.8937	1654.8864	1654.7733	68.4	2763	-	2775	0	---	K.NQEIDHLNEQIMR.L + Oxidation (M)
1655.8937	1654.8864	1654.7733	68.4	2763	-	2775	0	---	K.NQEIDHLNEQIMR.L + Oxidation (M)
1667.8373	1666.8300	1666.8097	12.2	3068	-	3080	1	---	K.TELYTECQALRQR.E
1670.8447	1669.8374	1669.8999	-37.40	2966	-	2979	1	---	R.QREAQLVETELQVK.T
1683.9177	1682.9104	1682.8410	41.3	3675	-	3688	1	---	R.AHLRTEQEAIVCELK.K
1689.8406	1688.8333	1688.8581	-14.65	229	-	243	1	---	K.DQSSQLDSLQKEALK.L
1790.8779	1789.8706	1789.8264	24.7	2145	-	2159	1	---	R.ERENEEDGNLVAMLR.A + Oxidation (M)
1791.8766	1790.8693	1790.8720	-1.48	2129	-	2143	1	---	K.EMEAKDSELETLLQR.R
1794.9020	1793.8947	1793.8445	28.0	2501	-	2514	1	---	R.HFIDEQAVEREHER.D
1852.9092	1851.9019	1851.9214	-10.50	2816	-	2830	1	---	R.NKEEEVEQLHEVIEK.L
1888.9403	1887.9330	1887.9537	-10.97	449	-	466	1	---	R.EKETALAQLAESSDGALR.L
2117.0503	2116.0430	2116.0648	-10.27	2968	-	2985	1	---	R.EAQLVETELQVKTSEEQR.D
2208.0913	2207.0840	2207.0012	37.5	2415	-	2434	1	---	R.DALTGSMDDNQGLLEEAER.L + Oxidation (M)
2225.1460	2224.1387	2224.1937	-24.72	4036	-	4054	1	---	R.ELTSHRLQQAHTPNLRPAR.D
3211.5742	3210.5669	3210.5966	-9.23	3430	-	3459	0	---	R.GMTLPDDNSISQSAVKPEEDISPQLGLLK.K

No match to: 884.4629, 884.4629, 983.5128, 983.5128, 1173.5913, 1240.5980, 1268.6426, 1278.6090, 1404.7360, 1412.7136, 1435.7228, 1498.7124, 1526.7263, 1597.7627, 1599.7936, 1601.8167, 1609.8295, 1613.7913, 1622.8384, 1623.8735, 1638.8503, 1646.7770, 1653.8228, 1656.8927, 1698.8608, 1712.8848, 1749.8521, 1763.8978, 2126.0847, 2218.0398, 2330.1763

5. [gi|973173881](#) Mass: 512464 Score: 98 Expect: 0.014 Matches: 39

PREDICTED: pericentrin isoform X4 [Lepisosteus oculatus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
1104.5879	1103.5806	1103.5822	-1.44	2966	-	2974	1	---	K.KSETEELLR.L
1166.6063	1165.5990	1165.5397	50.9	1090	-	1099	0	---	R.SQESAMLQTR.M + Oxidation (M)
1179.6006	1178.5933	1178.6659	-61.57	610	-	619	0	---	K.HLEILQAEVK.E
1229.6768	1228.6695	1228.6663	2.63	2572	-	2581	1	---	K.KIEQDLLQDK.D
1237.6604	1236.6531	1236.6285	19.9	1100	-	1108	1	---	R.MQFELERLR.E + Oxidation (M)
1264.5802	1263.5729	1263.6129	-31.61	899	-	908	1	---	K.LKESMVEQER.V + Oxidation (M)
1264.5802	1263.5729	1263.6129	-31.61	899	-	908	1	---	K.LKESMVEQER.V + Oxidation (M)
1276.6123	1275.6050	1275.6935	-69.36	2942	-	2954	0	---	R.DAALANLGHLPKG.V

1279.6028	1278.5955	1278.6026	-5.57	947	-	956	0	---	K.VEEHHQMEIK.E
1359.7040	1358.6967	1358.7154	-13.72	2083	-	2093	1	---	K.DSELETLQR.R
1359.7040	1358.6967	1358.7154	-13.72	2083	-	2093	1	10	K.DSELETLQR.R
1376.7080	1375.7007	1375.7095	-6.40	1715	-	1725	1	---	K.ENQLREEFALK.Q
1402.6704	1401.6631	1401.6848	-15.45	1626	-	1636	1	---	K.ELQTRREEVNR.L
1444.7155	1443.7082	1443.7205	-8.50	1691	-	1703	0	---	R.ELNAALQEQTAK.L
1480.7465	1479.7392	1479.7681	-19.52	3037	-	3048	1	---	R.EGHLQEIERLK.N
1553.7404	1552.7331	1552.7984	-42.06	4137	-	4150	0	---	R.DQLEPADIVPLSEK.L
1581.7969	1580.7896	1580.7583	19.8	3696	-	3707	0	---	K.IWELQHDLDQER.L
1583.7972	1582.7899	1582.7232	42.2	945	-	956	1	---	K.CKVEHHQMEIK.E + Oxidation (M)
1585.7628	1584.7555	1584.8008	-28.59	3501	-	3513	1	---	R.DWLRLSELHSSSR.G
1585.7628	1584.7555	1584.8008	-28.59	3501	-	3513	1	6	R.DWLRLSELHSSSR.G
1603.8350	1602.8277	1602.8287	-0.58	628	-	641	1	---	K.ASEELVMRLEVAQ.Q
1617.7798	1616.7725	1616.8886	-71.80	4329	-	4343	1	---	R.SLVSVQVSSPKSPFR.L
1642.8019	1641.7946	1641.8573	-38.18	2620	-	2634	1	---	K.EQLEAGQEALIGKEK.Q
1645.7986	1644.7913	1644.8318	-24.64	3645	-	3659	1	---	K.KELSSSSQELHTATK.A
1651.8420	1650.8347	1650.8035	18.9	1573	-	1586	1	---	R.EEGEMVTRQFLGQK.E
1655.8937	1654.8864	1654.7733	68.4	2719	-	2731	0	---	K.NQIDHLNEQIMR.L + Oxidation (M)
1655.8937	1654.8864	1654.7733	68.4	2719	-	2731	0	---	K.NQIDHLNEQIMR.L + Oxidation (M)
1667.8373	1666.8300	1666.8097	12.2	3024	-	3036	1	---	K.TELYTECQALRQR.E
1670.8447	1669.8374	1669.8999	-37.40	2922	-	2935	1	---	R.QREAQLVETELQVK.T
1683.9177	1682.9104	1682.8410	41.3	3631	-	3644	1	---	R.AHLRTEQEAVALCK.K
1790.8779	1789.8706	1789.8264	24.7	2094	-	2108	1	---	R.ERNEEGDNLVAMLR.A + Oxidation (M)
1791.8766	1790.8693	1790.8720	-1.48	2078	-	2092	1	---	K.EMEAKDSELETLQR.R
1794.9020	1793.8947	1793.8445	28.0	2450	-	2463	1	---	R.HFIDEQAVEREHER.D
1852.9092	1851.9019	1851.9214	-10.50	2772	-	2786	1	---	R.NKEEEVEQLHEVIEK.L
1888.9403	1887.9330	1887.9537	-10.97	398	-	415	1	---	R.EKETALQAESSDGLR.L
2117.0503	2116.0430	2116.0648	-10.27	2924	-	2941	1	---	R.EAQLVETELQVKTSEEQR.D
2208.0913	2207.0840	2207.0012	37.5	2364	-	2383	1	---	R.DALTGSMDDNQKGLLEAER.L + Oxidation (M)
2225.1460	2224.1387	2224.1937	-24.72	3992	-	4010	1	---	R.ELTSHRLQQAHTPNLRPAR.D
3211.5742	3210.5669	3210.5966	-9.23	3386	-	3415	0	---	R.GMTLPDDNSISQSAVKPEEDISPQLLK.K
No match to: 884.4629, 884.4629, 983.5128, 983.5128, 1173.5913, 1240.5980, 1268.6426, 1278.6090, 1404.7360, 1412.7136, 1435.7228, 1498.7124, 1526.7263, 1597.7627, 1599.7936, 1601.8167, 1609.8295, 1613.7913, 1622.8384, 1623.8735, 1638.8503, 1646.7770, 1653.8228, 1656.8927, 1689.8406, 1698.8608, 1712.8848, 1749.8521, 1763.8978, 2126.0847, 2218.0398, 2330.1763									

6. [gi|676388977](#) Mass: 235879 Score: 94 Expect: 0.034 Matches: 29

hypothetical protein AURANDRAFT_71752 [Aureococcus anophagefferens]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
884.4629	883.4556	883.4763	-23.42	1201	- 1209	0	---	R.DVANGALPK.D
884.4629	883.4556	883.4763	-23.42	1201	- 1209	0	---	R.DVANGALPK.D
1104.5879	1103.5806	1103.5757	4.44	122	- 132	0	---	K.MGTGTAAVQR.A
1173.5913	1172.5840	1172.5686	13.1	1488	- 1498	1	---	K.AGAKGNQDAWR.R
1229.6768	1228.6695	1228.6299	32.2	1840	- 1851	0	---	R.AIDADLGDAKQK.I
1240.5980	1239.5907	1239.6758	-68.59	466	- 476	1	---	R.GLLKLGNHMNK.E + Oxidation (M)
1264.5802	1263.5729	1263.6572	-66.65	92	- 103	1	---	R.QSSVSFRTPAGK.R
1264.5802	1263.5729	1263.6572	-66.65	92	- 103	1	---	R.QSSVSFRTPAGK.R
1268.6426	1267.6353	1267.6449	-7.52	2033	- 2044	0	---	R.AAFGDDVVAYLK.A
1376.7080	1375.7007	1375.7095	-6.41	968	- 980	0	---	R.VEEAAPPKPEGR.M
1402.6704	1401.6631	1401.7140	-36.27	105	- 118	0	---	R.SPAAADDAALAPYLK.M
1412.7136	1411.7063	1411.6224	59.4	606	- 616	1	---	R.FVVEADKCCER.A
1444.7155	1443.7082	1443.7180	-6.79	232	- 243	0	---	K.TCHFKPLDEAVK.V
1553.7404	1552.7331	1552.7569	-15.29	1257	- 1268	1	---	R.FSTHQYTMNRNL.C
1581.7969	1580.7896	1580.7763	8.44	841	- 855	1	---	R.TATAMRGAMTAISQR.G + Oxidation (M)
1597.7627	1596.7554	1596.7712	-9.88	841	- 855	1	---	R.TATAMRGAMTAISQR.G + 2 Oxidation (M)
1617.7798	1616.7725	1616.7518	12.8	1531	- 1544	1	---	K.TGGFSRAWPEPCR.R
1622.8384	1621.8311	1621.7292	62.8	1315	- 1334	0	---	R.SGSGGAASPGGAGATSSSTR.D
1645.7986	1644.7913	1644.7890	1.43	831	- 846	1	---	K.GPTTPPDASRTATAMR.G + Oxidation (M)
1646.7770	1645.7697	1645.7961	-16.02	923	- 939	1	---	R.DGYFGAAPAPAPGGRSR.T
1651.8420	1650.8347	1650.8941	-35.94	355	- 370	0	---	R.SLQPLLPATADEAAVR.A
1653.8228	1652.8155	1652.8093	3.77	1269	- 1281	1	---	R.CRYVHLTNYSVKN.K
1655.8937	1654.8864	1654.7872	60.0	1372	- 1386	0	---	K.TLIAAESEMTPASYSR.A + Oxidation (M)
1655.8937	1654.8864	1654.7872	60.0	1372	- 1386	0	---	K.TLIAAESEMTPASYSR.A + Oxidation (M)
1698.8608	1697.8535	1697.8234	17.8	1717	- 1731	1	---	R.APRPSQKSSDADHFR.I
1790.8779	1789.8706	1789.9284	-32.26	105	- 121	1	---	R.SPAAADDAALAPYLKMLK.M + Oxidation (M)
1791.8766	1790.8693	1790.7807	49.5	289	- 306	1	---	R.AGPSGSLDGGDDDDTVKK.V
1888.9403	1887.9330	1887.9439	-5.76	371	- 390	1	---	R.AYVAAQGAPTPGTRGTDAK.V
3211.5742	3210.5669	3210.4888	24.3	1500	- 1527	1	---	R.SGRPDDIALDKLSGEDWDLVCHAEDEL.R
No match to: 983.5128, 983.5128, 1166.6063, 1179.6006, 1237.6604, 1276.6123, 1278.6090, 1279.6028, 1359.7040, 1359.7040, 1404.7360, 1435.7228, 1480.7465, 1498.7124, 1526.7263, 1583.7972, 1585.7628, 1585.7628, 1599.7936, 1601.8167, 1603.8350, 1609.8295, 1613.7913, 1623.8735, 1638.8503, 1642.8019, 1656.8927, 1667.8373, 1670.8447, 1683.9177, 1689.8406, 1712.8848, 1749.8521, 1763.8978, 1794.9020, 1852.9092, 2117.0503, 2126.0847, 2208.0913, 2218.0398, 2225.1460, 2330.1763								

7. [gi|572314937](#) Mass: 108011 Score: 92 Expect: 0.048 Matches: 19

PREDICTED: uncharacterized protein LOC102672997 [Apis dorsata]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
884.4629	883.4556	883.4664	-12.25	185	-	192	0 ---	R.IPGGTFHR.S
884.4629	883.4556	883.4664	-12.25	185	-	192	0 ---	R.IPGGTFHR.S
1104.5879	1103.5806	1103.5611	17.7	896	-	906	0 ---	R.VFPGGQADVSK.S

1166.6063	1165.5990	1165.5397	50.9	586	-	595	1	---	R.KNSETEGVMR.A + Oxidation (M)
1229.6768	1228.6695	1228.6088	49.4	358	-	368	0	---	K.TASEEHFPALK.I
1237.6604	1236.6531	1236.6462	5.58	166	-	176	0	---	K.TEKPLQAEHGK.L
1444.7155	1443.7082	1443.7140	-3.99	37	-	49	0	---	R.DNCQSISPAALLR.V
1480.7465	1479.7392	1479.7834	-29.87	868	-	882	0	---	K.GYGKPSLGFSVVGGR.D
1583.7972	1582.7899	1582.7951	-3.27	369	-	382	1	---	K.IEDTYTGTTTLGRR.R
1585.7628	1584.7555	1584.8359	-50.70	729	-	742	1	---	R.LGDEIVEVEGKELR.T
1585.7628	1584.7555	1584.8359	-50.70	729	-	742	1	6	R.LGDEIVEVEGKELR.T
1599.7936	1598.7863	1598.7536	20.5	252	-	266	0	---	K.GDDPSEGIDLQIANR.K
1617.7798	1616.7725	1616.8562	-51.76	355	-	368	1	---	R.LFKTASEEHFPALK.I
1790.8779	1789.8706	1789.8604	5.74	199	-	214	1	---	K.SFFIRMGSTGMLNSAR.G + Oxidation (M)
1888.9403	1887.9330	1888.0418	-57.61	907	-	923	1	---	K.SLFQGDILSLNGKVL.R
2117.0503	2116.0430	2116.0185	11.6	842	-	860	1	---	R.KGGESNLESATEPQHLYR.H
2126.0847	2125.0774	2125.0725	2.31	482	-	500	1	---	R.FSETSSLNVDLDMVATLRK.H
2208.0913	2207.0840	2207.2062	-55.36	705	-	723	1	---	R.LPELRYIVVQLESDGIAHR.D
2225.1460	2224.1387	2224.0165	54.9	547	-	566	0	---	K.CTDSSDTSSVVDSELEKPIR.S

No match to: 983.5128, 983.5128, 1173.5913, 1179.6006, 1240.5980, 1264.5802, 1264.5802, 1268.6426, 1276.6123, 1278.6090, 1279.6028, 1359.7040, 1359.7040, 1376.7080, 1402.6704, 1404.7360, 1412.7136, 1435.7228, 1498.7124, 1526.7263, 1553.7404, 1581.7969, 1597.7627, 1601.8167, 1603.8350, 1609.8295, 1613.7913, 1622.8384, 1623.8735, 1638.8503, 1642.8019, 1645.7986, 1646.7770, 1651.8420, 1653.8228, 1655.8937, 1655.8937, 1656.8927, 1667.8373, 1670.8447, 1683.9177, 1689.8406, 1698.8608, 1712.8848, 1749.8521, 1763.8978, 1791.8766, 1794.9020, 1852.9092, 2218.0398, 2330.1763, 3211.5742

8. [gi|939160742](#) Mass: 18287 Score: 87 Expect: 0.17 Matches: 12

hypothetical protein [Sulfolobus sp. JCM 16833]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
884.4629	883.4556	883.3970	66.3	14	-	19	1 ---	K.RYQMDR.F + Oxidation (M)
884.4629	883.4556	883.3970	66.3	14	-	19	1 ---	K.RYQMDR.F + Oxidation (M)
1279.6028	1278.5955	1278.6091	-10.65	22	-	32	0 ---	K.EALYADLAER.F
1359.7040	1358.6967	1358.7268	-22.13	84	-	95	0 ---	R.VDWIIAIMPSSK.L
1359.7040	1358.6967	1358.7268	-22.13	84	-	95	0 ---	R.VDWIIAIMPSSK.L
1376.7080	1375.7007	1375.6653	25.7	98	-	109	0 ---	R.EIVSIMGDDEL.R
1404.7360	1403.7287	1403.7521	-16.65	33	-	45	1 ---	R.FLNDGLIRNSAGK.V
1553.7404	1552.7331	1552.7443	-7.20	1	-	13	0 ---	-.MTESITKPWTDTK.R + Oxidation (M)
1609.8295	1608.8222	1608.7995	14.1	129	-	142	1 ---	R.DAEISRYTGEELVK.K
1645.7986	1644.7913	1644.8505	-35.96	96	-	109	1 ---	K.LREIVSIMGDDEL.R
1888.9403	1887.9330	1888.0319	-52.37	46	-	62	1 ---	K.VYQAVKAYIAGISVNH.R
2208.0913	2207.0840	2207.1222	-17.29	22	-	40	1 ---	K.EALYADLAERFLNDGLIR.N

No match to: 983.5128, 983.5128, 1104.5879, 1166.6063, 1173.5913, 1179.6006, 1229.6768, 1237.6604, 1240.5980, 1264.5802, 1264.5802, 1268.6426, 1276.6123, 1278.6090, 1402.6704, 1412.7136, 1435.7228, 1444.7155, 1480.7465, 1498.7124, 1526.7263, 1553.7404, 1581.7969, 1583.7972, 1585.7628, 1597.7627, 1599.7936, 1601.8167, 1603.8350, 1613.7913, 1617.7798, 1622.8384, 1623.8735, 1638.8503, 1642.8019, 1646.7770, 1651.8420, 1653.8228, 1655.8937, 1655.8937, 1656.8927, 1667.8373, 1670.8447, 1683.9177, 1689.8406, 1698.8608, 1712.8848, 1749.8521, 1763.8978, 1790.8779, 1791.8766, 1794.9020, 1852.9092, 2117.0503, 2126.0847, 2218.0398, 2225.1460, 2330.1763, 3211.5742

9. [gi|973924294](#) Mass: 2113274 Score: 86 Expect: 0.22 Matches: 63

hypothetical protein AQJ67_40475 [Streptomyces caeruleatus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
884.4629	883.4556	883.4399	17.8	13861	- 13868	0	---	R.EPVGTEPR.A
884.4629	883.4556	883.4399	17.8	13861	- 13868	0	4	R.EPVGTEPR.A
1104.5879	1103.5806	1103.5095	64.5	3169	- 3177	0	---	R.LDEDTQIDR.T
1173.5913	1172.5840	1172.5648	16.4	15921	- 15931	0	---	R.FGPDGALMPPR.Q + Oxidation (M)
1229.6768	1228.6695	1228.5909	64.0	2140	- 2150	0	---	R.QSRPGQGQTD.R.A
1237.6604	1236.6531	1236.5946	47.3	19569	- 19581	0	---	K.GTTTADATATTAR.D
1240.5980	1239.5907	1239.6724	-65.88	5761	- 5771	0	---	R.LDAPLPQPHPR.E
1264.5802	1263.5729	1263.6095	-28.96	3011	- 3021	0	---	R.ESAEDVFLQAR.K
1264.5802	1263.5729	1263.6095	-28.96	3011	- 3021	0	---	R.ESAEDVFLQAR.K
1268.6426	1267.6353	1267.6309	3.46	9873	- 9883	0	---	R.IGADDSLHVWR.T
1276.6123	1275.6050	1275.6935	-69.36	14591	- 14601	1	---	R.ELFARVDLSAR.I
1279.6028	1278.5955	1278.6125	-13.30	9645	- 9656	1	---	R.EGMPSSSEKASLK.K + Oxidation (M)
1359.7040	1358.6967	1358.6983	-1.14	15331	- 15341	1	---	R.WTVTPAYHEKK.V
1359.7040	1358.6967	1358.7154	-13.72	12866	- 12877	1	7	R.VLEETVAASRER.G
1376.7080	1375.7007	1375.6150	62.3	915	- 926	1	---	R.RMEAADSPQEAR.A + Oxidation (M)
1402.6704	1401.6631	1401.6525	7.60	13271	- 13284	0	---	R.GPGVAAYDPVDDAR.Q
1412.7136	1411.7063	1411.7419	-25.22	12834	- 12846	1	---	R.TEPEGDGR LAVIR.T
1444.7155	1443.7082	1443.7028	3.79	6990	- 7002	0	---	R.EAIELSMTPQGR.S + Oxidation (M)
1480.7465	1479.7392	1479.7093	20.2	18032	- 18044	0	---	R.ELVENAFSDESIK.A
1498.7124	1497.7051	1497.8052	-66.82	6898	- 6912	0	---	R.GKPLAGGWL AGNTT.R.I
1526.7263	1525.7190	1525.8286	-71.82	10792	- 10804	1	---	R.IEKELALHTAMVR.D + Oxidation (M)
1553.7404	1552.7331	1552.7270	3.93	6409	- 6423	0	---	K.SAATSFGWQASVEGR.A
1581.7969	1580.7896	1580.7671	14.3	9732	- 9744	1	---	R.ADFMGHFFLGRQR.R
1585.7628	1584.7555	1584.7420	8.53	7599	- 7612	1	---	R.SGYKDVYVDPETGR.E
1585.7628	1584.7555	1584.7420	8.53	7599	- 7612	1	---	R.SGYKDVYVDPETGR.E
1597.7627	1596.7554	1596.7620	-4.10	9732	- 9744	1	---	R.ADFMGHFFLGRQR.R + Oxidation (M)
1599.7936	1598.7863	1598.8165	-18.87	14607	- 14620	1	---	R.ILAVDEEHRFGGTR.F
1601.8167	1600.8094	1600.8759	-41.52	2768	- 2781	1	---	R.MYRSVPLPLAELR.E
1603.8350	1602.8277	1602.7824	28.3	18714	- 18729	0	---	R.GTVAEMLAAPGGTSWR.E
1609.8295	1608.8222	1608.7757	28.9	18824	- 18837	1	---	R.VLARDDEHHFGGTR.F
1613.7913	1612.7840	1612.8825	-61.03	10739	- 10753	0	---	R.YLDGADLPVVPVSLR.R
1617.7798	1616.7725	1616.8708	-60.79	2768	- 2781	1	---	R.MYRSVPLPLAELR.E + Oxidation (M)

1622.8384	1621.8311	1621.8424	-6.93	11343	-	11358	0	---	R.EQGPELPQSALAGLGR.A
1623.8735	1622.8662	1622.8317	21.2	9078	-	9091	1	---	R.FEARLGAFANQPR.A
1638.8503	1637.8430	1637.8121	18.9	18321	-	18335	1	---	R.TVGAQSTSEQGYVRR.A
1642.8019	1641.7946	1641.7495	27.5	895	-	908	1	---	R.FEELRGDGS HQDPR.E
1645.7986	1644.7913	1644.7889	1.45	547	-	561	1	---	R.LGRLAQSDPESDAMR.R
1646.7770	1645.7697	1645.8497	-48.62	12387	-	12401	1	---	R.EFRLVDAPAEAGLK.V
1651.8420	1650.8347	1650.8590	-14.73	18599	-	18613	1	---	K.VGFEQLGGGERIHR.F
1653.8228	1652.8155	1652.8383	-13.79	7555	-	7569	1	---	R.TYHPTPDGGVVRAR.A
1655.8937	1654.8864	1654.8427	26.4	10641	-	10655	1	---	R.LWEPGGEAVRDAISR.R
1655.8937	1654.8864	1654.8427	26.4	10641	-	10655	1	---	R.LWEPGGEAVRDAISR.R
1656.8927	1655.8854	1655.8883	-1.71	2948	-	2961	0	---	R.FQEVVDQLLPAIER.E
1667.8373	1666.8300	1666.8427	-7.60	3440	-	3453	1	---	R.LFEVLDEAHPGERR.Q
1670.8447	1669.8374	1669.8999	-37.40	4642	-	4656	1	---	R.LDTTELAAPSVELRR.F
1683.9177	1682.9104	1682.8224	52.3	1486	-	1502	0	---	R.QAPNSEVSSAVTTGHAK.E
1689.8406	1688.8333	1688.8006	19.4	15797	-	15813	0	---	R.FAAGEDGPELSVVGEGR.Y
1698.8608	1697.8535	1697.8889	-20.85	15327	-	15340	1	---	R.LTPRWTVTPAYHEK.K
1712.8848	1711.8775	1711.9396	-36.27	15730	-	15745	0	---	R.YELLGLPAVPEVVDAL.L
1749.8521	1748.8448	1748.8581	-7.58	18764	-	18779	0	---	R.NASLDVLETFTSPEAR.M
1763.8978	1762.8905	1762.9829	-52.40	13162	-	13179	0	---	R.TGGLIASGISGTTQIFLK.E
1790.8779	1789.8706	1789.9798	-61.02	661	-	676	1	---	R.QLNALREGLLPADPQR.E
1791.8766	1790.8693	1790.8370	18.1	5061	-	5078	1	---	R.GRDYPSGMSAADGPAALR.R
1794.9020	1793.8947	1793.8598	19.5	17613	-	17627	0	---	R.FPQRPEDGHVDGWVR.V
1852.9092	1851.9019	1851.9843	-44.46	8281	-	8297	1	---	R.AAFAAPDSTYTLRSLR.D
1888.9403	1887.9330	1887.8864	24.7	17188	-	17205	0	---	R.AHSGAAFLWQNTSGDAK.Y
2117.0503	2116.0430	2116.0371	2.80	8449	-	8468	0	---	K.ADAVPSLAGRPLDDAAQMYR.S
2126.0847	2125.0774	2125.0764	0.50	12811	-	12831	1	---	R.LGDDVEATLVGSRGPVAGEQR.L
2208.0913	2207.0840	2207.1182	-15.50	19281	-	19302	1	---	R.STVPADEVLPARADADTPGAVR.V
2218.0398	2217.0325	2217.0451	-5.67	1672	-	1690	1	---	R.TWHTVDLDDVDASAVARFR.D
2225.1460	2224.1387	2224.0616	34.7	4297	-	4317	1	---	R.TAGMLPSLAGDALEDAARMYR.S + Oxidation (M)
2330.1763	2329.1690	2329.1736	-1.98	6982	-	7002	1	---	R.LTPVFDGREAIELSMTPQGR.S + Oxidation (M)
3211.5742	3210.5669	3210.5842	-5.38	18857	-	18886	1	---	K.LGGGVMAEIRHVLGYFGPDLDTAAMYSQVK.G + Oxidation (M)
No match to: 983.5128, 983.5128, 1166.6063, 1179.6006, 1278.6090, 1404.7360, 1435.7228, 1583.7972									

10. [gi|746319218](#) Mass: 77916 Score: 84 Expect: 0.29 Matches: 16

hypothetical protein [Pandoraaea pnomenusa]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1173.5913	1172.5840	1172.6050	-17.92	488	- 497	1	---	R.RDAITFHASR.D
1179.6006	1178.5933	1178.5931	0.18	83	- 92	0	---	R.YAELLNTAER.D
1268.6426	1267.6353	1267.5979	29.5	328	- 339	1	---	K.KGDGGISMFNAR.A + Oxidation (M)
1376.7080	1375.7007	1375.7823	-59.31	144	- 155	1	---	K.LEPLLARQPPDK.R
1404.7360	1403.7287	1403.7408	-8.63	240	- 251	1	---	R.FDEAIALNDKLR.A
1444.7155	1443.7082	1443.7218	-9.43	267	- 278	1	---	R.IAQSQRHYNEAK.G
1585.7628	1584.7555	1584.7784	-14.40	315	- 328	1	---	R.NSYVAAGYEIDQKK.G
1585.7628	1584.7555	1584.7784	-14.40	315	- 328	1	---	R.NSYVAAGYEIDQKK.G
1599.7936	1598.7863	1598.8012	-9.33	184	- 197	1	---	R.QDPSDQDARLSLVR.V
1603.8350	1602.8277	1602.7766	31.9	668	- 679	1	---	R.FLVYMRHYFDGR.R
1613.7913	1612.7840	1612.7845	-0.30	314	- 327	1	---	R.RNSYVAAGYEIDQK.K
1646.7770	1645.7697	1645.8536	-50.98	252	- 266	1	---	R.AQFPETSAVTVQRGR.I
1653.8228	1652.8155	1652.8311	-9.41	498	- 512	1	---	R.DFAKWGVFAEASVAR.L
1689.8406	1688.8333	1688.7828	29.9	157	- 170	1	---	R.AMSTLGDIFYDERR.Y + Oxidation (M)
1794.9020	1793.8947	1793.8559	21.6	660	- 673	1	---	R.SDYYPNRFVLYMR.Y
1852.9092	1851.9019	1851.9036	-0.92	234	- 249	1	---	R.LTSMERFDEAIALNDK.L
No match to: 884.4629, 884.4629, 983.5128, 983.5128, 1104.5879, 1166.6063, 1229.6768, 1237.6604, 1240.5980, 1264.5802, 1264.5802, 1276.6123, 1278.6090, 1279.6028, 1359.7040, 1359.7040, 1402.6704, 1412.7136, 1435.7228, 1480.7465, 1498.7124, 1526.7263, 1553.7404, 1581.7969, 1583.7972, 1597.7627, 1601.8167, 1609.8295, 1617.7798, 1622.8384, 1623.8735, 1638.8503, 1642.8019, 1645.7986, 1651.8420, 1655.8937, 1655.8937, 1656.8927, 1667.8373, 1670.8447, 1683.9177, 1698.8608, 1712.8848, 1749.8521, 1763.8978, 1790.8779, 1791.8766, 1888.9403, 2117.0503, 2126.0847, 2208.0913, 2218.0398, 2225.1460, 2330.1763, 3211.5742								

11. [gi|170045812](#) Mass: 53335 Score: 84 Expect: 0.3 Matches: 2

lysosomal pro-X carboxypeptidase [Culex quinquefasciatus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1655.8937	1654.8864	1654.9043	-10.78	56	-	71	0 ---	K.GPIFVIVGSNGPIETR.Y
1655.8937	1654.8864	1654.9043	-10.78	56	-	71	0 84	K.GPIFVIVGSNGPIETR.Y
No match to: 884.4629, 884.4629, 983.5128, 983.5128, 1104.5879, 1166.6063, 1173.5913, 1179.6006, 1229.6768, 1237.6604, 1240.5980, 1264.5802, 1264.5802, 1268.6426, 1276.6123, 1278.6090, 1279.6028, 1359.7040, 1359.7040, 1376.7080, 1402.6704, 1404.7360, 1412.7136, 1435.7228, 1444.7155, 1480.7465, 1498.7124, 1526.7263, 1553.7404, 1581.7969, 1583.7972, 1585.7628, 1585.7628, 1597.7627, 1599.7936, 1601.8167, 1603.8350, 1609.8295, 1613.7913, 1617.7798, 1622.8384, 1623.8735, 1638.8503, 1642.8019, 1645.7986, 1646.7770, 1651.8420, 1653.8228, 1656.8927, 1667.8373, 1670.8447, 1683.9177, 1689.8406, 1698.8608, 1712.8848, 1749.8521, 1763.8978, 1790.8779, 1791.8766, 1794.9020, 1852.9092, 1888.9403, 2117.0503, 2126.0847, 2208.0913, 2218.0398, 2225.1460, 2330.1763, 3211.5742								

12. [gi|740456478](#) Mass: 76742 Score: 84 Expect: 0.36 Matches: 16

B12-binding domain-containing radical SAM protein [[Clostridium] aminophilum]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
983.5128	982.5055	982.4944	11.3	144	151	1	---	R.DETGRIHR.N
983.5128	982.5055	982.4944	11.3	144	151	1	---	R.DETGRIHR.N
1173.5913	1172.5840	1172.6554	-60.84	133	143	0	---	K.DLSGIPGLVFR.D

1229.6768	1228.6695	1228.5836	69.9	560	-	569	1	---	R.LRGYAYDSR.Q
1276.6123	1275.6050	1275.5401	50.9	189	-	199	0	---	K.SQDMAEPDDL.R.N
1376.7080	1375.7007	1375.7500	-35.81	246	-	256	0	---	K.VLPQLQFFLDR.K
1404.7360	1403.7287	1403.7521	-16.65	588	-	600	1	---	R.LLNEAVKNGGFSR.N
1553.7404	1552.7331	1552.8144	-52.34	337	-	349	1	---	R.VMDLGILHRNVDR.I + Oxidation (M)
1599.7936	1598.7863	1598.8093	-14.36	457	-	470	1	---	R.LLADAKGSPYDFFR.A
1651.8420	1650.8347	1650.8253	5.71	424	-	436	0	---	R.TNWSYEDILELR.G
1791.8766	1790.8693	1790.9931	-69.09	242	-	256	1	---	R.SLSKVLPELQFFLDR.K
1852.9092	1851.9019	1851.9367	-18.77	612	-	626	1	---	K.EETPVDRTIVLFDYR.R
1888.9403	1887.9330	1887.8745	31.0	189	-	204	1	---	K.SQDMAEPDDLRLNTLQR.N
2208.0913	2207.0840	2206.9776	48.2	570	-	587	0	---	R.QMEHMTAETFTDPYVVR.L + Oxidation (M)
2218.0398	2217.0325	2217.0360	-1.58	263	-	280	1	---	K.FVDRFTFNCNHAHAMAIIWK.Y
3211.5742	3210.5669	3210.6190	-16.24	303	-	332	1	---	R.EDEMDVLGLRSGAVQLGIVQSVNPDTIR.A

No match to: 884.4629, 884.4629, 1104.5879, 1166.6063, 1179.6006, 1237.6604, 1240.5980, 1264.5802, 1268.6426, 1278.6090, 1279.6028, 1359.7040, 1359.7040, 1402.6704, 1412.7136, 1435.7228, 1444.7155, 1480.7465, 1498.7124, 1526.7263, 1581.7969, 1583.7972, 1585.7628, 1585.7628, 1597.7627, 1601.8167, 1603.8350, 1609.8295, 1613.7913, 1617.7798, 1622.8384, 1623.8735, 1638.8503, 1642.8019, 1645.7986, 1646.7770, 1653.8228, 1655.8937, 1655.8937, 1656.8927, 1667.8373, 1670.8447, 1683.9177, 1689.8406, 1698.8608, 1712.8848, 1749.8521, 1763.8978, 1790.8779, 1794.9020, 2117.0503, 2126.0847, 2225.1460, 2330.1763

13. [gi|440208481](#) Mass: 16760 Score: 83 Expect: 0.38 Matches: 10

his-tRNA synthetase, partial [Hypobapta xenomorpha]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1229.6768	1228.6695	1228.7027	-26.97	113	- 124	1	---	K.TKAAIEGLEGIK.L
1237.6604	1236.6531	1236.6020	41.3	54	- 64	1	---	R.TACSTVDKLDK.S
1581.7969	1580.7896	1580.6851	66.1	1	- 14	0	---	-.GAYDPMVPDAECLK.V + Oxidation (M)
1622.8384	1621.8311	1621.7480	51.2	37	- 51	0	---	R.LLDGMFEACGVPADK.F
1638.8503	1637.8430	1637.7429	61.1	37	- 51	0	---	R.LLDGMFEACGVPADK.F + Oxidation (M)
1646.7770	1645.7697	1645.8424	-44.13	79	- 93	1	---	K.GITPEAADRIGEYVR.L
1698.8608	1697.8535	1697.9062	-31.03	125	- 138	1	---	K.LLLSYCELFGIKDK.I
1763.8978	1762.8905	1762.8196	40.3	65	- 78	1	---	K.SPWEVVRTEMINER.G + Oxidation (M)
1790.8779	1789.8706	1789.8516	10.6	72	- 87	1	---	R.TEMINEKGITPEAADR.I + Oxidation (M)
1794.9020	1793.8947	1793.8440	28.3	36	- 51	1	---	R.LLDGMFEACGVPADK.F + Oxidation (M)

No match to: 884.4629, 884.4629, 983.5128, 983.5128, 1104.5879, 1166.6063, 1173.5913, 1179.6006, 1240.5980, 1264.5802, 1268.6426, 1276.6123, 1278.6090, 1279.6028, 1359.7040, 1359.7040, 1376.7080, 1402.6704, 1404.7360, 1412.7136, 1435.7228, 1444.7155, 1480.7465, 1498.7124, 1526.7263, 1553.7404, 1581.7969, 1583.7972, 1585.7628, 1585.7628, 1597.7627, 1599.7936, 1601.8167, 1603.8350, 1609.8295, 1613.7913, 1617.7798, 1623.8735, 1642.8019, 1645.7986, 1651.8420, 1653.8228, 1655.8937, 1655.8937, 1656.8927, 1667.8373, 1670.8447, 1683.9177, 1689.8406, 1712.8848, 1749.8521, 1791.8766, 1852.9092, 1888.9403, 2117.0503, 2126.0847, 2208.0913, 2218.0398, 2225.1460, 2330.1763, 3211.5742

14. [gi|358639159](#) Mass: 52503 Score: 83 Expect: 0.41 Matches: 11

radical SAM family protein [Azoarcus sp. KH32C]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1240.5980	1239.5907	1239.5376	42.8	396	- 405	0	---	R.FAPCDTCTIR.H
1412.7136	1411.7063	1411.7320	-18.19	72	- 83	1	---	R.ANDFARELHALR.F
1526.7263	1525.7190	1525.7599	-26.78	131	- 143	1	---	R.LKDYFATVMPADR.K
1585.7628	1584.7555	1584.8471	-57.79	52	- 66	1	---	R.KDQLAASLDGDELLR.S
1585.7628	1584.7555	1584.8471	-57.79	52	- 66	1	32	R.KDQLAASLDGDELLR.S
1597.7627	1596.7554	1596.8657	-69.07	1	- 16	0	---	-.MSAAVIEKPLAPSAGR.Y
1613.7913	1612.7840	1612.8606	-47.50	1	- 16	0	---	-.MSAAVIEKPLAPSAGR.Y + Oxidation (M)
1749.8521	1748.8448	1748.9097	-37.10	84	- 98	0	---	R.FELKPSAVVYNPTER.C
1763.8978	1762.8905	1762.9730	-46.78	249	- 263	0	---	K.NLDQLVPLVELFHAR.G
2126.0847	2125.0774	2125.2445	-78.62	311	- 330	1	---	R.KMVANFANILLAILAPTAR.R
2218.0398	2217.0325	2217.0082	11.0	229	- 248	0	---	R.AMDALQGYASWSVIATCTEK.N + Oxidation

No match to: 884.4629, 884.4629, 983.5128, 983.5128, 1104.5879, 1166.6063, 1173.5913, 1179.6006, 1229.6768, 1237.6604, 1264.5802, 1268.6426, 1276.6123, 1278.6090, 1279.6028, 1359.7040, 1359.7040, 1376.7080, 1402.6704, 1404.7360, 1435.7228, 1444.7155, 1480.7465, 1498.7124, 1553.7404, 1581.7969, 1583.7972, 1599.7936, 1601.8167, 1603.8350, 1609.8295, 1617.7798, 1622.8384, 1623.8735, 1638.8503, 1642.8019, 1645.7986, 1646.7770, 1651.8420, 1653.8228, 1655.8937, 1655.8937, 1656.8927, 1667.8373, 1670.8447, 1683.9177, 1689.8406, 1698.8608, 1712.8848, 1749.8521, 1791.8766, 1794.9020, 1852.9092, 1888.9403, 2117.0503, 2208.0913, 2225.1460, 2330.1763, 3211.5742

15. [gi|239787450](#) Mass: 174337 Score: 82 Expect: 0.48 Matches: 24

Sensor protein [uncultured bacterium]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1104.5879	1103.5806	1103.5757	4.44	1136	- 1144	0	---	R.VTMQNLVQR.L + Oxidation (M)
1179.6006	1178.5933	1178.6118	-15.65	648	- 658	0	---	R.SLLFEAGVMGR.D
1237.6604	1236.6531	1236.6285	19.9	1019	- 1030	0	---	R.YGGTGLGLAICR.N
1240.5980	1239.5907	1239.5587	25.8	443	- 453	1	---	R.VSKGAMEEAMR.V + 2 Oxidation (M)
1268.6426	1267.6353	1267.5615	58.2	1369	- 1378	1	---	R.CEGDEALYRR.L
1278.6090	1277.6017	1277.6616	-46.83	963	- 974	0	---	K.FTEAGEVAVSIR.L
1359.7040	1358.6967	1358.7042	-5.49	794	- 806	0	---	R.EDGEVTGLVVVS.R.D
1359.7040	1358.6967	1358.7042	-5.49	794	- 806	0	---	R.EDGEVTGLVVVS.R.D
1585.7628	1584.7555	1584.7864	-19.51	1494	- 1505	1	---	R.ELCILLHNRDMR.C + Oxidation (M)
1585.7628	1584.7555	1584.7864	-19.51	1494	- 1505	1	4	R.ELCILLHNRDMR.C + Oxidation (M)
1601.8167	1600.8094	1600.7344	46.9	709	- 721	0	---	R.DHMAFIDTGYIYR.A
1617.7798	1616.7725	1616.7293	26.7	709	- 721	0	---	R.DHMAFIDTGYIYR.A + Oxidation (M)
1642.8019	1641.7946	1641.8223	-16.85	1385	- 1399	1	---	R.SEFAHAARGIDEALR.Q
1646.7770	1645.7697	1645.7572	7.60	782	- 793	1	---	K.RWMDVSYPFPHR.E + Oxidation (M)
1655.8937	1654.8864	1654.9155	-17.54	868	- 882	1	---	R.GYLEIKIQGASHALLR.L
1655.8937	1654.8864	1654.9155	-17.54	868	- 882	1	---	R.GYLEIKIQGASHALLR.L

1670.8447 1669.8374 1669.8147 13.6 208 - 220 1 --- R.DMWHVLVAEGRWR.G + Oxidation (M)
 1683.9177 1682.9104 1682.8641 27.5 1379 - 1392 1 --- R.LLEHFRSEFAHAAR.G
 1689.8406 1688.8333 1688.9097 -45.23 883 - 897 1 --- R.LINDILDFSRIDAGK.L
 1712.8848 1711.8775 1711.8252 30.5 634 - 647 1 --- R.EMWAEHWAALKANR.S
 1763.8978 1762.8905 1762.9155 -14.16 768 - 782 1 --- R.INYQGWIDFPVAGKR.W
 1794.9020 1793.8947 1793.8935 0.70 556 - 571 0 --- R.LDTGEIVAIYDDLTEK.R
 2117.0503 2116.0430 2116.0185 11.6 1329 - 1350 0 --- K.VNGWIGSGAGPASVTEGSSVER.A
 2218.0398 2217.0325 2216.9988 15.2 529 - 546 1 --- R.TGESAYHPVSWYQDERHR.G
 No match to: 884.4629, 884.4629, 983.5128, 983.5128, 1166.6063, 1173.5913, 1229.6768, 1264.5802, 1264.5802, 1276.6123, 1279.6028, 1376.7080, 1402.6704, 1404.7360, 1412.7136, 1435.7228, 1444.7155, 1480.7465, 1498.7124, 1526.7263, 1553.7404, 1581.7969, 1583.7972, 1597.7627, 1599.7936, 1603.8350, 1609.8295, 1613.7913, 1622.8384, 1623.8735, 1638.8503, 1645.7986, 1651.8420, 1653.8228, 1656.8927, 1667.8373, 1698.8608, 1749.8521, 1790.8779, 1791.8766, 1852.9092, 1888.9403, 2126.0847, 2208.0913, 2225.1460, 2330.1763, 3211.5742

16. [gi|649503612](#) Mass: 21793 Score: 82 Expect: 0.5 Matches: 10

hypothetical protein M082_5993 [Bacteroides fragilis str. 3725 D9 ii]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
983.5128	982.5055	982.5124	-6.96	63	70	0	---	K.IGLNYFEK.S
983.5128	982.5055	982.5124	-6.96	63	70	0	---	K.IGLNYFEK.S
1583.7972	1582.7899	1582.7151	47.3	130	142	0	---	K.EENNEYEYLVGPK.I
1638.8503	1637.8430	1637.8089	20.8	92	104	1	---	R.IARDYYVDVAVYK.T
1646.7770	1645.7697	1645.8504	-49.03	58	70	1	---	R.TTFWKIGLNYFEK.S
1651.8420	1650.8347	1650.8042	18.5	63	75	1	---	K.IGLNYFEKSFDYR.Y
1888.9403	1887.9330	1888.0247	-48.56	171	186	1	---	K.SPWNVTWNVGKIVLLY.-
2117.0503	2116.0430	2116.0113	15.0	71	87	1	---	K.SFDYRYEDLSLEVPEVR.T
2218.0398	2217.0325	2217.0025	13.5	6	23	0	---	K.MTFILIMCGCMHGLYAQR.H + Oxidation (M)
2330.1763	2329.1690	2329.1026	28.5	5	23	1	---	K.KMTFILIMCGCMHGLYAQR.H

No match to: 884.4629, 884.4629, 1104.5879, 1166.6063, 1173.5913, 1179.6006, 1229.6768, 1237.6604, 1240.5980, 1264.5802, 1264.5802, 1268.6426, 1276.6123, 1278.6090, 1279.6028, 1359.7040, 1359.7040, 1376.7080, 1402.6704, 1404.7360, 1412.7136, 1435.7228, 1444.7155, 1480.7465, 1498.7124, 1526.7263, 1553.7404, 1581.7969, 1585.7628, 1585.7628, 1597.7627, 1599.7936, 1601.8167, 1603.8350, 1609.8295, 1613.7913, 1617.7798, 1622.8384, 1623.8735, 1642.8019, 1645.7986, 1653.8228, 1655.8937, 1655.8937, 1656.8927, 1667.8373, 1670.8447, 1683.9177, 1689.8406, 1698.8608, 1712.8848, 1749.8521, 1763.8978, 1790.8779, 1791.8766, 1794.9020, 1852.9092, 2126.0847, 2208.0913, 2225.1460, 3211.5742

17. [gi|913754691](#) Mass: 22021 Score: 80 Expect: 0.71 Matches: 10

MULTISPECIES: hypothetical protein [Bacteroides]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
983.5128	982.5055	982.5124	-6.96	65	72	0	---	K.IGLNYFEK.S
983.5128	982.5055	982.5124	-6.96	65	72	0	---	K.IGLNYFEK.S
1583.7972	1582.7899	1582.7151	47.3	132	144	0	---	K.EENNEYEYLVGPK.I
1638.8503	1637.8430	1637.8089	20.8	94	106	1	---	R.IARDYYVDVAVYK.T
1646.7770	1645.7697	1645.8504	-49.03	60	72	1	---	R.TTFWKIGLNYFEK.S
1651.8420	1650.8347	1650.8042	18.5	65	77	1	---	K.IGLNYFEKSFDYR.Y
1888.9403	1887.9330	1888.0247	-48.56	173	188	1	---	K.SPWNVTWNVGKIVLLY.-
2117.0503	2116.0430	2116.0113	15.0	73	89	1	---	K.SFDYRYEDLSLEVPEVR.T
2218.0398	2217.0325	2217.0025	13.5	8	25	0	---	K.MTFILIMCGCMHGLYAQR.H + Oxidation (M)
2330.1763	2329.1690	2329.1026	28.5	7	25	1	---	K.KMTFILIMCGCMHGLYAQR.H

No match to: 884.4629, 884.4629, 1104.5879, 1166.6063, 1173.5913, 1179.6006, 1229.6768, 1237.6604, 1240.5980, 1264.5802, 1264.5802, 1268.6426, 1276.6123, 1278.6090, 1279.6028, 1359.7040, 1359.7040, 1376.7080, 1402.6704, 1404.7360, 1412.7136, 1435.7228, 1444.7155, 1480.7465, 1498.7124, 1526.7263, 1553.7404, 1581.7969, 1585.7628, 1585.7628, 1597.7627, 1599.7936, 1601.8167, 1603.8350, 1609.8295, 1613.7913, 1617.7798, 1622.8384, 1623.8735, 1642.8019, 1645.7986, 1653.8228, 1655.8937, 1655.8937, 1656.8927, 1667.8373, 1670.8447, 1683.9177, 1689.8406, 1698.8608, 1712.8848, 1749.8521, 1763.8978, 1790.8779, 1791.8766, 1794.9020, 1852.9092, 2126.0847, 2208.0913, 2225.1460, 3211.5742

18. [gi|759928248](#) Mass: 34237 Score: 80 Expect: 0.71 Matches: 14

LysR family transcriptional regulator [Ensifer sp. ZNC0028]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
884.4629	883.4556	883.4512	5.04	56	63	0	---	K.LTATEHGR.V
884.4629	883.4556	883.4512	5.04	56	63	0	12	K.LTATEHGR.V
1166.6063	1165.5990	1165.5154	71.7	155	163	1	---	R.MRGIMNCER.V
1173.5913	1172.5840	1172.5206	54.1	286	294	0	---	R.LMIDYMAER.C + 2 Oxidation (M)
1240.5980	1239.5907	1239.5958	-4.09	164	174	0	---	R.VVCGAPAYFEK.R
1412.7136	1411.7063	1411.6952	7.91	284	294	1	---	K.VRLMIDYMAER.C + Oxidation (M)
1498.7124	1497.7051	1497.7762	-47.46	1	12	1	---	-.MSYLDNVRVFR.V
1585.7628	1584.7555	1584.7211	21.8	286	297	1	---	R.LMIDYMAERCQR.L
1585.7628	1584.7555	1584.7211	21.8	286	297	1	---	R.LMIDYMAERCQR.L
1601.8167	1600.8094	1600.7160	58.4	286	297	1	---	R.LMIDYMAERCQR.L + Oxidation (M)
1617.7798	1616.7725	1616.7109	38.1	286	297	1	---	R.LMIDYMAERCQR.L + 2 Oxidation (M)
1763.8978	1762.8905	1762.9002	-5.51	56	71	1	---	K.LTATEHGRVFDGAVK.I
2117.0503	2116.0430	2115.9540	42.1	157	174	1	---	R.GIMNCERVVCGAPAYFEK.R + Oxidation (M)
2208.0913	2207.0840	2207.0357	21.9	196	213	1	---	R.YPGSKEYFWTLQTMGVR.K + Oxidation (M)

No match to: 983.5128, 983.5128, 1104.5879, 1179.6006, 1229.6768, 1237.6604, 1264.5802, 1264.5802, 1268.6426, 1276.6123, 1278.6090, 1279.6028, 1359.7040, 1359.7040, 1376.7080, 1402.6704, 1404.7360, 1435.7228, 1444.7155, 1480.7465, 1526.7263, 1553.7404, 1581.7969, 1583.7972, 1597.7627, 1599.7936, 1603.8350, 1609.8295, 1613.7913, 1622.8384, 1623.8735, 1638.8503, 1642.8019, 1645.7986, 1646.7770, 1651.8420, 1653.8228, 1655.8937, 1655.8937, 1656.8927, 1667.8373, 1670.8447, 1683.9177, 1689.8406, 1698.8608, 1712.8848, 1749.8521, 1790.8779, 1791.8766, 1794.9020, 1852.9092, 1888.9403, 2126.0847, 2218.0398, 2225.1460, 2330.1763, 3211.5742

19. [gi|506413224](#) Mass: 307019 Score: 80 Expect: 0.71 Matches: 29

hypothetical protein [Methylobacterium nodulans]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1104.5879	1103.5806	1103.5869	-5.73	96	- 105	1	---	R.GIGAMRQSLR.V + Oxidation (M)
1173.5913	1172.5840	1172.6149	-26.34	2524	- 2535	0	---	R.QASSLAAALDAR.G
1179.6006	1178.5933	1178.5204	61.9	2212	- 2222	0	---	R.GEALADAFDDR.S
1229.6768	1228.6695	1228.6776	-6.53	1381	- 1392	0	---	R.DIVLAVTSQGAR.V
1268.6426	1267.6353	1267.7360	-79.43	2266	- 2277	1	---	R.RAAALAAALIDQR.S
1359.7040	1358.6967	1358.6976	-0.63	1686	- 1696	1	---	R.AEMLNRLVEER.T
1359.7040	1358.6967	1358.6976	-0.63	1686	- 1696	1	3	R.AEMLNRLVEER.T
1402.6704	1401.6631	1401.7212	-41.41	1302	- 1314	1	---	R.VAARTTEADEALR.R
1444.7155	1443.7082	1443.7106	-1.67	1785	- 1797	1	---	R.GASVDHAFEDRLK.R
1581.7969	1580.7896	1580.7100	50.4	1587	- 1600	1	---	R.TEELTERMDAGASR.F + Oxidation (M)
1585.7628	1584.7555	1584.7719	-10.30	2855	- 2867	0	---	R.MIDHQAAVTLWER.Y + Oxidation (M)
1585.7628	1584.7555	1584.7719	-10.30	2855	- 2867	0	---	R.MIDHQAAVTLWER.Y + Oxidation (M)
1609.8295	1608.8222	1608.7719	31.3	2941	- 2955	1	---	K.VYTMHAHASGRFEGA.-
1623.8735	1622.8662	1622.7900	47.0	952	- 967	0	---	R.IGSVASTFSQAAEEAR.G
1638.8503	1637.8430	1637.7798	38.6	2896	- 2908	1	---	R.YQAEPEFQRTVDR.Y
1646.7770	1645.7697	1645.8457	-46.17	1560	- 1575	0	---	R.AITAQSQAMSDALLAR.A
1651.8420	1650.8347	1650.8326	1.32	1440	- 1454	1	---	R.IARDTGEFSQTVATR.L
1655.8937	1654.8864	1654.8638	13.7	1545	- 1559	1	---	R.EVAQALDARADELVR.A
1655.8937	1654.8864	1654.8638	13.7	1545	- 1559	1	---	R.EVAQALDARADELVR.A
1656.8927	1655.8854	1655.8955	-6.07	1758	- 1773	1	---	R.TLEAGGTRLQEGVVAR.T
1670.8447	1669.8374	1669.8635	-15.62	1845	- 1861	0	---	R.GLLDQGAGALGSVLDER.G
1683.9177	1682.9104	1682.8488	36.6	1670	- 1685	1	---	R.DLAGHAEAIRAAFEGR.A
1689.8406	1688.8333	1688.8733	-23.69	1622	- 1636	0	---	R.LIEDTFGGQAQEILR.Q
1698.8608	1697.8535	1697.9424	-52.35	1461	- 1476	1	---	R.VITVQGRAVAESIAER.T
1852.9092	1851.9019	1851.8962	3.08	237	- 252	1	---	R.GEISTLERAYSONEIR.I
1888.9403	1887.9330	1887.9414	-4.42	2855	- 2869	1	---	R.MIDHQAAVTLWERYR.Q
2208.0913	2207.0840	2207.1182	-15.49	1086	- 1107	1	---	R.SADSATGTVDARLAGLAESFLR.A
2225.1460	2224.1387	2224.1811	-19.06	2284	- 2305	1	---	R.SLAETARELVQALDGPAAALSR.S
2330.1763	2329.1690	2329.2059	-15.85	1554	- 1575	1	---	R.ADELVRAITAQSQAMSDALLAR.A
No match to: 884.4629, 884.4629, 983.5128, 983.5128, 1166.6063, 1237.6604, 1240.5980, 1264.5802, 1264.5802, 1276.6123, 1278.6090, 1279.6028, 1376.7080, 1404.7360, 1412.7136, 1435.7228, 1480.7465, 1498.7124, 1526.7263, 1553.7404, 1583.7972, 1597.7627, 1599.7936, 1601.8167, 1603.8350, 1613.7913, 1617.7798, 1622.8384, 1642.8019, 1645.7986, 1653.8228, 1667.8373, 1712.8848, 1749.8521, 1763.8978, 1790.8779, 1791.8766, 1794.9020, 2117.0503, 2126.0847, 2218.0398, 3211.5742								

20. [gi|736079929](#) Mass: 169685 Score: 80 Expect: 0.8 Matches: 22
hypothetical protein [Actinoplanes subtropicus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1240.5980	1239.5907	1239.6823	-73.87	868	- 879	0	---	K.AATHEVTAVITK.E
1268.6426	1267.6353	1267.6819	-36.73	920	- 932	1	---	K.ALAATAAGKMAHR.N
1278.6090	1277.6017	1277.6252	-18.34	568	- 578	0	---	K.EVDELVAAYNR.L
1279.6028	1278.5955	1278.6330	-29.29	1298	- 1308	1	---	R.HRWAGASPNQR.A
1359.7040	1358.6967	1358.6500	34.4	1227	- 1239	0	---	R.EVMAGDVVTGPER.T
1359.7040	1358.6967	1358.6500	34.4	1227	- 1239	0	---	R.EVMAGDVVTGPER.T
1404.7360	1403.7287	1403.7885	-42.57	1520	- 1532	1	---	R.LGGLVGRLETAYR.D
1435.7228	1434.7155	1434.6337	57.1	85	- 96	0	---	R.AIDSEQYTYAMK.S + Oxidation (M)
1444.7155	1443.7082	1443.7034	3.32	135	- 145	1	---	K.RVEEVFFDFEK.I
1553.7404	1552.7331	1552.8283	-61.29	999	- 1012	1	---	R.SPKQMLLDNGIPPK.S + Oxidation (M)
1585.7628	1584.7555	1584.7454	6.40	1	- 15	0	---	-.MSTLDHDVEPGSAVK.A
1585.7628	1584.7555	1584.7454	6.40	1	- 15	0	---	-.MSTLDHDVEPGSAVK.A
1599.7936	1598.7863	1598.7875	-0.74	265	- 278	0	---	K.EHGP GTVELMLNFR.L
1601.8167	1600.8094	1600.7403	43.2	1	- 15	0	---	-.MSTLDHDVEPGSAVK.A + Oxidation (M)
1653.8228	1652.8155	1652.8331	-10.66	905	- 919	0	---	K.VMTGDFGLTVEEVVK.A + Oxidation (M)
1655.8937	1654.8864	1654.8890	-1.54	868	- 883	1	---	K.AATHEVTAVITKESAK.T
1655.8937	1654.8864	1654.8348	31.2	1081	- 1095	0	7	K.LPSQQILDAMTPDAR.Q
1670.8447	1669.8374	1669.8383	-0.54	1272	- 1287	1	---	R.RSATAPDPATEAQSIR.I
1791.8766	1790.8693	1790.9349	-36.60	179	- 194	0	---	R.GTRPEIPPEVMAELR.T
1794.9020	1793.8947	1793.9999	-58.63	163	- 178	1	---	K.ADLTPEQVARLEALLR.G
2208.0913	2207.0840	2207.1270	-19.45	265	- 284	1	---	K.EHGP GTVELMLNFR LGGPQR.R
2330.1763	2329.1690	2329.2238	-23.50	381	- 404	1	---	R.AVLGTQTGEGGGLDSGLQRTLAK.E
No match to: 884.4629, 884.4629, 983.5128, 983.5128, 1104.5879, 1166.6063, 1173.5913, 1179.6006, 1229.6768, 1237.6604, 1264.5802, 1264.5802, 1276.6123, 1376.7080, 1402.6704, 1412.7136, 1480.7465, 1498.7124, 1526.7263, 1581.7969, 1583.7972, 1597.7627, 1603.8350, 1609.8295, 1613.7913, 1617.7798, 1622.8384, 1623.8735, 1638.8503, 1642.8019, 1645.7986, 1646.7770, 1651.8420, 1656.8927, 1667.8373, 1683.9177, 1689.8406, 1698.8608, 1712.8848, 1749.8521, 1763.8978, 1790.8779, 1852.9092, 1888.9403, 2117.0503, 2126.0847, 2218.0398, 2225.1460, 3211.5742								

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : [Carbamidomethyl \(C\)](#)
Variable modifications : [Oxidation \(M\)](#)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 80 ppm
Fragment Mass Tolerance : ± 0.3 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Query1 (884.4629,1+) : <no title>

Query2 (884.4629,1+) : MaldiWellID: 60692, SpectrumID: 127290,
Query3 (983.5128,1+) : <no title>
Query4 (983.5128,1+) : MaldiWellID: 60692, SpectrumID: 127291,
Query5 (1104.5879,1+) : <no title>
Query6 (1166.6063,1+) : <no title>
Query7 (1173.5913,1+) : <no title>
Query8 (1179.6006,1+) : <no title>
Query9 (1229.6768,1+) : <no title>
Query10 (1237.6604,1+) : <no title>
Query11 (1240.5980,1+) : <no title>
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Query14 (1268.6426,1+) : <no title>
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Query17 (1279.6028,1+) : <no title>
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Query45 (1645.7986,1+) : <no title>
Query46 (1646.7770,1+) : <no title>
Query47 (1651.8420,1+) : <no title>
Query48 (1653.8228,1+) : <no title>
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Query51 (1656.8927,1+) : <no title>
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Query61 (1791.8766,1+) : <no title>
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Query63 (1852.9092,1+) : <no title>
Query64 (1888.9403,1+) : <no title>
Query65 (2117.0503,1+) : <no title>
Query66 (2126.0847,1+) : <no title>
Query67 (2208.0913,1+) : <no title>
Query68 (2218.0398,1+) : <no title>
Query69 (2225.1460,1+) : <no title>
Query70 (2330.1763,1+) : <no title>
Query71 (3211.5742,1+) : <no title>

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