Electronic Supplementary Material (ESI) for Metallomics.

In vivo metal selectivity of metal-dependent biosynthesis of Co-type nitrile hydratase in *Rhodococcus* bacteria: a new look at the nitrile hydratase maturation mechanism?

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Supplementary materials

Table S1. Primers used in this work.

Primer	Sequence	Template
Primers for RT-qPCR detection		
gyrB-M8-F	5′-GCCGAGGAACAGGAACAGG	The chromosomal DNAs of *R. rhodochrous* strains M8, M33, M33 aam and *R. aetherivorans* strain VKPM AC-2063
gyrB-M8-R	5′-CCTGTTCCTGTTCCTCGGC	-||-
gyrB-J1-F	5′-TCGCCAACACCATCAACACC	The chromosomal DNA of *R. rhodochrous* strain J1
gyrB-J1-R	5′-ATGTCGTCGCCCGTGAGGTT	-||-
nhmG-F	5′-ATCGGTGTCAGTAATGCG	The chromosomal DNAs of *R. rhodochrous* strains M8, M33, M33 aam, J1 and *R. aetherivorans* strain VKPM AC-2063
nhmG-R	5′-GTGCGGCGGTCCCAGT	-||-
Primers for cloning		
Sh1-F	5′ATGGGATCCATCGTTGCGGACGATGATGTC	The chromosomal DNA of *R. rhodochrous* strain M33 aam
Sh1-R	5′CGCCAAGGGCCTATCTACCGCCGCCACGACTGTTGGCTGT	-||-
Sh2-F	5′CGGTAGATAGGCCCTTGGCG	-||-
Sh2-R	5′GTGGAATTCTTGGGTGGGGCCCGACT	-||-
Sh3-F	5′ CACGGTACCTCGCTGTACCGGCGGCCTCA	-||-
Sh3-R	5′ CGACCTCTAGAGGATCCCCGTGCCTGTTCCTGCGTGCTGC	-||-
F1	5′CGGGGATCCTCTAGAGGTCGA (2Tfd-F)	-||-
R1	5′ GTGGAATTCTTGGGTGGGGCCCGACTACGGAAATGGCGC	-||-
R2	5′ GTGGAATTCCTTGCCATGAACGCCTACAGCGTCACCGCG	-||-
R3	5′ CACCGATCATCGAGTCGAGC	-||-
cblA-F	5′ GCTCGACTCGATGATCGGTGGAGCGCATGGAATCGATGGC	-||-
F6-del	5′CACACGCGTTTGGACGACCACGGTTGCTAC	-||-
R6-del	5′GTGGAATTCGCCATGAACGCCTACAGCGTC	-||-
2Tfd-F	5′CGGGGATCCTCTAGAGGTCGA	pM17 plasmid (obtained from Prof. S.V. Mashko[1]
2Tfd-R	5′CGCTACGTGACTGGGTC	-||-

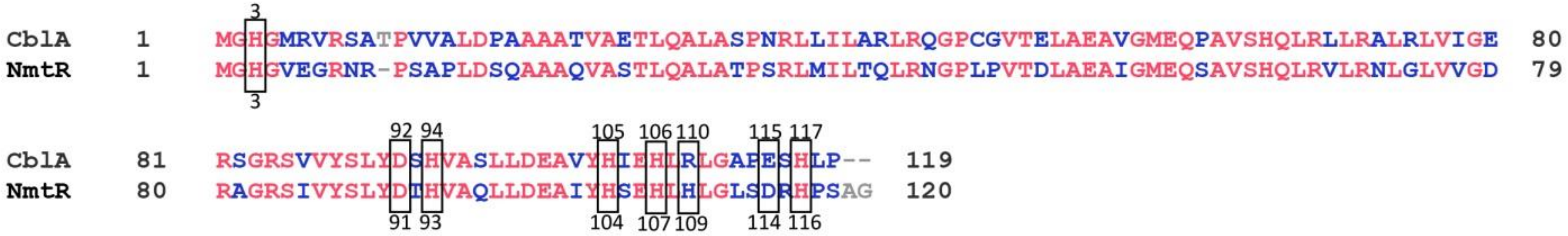

Figure S1. Alignment of amino acid sequences of NmtR and CblA. The amino acids, responsible for nickel coordinating in NmtR[2], are numbered, and marked with rectangles.

Additional discussion

The presumptive CblA binding preference can be sequence dependent. In this view, it is interesting to compare CblA with its closest experimentally studied relative - NmtR from *Mycobacterium tuberculosis* (64% of identical aminoacids). Mutation analysis revealed that H3, D91, H93, H104, H107 positions are critical for metal binding of NmtR, and H109, D114, H116 positions also affect it[2]. Moreover, deletion of 9 aminoacids at the C-end of NmtR (containing D114 and H116) reverts its metal preference from Ni to Co, making the regulator more responsive to the latter. The deduced sequence of CblA contains the same aminoacids at H3, D91, H93, H104, H107, H116 positions, but other aminoacids at H109 and D114 positions (R and E, correspondingly). These amino acid differences, together with the differences in non-conserved aminoacids at C-end (Fig. S1), can be the cause of Co preference of CblA. Further mutation analysis coupled with *in vitro* measurements are needed for direct estimation of CblA metal preferences. Similar sequence-dependent shift of Ni/Co preference was also obtained for an extensively studied RcnR regulator from *E. coli*, the member of RcnR/CsoR family[3-6].

References

1. V. Z. Akhverdyan, E. R. Gak, I. L. Tokmakova, N. V. Stoynova, Y. A. Yomantas and S. V. Mashko, Application of the bacteriophage Mu-driven system for the integration/amplification of target genes in the chromosomes of engineered Gram-negative bacteria--mini review, *Applied microbiology and biotechnology*, 2011, **91**, 857-871.

2. H. Reyes-Caballero, C. W. Lee and D. P. Giedroc, Mycobacterium tuberculosis NmtR harbors a nickel sensing site with parallels to Escherichia coli RcnR, *Biochemistry*, 2011, **50**, 7941-7952.
3. J. S. Iwig, S. Leitch, R. W. Herbst, M. J. Maroney and P. T. Chivers, Ni(II) and Co(II) sensing by Escherichia coli RcnR, *Journal of the American Chemical Society*, 2008, **130**, 7592-7606.
4. D. Blaha, S. Arous, C. Bleriot, C. Dorel, M. A. Mandrand-Berthelot and A. Rodrigue, The Escherichia coli metallo-regulator RcnR represses rcnA and rcnR transcription through binding on a shared operator site: Insights into regulatory specificity towards nickel and cobalt, *Biochimie*, 2011, **93**, 434-439.
5. K. A. Higgins, P. T. Chivers and M. J. Maroney, Role of the N-terminus in determining metal-specific responses in the E. coli Ni- and Co-responsive metalloregulator, RcnR, *Journal of the American Chemical Society*, 2012, **134**, 7081-7093.
6. C. E. Carr, F. Musiani, H.-T. Huang, P. T. Chivers, S. Ciurli and M. J. Maroney, Glutamate Ligation in the Ni(II)- and Co(II)-Responsive Escherichia coli Transcriptional Regulator, RcnR, *Inorganic Chemistry*, 2017, **56**, 6459-6476.

The results of MALDI-TOF analysis of NHase bands from the SDS-PAGE gel (see Figure 7 in the article).

1. The protein band of approx. 27 kDa, obtained from the crude extract of *R. rhodochrous* M33 cells, grown on the medium with cobalt.

MATRIX SCIENCE Mascot Search Results

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User             : toropygin
Email            : toropygin@rambler.ru
Search title     : 01
Database         : NCBIprot 20180429 (152462470 sequences; 55858910152 residues)
Timestamp        : 1 Sep 2018 at 16:07:01 GMT
Top Score        : 226 for WP_072636260.1, nitrile hydratase subunit beta [Rhodococcus sp. M8]
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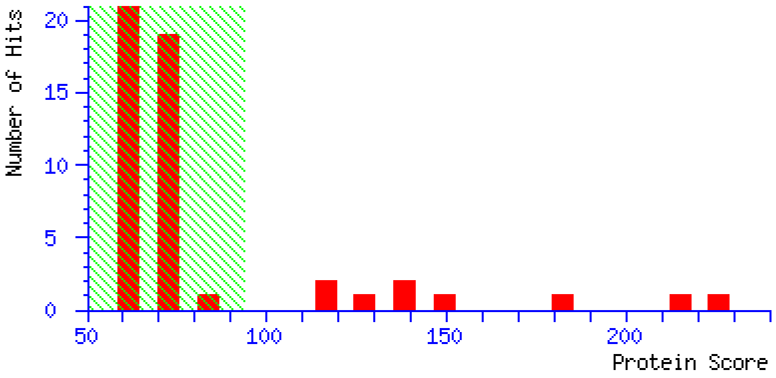
Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 94 are significant (p<0.05).



Protein Summary Report

Format As	Protein Summary	Help
	Significance threshold p< 0.05	Max. number of hits 20
	Preferred taxonomy All entries	

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-

-Accession- -Sequence-

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
☑ 842.5082 (1+)																				
☑ 880.4031 (1+)																				
☑ 889.4699 (1+)	●	●	●	●	●	●	●	●	●			●		●	●	●	●	●	●	
☑ 909.4110 (1+)	●		●										●		●					
☑ 925.3929 (1+)	●		●																	
☑ 931.4111 (1+)																				
☑ 943.5581 (1+)	●	●	●	●	●	●	●	●	●		●			●	●					
☑ 965.5374 (1+)																				
☑ 1008.5309 (1+)	●	●	●														●	●	●	●
☑ 1017.6068 (1+)	●	●	●	●	●	●	●	●	●											●
☑ 1032.5397 (1+)																				
☑ 1039.5621 (1+)	●	●	●								●					●				●
☑ 1050.5640 (1+)													●							
☑ 1055.5539 (1+)	●	●	●																	
☑ 1069.6765 (1+)																				
☑ 1076.6177 (1+)	●	●	●									●								
☑ 1085.6909 (1+)																				
☑ 1098.6115 (1+)															●					
☑ 1138.6869 (1+)																				

☑ 1145.6225 (1+)																				
☑ 1236.7658 (1+)	●	●	●	●	●	●	●	●	●											
☑ 1289.7106 (1+)																				
☑ 1342.8443 (1+)	●	●	●	●	●	●	●	●	●											
☑ 1358.8283 (1+)	●	●	●	●	●	●	●	●	●						●					
☑ 1364.8303 (1+)																				
☑ 1411.7877 (1+)																				
☑ 1528.9494 (1+)	●	●	●	●	●	●	●	●	●											
☑ 1537.7721 (1+)																				
☑ 1554.7745 (1+)	●	●	●	●	●	●	●	●		●										
☑ 1570.7627 (1+)	●	●	●	●	●	●	●	●		●			●		●					
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☑ 1582.8187 (1+)										●		●	●	●			●	●	●	
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☑ 1633.7985 (1+)																				
☑ 1639.8241 (1+)											●									

☑ 1641.8427 (1+)																				
☑ 1657.0650 (1+)																	●	●	●	
☑ 1679.0464 (1+)																				
☑ 1867.8974 (1+)														●		●				●
☑ 2004.9863 (1+)	●	●	●	●	●	●	●	●				●								
☑ 2123.9740 (1+)	●	●	●	●	●	●	●		●							●	●	●	●	
☑ 2139.9640 (1+)	●	●	●	●	●	●	●		●			●				●				●
☑ 2145.9803 (1+)																				
☑ 2202.1298 (1+)	●	●		●	●	●		●	●		●	●	●		●	●				
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☑ 2224.1306 (1+)											●			●	●				●	
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☑ 3716.1966 (1+)																	●	●	●	

Search Selected

Index

	Accession	Mass	Score	Description
1.	WP_072636260.1	26277	226	nitrile hydratase subunit beta [Rhodococcus sp. M8]
2.	AAN71592.1	26259	212	nitrile hydratase beta subunit [Nocardia sp. JBRs]
3.	WP_006940501.1	26305	183	nitrile hydratase subunit beta [Rhodococcus sp. EsD8]
4.	CAC83637.1	22560	150	nitrile hydratase beta chain, partial [uncultured bacterium SP1]
5.	BAE75932.1	26335	141	nitrile hydratase beta subunit [Rhodococcus pyridinivorans]
6.	P21220.2	26305	141	RecName: Full=High-molecular weight cobalt-containing nitrile hydratase subunit beta; Short=H-NHase; Short=H-nitrilase
7.	AEB00726.1	26303	122	nitrile hydratase beta subunit [Rhodococcus sp. BX2]
8.	CAE46767.1	26349	120	nitrile hydratase beta subunit [Rhodococcus pyridinivorans]
9.	CAC83638.1	19344	119	nitrile hydratase beta chain, partial [uncultured bacterium BD2]
10.	AIE75022.1	12588	79	hypothetical protein D082_24940 [Synechocystis sp. PCC 6714]
11.	OGC51977.1	24781	74	macrolide ABC transporter ATP-binding protein [candidate division WWE3 bacterium RIFCSPLOWO2_01_FULL_39_13]
12.	PPC88533.1	40463	74	8-amino-7-oxononanoate synthase [Hyphomicrobium sp.]
13.	AOK07627.1	11710	72	hypothetical protein WK25_24445 [Burkholderia latens]
14.	KUK80951.1	28382	71	Flagellar hook protein FlgE [Pelotomaculum thermopropionicum]
15.	WP_038563067.1	40788	71	CapA family protein [Draconibacterium orientale]
16.	WP_048896976.1	26861	71	arginyltransferase [Photobacterium swingsii]

17	**WP_053874729.1**	53645	70	aldehyde dehydrogenase [Staphylococcus aureus]
18	**WP_107364903.1**	53598	70	aldehyde dehydrogenase [Staphylococcus aureus]
19	**WP_031788062.1**	53650	70	MULTISPECIES: aldehyde dehydrogenase [Staphylococcus]
20	**WP_090000046.1**	17896	69	DUF1572 domain-containing protein [Chryseobacterium taichungense]

Results List

1. WP_072636260.1 **Mass:** 26277 **Score:** 226 **Expect:** 3.8e-15 **Matches:** 22

nitrile hydratase subunit beta [Rhodococcus sp. M8]

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 Observed    Mr(expt)   Mr(calc)    ppm  Start   End Miss  Peptide
 889.4699   888.4626   888.4552    8.31    88 -  94   0    K.IITEEER.K
 909.4110   908.4037   908.3851    20.5    44 -  50   0    K.GMSWWDK.S
 925.3929   924.3857   924.3800    6.14    44 -  50   0    K.GMSWWDK.S + Oxidation (M)
 943.5581   942.5508   942.5134    39.6    98 - 105   0    R.VQEILEGR.Y
1008.5309  1007.5236  1007.4784    44.8   106 - 113   1    R.YTDRNPSR.K
1017.6068  1016.5995  1016.5502    48.5    88 -  95   1    K.IITEEERK.H
1039.5621  1038.5548  1038.5029    50.0   152 - 160   0    K.NMNPLGHTR.C
1055.5539  1054.5467  1054.4978    46.3   152 - 160   0    K.NMNPLGHTR.C + Oxidation (M)
1076.6177  1075.6104  1075.5549    51.5   114 - 122   1    R.KFDPAEIEK.A
1236.7658  1235.7585  1235.6734    68.9    96 - 105   1    K.HRVQEILEGR.Y
1342.8443  1341.8370  1341.7479    66.4    33 -  43   0    R.TLSILTWMHLK.G
1358.8283  1357.8210  1357.7428    57.6    33 -  43   0    R.TLSILTWMHLK.G + Oxidation (M)
1528.9494  1527.9422  1527.8508    59.8    82 -  94   1    R.ILVADKIITEEER.K
1554.7745  1553.7672  1553.6780    57.4    56 -  68   0    R.ESMGNENYVNEIR.N
1570.7627  1569.7554  1569.6729    52.6    56 -  68   0    R.ESMGNENYVNEIR.N + Oxidation (M)
1597.8453  1596.8380  1596.7321    66.4    69 -  81   0    R.NSYYTHWLSAAER.I
1611.7977  1610.7904  1610.6790    69.2    21 -  32   0    K.DEPFFHYEWEGR.T
2004.9863  2003.9790  2003.9159    31.5    53 -  68   1    R.FFRESMGNENYVNEIR.N
2123.9740  2122.9667  2122.9452    10.1     1 -  20   0    -.MDGIHDTGGMTGYGPVPYQK.D
2139.9640  2138.9567  2138.9402    7.73     1 -  20   0    -.MDGIHDTGGMTGYGPVPYQK.D + Oxidation (M)
2202.1298  2201.1225  2201.1117    4.94   127 - 147   0    R.LHEPHSLALPGAEPSFSLGDK.V
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No match to: 842.5082, 880.4031, 931.4111, 965.5374, 1032.5397, 1050.5640, 1069.6765, 1085.6909, 1098.6115,
1138.6869, 1145.6225, 1289.7106, 1364.8303, 1411.7877, 1537.7721, 1576.7774, 1582.8187, 1600.5682, 1619.8359,
1633.7985, 1639.8241, 1641.8427, 1657.0650, 1679.0464, 1867.8974, 2145.9803, 2211.1003, 2224.1306, 2230.1580,
2246.0893, 2350.1988, 2451.2369, 3716.1966

2.    AAN71592.1     Mass: 26259     Score: 212     Expect: 9.6e-14   Matches: 20
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       Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
       889.4699    888.4626    888.4552     8.31    88 -   94    0    K.IITEEER.K
       943.5581    942.5508    942.5134     39.6    98 - 105    0    R.VQEILEGR.Y
      1008.5309   1007.5236   1007.4784     44.8   106 - 113    1    R.YTDRNPSR.K
      1017.6068   1016.5995   1016.5502     48.5    88 -   95    1    K.IITEEERK.H
      1039.5621   1038.5548   1038.5029     50.0   152 - 160    0    K.NMNPLGHTR.C
      1055.5539   1054.5467   1054.4978     46.3   152 - 160    0    K.NMNPLGHTR.C + Oxidation (M)
      1076.6177   1075.6104   1075.5549     51.5   114 - 122    1    R.KFDPAEIEK.A
      1236.7658   1235.7585   1235.6734     68.9    96 - 105    1    K.HRVQEILEGR.Y
      1342.8443   1341.8370   1341.7479     66.4    33 -   43    0    R.TLSILTWMHLK.G
      1358.8283   1357.8210   1357.7428     57.6    33 -   43    0    R.TLSILTWMHLK.G + Oxidation (M)
      1528.9494   1527.9422   1527.8508     59.8    82 -   94    1    R.ILVADKIITEEER.K
      1554.7745   1553.7672   1553.6780     57.4    56 -   68    0    R.ESMGNENYVNEIR.N
      1570.7627   1569.7554   1569.6729     52.6    56 -   68    0    R.ESMGNENYVNEIR.N + Oxidation (M)
      1597.8453   1596.8380   1596.7321     66.4    69 -   81    0    R.NSYYTHWLSAAER.I
      1611.7977   1610.7904   1610.6790     69.2    21 -   32    0    K.DEPFFHYEWEGR.T
      2004.9863   2003.9790   2003.9159     31.5    53 -   68    1    R.FFRESMGNENYVNEIR.N
      2123.9740   2122.9667   2122.9452     10.1     1 -   20    0    -.MDGIHDTGGMTGYGPVPYQK.D
      2139.9640   2138.9567   2138.9402     7.73     1 -   20    0    -.MDGIHDTGGMTGYGPVPYQK.D + Oxidation (M)
      2202.1298   2201.1225   2201.1117     4.94   127 - 147    0    R.LHEPHSLALPGAEPSFSLGDK.V
      2429.2429   2428.2356   2428.2750   -16.24   127 - 149    1    R.LHEPHSLALPGAEPSFSLGDKVK.V
      No match to: 842.5082, 880.4031, 909.4110, 925.3929, 931.4111, 965.5374, 1032.5397, 1050.5640, 1069.6765,
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      1600.5682, 1619.8359, 1633.7985, 1639.8241, 1641.8427, 1657.0650, 1679.0464, 1867.8974, 2145.9803, 2211.1003,
      2224.1306, 2230.1580, 2246.0893, 2350.1988, 2451.2369, 3716.1966

3.    WP_006940501.1     Mass: 26305     Score: 183     Expect: 7.6e-11   Matches: 21
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     nitrile hydratase subunit beta [Rhodococcus sp. EsD8]
      Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss    Peptide
      889.4699    888.4626    888.4552    8.31     88 -   94    0    K.IITEEER.K
      909.4110    908.4037    908.3851    20.5     44 -   50    0    K.GMSWWDK.S
      925.3929    924.3857    924.3800    6.14     44 -   50    0    K.GMSWWDK.S + Oxidation (M)
      943.5581    942.5508    942.5134    39.6     98 -  105    0    R.VQEILEGR.Y
     1008.5309   1007.5236   1007.4784    44.8    106 -  113    1    R.YTDRNPSR.K
     1017.6068   1016.5995   1016.5502    48.5     88 -   95    1    K.IITEEERK.H
     1039.5621   1038.5548   1038.5029    50.0    152 -  160    0    K.NMNPLGHTR.C
     1055.5539   1054.5467   1054.4978    46.3    152 -  160    0    K.NMNPLGHTR.C + Oxidation (M)
     1076.6177   1075.6104   1075.5549    51.5    114 -  122    1    R.KFDPAEIEK.A
     1236.7658   1235.7585   1235.6734    68.9     96 -  105    1    K.HRVQEILEGR.Y
     1342.8443   1341.8370   1341.7479    66.4     33 -   43    0    R.TLSILTWMHLK.G
     1358.8283   1357.8210   1357.7428    57.6     33 -   43    0    R.TLSILTWMHLK.G + Oxidation (M)
     1528.9494   1527.9422   1527.8508    59.8     82 -   94    1    R.ILVADKIITEEER.K
     1554.7745   1553.7672   1553.6780    57.4     56 -   68    0    R.ESMGNENYVNEIR.N
     1570.7627   1569.7554   1569.6729    52.6     56 -   68    0    R.ESMGNENYVNEIR.N + Oxidation (M)
     1597.8453   1596.8380   1596.7321    66.4     69 -   81    0    R.NSYYTHWLSAAER.I
     1611.7977   1610.7904   1610.6790    69.2     21 -   32    0    K.DEPFFHYEWEGR.T
     2004.9863   2003.9790   2003.9159    31.5     53 -   68    1    R.FFRESMGNENYVNEIR.N
     2123.9740   2122.9667   2122.9452    10.1      1 -   20    0    -.MDGIHDTGGMTGYGPVPYQK.D
     2139.9640   2138.9567   2138.9402    7.73      1 -   20    0    -.MDGIHDTGGMTGYGPVPYQK.D + Oxidation (M)
     2230.1580   2229.1507   2229.1430    3.46    127 -  147    0    R.LHEPHSLVLPGAEPSFSLGDK.V
     No match to: 842.5082, 880.4031, 931.4111, 965.5374, 1032.5397, 1050.5640, 1069.6765, 1085.6909, 1098.6115,
     1138.6869, 1145.6225, 1289.7106, 1364.8303, 1411.7877, 1537.7721, 1576.7774, 1582.8187, 1600.5682, 1619.8359,
     1633.7985, 1639.8241, 1641.8427, 1657.0650, 1679.0464, 1867.8974, 2145.9803, 2202.1298, 2211.1003, 2224.1306,
     2246.0893, 2350.1988, 2429.2429, 2451.2369, 3716.1966
```

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4.   CAC83637.1     Mass: 22560     Score: 150     Expect: 1.5e-07  Matches: 15
     nitrile hydratase beta chain, partial [uncultured bacterium SP1]
      Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss    Peptide
      889.4699    888.4626    888.4552    8.31     88 -   94    0    K.IITEEER.K
      943.5581    942.5508    942.5134    39.6     98 -  105    0    R.VQEILEGR.Y
     1017.6068   1016.5995   1016.5502    48.5     88 -   95    1    K.IITEEERK.H
```

```
1236.7658  1235.7585  1235.6734   68.9     96 - 105    1    K.HRVQEILEGR.Y
1342.8443  1341.8370  1341.7479   66.4     33 -  43    0    R.TLSILTWMHLK.G
1358.8283  1357.8210  1357.7428   57.6     33 -  43    0    R.TLSILTWMHLK.G + Oxidation (M)
1528.9494  1527.9422  1527.8508   59.8     82 -  94    1    R.ILVADKIITEEER.K
1554.7745  1553.7672  1553.6780   57.4     56 -  68    0    R.ESMGNENYVNEIR.N
1570.7627  1569.7554  1569.6729   52.6     56 -  68    0    R.ESMGNENYVNEIR.N + Oxidation (M)
1597.8453  1596.8380  1596.7321   66.4     69 -  81    0    R.NSYYTHWLSAAER.I
1611.7977  1610.7904  1610.6790   69.2     21 -  32    0    K.DEPFFHYEWEGR.T
2004.9863  2003.9790  2003.9159   31.5     53 -  68    1    R.FFRESMGNENYVNEIR.N
2123.9740  2122.9667  2122.9452   10.1      1 -  20    0    -.MDGIHDTGGMTGYGPVPYQK.D
2139.9640  2138.9567  2138.9402   7.73      1 -  20    0    -.MDGIHDTGGMTGYGPVPYQK.D + Oxidation (M)
2202.1298  2201.1225  2201.1117   4.94    127 - 147    0    R.LHEPHSLALPGAEPSFSLGDK.I
```

No match to: 842.5082, 880.4031, 909.4110, 925.3929, 931.4111, 965.5374, 1008.5309, 1032.5397, 1039.5621, 1050.5640, 1055.5539, 1069.6765, 1076.6177, 1085.6909, 1098.6115, 1138.6869, 1145.6225, 1289.7106, 1364.8303, 1411.7877, 1537.7721, 1576.7774, 1582.8187, 1600.5682, 1619.8359, 1633.7985, 1639.8241, 1641.8427, 1657.0650, 1679.0464, 1867.8974, 2145.9803, 2211.1003, 2224.1306, 2230.1580, 2246.0893, 2350.1988, 2429.2429, 2451.2369, 3716.1966

5. BAE75932.1 **Mass:** 26335 **Score:** **141** **Expect:** 1.2e-06 **Matches:** 15

nitrile hydratase beta subunit [Rhodococcus pyridinivorans]

```
 Observed   Mr(expt)   Mr(calc)    ppm  Start   End Miss   Peptide
 889.4699   888.4626   888.4552   8.31     88 -  94    0    K.IITEEER.K
 943.5581   942.5508   942.5134   39.6     98 - 105    0    R.VQEILEGR.Y
1017.6068  1016.5995  1016.5502   48.5     88 -  95    1    K.IITEEERK.H
1236.7658  1235.7585  1235.6734   68.9     96 - 105    1    K.HRVQEILEGR.Y
1342.8443  1341.8370  1341.7479   66.4     33 -  43    0    R.TLSILTWMHLK.G
1358.8283  1357.8210  1357.7428   57.6     33 -  43    0    R.TLSILTWMHLK.G + Oxidation (M)
1528.9494  1527.9422  1527.8508   59.8     82 -  94    1    R.ILVADKIITEEER.K
1554.7745  1553.7672  1553.6780   57.4     56 -  68    0    R.ESMGNENYVNEIR.N
1570.7627  1569.7554  1569.6729   52.6     56 -  68    0    R.ESMGNENYVNEIR.N + Oxidation (M)
1597.8453  1596.8380  1596.7321   66.4     69 -  81    0    R.NSYYTHWLSAAER.I
1611.7977  1610.7904  1610.6790   69.2     21 -  32    0    K.DEPFFHYEWEGR.T
2004.9863  2003.9790  2003.9159   31.5     53 -  68    1    R.FFRESMGNENYVNEIR.N
2123.9740  2122.9667  2122.9452   10.1      1 -  20    0    -.MDGIHDTGGMTGYGPVPYQK.D
```

2139.9640	2138.9567	2138.9402	7.73	1 -	20	0	-.MDGIHDTGGMTGYGPVPYQK.D + Oxidation (M)
2202.1298	2201.1225	2201.1117	4.94	127 -	147	0	R.LHEPHSLALPGAEPSFSLGDK.I

No match to: 842.5082, 880.4031, 909.4110, 925.3929, 931.4111, 965.5374, 1008.5309, 1032.5397, 1039.5621, 1050.5640, 1055.5539, 1069.6765, 1076.6177, 1085.6909, 1098.6115, 1138.6869, 1145.6225, 1289.7106, 1364.8303, 1411.7877, 1537.7721, 1576.7774, 1582.8187, 1600.5682, 1619.8359, 1633.7985, 1639.8241, 1641.8427, 1657.0650, 1679.0464, 1867.8974, 2145.9803, 2211.1003, 2224.1306, 2230.1580, 2246.0893, 2350.1988, 2429.2429, 2451.2369, 3716.1966

6. P21220.2 **Mass:** 26305 **Score:** 141 **Expect:** 1.2e-06 **Matches:** 15

RecName: Full=High-molecular weight cobalt-containing nitrile hydratase subunit beta; Short=H-NHase; Short=H-nitrilase

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
889.4699	888.4626	888.4552	8.31	88 -	94	0	K.IITEEER.K
943.5581	942.5508	942.5134	39.6	98 -	105	0	R.VQEILEGR.Y
1017.6068	1016.5995	1016.5502	48.5	88 -	95	1	K.IITEEERK.H
1236.7658	1235.7585	1235.6734	68.9	96 -	105	1	K.HRVQEILEGR.Y
1342.8443	1341.8370	1341.7479	66.4	33 -	43	0	R.TLSILTWMHLK.G
1358.8283	1357.8210	1357.7428	57.6	33 -	43	0	R.TLSILTWMHLK.G + Oxidation (M)
1528.9494	1527.9422	1527.8508	59.8	82 -	94	1	R.ILVADKIITEEER.K
1554.7745	1553.7672	1553.6780	57.4	56 -	68	0	R.ESMGNENYVNEIR.N
1570.7627	1569.7554	1569.6729	52.6	56 -	68	0	R.ESMGNENYVNEIR.N + Oxidation (M)
1597.8453	1596.8380	1596.7321	66.4	69 -	81	0	R.NSYYTHWLSAAER.I
1611.7977	1610.7904	1610.6790	69.2	21 -	32	0	K.DEPFFHYEWEGR.T
2004.9863	2003.9790	2003.9159	31.5	53 -	68	1	R.FFRESMGNENYVNEIR.N
2123.9740	2122.9667	2122.9452	10.1	1 -	20	0	-.MDGIHDTGGMTGYGPVPYQK.D
2139.9640	2138.9567	2138.9402	7.73	1 -	20	0	-.MDGIHDTGGMTGYGPVPYQK.D + Oxidation (M)
2202.1298	2201.1225	2201.1117	4.94	127 -	147	0	R.LHEPHSLALPGAEPSFSLGDK.I

No match to: 842.5082, 880.4031, 909.4110, 925.3929, 931.4111, 965.5374, 1008.5309, 1032.5397, 1039.5621, 1050.5640, 1055.5539, 1069.6765, 1076.6177, 1085.6909, 1098.6115, 1138.6869, 1145.6225, 1289.7106, 1364.8303, 1411.7877, 1537.7721, 1576.7774, 1582.8187, 1600.5682, 1619.8359, 1633.7985, 1639.8241, 1641.8427, 1657.0650, 1679.0464, 1867.8974, 2145.9803, 2211.1003, 2224.1306, 2230.1580, 2246.0893, 2350.1988, 2429.2429, 2451.2369, 3716.1966

7. AEB00726.1 **Mass:** 26303 **Score:** 122 **Expect:** 9.6e-05 **Matches:** 14

nitrile hydratase beta subunit [Rhodococcus sp. BX2]

```
 Observed   Mr(expt)   Mr(calc)    ppm  Start    End Miss   Peptide
  889.4699   888.4626   888.4552   8.31    88 -   94    0    K.IITEEER.K
  943.5581   942.5508   942.5134   39.6    98 -  105    0    R.VQEILEGR.Y
 1017.6068  1016.5995  1016.5502   48.5    88 -   95    1    K.IITEEERK.H
 1236.7658  1235.7585  1235.6734   68.9    96 -  105    1    K.HRVQEILEGR.Y
 1342.8443  1341.8370  1341.7479   66.4    33 -   43    0    R.TLSILTWMHLK.G
 1358.8283  1357.8210  1357.7428   57.6    33 -   43    0    R.TLSILTWMHLK.G + Oxidation (M)
 1528.9494  1527.9422  1527.8508   59.8    82 -   94    1    R.ILVADKIITEEER.K
 1554.7745  1553.7672  1553.6780   57.4    56 -   68    0    R.ESMGNENYVNEIR.N
 1570.7627  1569.7554  1569.6729   52.6    56 -   68    0    R.ESMGNENYVNEIR.N + Oxidation (M)
 1597.8453  1596.8380  1596.7321   66.4    69 -   81    0    R.NSYYTHWLSAAER.I
 1611.7977  1610.7904  1610.6790   69.2    21 -   32    0    K.DEPFFHYEWEGR.T
 2004.9863  2003.9790  2003.9159   31.5    53 -   68    1    R.FFRESMGNENYVNEIR.N
 2123.9740  2122.9667  2122.9452   10.1     1 -   20    0    -.MDGIHDTGGMTGYGPVPYQK.D
 2139.9640  2138.9567  2138.9402   7.73     1 -   20    0    -.MDGIHDTGGMTGYGPVPYQK.D + Oxidation (M)
No match to: 842.5082, 880.4031, 909.4110, 925.3929, 931.4111, 965.5374, 1008.5309, 1032.5397, 1039.5621,
1050.5640, 1055.5539, 1069.6765, 1076.6177, 1085.6909, 1098.6115, 1138.6869, 1145.6225, 1289.7106, 1364.8303,
1411.7877, 1537.7721, 1576.7774, 1582.8187, 1600.5682, 1619.8359, 1633.7985, 1639.8241, 1641.8427, 1657.0650,
1679.0464, 1867.8974, 2145.9803, 2202.1298, 2211.1003, 2224.1306, 2230.1580, 2246.0893, 2350.1988, 2429.2429,
2451.2369, 3716.1966
```

```
8.    CAE46767.1    Mass: 26349    Score: 120    Expect: 0.00015  Matches: 13
      nitrile hydratase beta subunit [Rhodococcus pyridinivorans]
 Observed   Mr(expt)   Mr(calc)    ppm  Start    End Miss   Peptide
  889.4699   888.4626   888.4552   8.31    88 -   94    0    K.IITEEER.K
  943.5581   942.5508   942.5134   39.6    98 -  105    0    R.VQEILEGR.Y
 1017.6068  1016.5995  1016.5502   48.5    88 -   95    1    K.IITEEERK.H
 1236.7658  1235.7585  1235.6734   68.9    96 -  105    1    K.HRVQEILEGR.Y
 1342.8443  1341.8370  1341.7479   66.4    33 -   43    0    R.TLSILTWMHLK.G
 1358.8283  1357.8210  1357.7428   57.6    33 -   43    0    R.TLSILTWMHLK.G + Oxidation (M)
 1528.9494  1527.9422  1527.8508   59.8    82 -   94    1    R.ILVADKIITEEER.K
 1554.7745  1553.7672  1553.6780   57.4    56 -   68    0    R.ESMGNENYVNEIR.N
 1570.7627  1569.7554  1569.6729   52.6    56 -   68    0    R.ESMGNENYVNEIR.N + Oxidation (M)
 1597.8453  1596.8380  1596.7321   66.4    69 -   81    0    R.NSYYTHWLSAAER.I
 1611.7977  1610.7904  1610.6790   69.2    21 -   32    0    K.DEPFFHYEWEGR.T
```

```
         2004.9863  2003.9790  2003.9159   31.5     53 -  68    1    R.FFRESMGNENYVNEIR.N
         2202.1298  2201.1225  2201.1117   4.94   127 - 147    0    R.LHEPHSLALPGAEPSFSLGDK.I
         No match to: 842.5082, 880.4031, 909.4110, 925.3929, 931.4111, 965.5374, 1008.5309, 1032.5397, 1039.5621,
         1050.5640, 1055.5539, 1069.6765, 1076.6177, 1085.6909, 1098.6115, 1138.6869, 1145.6225, 1289.7106, 1364.8303,
         1411.7877, 1537.7721, 1576.7774, 1582.8187, 1600.5682, 1619.8359, 1633.7985, 1639.8241, 1641.8427, 1657.0650,
         1679.0464, 1867.8974, 2123.9740, 2139.9640, 2145.9803, 2211.1003, 2224.1306, 2230.1580, 2246.0893, 2350.1988,
         2429.2429, 2451.2369, 3716.1966

9.       CAC83638.1     Mass: 19344     Score: 119     Expect: 0.00019  Matches: 12
         nitrile hydratase beta chain, partial [uncultured bacterium BD2]
          Observed    Mr(expt)    Mr(calc)    ppm  Start    End Miss    Peptide
          889.4699    888.4626    888.4552    8.31     88 -  94    0    K.IITEEER.K
          943.5581    942.5508    942.5134    39.6     98 - 105    0    R.VQEILEGR.Y
         1017.6068  1016.5995  1016.5502   48.5     88 -  95    1    K.IITEEERK.H
         1236.7658  1235.7585  1235.6734   68.9     96 - 105    1    K.HRVQEILEGR.Y
         1342.8443  1341.8370  1341.7479   66.4     33 -  43    0    R.TLSILTWMHLK.G
         1358.8283  1357.8210  1357.7428   57.6     33 -  43    0    R.TLSILTWMHLK.G + Oxidation (M)
         1528.9494  1527.9422  1527.8508   59.8     82 -  94    1    R.ILVADKIITEEER.K
         1597.8453  1596.8380  1596.7321   66.4     69 -  81    0    R.NSYYTHWLSAAER.I
         1611.7977  1610.7904  1610.6790   69.2     21 -  32    0    K.DEPFFHYEWEGR.T
         2123.9740  2122.9667  2122.9452   10.1      1 -  20    0    -.MDGIHDTGGMTGYGPVPYQK.D
         2139.9640  2138.9567  2138.9402   7.73      1 -  20    0    -.MDGIHDTGGMTGYGPVPYQK.D + Oxidation (M)
         2202.1298  2201.1225  2201.1117   4.94    127 - 147    0    R.LHEPHSLALPGAEPSFSLGDK.N
         No match to: 842.5082, 880.4031, 909.4110, 925.3929, 931.4111, 965.5374, 1008.5309, 1032.5397, 1039.5621,
         1050.5640, 1055.5539, 1069.6765, 1076.6177, 1085.6909, 1098.6115, 1138.6869, 1145.6225, 1289.7106, 1364.8303,
         1411.7877, 1537.7721, 1554.7745, 1570.7627, 1576.7774, 1582.8187, 1600.5682, 1619.8359, 1633.7985, 1639.8241,
         1641.8427, 1657.0650, 1679.0464, 1867.8974, 2004.9863, 2145.9803, 2211.1003, 2224.1306, 2230.1580, 2246.0893,
         2350.1988, 2429.2429, 2451.2369, 3716.1966

10.      AIE75022.1     Mass: 12588     Score: 79      Expect: 1.9  Matches: 7
         hypothetical protein D082_24940 [Synechocystis sp. PCC 6714]
          Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss    Peptide
         1554.7745  1553.7672  1553.7548     7.99     44 -  56    1    R.SQSYEFCIPPQKK.S
         1570.7627  1569.7554  1569.8191   -40.58    103 - 115    1    R.LSYIEKIVPHWGE.-
         1582.8187  1581.8114  1581.7609     31.9     43 -  55    1    K.RSQSYEFCIPPQK.K
```

1619.8359	1618.8286	1618.7735	34.1	1 -	15	0	-.MDLAIAADFPEPMAK.V
2230.1580	2229.1507	2229.1351	6.99	2 -	22	1	M.DLAIAADFPEPMAKVANTLDK.I
2246.0893	2245.0820	2245.1300	-21.39	2 -	22	1	M.DLAIAADFPEPMAKVANTLDK.I + Oxidation (M)
2350.1988	2349.1916	2349.3090	-49.99	57 -	79	1	K.SAVLAIDPSLQISPSPGRIVCVK.G

No match to: 842.5082, 880.4031, 889.4699, 909.4110, 925.3929, 931.4111, 943.5581, 965.5374, 1008.5309, 1017.6068, 1032.5397, 1039.5621, 1050.5640, 1055.5539, 1069.6765, 1076.6177, 1085.6909, 1098.6115, 1138.6869, 1145.6225, 1236.7658, 1289.7106, 1342.8443, 1358.8283, 1364.8303, 1411.7877, 1528.9494, 1537.7721, 1576.7774, 1597.8453, 1600.5682, 1611.7977, 1633.7985, 1639.8241, 1641.8427, 1657.0650, 1679.0464, 1867.8974, 2004.9863, 2123.9740, 2139.9640, 2145.9803, 2202.1298, 2211.1003, 2224.1306, 2429.2429, 2451.2369, 3716.1966

11. OGC51977.1 **Mass:** 24781 **Score:** 74 **Expect:** 6.7 **Matches:** 8

macrolide ABC transporter ATP-binding protein [candidate division WWE3 bacterium RIFCSPLOWO2_01_FULL_39_13]

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
943.5581	942.5508	942.5247	27.7	28 -	35	0	K.NISVQINR.S
1039.5621	1038.5548	1038.5419	12.4	184 -	191	1	R.EIMDLFKK.L + Oxidation (M)
1597.8453	1596.8380	1596.8293	5.45	127 -	140	1	K.ADEMLEIVGLSHRK.Y
1611.7977	1610.7904	1610.8516	-37.97	196 -	210	0	K.GTTVIIVTHDEDIAK.Q
1639.8241	1638.8168	1638.9127	-58.47	1 -	14	1	-.MQSKLILEAQHITK.T
2202.1298	2201.1225	2201.1362	-6.20	45 -	66	1	K.SGSGKSTLMHIIGLLDSPTSGK.I + Oxidation (M)
2224.1306	2223.1233	2223.1383	-6.73	160 -	180	0	R.ALVNDPSIILADEPTGNLDTR.T
2429.2429	2428.2356	2428.3002	-26.59	103 -	124	1	R.ATALENVLLPLKYSNVPGSEWK.N

No match to: 842.5082, 880.4031, 889.4699, 909.4110, 925.3929, 931.4111, 965.5374, 1008.5309, 1017.6068, 1032.5397, 1050.5640, 1055.5539, 1069.6765, 1076.6177, 1085.6909, 1098.6115, 1138.6869, 1145.6225, 1236.7658, 1289.7106, 1342.8443, 1358.8283, 1364.8303, 1411.7877, 1528.9494, 1537.7721, 1554.7745, 1570.7627, 1576.7774, 1582.8187, 1600.5682, 1619.8359, 1633.7985, 1641.8427, 1657.0650, 1679.0464, 1867.8974, 2004.9863, 2123.9740, 2139.9640, 2145.9803, 2211.1003, 2230.1580, 2246.0893, 2350.1988, 2451.2369, 3716.1966

12. PPC88533.1 **Mass:** 40463 **Score:** 74 **Expect:** 6.8 **Matches:** 8

8-amino-7-oxononanoate synthase [Hyphomicrobium sp.]

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
889.4699	888.4626	888.4739	-12.66	319 -	327	0	R.AVALADAMK.A
1076.6177	1075.6104	1075.5444	61.3	45 -	53	1	R.DAVMRALER.G + Oxidation (M)
1582.8187	1581.8114	1581.8045	4.34	1 -	14	1	-.MSANHDRALDALLR.R
1619.8359	1618.8286	1618.9267	-60.59	335 -	349	1	R.AVRPPTVPEGTARLR.M
2004.9863	2003.9790	2004.1156	-68.17	250 -	268	1	R.ARSFIYATAPSPLIAATVR.E

```
2139.9640  2138.9567  2139.0419  -39.81   109 - 127   0   R.GDLIIYDELIHASAHEGMR.L
2202.1298  2201.1225  2201.1090    6.15   135 - 152   1   R.SVRHNDVQHIEDVIQAWR.E
2429.2429  2428.2356  2428.0853    61.9   153 - 174   0   R.EDGATGQIWIAVESLYSMDGDR.A + Oxidation (M)
No match to: 842.5082, 880.4031, 909.4110, 925.3929, 931.4111, 943.5581, 965.5374, 1008.5309, 1017.6068,
1032.5397, 1039.5621, 1050.5640, 1055.5539, 1069.6765, 1085.6909, 1098.6115, 1138.6869, 1145.6225, 1236.7658,
1289.7106, 1342.8443, 1358.8283, 1364.8303, 1411.7877, 1528.9494, 1537.7721, 1554.7745, 1570.7627, 1576.7774,
1597.8453, 1600.5682, 1611.7977, 1633.7985, 1639.8241, 1641.8427, 1657.0650, 1679.0464, 1867.8974, 2123.9740,
2145.9803, 2211.1003, 2224.1306, 2230.1580, 2246.0893, 2350.1988, 2451.2369, 3716.1966

13.  AOK07627.1     Mass: 11710     Score: 72      Expect: 10  Matches: 6
     hypothetical protein WK25_24445 [Burkholderia latens]
      Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
      909.4110   908.4037   908.4386  -38.35    72 -  80   0   R.VAGATSTMR.T + Oxidation (M)
     1050.5640  1049.5567  1049.5553    1.36     9 -  17   1   R.RLPAMHPGR.D + Oxidation (M)
     1570.7627  1569.7554  1569.7787  -14.86    18 -  32   0   R.DFGDALPPAQIDVGR.H
     1582.8187  1581.8114  1581.8587  -29.90    95 - 111   1   R.ATPAARRPVSVATAGSA.-
     2202.1298  2201.1225  2201.0497    33.1    47 -  66   0   R.IDGDIVPLCDGWIGVDVEMR.V
     2429.2429  2428.2356  2428.1879    19.6    45 -  66   1   R.ARIDGDIVPLCDGWIGVDVEMR.V
     No match to: 842.5082, 880.4031, 889.4699, 925.3929, 931.4111, 943.5581, 965.5374, 1008.5309, 1017.6068,
     1032.5397, 1039.5621, 1055.5539, 1069.6765, 1076.6177, 1085.6909, 1098.6115, 1138.6869, 1145.6225, 1236.7658,
     1289.7106, 1342.8443, 1358.8283, 1364.8303, 1411.7877, 1528.9494, 1537.7721, 1554.7745, 1576.7774, 1597.8453,
     1600.5682, 1611.7977, 1619.8359, 1633.7985, 1639.8241, 1641.8427, 1657.0650, 1679.0464, 1867.8974, 2004.9863,
     2123.9740, 2139.9640, 2145.9803, 2211.1003, 2224.1306, 2230.1580, 2246.0893, 2350.1988, 2451.2369, 3716.1966

14.  KUK80951.1     Mass: 28382     Score: 71      Expect: 11  Matches: 7
     Flagellar hook protein FlgE [Pelotomaculum thermopropionicum]
      Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
      889.4699   888.4626   888.4665   -4.39   205 - 212   0   R.QADVTTVR.Q
      943.5581   942.5508   942.5247    27.7   254 - 262   0   K.AVNQVGSLR.-
     1582.8187  1581.8114  1581.7570    34.4   160 - 175   0   K.VNHDGTVVSGGMPQGK.L
     1597.8453  1596.8380  1596.7268    69.7   190 - 204   0   K.ETDSIFVDTTGEAGR.Q
     1867.8974  1866.8901  1866.9371  -25.13   160 - 177   1   K.VNHDGTVVSGGMPQGKLR.L + Oxidation (M)
     2224.1306  2223.1233  2223.0817    18.7    95 - 114   1   R.NPTDMMLKGPGFFAVNVPTR.E + 2 Oxidation (M)
     2451.2369  2450.2296  2450.3282  -40.21    36 -  57   1   K.KDVVQAQSFPELLLIQQGGPQR.R
     No match to: 842.5082, 880.4031, 909.4110, 925.3929, 931.4111, 965.5374, 1008.5309, 1017.6068, 1032.5397,
     1039.5621, 1050.5640, 1055.5539, 1069.6765, 1076.6177, 1085.6909, 1098.6115, 1138.6869, 1145.6225, 1236.7658,
```

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        1289.7106, 1342.8443, 1358.8283, 1364.8303, 1411.7877, 1528.9494, 1537.7721, 1554.7745, 1570.7627, 1576.7774,
        1600.5682, 1611.7977, 1619.8359, 1633.7985, 1639.8241, 1641.8427, 1657.0650, 1679.0464, 2004.9863, 2123.9740,
        2139.9640, 2145.9803, 2202.1298, 2211.1003, 2230.1580, 2246.0893, 2350.1988, 2429.2429, 3716.1966

15.     WP_038563067.1     Mass: 40788     Score: 71      Expect: 13  Matches: 8
        CapA family protein [Draconibacterium orientale]
         Observed    Mr(expt)    Mr(calc)     ppm   Start    End Miss    Peptide
         889.4699    888.4626    888.4916  -32.67     93 - 100    1     R.KGIEDTVK.I
         909.4110    908.4037    908.4603  -62.32    145 - 152    0     K.GVNTLDYK.E
         943.5581    942.5508    942.5651  -15.15    189 - 196    1     K.FSHLLAKK.N
        1098.6115   1097.6042   1097.6444  -36.63     64 -  73    0     R.SPSININLLK.Y
        1358.8283   1357.8210   1357.8333   -9.03      2 -  14    1     M.KIAFLGDIALIGK.Y
        1570.7627   1569.7554   1569.7311    15.5    250 - 262    0     R.ESFIFDVSIDENR.I
        2202.1298   2201.1225   2201.1004    10.0    250 - 267    1     R.ESFIFDVSIDENRIINYK.T
        2224.1306   2223.1233   2223.1072    7.23     74 -  92    0     K.YLNINIVSLANNHTYDFGR.K
        No match to: 842.5082, 880.4031, 925.3929, 931.4111, 965.5374, 1008.5309, 1017.6068, 1032.5397, 1039.5621,
        1050.5640, 1055.5539, 1069.6765, 1076.6177, 1085.6909, 1138.6869, 1145.6225, 1236.7658, 1289.7106, 1342.8443,
        1364.8303, 1411.7877, 1528.9494, 1537.7721, 1554.7745, 1576.7774, 1582.8187, 1597.8453, 1600.5682, 1611.7977,
        1619.8359, 1633.7985, 1639.8241, 1641.8427, 1657.0650, 1679.0464, 1867.8974, 2004.9863, 2123.9740, 2139.9640,
        2145.9803, 2211.1003, 2230.1580, 2246.0893, 2350.1988, 2429.2429, 2451.2369, 3716.1966

16.     WP_048896976.1     Mass: 26861     Score: 71      Expect: 13  Matches: 7
        arginyltransferase [Photobacterium swingsii]
         Observed    Mr(expt)    Mr(calc)     ppm   Start    End Miss    Peptide
         889.4699    888.4626    888.4851  -25.30     85 -  91    1     R.QLNQMKK.L
        1039.5621   1038.5548   1038.5723  -16.83    215 - 222    1     K.VRFQPHQK.L
        1611.7977   1610.7904   1610.7616    17.9     98 - 110    0     K.SELDPNWFALYEK.Y
        1867.8974   1866.8901   1866.8976   -4.02     54 -  70    0     K.AIYKPMCTACQACVPLR.V
        2123.9740   2122.9667   2122.9492    8.25    198 - 214    1     R.WLYPGYQIDDCKAMNYK.V + Oxidation (M)
        2139.9640   2138.9567   2139.0461  -41.79     51 -  70    1     R.SGKAIYKPMCTACQACVPLR.V
        2202.1298   2201.1225   2201.0469    34.4     94 - 110    1     R.WEFKSELDPNWFALYEK.Y
        No match to: 842.5082, 880.4031, 909.4110, 925.3929, 931.4111, 943.5581, 965.5374, 1008.5309, 1017.6068,
        1032.5397, 1050.5640, 1055.5539, 1069.6765, 1076.6177, 1085.6909, 1098.6115, 1138.6869, 1145.6225, 1236.7658,
        1289.7106, 1342.8443, 1358.8283, 1364.8303, 1411.7877, 1528.9494, 1537.7721, 1554.7745, 1570.7627, 1576.7774,
        1582.8187, 1597.8453, 1600.5682, 1619.8359, 1633.7985, 1639.8241, 1641.8427, 1657.0650, 1679.0464, 2004.9863,
        2145.9803, 2211.1003, 2224.1306, 2230.1580, 2246.0893, 2350.1988, 2429.2429, 2451.2369, 3716.1966
```

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17.    WP_053874729.1    Mass: 53645    Score: 70     Expect: 14  Matches: 8
       aldehyde dehydrogenase [Staphylococcus aureus]
        Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
        889.4699    888.4626    888.4552    8.29    362 - 369    0    R.LTENGLDK.G
       1008.5309   1007.5236   1007.5287   -5.10    341 - 349    0    K.IQSYIDAAK.E
       1582.8187   1581.8114   1581.7675    27.8     58 -  71    0    K.VAQEAFESWSLTSK.S
       1657.0650   1656.0578   1655.9498    65.2    387 - 401    0    K.LAQEEIFGPVLTVIK.V
       2123.9740   2122.9667   2123.0607  -44.26    350 - 369    1    K.ESDAQILAGGHRLTENGLDK.G
       2429.2429   2428.2356   2428.1758    24.6    225 - 248    1    R.DGVDKLSFTGSTDVGYQVAEAAAK.H
       2451.2369   2450.2296   2450.1390    37.0    118 - 138    0    R.HFHYFASVIETEEGTVNDIDK.D
       3716.1966   3715.1894   3715.1175    19.3    169 - 204    1    K.IAPAIAAGNTIVIQPSSSTPLSLLEVAKIFQEVLPK.G
       No match to: 842.5082, 880.4031, 909.4110, 925.3929, 931.4111, 943.5581, 965.5374, 1017.6068, 1032.5397,
       1039.5621, 1050.5640, 1055.5539, 1069.6765, 1076.6177, 1085.6909, 1098.6115, 1138.6869, 1145.6225, 1236.7658,
       1289.7106, 1342.8443, 1358.8283, 1364.8303, 1411.7877, 1528.9494, 1537.7721, 1554.7745, 1570.7627, 1576.7774,
       1597.8453, 1600.5682, 1611.7977, 1619.8359, 1633.7985, 1639.8241, 1641.8427, 1679.0464, 1867.8974, 2004.9863,
       2139.9640, 2145.9803, 2202.1298, 2211.1003, 2224.1306, 2230.1580, 2246.0893, 2350.1988

18.    WP_107364903.1    Mass: 53598    Score: 70     Expect: 15  Matches: 8
       aldehyde dehydrogenase [Staphylococcus aureus]
        Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
        889.4699    888.4626    888.4552    8.29    362 - 369    0    R.LTENGLDK.G
       1008.5309   1007.5236   1007.5287   -5.10    341 - 349    0    K.IQSYIDAAK.E
       1582.8187   1581.8114   1581.7675    27.8     58 -  71    0    K.VAQEAFESWSLTSK.S
       1657.0650   1656.0578   1655.9498    65.2    387 - 401    0    K.LAQEEIFGPVLTVIK.V
       2123.9740   2122.9667   2123.0607  -44.26    350 - 369    1    K.ESDAQILAGGHRLTENGLDK.G
       2429.2429   2428.2356   2428.1718    26.3     24 -  46    0    K.ASSDETIEVTNPATGETLSHITR.A
       2451.2369   2450.2296   2450.1390    37.0    118 - 138    0    R.HFHYFASVIETEEGTVNDIDK.D
       3716.1966   3715.1894   3715.1175    19.3    169 - 204    1    K.IAPAIAAGNTIVIQPSSSTPLSLLEVAKIFQEVLPK.G
       No match to: 842.5082, 880.4031, 909.4110, 925.3929, 931.4111, 943.5581, 965.5374, 1017.6068, 1032.5397,
       1039.5621, 1050.5640, 1055.5539, 1069.6765, 1076.6177, 1085.6909, 1098.6115, 1138.6869, 1145.6225, 1236.7658,
       1289.7106, 1342.8443, 1358.8283, 1364.8303, 1411.7877, 1528.9494, 1537.7721, 1554.7745, 1570.7627, 1576.7774,
       1597.8453, 1600.5682, 1611.7977, 1619.8359, 1633.7985, 1639.8241, 1641.8427, 1679.0464, 1867.8974, 2004.9863,
       2139.9640, 2145.9803, 2202.1298, 2211.1003, 2224.1306, 2230.1580, 2246.0893, 2350.1988
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19.   WP_031788062.1     Mass: 53650    Score: 70     Expect: 17  Matches: 8
      MULTISPECIES: aldehyde dehydrogenase [Staphylococcus]
       Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss  Peptide
       889.4699    888.4626    888.4552    8.29   362 - 369    0    R.LTENGLDK.G
      1008.5309   1007.5236   1007.5287   -5.10   341 - 349    0    K.IQSYIDAAK.E
      1582.8187   1581.8114   1581.7675    27.8    58 -  71    0    K.VAQEAFESWSLTSK.T
      1657.0650   1656.0578   1655.9498    65.2   387 - 401    0    K.LAQEEIFGPVLTVIK.V
      2123.9740   2122.9667   2123.0607  -44.26   350 - 369    1    K.ESDAQILAGGHRLTENGLDK.G
      2224.1306   2223.1233   2223.1477  -10.95   443 - 462    1    R.IWINTYNQVPAGAPFGGYKK.S
      2451.2369   2450.2296   2450.1390    37.0   118 - 138    0    R.HFHYFASVIETEEGTVNDIDK.D
      3716.1966   3715.1894   3715.1175    19.3   169 - 204    1    K.IAPAIAAGNTIVIQPSSSTPLSLLEVAKIFQEVLPK.G
      No match to: 842.5082, 880.4031, 909.4110, 925.3929, 931.4111, 943.5581, 965.5374, 1017.6068, 1032.5397,
      1039.5621, 1050.5640, 1055.5539, 1069.6765, 1076.6177, 1085.6909, 1098.6115, 1138.6869, 1145.6225, 1236.7658,
      1289.7106, 1342.8443, 1358.8283, 1364.8303, 1411.7877, 1528.9494, 1537.7721, 1554.7745, 1570.7627, 1576.7774,
      1597.8453, 1600.5682, 1611.7977, 1619.8359, 1633.7985, 1639.8241, 1641.8427, 1679.0464, 1867.8974, 2004.9863,
      2139.9640, 2145.9803, 2202.1298, 2211.1003, 2230.1580, 2246.0893, 2350.1988, 2429.2429

20.   WP_090000046.1     Mass: 17896    Score: 69     Expect: 20  Matches: 6
      DUF1572 domain-containing protein [Chryseobacterium taichungense]
       Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss  Peptide
      1008.5309   1007.5236   1007.5321   -8.47     1 -   9    0    -.MSTTLQLAK.R + Oxidation (M)
      1017.6068   1016.5995   1016.5978    1.66     2 -  10    1    M.STTLQLAKR.F
      1039.5621   1038.5548   1038.5386    15.6    77 -  85    0    K.YSFDLPAVK.S
      1867.8974   1866.8901   1866.8458    23.8   116 - 130    1    K.MNESFVDEKYGTYLR.N + Oxidation (M)
      2139.9640   2138.9567   2139.0558  -46.32    97 - 115    1    K.LFSDAEKFASLLEQMPDAK.M
      2429.2429   2428.2356   2428.1290    43.9   104 - 124    1    K.FASLLEQMPDAKMNESFVDEK.Y
      No match to: 842.5082, 880.4031, 889.4699, 909.4110, 925.3929, 931.4111, 943.5581, 965.5374, 1032.5397, 1050.5640,
      1055.5539, 1069.6765, 1076.6177, 1085.6909, 1098.6115, 1138.6869, 1145.6225, 1236.7658, 1289.7106, 1342.8443,
      1358.8283, 1364.8303, 1411.7877, 1528.9494, 1537.7721, 1554.7745, 1570.7627, 1576.7774, 1582.8187, 1597.8453,
      1600.5682, 1611.7977, 1619.8359, 1633.7985, 1639.8241, 1641.8427, 1657.0650, 1679.0464, 2004.9863, 2123.9740,
      2145.9803, 2202.1298, 2211.1003, 2224.1306, 2230.1580, 2246.0893, 2350.1988, 2451.2369, 3716.1966
```

Search Parameters

```
Type of search         : Peptide Mass Fingerprint
Enzyme                 : Trypsin
Variable modifications : Oxidation (M)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Peptide Charge State   : 1+
Max Missed Cleavages   : 1
Number of queries      : 55
Selected for scoring   : 35
```

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

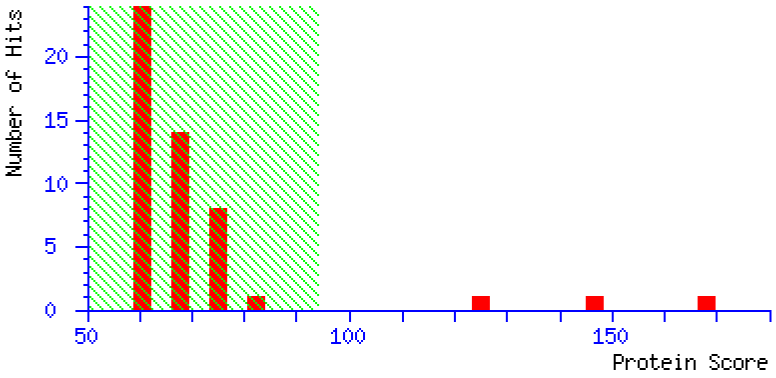
2. The protein band of approx. 24 kDa, obtained from the crude extract of *R. rhodochrous* M33 cells, grown on the medium with cobalt.

MATRIX SCIENCE Mascot Search Results

```
User           : toropygin
Email          : toropygin@rambler.ru
Search title   : 02
Database       : NCBIprot 20180429 (152462470 sequences; 55858910152 residues)
Timestamp      : 1 Sep 2018 at 16:28:39 GMT
Top Score      : 168 for WP_006940500.1, MULTISPECIES: nitrile hydratase subunit alpha [Rhodococcus]
```

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 94 are significant ($p<0.05$).



Protein Summary Report

Format As	Protein Summary ▾	Help
	Significance threshold p< 0.05	Max. number of hits 20
	Preferred taxonomy All entries ▾	

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-
-Accession- -Sequence-

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
☑ 889.5150 (1+)														●						
☑ 908.4816 (1+)																●				
☑ 931.4470 (1+)	●	●	●			●				●	●	●	●		●				●	
☑ 1012.6227 (1+)	●	●	●																	
☑ 1034.5371 (1+)						●				●		●								
☑ 1051.5204 (1+)	●	●	●	●	●	●		●	●	●		●			●		●	●		●
☑ 1060.5250 (1+)																	●			
☑ 1063.6041 (1+)					●															
☑ 1069.3880 (1+)																				
☑ 1073.5195 (1+)																	●			
☑ 1078.5660 (1+)	●	●	●	●	●	●		●	●	●	●	●	●		●		●	●	●	●
☑ 1089.4628 (1+)																				
☑ 1091.6424 (1+)											●									
☑ 1100.5534 (1+)						●				●	●	●					●			
☑ 1107.6693 (1+)	●	●			●						●								●	
☑ 1116.5044 (1+)																				
☑ 1129.6426 (1+)											●									
☑ 1135.6690 (1+)								●	●											
☑ 1145.5679 (1+)																				

☑ 1164.6447 (1+)																				
☑ 1179.6335 (1+)	●	●	●	●	●		●	●	●						●		●	●	●	●
☑ 1188.7314 (1+)					●											●	●		●	
☑ 1201.6313 (1+)				●	●		●							●		●	●			
☑ 1214.6924 (1+)																				
☑ 1217.6072 (1+)					●												●			
☑ 1239.5902 (1+)																	●			
☑ 1305.7046 (1+)																				
☑ 1438.0931 (1+)																				
☑ 1475.6807 (1+)															●					
☑ 1522.7371 (1+)																	●			
☑ 1537.7261 (1+)	●	●	●	●	●	●		●	●	●	●	●	●	●	●		●	●		●
☑ 1553.7615 (1+)				●										●				●		
☑ 1559.7352 (1+)																				
☑ 1565.7611 (1+)																				
☑ 1575.7735 (1+)						●				●		●								
☑ 1581.7207 (1+)																				
☑ 1625.7823 (1+)	●	●	●								●			●						●
☑ 1673.7665 (1+)															●					

☑ 1678.8700 (1+)																				
☑ 1693.8244 (1+)	●	●	●	●		●		●	●	●	●	●		●	●					●
☑ 1713.8084 (1+)	●	●	●				●							●		●	●			
☑ 1729.8158 (1+)	●	●	●											●	●	●	●		●	
☑ 1735.8188 (1+)				●	●		●				●		●			●	●	●		●
☑ 1751.7956 (1+)					●						●								●	●
☑ 1757.8117 (1+)																				
☑ 1772.8791 (1+)	●	●	●																	
☑ 1794.8996 (1+)																				
☑ 1810.8908 (1+)																				
☑ 2005.0171 (1+)																				
☑ 2211.0100 (1+)																				
☑ 2234.3806 (1+)																				
☑ 2327.9891 (1+)																				
☑ 2331.0385 (1+)						●				●		●								
☑ 2346.0194 (1+)	●			●		●				●	●	●			●	●				
☑ 2362.0439 (1+)				●		●	●			●		●		●						
☑ 2368.0227 (1+)											●		●				●			
☑ 2374.0601 (1+)						●				●		●								

☑	2378.0243 (1+)				●		●				●		●		●						
☑	2384.0056 (1+)																				
☑	2390.0201 (1+)																				
☑	2482.0317 (1+)				●									●					●		

Search Selected

Index

	Accession	Mass	Score	Description
1.	WP_006940500.1	22776	168	MULTISPECIES: nitrile hydratase subunit alpha [Rhodococcus]
2.	P21219.3	22820	147	RecName: Full=High-molecular weight cobalt-containing nitrile hydratase subunit alpha; Short=H-NHase; Short=H-nitrilase
3.	CAC83635.1	20309	128	nitrile hydratase alpha chain, partial [uncultured bacterium SP1]
4.	XP_022160284.1	56268	83	piggyBac transposable element-derived protein 4-like [Myzus persicae]
5.	WP_072352678.1	60211	74	peptide chain release factor 3 [Flavobacteriaceae bacterium A100]
6.	XP_014914961.1	53651	73	PREDICTED: zinc finger protein OZF-like [Poecilia latipinna]
7.	AUE22959.1	11083	73	hypothetical protein Cf1_00086 [Citrobacter phage CF1]
8.	KRZ52036.1	7760	73	hypothetical protein T02_6964 [Trichinella nativa]
9.	KRZ94483.1	7732	73	hypothetical protein T08_6364 [Trichinella sp. T8]
10.	XP_007540545.1	53847	72	PREDICTED: zinc finger protein OZF-like [Poecilia formosa]
11.	XP_012503418.1	100406	72	PREDICTED: zinc finger protein 252-like [Propithecus coquereli]

12	**XP_023206789.1**	53820	72	zinc finger protein OZF-like isoform X1 [Xiphophorus maculatus]
13	**XP_009635910.1**	27284	70	PREDICTED: calpain small subunit 2 [Egretta garzetta]
14	**WP_065353684.1**	21584	69	malonic semialdehyde reductase [Candidatus Thioglobus singularis]
15	**WP_073033850.1**	65303	68	hypothetical protein [Roseovarius pacificus]
16	**XP_001652380.1**	29108	68	cation-dependent mannose-6-phosphate receptor [Aedes aegypti]
17	**EEX28339.1**	153819	67	tape measure domain protein, partial [Lactobacillus crispatus MV-3A-US]
18	**WP_054693860.1**	28485	67	hypothetical protein [Syntrophomonas palmitatica]
19	**PIQ35028.1**	23072	67	YigZ family protein [Bacteroidetes bacterium CG18_big_fil_WC_8_21_14_2_50_41_14]
20	**ART89119.1**	29503	66	coat protein [Tomato leaf curl Joydebpur virus]

Results List

1. WP_006940500.1 **Mass:** 22776 **Score:** 168 **Expect:** 2.4e-09 **Matches:** 13

MULTISPECIES: nitrile hydratase subunit alpha [Rhodococcus]

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
931.4470	930.4398	930.4083	33.8	8 -	14	0	K.YTEYEAR.T
1012.6227	1011.6155	1011.5713	43.7	26 -	35	0	R.GLITPAAVDR.V
1051.5204	1050.5131	1050.4771	34.3	56 -	63	0	K.SWVDPEYR.K
1078.5660	1077.5587	1077.5091	46.1	153 -	161	0	R.VWDSSSEIR.Y
1107.6693	1106.6621	1106.5971	58.7	17 -	25	0	K.AIETLLYER.G
1179.6335	1178.6262	1178.5720	46.0	56 -	64	1	K.SWVDPEYRK.W
1537.7261	1536.7188	1536.7097	5.96	140 -	152	0	R.DFGFDIPDEVEVR.V
1625.7823	1624.7750	1624.7481	16.6	2 -	14	1	M.SEHVNKYTEYEAR.T
1693.8244	1692.8171	1692.8108	3.73	139 -	152	1	K.RDFGFDIPDEVEVR.V
1713.8084	1712.8011	1712.8080	-3.99	36 -	51	0	R.VVSYYENEIGPMGGAK.V
1729.8158	1728.8085	1728.8029	3.25	36 -	51	0	R.VVSYYENEIGPMGGAK.V + Oxidation (M)
1772.8791	1771.8719	1771.9026	-17.34	187 -	203	0	R.DSMIGVSNALTPQEVIV.-
2346.0194	2345.0122	2345.1539	-60.45	162 -	182	0	R.YIVIPERPAGTDGWSEDELAK.L

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No match to: 889.5150, 908.4816, 1034.5371, 1060.5250, 1063.6041, 1069.3880, 1073.5195, 1089.4628, 1091.6424,
1100.5534, 1116.5044, 1129.6426, 1135.6690, 1145.5679, 1164.6447, 1188.7314, 1201.6313, 1214.6924, 1217.6072,
1239.5902, 1305.7046, 1438.0931, 1475.6807, 1522.7371, 1553.7615, 1559.7352, 1565.7611, 1575.7735, 1581.7207,
1673.7665, 1678.8700, 1735.8188, 1751.7956, 1757.8117, 1794.8996, 1810.8908, 2005.0171, 2211.0100, 2234.3806,
2327.9891, 2331.0385, 2362.0439, 2368.0227, 2374.0601, 2378.0243, 2384.0056, 2390.0201, 2482.0317

2.     P21219.3    Mass: 22820    Score: 147    Expect: 3e-07  Matches: 12
       RecName: Full=High-molecular weight cobalt-containing nitrile hydratase subunit alpha; Short=H-NHase; Short=H-
       nitrilase
        Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
        931.4470    930.4398    930.4083    33.8      8 -   14    0   K.YTEYEAR.T
       1012.6227   1011.6155   1011.5713    43.7     26 -   35    0   R.GLITPAAVDR.V
       1051.5204   1050.5131   1050.4771    34.3     56 -   63    0   K.SWVDPEYR.K
       1078.5660   1077.5587   1077.5091    46.1    153 -  161    0   R.VWDSSSEIR.Y
       1107.6693   1106.6621   1106.5971    58.7     17 -   25    0   K.AIETLLYER.G
       1179.6335   1178.6262   1178.5720    46.0     56 -   64    1   K.SWVDPEYRK.W
       1537.7261   1536.7188   1536.7097    5.96    140 -  152    0   R.DFGFDIPDEVEVR.V
       1625.7823   1624.7750   1624.7481    16.6      2 -   14    1   M.SEHVNKYTEYEAR.T
       1693.8244   1692.8171   1692.8108    3.73    139 -  152    1   K.RDFGFDIPDEVEVR.V
       1713.8084   1712.8011   1712.8080   -3.99     36 -   51    0   R.VVSYYENEIGPMGGAK.V
       1729.8158   1728.8085   1728.8029    3.25     36 -   51    0   R.VVSYYENEIGPMGGAK.V + Oxidation (M)
       1772.8791   1771.8719   1771.9026  -17.34    187 -  203    0   R.DSMIGVSNALTPQEVIV.-
       No match to: 889.5150, 908.4816, 1034.5371, 1060.5250, 1063.6041, 1069.3880, 1073.5195, 1089.4628, 1091.6424,
       1100.5534, 1116.5044, 1129.6426, 1135.6690, 1145.5679, 1164.6447, 1188.7314, 1201.6313, 1214.6924, 1217.6072,
       1239.5902, 1305.7046, 1438.0931, 1475.6807, 1522.7371, 1553.7615, 1559.7352, 1565.7611, 1575.7735, 1581.7207,
       1673.7665, 1678.8700, 1735.8188, 1751.7956, 1757.8117, 1794.8996, 1810.8908, 2005.0171, 2211.0100, 2234.3806,
       2327.9891, 2331.0385, 2346.0194, 2362.0439, 2368.0227, 2374.0601, 2378.0243, 2384.0056, 2390.0201, 2482.0317

3.     CAC83635.1    Mass: 20309    Score: 128    Expect: 2.4e-05  Matches: 11
       nitrile hydratase alpha chain, partial [uncultured bacterium SP1]
        Observed    Mr(expt)    Mr(calc)   ppm  Start    End Miss   Peptide
        931.4470    930.4398    930.4083  33.8      8 -   14    0   K.YTEYEAR.T
       1012.6227   1011.6155   1011.5713  43.7     26 -   35    0   R.GLITPAAVDR.V
       1051.5204   1050.5131   1050.4771  34.3     56 -   63    0   K.SWVDPEYR.K
       1078.5660   1077.5587   1077.5091  46.1    141 -  149    0   R.VWDSSSEIR.Y
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1179.6335  1178.6262  1178.5720   46.0    56 -  64   1   K.SWVDPEYRK.W
1537.7261  1536.7188  1536.7097   5.96   128 - 140   0   R.DFGFDIPDEVEVR.V
1625.7823  1624.7750  1624.7481   16.6     2 -  14   1   M.SEHVNKYTEYEAR.T
1693.8244  1692.8171  1692.8108   3.73   127 - 140   1   K.RDFGFDIPDEVEVR.V
1713.8084  1712.8011  1712.8080  -3.99    36 -  51   0   R.VVSYYENEIGPMGGAK.V
1729.8158  1728.8085  1728.8029   3.25    36 -  51   0   R.VVSYYENEIGPMGGAK.V + Oxidation (M)
1772.8791  1771.8719  1771.7835   49.9     1 -  14   1   -.MSEHVNKYTEYEAR.T + Oxidation (M)
 No match to: 889.5150, 908.4816, 1034.5371, 1060.5250, 1063.6041, 1069.3880, 1073.5195, 1089.4628, 1091.6424,
 1100.5534, 1107.6693, 1116.5044, 1129.6426, 1135.6690, 1145.5679, 1164.6447, 1188.7314, 1201.6313, 1214.6924,
 1217.6072, 1239.5902, 1305.7046, 1438.0931, 1475.6807, 1522.7371, 1553.7615, 1559.7352, 1565.7611, 1575.7735,
 1581.7207, 1673.7665, 1678.8700, 1735.8188, 1751.7956, 1757.8117, 1794.8996, 1810.8908, 2005.0171, 2211.0100,
 2234.3806, 2327.9891, 2331.0385, 2346.0194, 2362.0439, 2368.0227, 2374.0601, 2378.0243, 2384.0056, 2390.0201,
 2482.0317

4.   XP_022160284.1     Mass: 56268     Score: 83     Expect: 0.7  Matches: 12
     piggyBac transposable element-derived protein 4-like [Myzus persicae]
 Observed    Mr(expt)    Mr(calc)     ppm   Start    End Miss   Peptide
1051.5204  1050.5131  1050.5386  -24.28     50 -  58    0   K.GPVDPYLYK.K
1078.5660  1077.5587  1077.5666   -7.33    431 - 441    1   K.DSTGSVKISGK.H
1179.6335  1178.6262  1178.6335   -6.20     50 -  59    1   K.GPVDPYLYKK.S
1201.6313  1200.6240  1200.6979  -61.52    442 - 451    1   K.HLAIKISTYR.R
1537.7261  1536.7188  1536.7606  -27.20    189 - 202    0   K.QLAIDESMVAFTGR.S
1553.7615  1552.7542  1552.7555   -0.87    189 - 202    0   K.QLAIDESMVAFTGR.S + Oxidation (M)
1693.8244  1692.8171  1692.7941    13.6      3 -  17    0   K.LLESEDSDIDELSTK.E
1735.8188  1734.8116  1734.7096    58.8    118 - 130    0   R.SYWSNDPNFFCER.V + Propionamide (C)
2346.0194  2345.0122  2345.0456  -14.28    341 - 360    1   R.YMGAVDRFDQYMSAYSVSQK.S
2362.0439  2361.0367  2361.0406   -1.65    341 - 360    1   R.YMGAVDRFDQYMSAYSVSQK.S + Oxidation (M)
2378.0243  2377.0170  2377.0355   -7.77    341 - 360    1   R.YMGAVDRFDQYMSAYSVSQK.S + 2 Oxidation (M)
2482.0317  2481.0245  2481.1859  -65.07    146 - 165    1   R.FLHLNDNLQMPPRNTEHFDK.L + Oxidation (M)
 No match to: 889.5150, 908.4816, 931.4470, 1012.6227, 1034.5371, 1060.5250, 1063.6041, 1069.3880, 1073.5195,
 1089.4628, 1091.6424, 1100.5534, 1107.6693, 1116.5044, 1129.6426, 1135.6690, 1145.5679, 1164.6447, 1188.7314,
 1214.6924, 1217.6072, 1239.5902, 1305.7046, 1438.0931, 1475.6807, 1522.7371, 1559.7352, 1565.7611, 1575.7735,
 1581.7207, 1625.7823, 1673.7665, 1678.8700, 1713.8084, 1729.8158, 1751.7956, 1757.8117, 1772.8791, 1794.8996,
 1810.8908, 2005.0171, 2211.0100, 2234.3806, 2327.9891, 2331.0385, 2368.0227, 2374.0601, 2384.0056, 2390.0201
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5.   WP_072352678.1    Mass: 60211    Score: 74    Expect: 5.7  Matches: 11
     peptide chain release factor 3 [Flavobacteriaceae bacterium A100]
      Observed   Mr(expt)   Mr(calc)    ppm  Start   End Miss  Peptide
     1051.5204  1050.5131  1050.5345  -20.43   187 - 195   0   K.INLFSSENK.Q
     1063.6041  1062.5969  1062.5631    31.8     1 -   9   0   -.MSLITELEK.R
     1078.5660  1077.5587  1077.5971  -35.62   178 - 186   1   K.GIYNIWGKK.I
     1107.6693  1106.6621  1106.6084    48.5    81 -  90   0   K.INILDTPGHK.D
     1179.6335  1178.6262  1178.6295   -2.76   186 - 195   1   K.KINLFSSENK.Q
     1188.7314  1187.7241  1187.6736    42.5   131 - 140   0   R.NIPMIVFINK.L
     1201.6313  1200.6240  1200.5849    32.6   290 - 299   1   K.EDKMTGFVFK.I
     1217.6072  1216.5999  1216.5798    16.5   290 - 299   1   K.EDKMTGFVFK.I + Oxidation (M)
     1537.7261  1536.7188  1536.7420  -15.09   372 - 385   0   K.IGDTLTEGESVNFR.G
     1735.8188  1734.8116  1734.8312  -11.32   144 - 158   1   R.EGKDAFDLLDEVEQK.L
     1751.7956  1750.7883  1750.8535  -37.24   293 - 307   1   K.MTGFVFKIHANMDPK.H + Oxidation (M)
     No match to: 889.5150, 908.4816, 931.4470, 1012.6227, 1034.5371, 1060.5250, 1069.3880, 1073.5195, 1089.4628,
     1091.6424, 1100.5534, 1116.5044, 1129.6426, 1135.6690, 1145.5679, 1164.6447, 1214.6924, 1239.5902, 1305.7046,
     1438.0931, 1475.6807, 1522.7371, 1553.7615, 1559.7352, 1565.7611, 1575.7735, 1581.7207, 1625.7823, 1673.7665,
     1678.8700, 1693.8244, 1713.8084, 1729.8158, 1757.8117, 1772.8791, 1794.8996, 1810.8908, 2005.0171, 2211.0100,
     2234.3806, 2327.9891, 2331.0385, 2346.0194, 2362.0439, 2368.0227, 2374.0601, 2378.0243, 2384.0056, 2390.0201,
     2482.0317
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6.   XP_014914961.1    Mass: 53651    Score: 73    Expect: 7.3  Matches: 13
     PREDICTED: zinc finger protein OZF-like [Poecilia latipinna]
      Observed   Mr(expt)   Mr(calc)    ppm  Start   End Miss  Peptide
      931.4470   930.4398   930.4406   -0.95    10 -  17   0   R.LDAAEEQR.H
     1034.5371  1033.5299  1033.4974    31.4   221 - 228   1   R.SLNCNEKR.K + Propionamide (C)
     1051.5204  1050.5131  1050.5393  -24.93   212 - 220   0   R.HMTGHSIIR.S
     1078.5660  1077.5587  1077.6295  -65.68   462 - 471   1   R.VHVEGRGVLL.-
     1100.5534  1099.5461  1099.5887  -38.67   310 - 318   1   R.FSQKAHLNR.H
     1537.7261  1536.7188  1536.6176    65.9   126 - 140   0   K.AESDEEDGEVAGSSR.R
     1575.7735  1574.7662  1574.6705    60.8   193 - 206   0   K.TLSCSECSNQFASK.R + Propionamide (C)
     1693.8244  1692.8171  1692.7422    44.2   294 - 308   0   R.IHTGDKPFCCDVCGK.R + Propionamide (C)
     2331.0385  2330.0312  2330.0759  -19.15   406 - 425   1   R.THTGMKPFACEVCGQRFGYK.S + Propionamide (C)
     2346.0194  2345.0122  2345.0650  -22.52   262 - 281   1   K.IHMRIHTGEKPFCCDVCGQR.F + Oxidation (M)
     2362.0439  2361.0367  2361.0929  -23.82   430 - 449   1   K.IHMRLHTGEKPFSCDFCGQR.F
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2374.0601  2373.0528  2373.1107  -24.38   378 - 397   1   R.LHSGEKPFGCDVCGQRFSHK.E + 2 Propionamide (C)
2378.0243  2377.0170  2377.0878  -29.78   430 - 449   1   K.IHMRLHTGEKPFSCDFCGQR.F + Oxidation (M)
No match to: 889.5150, 908.4816, 1012.6227, 1060.5250, 1063.6041, 1069.3880, 1073.5195, 1089.4628, 1091.6424,
1107.6693, 1116.5044, 1129.6426, 1135.6690, 1145.5679, 1164.6447, 1179.6335, 1188.7314, 1201.6313, 1214.6924,
1217.6072, 1239.5902, 1305.7046, 1438.0931, 1475.6807, 1522.7371, 1553.7615, 1559.7352, 1565.7611, 1581.7207,
1625.7823, 1673.7665, 1678.8700, 1713.8084, 1729.8158, 1735.8188, 1751.7956, 1757.8117, 1772.8791, 1794.8996,
1810.8908, 2005.0171, 2211.0100, 2234.3806, 2327.9891, 2368.0227, 2384.0056, 2390.0201, 2482.0317

7.    AUE22959.1     Mass: 11083     Score: 73     Expect: 8  Matches: 5
      hypothetical protein Cf1_00086 [Citrobacter phage CF1]
 Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
1179.6335  1178.6262  1178.5932    28.1    38 -  48    0   K.GIDFSVDAVTR.E
1201.6313  1200.6240  1200.5485    62.9    29 -  37    0   R.ICFQYAEEK.G + Propionamide (C)
1713.8084  1712.8011  1712.8192  -10.53    24 -  37    1   R.EINARICFQYAEEK.G
1735.8188  1734.8116  1734.8247   -7.55     2 -  16    0   M.NPFKPTNIAQSDEMK.A + Oxidation (M)
2362.0439  2361.0367  2361.1311  -39.99    29 -  48    1   R.ICFQYAEEKGIDFSVDAVTR.E + Propionamide (C)
No match to: 889.5150, 908.4816, 931.4470, 1012.6227, 1034.5371, 1051.5204, 1060.5250, 1063.6041, 1069.3880,
1073.5195, 1078.5660, 1089.4628, 1091.6424, 1100.5534, 1107.6693, 1116.5044, 1129.6426, 1135.6690, 1145.5679,
1164.6447, 1188.7314, 1214.6924, 1217.6072, 1239.5902, 1305.7046, 1438.0931, 1475.6807, 1522.7371, 1537.7261,
1553.7615, 1559.7352, 1565.7611, 1575.7735, 1581.7207, 1625.7823, 1673.7665, 1678.8700, 1693.8244, 1729.8158,
1751.7956, 1757.8117, 1772.8791, 1794.8996, 1810.8908, 2005.0171, 2211.0100, 2234.3806, 2327.9891, 2331.0385,
2346.0194, 2368.0227, 2374.0601, 2378.0243, 2384.0056, 2390.0201, 2482.0317

8.    KRZ52036.1     Mass: 7760      Score: 73     Expect: 8.2  Matches: 6
      hypothetical protein T02_6964 [Trichinella nativa]
 Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
1051.5204  1050.5131  1050.5280  -14.23    51 -  58    0   K.HIQLHMEK.K + Oxidation (M)
1078.5660  1077.5587  1077.5892  -28.35    60 -  68    0   K.QVATICFIL.- + Propionamide (C)
1135.6690  1134.6617  1134.6471    12.9    59 -  68    1   K.KQVATICFIL.-
1179.6335  1178.6262  1178.6230    2.76    51 -  59    1   K.HIQLHMEKK.Q + Oxidation (M)
1537.7261  1536.7188  1536.7831  -41.84    26 -  39    0   K.VMHHTNVGISGTIR.R + Oxidation (M)
1693.8244  1692.8171  1692.8842  -39.66    26 -  40    1   K.VMHHTNVGISGTIRR.N + Oxidation (M)
No match to: 889.5150, 908.4816, 931.4470, 1012.6227, 1034.5371, 1060.5250, 1063.6041, 1069.3880, 1073.5195,
1089.4628, 1091.6424, 1100.5534, 1107.6693, 1116.5044, 1129.6426, 1145.5679, 1164.6447, 1188.7314, 1201.6313,
1214.6924, 1217.6072, 1239.5902, 1305.7046, 1438.0931, 1475.6807, 1522.7371, 1553.7615, 1559.7352, 1565.7611,
1575.7735, 1581.7207, 1625.7823, 1673.7665, 1678.8700, 1713.8084, 1729.8158, 1735.8188, 1751.7956, 1757.8117,
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       1772.8791, 1794.8996, 1810.8908, 2005.0171, 2211.0100, 2234.3806, 2327.9891, 2331.0385, 2346.0194, 2362.0439,
       2368.0227, 2374.0601, 2378.0243, 2384.0056, 2390.0201, 2482.0317

9.     KRZ94483.1     Mass: 7732      Score: 73      Expect: 8.2  Matches: 6
       hypothetical protein T08_6364 [Trichinella sp. T8]
        Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
       1051.5204   1050.5131   1050.5280  -14.23     51 -   58    0   K.HIQLHMEK.K + Oxidation (M)
       1078.5660   1077.5587   1077.5892  -28.35     60 -   68    0   K.QVATICFIL.- + Propionamide (C)
       1135.6690   1134.6617   1134.6471    12.9     59 -   68    1   K.KQVATICFIL.-
       1179.6335   1178.6262   1178.6230    2.76     51 -   59    1   K.HIQLHMEKK.Q + Oxidation (M)
       1537.7261   1536.7188   1536.7831  -41.84     26 -   39    0   K.VMHHTNVGISGTIR.R + Oxidation (M)
       1693.8244   1692.8171   1692.8842  -39.66     26 -   40    1   K.VMHHTNVGISGTIRR.N + Oxidation (M)
       No match to: 889.5150, 908.4816, 931.4470, 1012.6227, 1034.5371, 1060.5250, 1063.6041, 1069.3880, 1073.5195,
       1089.4628, 1091.6424, 1100.5534, 1107.6693, 1116.5044, 1129.6426, 1145.5679, 1164.6447, 1188.7314, 1201.6313,
       1214.6924, 1217.6072, 1239.5902, 1305.7046, 1438.0931, 1475.6807, 1522.7371, 1553.7615, 1559.7352, 1565.7611,
       1575.7735, 1581.7207, 1625.7823, 1673.7665, 1678.8700, 1713.8084, 1729.8158, 1735.8188, 1751.7956, 1757.8117,
       1772.8791, 1794.8996, 1810.8908, 2005.0171, 2211.0100, 2234.3806, 2327.9891, 2331.0385, 2346.0194, 2362.0439,
       2368.0227, 2374.0601, 2378.0243, 2384.0056, 2390.0201, 2482.0317

10.    XP_007540545.1     Mass: 53847     Score: 72      Expect: 9.8  Matches: 13
       PREDICTED: zinc finger protein OZF-like [Poecilia formosa]
        Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
        931.4470    930.4398    930.4406   -0.95     10 -   17    0   R.LDAAEEQR.H
       1034.5371   1033.5299   1033.4974    31.4    222 -  229    1   R.SLNCNEKR.K + Propionamide (C)
       1051.5204   1050.5131   1050.5393  -24.93    213 -  221    0   R.HMTGHSIIR.S
       1078.5660   1077.5587   1077.6295  -65.68    463 -  472    1   R.VHVEGRGVLL.-
       1100.5534   1099.5461   1099.5887  -38.67    311 -  319    1   R.FSQKAHLNR.H
       1537.7261   1536.7188   1536.6176    65.9    127 -  141    0   K.AESDEEDGEVAGSSR.R
       1575.7735   1574.7662   1574.6705    60.8    194 -  207    0   K.TLSCSECSNQFASK.R + Propionamide (C)
       1693.8244   1692.8171   1692.7422    44.2    295 -  309    0   R.IHTGDKPFCCDVCGK.R + Propionamide (C)
       2331.0385   2330.0312   2330.0759  -19.15    407 -  426    1   R.THTGMKPFACEVCGQRFGYK.S + Propionamide (C)
       2346.0194   2345.0122   2345.0650  -22.52    263 -  282    1   K.IHMRIHTGEKPFCCDVCGQR.F + Oxidation (M)
       2362.0439   2361.0367   2361.0929  -23.82    431 -  450    1   K.IHMRLHTGEKPFSCDFCGQR.F
       2374.0601   2373.0528   2373.1107  -24.38    379 -  398    1   R.LHSGEKPFGCDVCGQRFSHK.E + 2 Propionamide (C)
       2378.0243   2377.0170   2377.0878  -29.78    431 -  450    1   K.IHMRLHTGEKPFSCDFCGQR.F + Oxidation (M)
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        No match to: 889.5150, 908.4816, 1012.6227, 1060.5250, 1063.6041, 1069.3880, 1073.5195, 1089.4628, 1091.6424,
        1107.6693, 1116.5044, 1129.6426, 1135.6690, 1145.5679, 1164.6447, 1179.6335, 1188.7314, 1201.6313, 1214.6924,
        1217.6072, 1239.5902, 1305.7046, 1438.0931, 1475.6807, 1522.7371, 1553.7615, 1559.7352, 1565.7611, 1581.7207,
        1625.7823, 1673.7665, 1678.8700, 1713.8084, 1729.8158, 1735.8188, 1751.7956, 1757.8117, 1772.8791, 1794.8996,
        1810.8908, 2005.0171, 2211.0100, 2234.3806, 2327.9891, 2368.0227, 2384.0056, 2390.0201, 2482.0317

    11. XP_012503418.1    Mass: 100406   Score: 72     Expect: 10  Matches: 13
        PREDICTED: zinc finger protein 252-like [Propithecus coquereli]
         Observed    Mr(expt)    Mr(calc)    ppm   Start   End Miss   Peptide
         931.4470    930.4398    930.4817  -45.11    271 - 277   1    R.QNRALCR.H + Propionamide (C)
        1078.5660   1077.5587   1077.4839    69.4     87 -  95   1    R.HKSEGYDSR.I
        1091.6424   1090.6351   1090.5996    32.6    300 - 308   1    R.HSVLSKHQR.I
        1100.5534   1099.5461   1099.5774  -28.46    477 - 485   0    R.IHTGEKPYR.C
        1107.6693   1106.6621   1106.6336    25.8    660 - 669   0    K.TFGQISTLIK.H
        1129.6426   1128.6353   1128.6040    27.8    688 - 697   0    K.AFSQSAHLIR.H
        1537.7261   1536.7188   1536.8049  -55.98    352 - 364   1    K.AFSTRSSYIQHLK.I
        1625.7823   1624.7750   1624.7151    36.9    179 - 193   0    K.FIVGENCSTDSNPSR.H
        1693.8244   1692.8171   1692.7348    48.6    819 - 832   1    R.SYTCNQCGKTFSQR.I + Propionamide (C)
        1735.8188   1734.8116   1734.7705    23.7    785 - 799   0    R.IHTGEKPYECAECGK.S + Propionamide (C)
        1751.7956   1750.7883   1750.7879    0.21    365 - 379   0    K.IHTGEKPHECNQCGK.A + Propionamide (C)
        2346.0194   2345.0122   2345.0238   -4.98    757 - 776   1    R.IHTGEKPYMCNECEKSFSAR.L + Oxidation (M)
        2368.0227   2367.0154   2367.1100  -39.95    505 - 524   1    R.IHTGEKPYVCNECGKSFSAR.L + 2 Propionamide (C)
        No match to: 889.5150, 908.4816, 1012.6227, 1034.5371, 1051.5204, 1060.5250, 1063.6041, 1069.3880, 1073.5195,
        1089.4628, 1116.5044, 1135.6690, 1145.5679, 1164.6447, 1179.6335, 1188.7314, 1201.6313, 1214.6924, 1217.6072,
        1239.5902, 1305.7046, 1438.0931, 1475.6807, 1522.7371, 1553.7615, 1559.7352, 1565.7611, 1575.7735, 1581.7207,
        1673.7665, 1678.8700, 1713.8084, 1729.8158, 1757.8117, 1772.8791, 1794.8996, 1810.8908, 2005.0171, 2211.0100,
        2234.3806, 2327.9891, 2331.0385, 2362.0439, 2374.0601, 2378.0243, 2384.0056, 2390.0201, 2482.0317

    12. XP_023206789.1    Mass: 53820    Score: 72     Expect: 11  Matches: 13
        zinc finger protein OZF-like isoform X1 [Xiphophorus maculatus]
         Observed    Mr(expt)    Mr(calc)    ppm   Start   End Miss   Peptide
         931.4470    930.4398    930.4406   -0.95     10 -  17   0    R.LDAAEEQR.H
        1034.5371   1033.5299   1033.4974    31.4    221 - 228   1    R.SLNCNEKR.K + Propionamide (C)
        1051.5204   1050.5131   1050.5393  -24.93    212 - 220   0    R.HMTGHSIIR.S
        1078.5660   1077.5587   1077.6295  -65.68    462 - 471   1    R.VHVEGRGVLL.-
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     1100.5534  1099.5461  1099.5887  -38.67   310 - 318   1   R.FSQKAHLNR.H
     1537.7261  1536.7188  1536.6176    65.9   126 - 140   0   K.AESDEEDGEVAGSSR.R
     1575.7735  1574.7662  1574.6705    60.8   193 - 206   0   K.TLSCSECSNQFASK.R + Propionamide (C)
     1693.8244  1692.8171  1692.7422    44.2   294 - 308   0   R.IHTGDKPFCCDVCGK.R + Propionamide (C)
     2331.0385  2330.0312  2330.0759  -19.15   406 - 425   1   R.THTGMKPFACEVCGQRFGYK.S + Propionamide (C)
     2346.0194  2345.0122  2345.0650  -22.52   262 - 281   1   K.IHMRIHTGEKPFCCDVCGQR.F + Oxidation (M)
     2362.0439  2361.0367  2361.0929  -23.82   430 - 449   1   K.IHMRLHTGEKPFSCDFCGQR.F
     2374.0601  2373.0528  2373.1107  -24.38   378 - 397   1   R.LHSGEKPFGCDVCGQRFSHK.E + 2 Propionamide (C)
     2378.0243  2377.0170  2377.0878  -29.78   430 - 449   1   K.IHMRLHTGEKPFSCDFCGQR.F + Oxidation (M)
     No match to: 889.5150, 908.4816, 1012.6227, 1060.5250, 1063.6041, 1069.3880, 1073.5195, 1089.4628, 1091.6424,
     1107.6693, 1116.5044, 1129.6426, 1135.6690, 1145.5679, 1164.6447, 1179.6335, 1188.7314, 1201.6313, 1214.6924,
     1217.6072, 1239.5902, 1305.7046, 1438.0931, 1475.6807, 1522.7371, 1553.7615, 1559.7352, 1565.7611, 1581.7207,
     1625.7823, 1673.7665, 1678.8700, 1713.8084, 1729.8158, 1735.8188, 1751.7956, 1757.8117, 1772.8791, 1794.8996,
     1810.8908, 2005.0171, 2211.0100, 2234.3806, 2327.9891, 2368.0227, 2384.0056, 2390.0201, 2482.0317

13.  XP_009635910.1     Mass: 27284    Score: 70     Expect: 16  Matches: 6
     PREDICTED: calpain small subunit 2 [Egretta garzetta]
      Observed   Mr(expt)   Mr(calc)     ppm  Start    End Miss   Peptide
      931.4470   930.4398   930.4883  -52.16     6 -  16   0   K.ALLSGGSGGGR.G
     1078.5660  1077.5587  1077.5971  -35.61   146 - 153   1   K.YLWNNIKK.W
     1537.7261  1536.7188  1536.8082  -58.19     1 -  16   1   -.MFLAKALLSGGSGGGR.G + Oxidation (M)
     1735.8188  1734.8116  1734.7995    6.93   111 - 125   1   R.HQDLKTDGFSLDTCR.S
     2368.0227  2367.0154  2367.0260   -4.47   196 - 215   1   R.RYADEDGSMDFNNFISCLVR.L + Oxidation (M)
     2482.0317  2481.0245  2481.0458   -8.61   116 - 138   1   K.TDGFSLDTCRSMVAVMDSDTNGK.L + 2 Oxidation (M)
     No match to: 889.5150, 908.4816, 1012.6227, 1034.5371, 1051.5204, 1060.5250, 1063.6041, 1069.3880, 1073.5195,
     1089.4628, 1091.6424, 1100.5534, 1107.6693, 1116.5044, 1129.6426, 1135.6690, 1145.5679, 1164.6447, 1179.6335,
     1188.7314, 1201.6313, 1214.6924, 1217.6072, 1239.5902, 1305.7046, 1438.0931, 1475.6807, 1522.7371, 1553.7615,
     1559.7352, 1565.7611, 1575.7735, 1581.7207, 1625.7823, 1673.7665, 1678.8700, 1693.8244, 1713.8084, 1729.8158,
     1751.7956, 1757.8117, 1772.8791, 1794.8996, 1810.8908, 2005.0171, 2211.0100, 2234.3806, 2327.9891, 2331.0385,
     2346.0194, 2362.0439, 2374.0601, 2378.0243, 2384.0056, 2390.0201

14.  WP_065353684.1     Mass: 21584    Score: 69     Expect: 18  Matches: 10
     malonic semialdehyde reductase [Candidatus Thioglobus singularis]
      Observed   Mr(expt)   Mr(calc)     ppm  Start    End Miss   Peptide
      889.5150   888.5078   888.4929    16.7   177 - 183   1   K.LYNRAPR.L
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      1201.6313  1200.6240  1200.6026    17.8    51 -  60   1   R.FTFVKSEESK.Q
      1537.7261  1536.7188  1536.7395  -13.46   163 - 176   0   K.AVFICGIGYGDHSK.L + Propionamide (C)
      1553.7615  1552.7542  1552.8097  -35.73     2 -  15   1   M.LSTDSTDILFSKAR.S
      1625.7823  1624.7750  1624.8204  -27.97    75 -  89   0   K.VMSAPCVVIISYDTK.F
      1693.8244  1692.8171  1692.8359  -11.11    90 - 104   0   K.FYESLSILSPHSDAK.S
      1713.8084  1712.8011  1712.7684    19.1   135 - 150   1   R.SAGLDCCPMLGFSKER.L
      1729.8158  1728.8085  1728.7633    26.1   135 - 150   1   R.SAGLDCCPMLGFSKER.L + Oxidation (M)
      2362.0439  2361.0367  2361.1787  -60.15   114 - 134   1   K.IKNTAEFNSSLQGAYFIMATR.S
      2378.0243  2377.0170  2377.1736  -65.87   114 - 134   1   K.IKNTAEFNSSLQGAYFIMATR.S + Oxidation (M)
      No match to: 908.4816, 931.4470, 1012.6227, 1034.5371, 1051.5204, 1060.5250, 1063.6041, 1069.3880, 1073.5195,
      1078.5660, 1089.4628, 1091.6424, 1100.5534, 1107.6693, 1116.5044, 1129.6426, 1135.6690, 1145.5679, 1164.6447,
      1179.6335, 1188.7314, 1214.6924, 1217.6072, 1239.5902, 1305.7046, 1438.0931, 1475.6807, 1522.7371, 1559.7352,
      1565.7611, 1575.7735, 1581.7207, 1673.7665, 1678.8700, 1735.8188, 1751.7956, 1757.8117, 1772.8791, 1794.8996,
      1810.8908, 2005.0171, 2211.0100, 2234.3806, 2327.9891, 2331.0385, 2346.0194, 2368.0227, 2374.0601, 2384.0056,
      2390.0201, 2482.0317

15.   WP_073033850.1    Mass: 65303    Score: 68     Expect: 23  Matches: 10
      hypothetical protein [Roseovarius pacificus]
       Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
       931.4470   930.4398   930.4957  -60.08   543 - 550   0   R.CATPLSIR.Y + Propionamide (C)
      1051.5204  1050.5131  1050.5532  -38.18    54 -  62   0   R.MSFADLIVR.K
      1078.5660  1077.5587  1077.5131    42.3   103 - 111   0   R.AYPWDGIEK.V
      1179.6335  1178.6262  1178.6481  -18.58    54 -  63   1   R.MSFADLIVRK.M
      1475.6807  1474.6734  1474.7569  -56.58    90 - 102   0   R.IETPGHAFTYIAR.A
      1537.7261  1536.7188  1536.7990  -52.19   280 - 291   0   R.WPHWVATWVTVR.E
      1673.7665  1672.7592  1672.7847  -15.25    30 -  42   0   R.VCALMRPEHEVMR.V + 2 Oxidation (M); Propionamide (C)
      1693.8244  1692.8171  1692.9345  -69.36   405 - 420   1   R.VADPAMPVGDLRAILR.R
      1729.8158  1728.8085  1728.8543  -26.52   167 - 182   1   R.SSRHFDAVVDALAEGR.Q
      2346.0194  2345.0122  2345.0892  -32.87    64 -  85   1   K.MAGENWRIVLLSSACDHDGAGK.F + Oxidation (M)
      No match to: 889.5150, 908.4816, 1012.6227, 1034.5371, 1060.5250, 1063.6041, 1069.3880, 1073.5195, 1089.4628,
      1091.6424, 1100.5534, 1107.6693, 1116.5044, 1129.6426, 1135.6690, 1145.5679, 1164.6447, 1188.7314, 1201.6313,
      1214.6924, 1217.6072, 1239.5902, 1305.7046, 1438.0931, 1522.7371, 1553.7615, 1559.7352, 1565.7611, 1575.7735,
      1581.7207, 1625.7823, 1678.8700, 1713.8084, 1735.8188, 1751.7956, 1757.8117, 1772.8791, 1794.8996, 1810.8908,
      2005.0171, 2211.0100, 2234.3806, 2327.9891, 2331.0385, 2362.0439, 2368.0227, 2374.0601, 2378.0243, 2384.0056,
      2390.0201, 2482.0317
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16. XP_001652380.1 **Mass:** 29108 **Score:** 68 **Expect:** 26 **Matches:** 7

cation-dependent mannose-6-phosphate receptor [Aedes aegypti]

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Peptide
908.4816	907.4743	907.4334	45.1	242	-	248	0	R.FLQNGCR.V + Propionamide (C)
1188.7314	1187.7241	1187.6948	24.7	136	-	145	0	K.VTSIQLLCLK.H + Propionamide (C)
1201.6313	1200.6240	1200.5411	69.1	100	-	109	0	R.FNNASQTYEK.L
1713.8084	1712.8011	1712.8733	-42.15	100	-	114	1	R.FNNASQTYEKLGTIK.D
1729.8158	1728.8085	1728.8512	-24.68	23	-	38	1	R.LAAAASGQCRQLNPCR.C + Propionamide (C)
1735.8188	1734.8116	1734.8424	-17.79	56	-	70	1	K.VENYLNTADPKTQDK.Y
2346.0194	2345.0122	2345.0747	-26.65	115	-	135	1	K.DSSFHTDGGGQQFLVYKMNAK.V + Oxidation (M)

No match to: 889.5150, 931.4470, 1012.6227, 1034.5371, 1051.5204, 1060.5250, 1063.6041, 1069.3880, 1073.5195, 1078.5660, 1089.4628, 1091.6424, 1100.5534, 1107.6693, 1116.5044, 1129.6426, 1135.6690, 1145.5679, 1164.6447, 1179.6335, 1214.6924, 1217.6072, 1239.5902, 1305.7046, 1438.0931, 1475.6807, 1522.7371, 1537.7261, 1553.7615, 1559.7352, 1565.7611, 1575.7735, 1581.7207, 1625.7823, 1673.7665, 1678.8700, 1693.8244, 1751.7956, 1757.8117, 1772.8791, 1794.8996, 1810.8908, 2005.0171, 2211.0100, 2234.3806, 2327.9891, 2331.0385, 2362.0439, 2368.0227, 2374.0601, 2378.0243, 2384.0056, 2390.0201, 2482.0317

17. EEX28339.1 **Mass:** 153819 **Score:** 67 **Expect:** 30 **Matches:** 16

tape measure domain protein, partial [Lactobacillus crispatus MV-3A-US]

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Peptide
1051.5204	1050.5131	1050.5015	11.0	424	-	433	1	R.GAGMSEDKLK.S + Oxidation (M)
1060.5250	1059.5177	1059.5600	-39.91	133	-	141	1	R.AKSSLTYYK.S
1073.5195	1072.5122	1072.4794	30.6	316	-	324	1	R.FKGMGMNTR.Q + 2 Oxidation (M)
1078.5660	1077.5587	1077.5050	49.8	1308	-	1317	1	K.NDSATASERK.R
1100.5534	1099.5461	1099.5622	-14.60	1166	-	1176	0	K.GLQDAAGNVQK.F
1179.6335	1178.6262	1178.6659	-33.67	1008	-	1018	1	K.QITSGIGKTFK.K
1188.7314	1187.7241	1187.6874	31.0	1078	-	1088	1	K.TLGQTAKTQLK.I
1201.6313	1200.6240	1200.6615	-31.24	567	-	577	1	K.SFGLIHGNTKK.T
1217.6072	1216.5999	1216.6411	-33.92	123	-	132	1	R.LESLTKQQDR.A
1239.5902	1238.5830	1238.5437	31.7	666	-	674	0	K.IHMWNMHDR.I
1522.7371	1521.7298	1521.7616	-20.88	1147	-	1158	1	K.NFWDDLWKGITK.T
1537.7261	1536.7188	1536.7858	-43.56	482	-	494	0	K.LEQTMTKPLFDAK.T + Oxidation (M)
1713.8084	1712.8011	1712.8668	-38.37	463	-	478	1	K.GFSSTQGGALKFMQVR.W
1729.8158	1728.8085	1728.8618	-30.81	463	-	478	1	K.GFSSTQGGALKFMQVR.W + Oxidation (M)

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1735.8188  1734.8116  1734.9152  -59.73   513 -  530   0   K.GAAAIGNALSTTIGYIDK.H
2368.0227  2367.0154  2367.1740  -67.01   273 -  296   0   R.EVFMGSALGNAVSNAVSNLGSSLK.S + Oxidation (M)
No match to: 889.5150, 908.4816, 931.4470, 1012.6227, 1034.5371, 1063.6041, 1069.3880, 1089.4628, 1091.6424,
1107.6693, 1116.5044, 1129.6426, 1135.6690, 1145.5679, 1164.6447, 1214.6924, 1305.7046, 1438.0931, 1475.6807,
1553.7615, 1559.7352, 1565.7611, 1575.7735, 1581.7207, 1625.7823, 1673.7665, 1678.8700, 1693.8244, 1751.7956,
1757.8117, 1772.8791, 1794.8996, 1810.8908, 2005.0171, 2211.0100, 2234.3806, 2327.9891, 2331.0385, 2346.0194,
2362.0439, 2374.0601, 2378.0243, 2384.0056, 2390.0201, 2482.0317

18.  WP_054693860.1    Mass: 28485    Score: 67     Expect: 33  Matches: 7
     hypothetical protein [Syntrophomonas palmitatica]
      Observed   Mr(expt)   Mr(calc)     ppm  Start    End Miss   Peptide
     1051.5204  1050.5131  1050.5862  -69.59   183 - 190    1   R.FLYDPKLR.M
     1078.5660  1077.5587  1077.5488    9.17    11 -  19    1   R.MTSTRLPEK.V + Oxidation (M)
     1179.6335  1178.6262  1178.5787    40.3     1 -  10    0   -.MSIGCIIEAR.M + Oxidation (M); Propionamide (C)
     1537.7261  1536.7188  1536.7752  -36.69     2 -  15    1   M.SIGCIIEARMTSTR.L
     1553.7615  1552.7542  1552.7701  -10.26     2 -  15    1   M.SIGCIIEARMTSTR.L + Oxidation (M)
     1735.8188  1734.8116  1734.9013  -51.72   145 - 159    1   R.VLQESARLTDDPVHR.E
     2482.0317  2481.0245  2481.1232  -39.79   205 - 223    0   R.IYEELYPQKPDFDLYDMMR.L + Oxidation (M)
     No match to: 889.5150, 908.4816, 931.4470, 1012.6227, 1034.5371, 1060.5250, 1063.6041, 1069.3880, 1073.5195,
     1089.4628, 1091.6424, 1100.5534, 1107.6693, 1116.5044, 1129.6426, 1135.6690, 1145.5679, 1164.6447, 1188.7314,
     1201.6313, 1214.6924, 1217.6072, 1239.5902, 1305.7046, 1438.0931, 1475.6807, 1522.7371, 1559.7352, 1565.7611,
     1575.7735, 1581.7207, 1625.7823, 1673.7665, 1678.8700, 1693.8244, 1713.8084, 1729.8158, 1751.7956, 1757.8117,
     1772.8791, 1794.8996, 1810.8908, 2005.0171, 2211.0100, 2234.3806, 2327.9891, 2331.0385, 2346.0194, 2362.0439,
     2368.0227, 2374.0601, 2378.0243, 2384.0056, 2390.0201

19.  PIQ35028.1    Mass: 23072    Score: 67     Expect: 33  Matches: 7
     YigZ family protein [Bacteroidetes bacterium CG18_big_fil_WC_8_21_14_2_50_41_14]
      Observed   Mr(expt)   Mr(calc)     ppm  Start    End Miss   Peptide
      931.4470   930.4398   930.5022  -67.10   158 - 165    0   K.EENLTVVK.Q
     1078.5660  1077.5587  1077.6005  -38.75   172 - 179    1   R.CKFIIEVR.V + Propionamide (C)
     1107.6693  1106.6621  1106.6336    25.8   109 - 119    0   K.LGVSGLVTAYK.T
     1179.6335  1178.6262  1178.5931    28.1    12 -  21    1   K.EQGQGLYKEK.G
     1188.7314  1187.7241  1187.7026    18.1   174 - 183    1   K.FIIEVRVGQK.N
     1729.8158  1728.8085  1728.8934  -49.11    25 -  39    0   K.FISIAIHVESEEEVK.A
     1751.7956  1750.7883  1750.8560  -38.66   158 - 171    1   K.EENLTVVKQEFEMR.C
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No match to: 889.5150, 908.4816, 1012.6227, 1034.5371, 1051.5204, 1060.5250, 1063.6041, 1069.3880, 1073.5195, 1089.4628, 1091.6424, 1100.5534, 1116.5044, 1129.6426, 1135.6690, 1145.5679, 1164.6447, 1201.6313, 1214.6924, 1217.6072, 1239.5902, 1305.7046, 1438.0931, 1475.6807, 1522.7371, 1537.7261, 1553.7615, 1559.7352, 1565.7611, 1575.7735, 1581.7207, 1625.7823, 1673.7665, 1678.8700, 1693.8244, 1713.8084, 1735.8188, 1757.8117, 1772.8791, 1794.8996, 1810.8908, 2005.0171, 2211.0100, 2234.3806, 2327.9891, 2331.0385, 2346.0194, 2362.0439, 2368.0227, 2374.0601, 2378.0243, 2384.0056, 2390.0201, 2482.0317

20. ART89119.1 **Mass:** 29503 **Score:** 66 **Expect:** 38 **Matches:** 8

coat protein [Tomato leaf curl Joydebpur virus]

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Peptide
1051.5204	1050.5131	1050.5056	7.15	120	-	127	0	K.IWMDETIK.T + Oxidation (M)
1078.5660	1077.5587	1077.5423	15.2	89	-	97	1	K.VMCVRDVTR.G
1179.6335	1178.6262	1178.6270	-0.67	31	-	40	1	R.VAAPMFRFPK.Q + Oxidation (M)
1537.7261	1536.7188	1536.7653	-30.28	81	-	93	1	R.HDVQHIGKVMCVR.D + Oxidation (M)
1625.7823	1624.7750	1624.7845	-5.85	205	-	218	0	R.VNNYVVYNQQEAGK.Y
1693.8244	1692.8171	1692.8770	-35.40	128	-	141	1	K.TKNHTNSVMFFLVR.D
1735.8188	1734.8116	1734.8624	-29.31	130	-	143	1	K.NHTNSVMFFLVRDR.R
1751.7956	1750.7883	1750.8573	-39.44	130	-	143	1	K.NHTNSVMFFLVRDR.R + Oxidation (M)

No match to: 889.5150, 908.4816, 931.4470, 1012.6227, 1034.5371, 1060.5250, 1063.6041, 1069.3880, 1073.5195, 1089.4628, 1091.6424, 1100.5534, 1107.6693, 1116.5044, 1129.6426, 1135.6690, 1145.5679, 1164.6447, 1188.7314, 1201.6313, 1214.6924, 1217.6072, 1239.5902, 1305.7046, 1438.0931, 1475.6807, 1522.7371, 1553.7615, 1559.7352, 1565.7611, 1575.7735, 1581.7207, 1673.7665, 1678.8700, 1713.8084, 1729.8158, 1757.8117, 1772.8791, 1794.8996, 1810.8908, 2005.0171, 2211.0100, 2234.3806, 2327.9891, 2331.0385, 2346.0194, 2362.0439, 2368.0227, 2374.0601, 2378.0243, 2384.0056, 2390.0201, 2482.0317

Search Parameters

Type of search	:	**Peptide Mass Fingerprint**
Enzyme	:	**Trypsin**
Variable modifications	:	**Oxidation (M),Propionamide (C)**
Mass values	:	**Monoisotopic**
Protein Mass	:	**Unrestricted**
Peptide Mass Tolerance	:	**± 70 ppm**
Peptide Charge State	:	**1+**
Max Missed Cleavages	:	**1**
Number of queries	:	**61**

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Selected for scoring   : 19
```

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

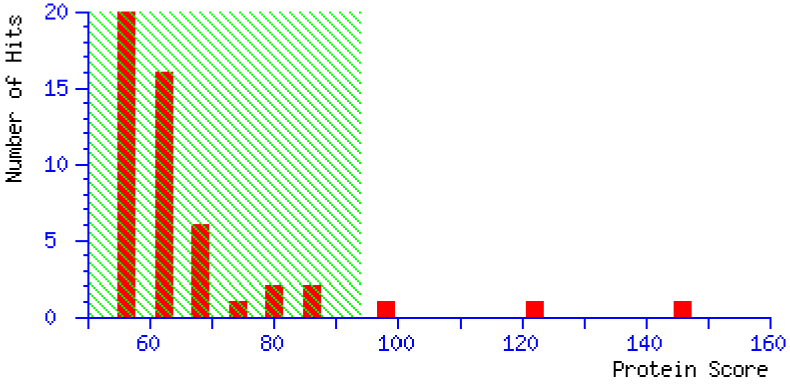
3. The protein band of approx. 27 kDa, obtained from the crude extract of *R. rhodochrous* M33 cells, grown on the medium with nickel.

MATRIX SCIENCE Mascot Search Results

User : toropygin
Email : toropygin@rambler.ru
Search title : 03
Database : NCBIprot 20180429 (152462470 sequences; 55858910152 residues)
Timestamp : 1 Sep 2018 at 16:32:20 GMT
Top Score : 146 for WP_072636260.1, nitrile hydratase subunit beta [Rhodococcus sp. M8]

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 94 are significant (p<0.05).



Protein Summary Report

Format As | Protein Summary ▾ | Help

	Significance threshold p< 0.05	Max. number of hits 20
	Preferred taxonomy All entries	

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-
-Accession- -Sequence-

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
☑ 805.4494 (1+)																				
☑ 842.5035 (1+)																●				
☑ 909.4046 (1+)	●		●																	
☑ 925.4130 (1+)	●		●																	
☑ 931.3994 (1+)																				
☑ 943.5490 (1+)	●	●	●	●	●	●	●		●									●		
☑ 1008.5232 (1+)	●	●	●																	
☑ 1017.5815 (1+)	●	●	●	●	●	●	●		●									●		
☑ 1039.5620 (1+)	●	●	●					●		●	●	●	●	●			●			

☑ 1050.5574 (1+)								●		●	●	●	●	●			●			●
☑ 1054.6213 (1+)								●		●	●	●	●	●			●			
☑ 1073.5667 (1+)															●					
☑ 1076.6081 (1+)	●	●	●																	
☑ 1085.6544 (1+)																				●
☑ 1100.5430 (1+)				●																
☑ 1117.5807 (1+)																				
☑ 1138.6538 (1+)																				
☑ 1145.6530 (1+)								●									●		●	
☑ 1152.5748 (1+)	●		●												●					
☑ 1168.5751 (1+)	●		●							●						●				
☑ 1221.7220 (1+)										●								●		
☑ 1236.7463 (1+)	●	●	●	●	●	●	●		●											
☑ 1330.7703 (1+)																				
☑ 1342.8198 (1+)	●	●	●	●	●	●	●		●						●					
☑ 1358.8120 (1+)	●	●	●	●	●	●	●		●							●				
☑ 1364.8023 (1+)																●		●		
☑ 1413.8359 (1+)															●				●	
☑ 1423.7457 (1+)																●		●		

☑	1528.9209 (1+)	●	●	●	●	●	●	●		●							●				
☑	1545.9066 (1+)															●					
☑	1554.7713 (1+)	●	●	●	●	●	●	●									●		●		
☑	1567.7853 (1+)										●										
☑	1570.7642 (1+)	●	●	●	●	●	●	●	●		●	●	●	●	●		●	●	●		
☑	1576.8616 (1+)																			●	●
☑	1597.8169 (1+)	●	●	●	●	●	●	●		●							●				
☑	1611.7590 (1+)	●	●	●	●	●	●	●		●						●	●				
☑	1657.0233 (1+)																				
☑	1678.9891 (1+)																				
☑	1687.9118 (1+)																●				
☑	1697.0138 (1+)																●				
☑	1759.8782 (1+)															●	●		●	●	
☑	1794.8836 (1+)								●			●	●	●	●			●			●
☑	1933.0507 (1+)								●			●	●	●	●			●			
☑	1950.1483 (1+)																				
☑	1956.0934 (1+)																				
☑	2003.1606 (1+)																				
☑	2005.0365 (1+)	●	●	●	●	●	●	●													

☑ 2202.1164 (1+)	●	●		●	●	●	●		●						●				●	●
☑ 2211.0972 (1+)																				
☑ 2224.0416 (1+)																●				
☑ 2229.1680 (1+)								●		●										●
☑ 2245.2213 (1+)								●			●	●	●	●			●			
☑ 2252.2275 (1+)								●			●	●	●	●	●			●		
☑ 2283.1447 (1+)																				●
☑ 2297.1105 (1+)								●			●	●	●	●	●		●			●
☑ 2301.2929 (1+)																				
☑ 2429.2478 (1+)	●	●																●	●	
☑ 2451.2298 (1+)										●										●
☑ 2518.1177 (1+)																				
☑ 2671.2164 (1+)	●	●		●	●	●	●	●	●		●	●	●	●	●		●			
☑ 2691.1981 (1+)																				
☑ 2874.4195 (1+)																				
☑ 2898.3838 (1+)															●			●	●	
☑ 3118.1300 (1+)																				
☑ 3133.1540 (1+)																				
☑ 3149.1353 (1+)																				

☑	3519.4917 (1+)									●											
☑	3583.2288 (1+)																				
☑	3716.2107 (1+)																				
☑	3728.4763 (1+)																				
☑	3732.2097 (1+)																				
☑	3748.1712 (1+)																				
☑	3794.3838 (1+)																				
☑	3808.3873 (1+)																				
☑	3955.6468 (1+)																				

Search Selected

Index

	Accession	Mass	Score	Description
1.	WP_072636260.1	26277	146	nitrile hydratase subunit beta [Rhodococcus sp. M8]
2.	AAN71592.1	26259	124	nitrile hydratase beta subunit [Nocardia sp. JBRs]
3.	WP_006940501.1	26305	101	nitrile hydratase subunit beta [Rhodococcus sp. EsD8]
4.	CAE46767.1	26349	89	nitrile hydratase beta subunit [Rhodococcus pyridinivorans]
5.	CAC83637.1	22560	87	nitrile hydratase beta chain, partial [uncultured bacterium SP1]

6. BAE75932.1	26335	78	nitrile hydratase beta subunit [Rhodococcus pyridinivorans]
7. P21220.2	26305	78	RecName: Full=High-molecular weight cobalt-containing nitrile hydratase subunit beta; Short=H-NHase; Short=H-nitrilase
8. WP_038342507.1	34588	75	LysR family transcriptional regulator [Acinetobacter sp. A47]
9. CAC83638.1	19344	70	nitrile hydratase beta chain, partial [uncultured bacterium BD2]
10. WP_047545807.1	30995	69	hypothetical protein [Psychroserpens sp. Hel_I_66]
11. WP_005145929.1	34512	66	LysR family transcriptional regulator [Acinetobacter sp. ANC 3929]
12. WP_005183230.1	34482	66	LysR family transcriptional regulator [Acinetobacter sp. ANC 4105]
13. WP_005295489.1	34482	66	LysR family transcriptional regulator [Acinetobacter sp. NIPH 2100]
14. WP_005213279.1	34512	66	LysR family transcriptional regulator [Acinetobacter sp. NIPH 1867]
15. WP_107654896.1	46639	65	DUF3558 domain-containing protein [Nocardia suismassiliense]
16. XP_004363930.1	63588	65	hypothetical protein CAOG_03091 [Capsaspora owczarzaki ATCC 30864]
17. WP_004880504.1	34674	64	MULTISPECIES: LysR family transcriptional regulator [Acinetobacter]
18. AJY18677.1	34526	64	bacterial regulatory helix-turn-helix, lysR family protein [Burkholderia multivorans ATCC BAA-247]
19. WP_066550229.1	13748	63	MULTISPECIES: nitrite reductase (NAD(P)H) small subunit [Sphingomonadales]
20. WP_069623671.1	27359	63	alpha/beta hydrolase [Methyloceanibacter marginalis]

Results List

1. WP_072636260.1 **Mass:** 26277 **Score:** 146 **Expect:** 3.8e-07 **Matches:** 21

nitrile hydratase subunit beta [Rhodococcus sp. M8]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
909.4046	908.3973	908.3851	13.5	44 -	50	0	K.GMSWWDK.S
925.4130	924.4057	924.3800	27.8	44 -	50	0	K.GMSWWDK.S + Oxidation (M)
943.5490	942.5417	942.5134	30.0	98 -	105	0	R.VQEILEGR.Y

```
1008.5232  1007.5160  1007.4784    37.3   106 - 113   1   R.YTDRNPSR.K
1017.5815  1016.5742  1016.5502    23.6    88 -  95   1   K.IITEEERK.H
1039.5620  1038.5547  1038.5029    49.9   152 - 160   0   K.NMNPLGHTR.C
1076.6081  1075.6008  1075.5549    42.6   114 - 122   1   R.KFDPAEIEK.A
1152.5748  1151.5676  1151.5182    42.9    44 -  52   1   K.GMSWWDKSR.F
1168.5751  1167.5679  1167.5131    46.9    44 -  52   1   K.GMSWWDKSR.F + Oxidation (M)
1236.7463  1235.7390  1235.6734    53.1    96 - 105   1   K.HRVQEILEGR.Y
1342.8198  1341.8125  1341.7479    48.2    33 -  43   0   R.TLSILTWMHLK.G
1358.8120  1357.8047  1357.7428    45.6    33 -  43   0   R.TLSILTWMHLK.G + Oxidation (M)
1528.9209  1527.9136  1527.8508    41.1    82 -  94   1   R.ILVADKIITEEER.K
1554.7713  1553.7640  1553.6780    55.4    56 -  68   0   R.ESMGNENYVNEIR.N
1570.7642  1569.7569  1569.6729    53.5    56 -  68   0   R.ESMGNENYVNEIR.N + Oxidation (M)
1597.8169  1596.8096  1596.7321    48.6    69 -  81   0   R.NSYYTHWLSAAER.I
1611.7590  1610.7517  1610.6790    45.1    21 -  32   0   K.DEPFFHYEWEGR.T
2005.0365  2004.0292  2003.9159    56.5    53 -  68   1   R.FFRESMGNENYVNEIR.N
2202.1164  2201.1091  2201.1117   -1.16   127 - 147   0   R.LHEPHSLALPGAEPSFSLGDK.V
2429.2478  2428.2405  2428.2750  -14.23   127 - 149   1   R.LHEPHSLALPGAEPSFSLGDKVK.V
2671.2164  2670.2091  2670.3765  -62.69   123 - 147   1   K.AIERLHEPHSLALPGAEPSFSLGDK.V
```

No match to: 805.4494, 842.5035, 931.3994, 1050.5574, 1054.6213, 1073.5667, 1085.6544, 1100.5430, 1117.5807, 1138.6538, 1145.6530, 1221.7220, 1330.7703, 1364.8023, 1413.8359, 1423.7457, 1545.9066, 1567.7853, 1576.8616, 1657.0233, 1678.9891, 1687.9118, 1697.0138, 1759.8782, 1794.8836, 1933.0507, 1950.1483, 1956.0934, 2003.1606, 2211.0972, 2224.0416, 2229.1680, 2245.2213, 2252.2275, 2283.1447, 2297.1105, 2301.2929, 2451.2298, 2518.1177, 2691.1981, 2874.4195, 2898.3838, 3118.1300, 3133.1540, 3149.1353, 3519.4917, 3583.2288, 3716.2107, 3728.4763, 3732.2097, 3748.1712, 3794.3838, 3808.3873, 3955.6468

2. AAN71592.1 **Mass:** 26259 **Score:** **124** **Expect:** 6.1e-05 **Matches:** 17

nitrile hydratase beta subunit [Nocardia sp. JBRs]

```
 Observed    Mr(expt)   Mr(calc)     ppm  Start   End Miss  Peptide
 943.5490   942.5417   942.5134    30.0    98 - 105   0   R.VQEILEGR.Y
1008.5232  1007.5160  1007.4784    37.3   106 - 113   1   R.YTDRNPSR.K
1017.5815  1016.5742  1016.5502    23.6    88 -  95   1   K.IITEEERK.H
1039.5620  1038.5547  1038.5029    49.9   152 - 160   0   K.NMNPLGHTR.C
1076.6081  1075.6008  1075.5549    42.6   114 - 122   1   R.KFDPAEIEK.A
1236.7463  1235.7390  1235.6734    53.1    96 - 105   1   K.HRVQEILEGR.Y
1342.8198  1341.8125  1341.7479    48.2    33 -  43   0   R.TLSILTWMHLK.G
```

```
1358.8120  1357.8047  1357.7428    45.6    33 -  43   0   R.TLSILTWMHLK.G + Oxidation (M)
1528.9209  1527.9136  1527.8508    41.1    82 -  94   1   R.ILVADKIITEEER.K
1554.7713  1553.7640  1553.6780    55.4    56 -  68   0   R.ESMGNENYVNEIR.N
1570.7642  1569.7569  1569.6729    53.5    56 -  68   0   R.ESMGNENYVNEIR.N + Oxidation (M)
1597.8169  1596.8096  1596.7321    48.6    69 -  81   0   R.NSYYTHWLSAAER.I
1611.7590  1610.7517  1610.6790    45.1    21 -  32   0   K.DEPFFHYEWEGR.T
2005.0365  2004.0292  2003.9159    56.5    53 -  68   1   R.FFRESMGNENYVNEIR.N
2202.1164  2201.1091  2201.1117   -1.16   127 - 147   0   R.LHEPHSLALPGAEPSFSLGDK.V
2429.2478  2428.2405  2428.2750  -14.23   127 - 149   1   R.LHEPHSLALPGAEPSFSLGDKVK.V
2671.2164  2670.2091  2670.3765  -62.69   123 - 147   1   K.AIERLHEPHSLALPGAEPSFSLGDK.V
No match to: 805.4494, 842.5035, 909.4046, 925.4130, 931.3994, 1050.5574, 1054.6213, 1073.5667, 1085.6544,
1100.5430, 1117.5807, 1138.6538, 1145.6530, 1152.5748, 1168.5751, 1221.7220, 1330.7703, 1364.8023, 1413.8359,
1423.7457, 1545.9066, 1567.7853, 1576.8616, 1657.0233, 1678.9891, 1687.9118, 1697.0138, 1759.8782, 1794.8836,
1933.0507, 1950.1483, 1956.0934, 2003.1606, 2211.0972, 2224.0416, 2229.1680, 2245.2213, 2252.2275, 2283.1447,
2297.1105, 2301.2929, 2451.2298, 2518.1177, 2691.1981, 2874.4195, 2898.3838, 3118.1300, 3133.1540, 3149.1353,
3519.4917, 3583.2288, 3716.2107, 3728.4763, 3732.2097, 3748.1712, 3794.3838, 3808.3873, 3955.6468
```

```
3.   WP_006940501.1    Mass: 26305    Score: 101    Expect: 0.012  Matches: 18
     nitrile hydratase subunit beta [Rhodococcus sp. EsD8]
      Observed    Mr(expt)   Mr(calc)    ppm  Start   End Miss   Peptide
      909.4046    908.3973   908.3851   13.5    44 -  50    0    K.GMSWWDK.S
      925.4130    924.4057   924.3800   27.8    44 -  50    0    K.GMSWWDK.S + Oxidation (M)
      943.5490    942.5417   942.5134   30.0    98 - 105    0    R.VQEILEGR.Y
     1008.5232   1007.5160  1007.4784   37.3   106 - 113    1    R.YTDRNPSR.K
     1017.5815   1016.5742  1016.5502   23.6    88 -  95    1    K.IITEEERK.H
     1039.5620   1038.5547  1038.5029   49.9   152 - 160    0    K.NMNPLGHTR.C
     1076.6081   1075.6008  1075.5549   42.6   114 - 122    1    R.KFDPAEIEK.A
     1152.5748   1151.5676  1151.5182   42.9    44 -  52    1    K.GMSWWDKSR.F
     1168.5751   1167.5679  1167.5131   46.9    44 -  52    1    K.GMSWWDKSR.F + Oxidation (M)
     1236.7463   1235.7390  1235.6734   53.1    96 - 105    1    K.HRVQEILEGR.Y
     1342.8198   1341.8125  1341.7479   48.2    33 -  43    0    R.TLSILTWMHLK.G
     1358.8120   1357.8047  1357.7428   45.6    33 -  43    0    R.TLSILTWMHLK.G + Oxidation (M)
     1528.9209   1527.9136  1527.8508   41.1    82 -  94    1    R.ILVADKIITEEER.K
     1554.7713   1553.7640  1553.6780   55.4    56 -  68    0    R.ESMGNENYVNEIR.N
     1570.7642   1569.7569  1569.6729   53.5    56 -  68    0    R.ESMGNENYVNEIR.N + Oxidation (M)
```

```
1597.8169  1596.8096  1596.7321   48.6     69 -  81   0   R.NSYYTHWLSAAER.I
1611.7590  1610.7517  1610.6790   45.1     21 -  32   0   K.DEPFFHYEWEGR.T
2005.0365  2004.0292  2003.9159   56.5     53 -  68   1   R.FFRESMGNENYVNEIR.N
No match to: 805.4494, 842.5035, 931.3994, 1050.5574, 1054.6213, 1073.5667, 1085.6544, 1100.5430, 1117.5807,
1138.6538, 1145.6530, 1221.7220, 1330.7703, 1364.8023, 1413.8359, 1423.7457, 1545.9066, 1567.7853, 1576.8616,
1657.0233, 1678.9891, 1687.9118, 1697.0138, 1759.8782, 1794.8836, 1933.0507, 1950.1483, 1956.0934, 2003.1606,
2202.1164, 2211.0972, 2224.0416, 2229.1680, 2245.2213, 2252.2275, 2283.1447, 2297.1105, 2301.2929, 2429.2478,
2451.2298, 2518.1177, 2671.2164, 2691.1981, 2874.4195, 2898.3838, 3118.1300, 3133.1540, 3149.1353, 3519.4917,
3583.2288, 3716.2107, 3728.4763, 3732.2097, 3748.1712, 3794.3838, 3808.3873, 3955.6468

4.    CAE46767.1     Mass: 26349     Score: 89     Expect: 0.21  Matches: 14
      nitrile hydratase beta subunit [Rhodococcus pyridinivorans]
       Observed    Mr(expt)   Mr(calc)     ppm  Start    End Miss   Peptide
        943.5490   942.5417   942.5134    30.0     98 - 105    0    R.VQEILEGR.Y
       1017.5815  1016.5742  1016.5502    23.6     88 -  95    1    K.IITEEERK.H
       1100.5430  1099.5357  1099.5080    25.2    152 - 160    0    K.SMNPLEHTR.C + Oxidation (M)
       1236.7463  1235.7390  1235.6734    53.1     96 - 105    1    K.HRVQEILEGR.Y
       1342.8198  1341.8125  1341.7479    48.2     33 -  43    0    R.TLSILTWMHLK.G
       1358.8120  1357.8047  1357.7428    45.6     33 -  43    0    R.TLSILTWMHLK.G + Oxidation (M)
       1528.9209  1527.9136  1527.8508    41.1     82 -  94    1    R.ILVADKIITEEER.K
       1554.7713  1553.7640  1553.6780    55.4     56 -  68    0    R.ESMGNENYVNEIR.N
       1570.7642  1569.7569  1569.6729    53.5     56 -  68    0    R.ESMGNENYVNEIR.N + Oxidation (M)
       1597.8169  1596.8096  1596.7321    48.6     69 -  81    0    R.NSYYTHWLSAAER.I
       1611.7590  1610.7517  1610.6790    45.1     21 -  32    0    K.DEPFFHYEWEGR.T
       2005.0365  2004.0292  2003.9159    56.5     53 -  68    1    R.FFRESMGNENYVNEIR.N
       2202.1164  2201.1091  2201.1117   -1.16    127 - 147    0    R.LHEPHSLALPGAEPSFSLGDK.I
       2671.2164  2670.2091  2670.3765  -62.69    123 - 147    1    K.AIERLHEPHSLALPGAEPSFSLGDK.I
      No match to: 805.4494, 842.5035, 909.4046, 925.4130, 931.3994, 1008.5232, 1039.5620, 1050.5574, 1054.6213,
      1073.5667, 1076.6081, 1085.6544, 1117.5807, 1138.6538, 1145.6530, 1152.5748, 1168.5751, 1221.7220, 1330.7703,
      1364.8023, 1413.8359, 1423.7457, 1545.9066, 1567.7853, 1576.8616, 1657.0233, 1678.9891, 1687.9118, 1697.0138,
      1759.8782, 1794.8836, 1933.0507, 1950.1483, 1956.0934, 2003.1606, 2211.0972, 2224.0416, 2229.1680, 2245.2213,
      2252.2275, 2283.1447, 2297.1105, 2301.2929, 2429.2478, 2451.2298, 2518.1177, 2691.1981, 2874.4195, 2898.3838,
      3118.1300, 3133.1540, 3149.1353, 3519.4917, 3583.2288, 3716.2107, 3728.4763, 3732.2097, 3748.1712, 3794.3838,
      3808.3873, 3955.6468

5.    CAC83637.1     Mass: 22560     Score: 87     Expect: 0.31  Matches: 13
```

nitrile hydratase beta chain, partial [uncultured bacterium SP1]

```
 Observed   Mr(expt)   Mr(calc)    ppm  Start    End Miss   Peptide
  943.5490   942.5417   942.5134   30.0     98 - 105    0   R.VQEILEGR.Y
 1017.5815  1016.5742  1016.5502   23.6     88 -  95    1   K.IITEEERK.H
 1236.7463  1235.7390  1235.6734   53.1     96 - 105    1   K.HRVQEILEGR.Y
 1342.8198  1341.8125  1341.7479   48.2     33 -  43    0   R.TLSILTWMHLK.G
 1358.8120  1357.8047  1357.7428   45.6     33 -  43    0   R.TLSILTWMHLK.G + Oxidation (M)
 1528.9209  1527.9136  1527.8508   41.1     82 -  94    1   R.ILVADKIITEEER.K
 1554.7713  1553.7640  1553.6780   55.4     56 -  68    0   R.ESMGNENYVNEIR.N
 1570.7642  1569.7569  1569.6729   53.5     56 -  68    0   R.ESMGNENYVNEIR.N + Oxidation (M)
 1597.8169  1596.8096  1596.7321   48.6     69 -  81    0   R.NSYYTHWLSAAER.I
 1611.7590  1610.7517  1610.6790   45.1     21 -  32    0   K.DEPFFHYEWEGR.T
 2005.0365  2004.0292  2003.9159   56.5     53 -  68    1   R.FFRESMGNENYVNEIR.N
 2202.1164  2201.1091  2201.1117  -1.16    127 - 147    0   R.LHEPHSLALPGAEPSFSLGDK.I
 2671.2164  2670.2091  2670.3765 -62.69    123 - 147    1   K.AIERLHEPHSLALPGAEPSFSLGDK.I
```

No match to: 805.4494, 842.5035, 909.4046, 925.4130, 931.3994, 1008.5232, 1039.5620, 1050.5574, 1054.6213, 1073.5667, 1076.6081, 1085.6544, 1100.5430, 1117.5807, 1138.6538, 1145.6530, 1152.5748, 1168.5751, 1221.7220, 1330.7703, 1364.8023, 1413.8359, 1423.7457, 1545.9066, 1567.7853, 1576.8616, 1657.0233, 1678.9891, 1687.9118, 1697.0138, 1759.8782, 1794.8836, 1933.0507, 1950.1483, 1956.0934, 2003.1606, 2211.0972, 2224.0416, 2229.1680, 2245.2213, 2252.2275, 2283.1447, 2297.1105, 2301.2929, 2429.2478, 2451.2298, 2518.1177, 2691.1981, 2874.4195, 2898.3838, 3118.1300, 3133.1540, 3149.1353, 3519.4917, 3583.2288, 3716.2107, 3728.4763, 3732.2097, 3748.1712, 3794.3838, 3808.3873, 3955.6468

6. BAE75932.1 **Mass:** 26335 **Score:** 78 **Expect:** 2.7 **Matches:** 13

nitrile hydratase beta subunit [Rhodococcus pyridinivorans]

```
 Observed   Mr(expt)   Mr(calc)    ppm  Start    End Miss   Peptide
  943.5490   942.5417   942.5134   30.0     98 - 105    0   R.VQEILEGR.Y
 1017.5815  1016.5742  1016.5502   23.6     88 -  95    1   K.IITEEERK.H
 1236.7463  1235.7390  1235.6734   53.1     96 - 105    1   K.HRVQEILEGR.Y
 1342.8198  1341.8125  1341.7479   48.2     33 -  43    0   R.TLSILTWMHLK.G
 1358.8120  1357.8047  1357.7428   45.6     33 -  43    0   R.TLSILTWMHLK.G + Oxidation (M)
 1528.9209  1527.9136  1527.8508   41.1     82 -  94    1   R.ILVADKIITEEER.K
 1554.7713  1553.7640  1553.6780   55.4     56 -  68    0   R.ESMGNENYVNEIR.N
 1570.7642  1569.7569  1569.6729   53.5     56 -  68    0   R.ESMGNENYVNEIR.N + Oxidation (M)
 1597.8169  1596.8096  1596.7321   48.6     69 -  81    0   R.NSYYTHWLSAAER.I
```

1611.7590	1610.7517	1610.6790	45.1	21	- 32	0	K.DEPFFHYEWEGR.T
2005.0365	2004.0292	2003.9159	56.5	53	- 68	1	R.FFRESMGNENYVNEIR.N
2202.1164	2201.1091	2201.1117	-1.16	127	- 147	0	R.LHEPHSLALPGAEPSFSLGDK.I
2671.2164	2670.2091	2670.3765	-62.69	123	- 147	1	K.AIERLHEPHSLALPGAEPSFSLGDK.I

No match to: 805.4494, 842.5035, 909.4046, 925.4130, 931.3994, 1008.5232, 1039.5620, 1050.5574, 1054.6213, 1073.5667, 1076.6081, 1085.6544, 1100.5430, 1117.5807, 1138.6538, 1145.6530, 1152.5748, 1168.5751, 1221.7220, 1330.7703, 1364.8023, 1413.8359, 1423.7457, 1545.9066, 1567.7853, 1576.8616, 1657.0233, 1678.9891, 1687.9118, 1697.0138, 1759.8782, 1794.8836, 1933.0507, 1950.1483, 1956.0934, 2003.1606, 2211.0972, 2224.0416, 2229.1680, 2245.2213, 2252.2275, 2283.1447, 2297.1105, 2301.2929, 2429.2478, 2451.2298, 2518.1177, 2691.1981, 2874.4195, 2898.3838, 3118.1300, 3133.1540, 3149.1353, 3519.4917, 3583.2288, 3716.2107, 3728.4763, 3732.2097, 3748.1712, 3794.3838, 3808.3873, 3955.6468

7. P21220.2 **Mass:** 26305 **Score:** 78 **Expect:** 2.7 **Matches:** 13

RecName: Full=High-molecular weight cobalt-containing nitrile hydratase subunit beta; Short=H-NHase; Short=H-nitrilase

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
943.5490	942.5417	942.5134	30.0	98	- 105	0	R.VQEILEGR.Y
1017.5815	1016.5742	1016.5502	23.6	88	- 95	1	K.IITEEERK.H
1236.7463	1235.7390	1235.6734	53.1	96	- 105	1	K.HRVQEILEGR.Y
1342.8198	1341.8125	1341.7479	48.2	33	- 43	0	R.TLSILTWMHLK.G
1358.8120	1357.8047	1357.7428	45.6	33	- 43	0	R.TLSILTWMHLK.G + Oxidation (M)
1528.9209	1527.9136	1527.8508	41.1	82	- 94	1	R.ILVADKIITEEER.K
1554.7713	1553.7640	1553.6780	55.4	56	- 68	0	R.ESMGNENYVNEIR.N
1570.7642	1569.7569	1569.6729	53.5	56	- 68	0	R.ESMGNENYVNEIR.N + Oxidation (M)
1597.8169	1596.8096	1596.7321	48.6	69	- 81	0	R.NSYYTHWLSAAER.I
1611.7590	1610.7517	1610.6790	45.1	21	- 32	0	K.DEPFFHYEWEGR.T
2005.0365	2004.0292	2003.9159	56.5	53	- 68	1	R.FFRESMGNENYVNEIR.N
2202.1164	2201.1091	2201.1117	-1.16	127	- 147	0	R.LHEPHSLALPGAEPSFSLGDK.I
2671.2164	2670.2091	2670.3765	-62.69	123	- 147	1	K.AIERLHEPHSLALPGAEPSFSLGDK.I

No match to: 805.4494, 842.5035, 909.4046, 925.4130, 931.3994, 1008.5232, 1039.5620, 1050.5574, 1054.6213, 1073.5667, 1076.6081, 1085.6544, 1100.5430, 1117.5807, 1138.6538, 1145.6530, 1152.5748, 1168.5751, 1221.7220, 1330.7703, 1364.8023, 1413.8359, 1423.7457, 1545.9066, 1567.7853, 1576.8616, 1657.0233, 1678.9891, 1687.9118, 1697.0138, 1759.8782, 1794.8836, 1933.0507, 1950.1483, 1956.0934, 2003.1606, 2211.0972, 2224.0416, 2229.1680, 2245.2213, 2252.2275, 2283.1447, 2297.1105, 2301.2929, 2429.2478, 2451.2298, 2518.1177, 2691.1981, 2874.4195,

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     2898.3838, 3118.1300, 3133.1540, 3149.1353, 3519.4917, 3583.2288, 3716.2107, 3728.4763, 3732.2097, 3748.1712,
     3794.3838, 3808.3873, 3955.6468

8.   WP_038342507.1     Mass: 34588     Score: 75     Expect: 4.7  Matches: 12
     LysR family transcriptional regulator [Acinetobacter sp. A47]
      Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
     1039.5620  1038.5547  1038.5419    12.3    243 - 250    0    R.ILYMDIQK.E + Oxidation (M)
     1050.5574  1049.5501  1049.5393    10.3    132 - 139    0    R.YIDLIEER.I
     1054.6213  1053.6140  1053.5753    36.7    285 - 293    1    K.VHRCIDALK.Q
     1145.6530  1144.6457  1144.6638  -15.80    140 - 149    1    R.IDIAVRMSLK.M
     1570.7642  1569.7569  1569.7821  -16.02     40 -  52    0    R.SLEQEMDVTLLHR.S
     1794.8836  1793.8763  1793.9168  -22.56      2 -  17    1    M.LDQLRAMGVFACVVEK.S + Oxidation (M)
     1933.0507  1932.0435  1931.9234    62.2      7 -  25    1    R.AMGVFACVVEKSSFSGAAR.D + Oxidation (M)
     2229.1680  2228.1607  2228.1558    2.22    232 - 250    1    K.ALCQQGHGIARILYMDIQK.E + Propionamide (C)
     2245.2213  2244.2140  2244.1507    28.2    232 - 250    1    K.ALCQQGHGIARILYMDIQK.E + Oxidation (M); Propionamide (C)
     2252.2275  2251.2202  2251.1557    28.7     18 -  39    1    K.SSFSGAARDLGITTSAVSQQIR.S
     2297.1105  2296.1033  2296.1600  -24.70    121 - 139    1    K.GLAIHFEADHRYIDLIEER.I
     2671.2164  2670.2091  2670.3145  -39.47     57 -  81    1    K.LSLTEAGQAFFLSCQEMLAAAERGK.I
     No match to: 805.4494, 842.5035, 909.4046, 925.4130, 931.3994, 943.5490, 1008.5232, 1017.5815, 1073.5667,
     1076.6081, 1085.6544, 1100.5430, 1117.5807, 1138.6538, 1152.5748, 1168.5751, 1221.7220, 1236.7463, 1330.7703,
     1342.8198, 1358.8120, 1364.8023, 1413.8359, 1423.7457, 1528.9209, 1545.9066, 1554.7713, 1567.7853, 1576.8616,
     1597.8169, 1611.7590, 1657.0233, 1678.9891, 1687.9118, 1697.0138, 1759.8782, 1950.1483, 1956.0934, 2003.1606,
     2005.0365, 2202.1164, 2211.0972, 2224.0416, 2283.1447, 2301.2929, 2429.2478, 2451.2298, 2518.1177, 2691.1981,
     2874.4195, 2898.3838, 3118.1300, 3133.1540, 3149.1353, 3519.4917, 3583.2288, 3716.2107, 3728.4763, 3732.2097,
     3748.1712, 3794.3838, 3808.3873, 3955.6468

9.   CAC83638.1     Mass: 19344     Score: 70     Expect: 15  Matches: 10
     nitrile hydratase beta chain, partial [uncultured bacterium BD2]
      Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
      943.5490   942.5417   942.5134    30.0     98 - 105    0    R.VQEILEGR.Y
     1017.5815  1016.5742  1016.5502    23.6     88 -  95    1    K.IITEEERK.H
     1236.7463  1235.7390  1235.6734    53.1     96 - 105    1    K.HRVQEILEGR.Y
     1342.8198  1341.8125  1341.7479    48.2     33 -  43    0    R.TLSILTWMHLK.G
     1358.8120  1357.8047  1357.7428    45.6     33 -  43    0    R.TLSILTWMHLK.G + Oxidation (M)
     1528.9209  1527.9136  1527.8508    41.1     82 -  94    1    R.ILVADKIITEEER.K
```

1597.8169	1596.8096	1596.7321	48.6	69 - 81	0	R.NSYYTHWLSAAER.I
1611.7590	1610.7517	1610.6790	45.1	21 - 32	0	K.DEPFFHYEWEGR.T
2202.1164	2201.1091	2201.1117	-1.16	127 - 147	0	R.LHEPHSLALPGAEPSFSLGDK.N
2671.2164	2670.2091	2670.3765	-62.69	123 - 147	1	K.AIERLHEPHSLALPGAEPSFSLGDK.N

No match to: 805.4494, 842.5035, 909.4046, 925.4130, 931.3994, 1008.5232, 1039.5620, 1050.5574, 1054.6213, 1073.5667, 1076.6081, 1085.6544, 1100.5430, 1117.5807, 1138.6538, 1145.6530, 1152.5748, 1168.5751, 1221.7220, 1330.7703, 1364.8023, 1413.8359, 1423.7457, 1545.9066, 1554.7713, 1567.7853, 1570.7642, 1576.8616, 1657.0233, 1678.9891, 1687.9118, 1697.0138, 1759.8782, 1794.8836, 1933.0507, 1950.1483, 1956.0934, 2003.1606, 2005.0365, 2211.0972, 2224.0416, 2229.1680, 2245.2213, 2252.2275, 2283.1447, 2297.1105, 2301.2929, 2429.2478, 2451.2298, 2518.1177, 2691.1981, 2874.4195, 2898.3838, 3118.1300, 3133.1540, 3149.1353, 3519.4917, 3583.2288, 3716.2107, 3728.4763, 3732.2097, 3748.1712, 3794.3838, 3808.3873, 3955.6468

10. WP_047545807.1 **Mass:** 30995 **Score:** 69 **Expect:** 19 **Matches:** 10

hypothetical protein [Psychroserpens sp. Hel_I_66]

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
1039.5620	1038.5547	1038.5498	4.74	188	- 195	1	R.KFFENVQK.T
1050.5574	1049.5501	1049.5618	-11.07	196	- 204	1	K.TRAFEISAR.N
1054.6213	1053.6140	1053.6797	-62.39	147	- 155	0	K.IIETIKPIK.N
1168.5751	1167.5679	1167.6037	-30.65	189	- 197	1	K.FFENVQKTR.A
1221.7220	1220.7148	1220.6401	61.2	22	- 32	0	K.GAIYSELVDVR.I
1567.7853	1566.7781	1566.7559	14.1	251	- 266	0	K.SDNSTVGSASTLMGLK.I
1570.7642	1569.7569	1569.7021	34.9	215	- 227	0	K.YCDAINFEIPEEK.R
2229.1680	2228.1607	2228.1776	-7.58	118	- 137	0	R.VATSFPVLDVFVNVACHIAR.G + Propionamide (C)
2451.2298	2450.2225	2450.2369	-5.88	229	- 250	1	R.YDEGKGLVVFNSSGYLEIAVYK.S
3519.4917	3518.4844	3518.6454	-45.76	79	- 108	0	K.HIAVQLDDHYFICANNGIMSMICSEIAPQK.I + Oxidation (M); 2 Propionamide (C)

No match to: 805.4494, 842.5035, 909.4046, 925.4130, 931.3994, 943.5490, 1008.5232, 1017.5815, 1073.5667, 1076.6081, 1085.6544, 1100.5430, 1117.5807, 1138.6538, 1145.6530, 1152.5748, 1236.7463, 1330.7703, 1342.8198, 1358.8120, 1364.8023, 1413.8359, 1423.7457, 1528.9209, 1545.9066, 1554.7713, 1576.8616, 1597.8169, 1611.7590,

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        1657.0233, 1678.9891, 1687.9118, 1697.0138, 1759.8782, 1794.8836, 1933.0507, 1950.1483, 1956.0934, 2003.1606,
        2005.0365, 2202.1164, 2211.0972, 2224.0416, 2245.2213, 2252.2275, 2283.1447, 2297.1105, 2301.2929, 2429.2478,
        2518.1177, 2671.2164, 2691.1981, 2874.4195, 2898.3838, 3118.1300, 3133.1540, 3149.1353, 3583.2288, 3716.2107,
        3728.4763, 3732.2097, 3748.1712, 3794.3838, 3808.3873, 3955.6468

11.     WP_005145929.1    Mass: 34512    Score: 66     Expect: 41  Matches: 10
        LysR family transcriptional regulator [Acinetobacter sp. ANC 3929]
         Observed   Mr(expt)   Mr(calc)    ppm  Start   End Miss  Peptide
        1039.5620  1038.5547  1038.5419    12.3   243 - 250    0   R.ILYMDIQK.E + Oxidation (M)
        1050.5574  1049.5501  1049.5393    10.3   132 - 139    0   R.YIDLIEER.I
        1054.6213  1053.6140  1053.5753    36.7   285 - 293    1   K.VHRCIDALK.Q
        1570.7642  1569.7569  1569.7821  -16.02    40 -  52    0   R.SLEQEMDVTLLHR.S
        1794.8836  1793.8763  1793.9168  -22.56     2 -  17    1   M.LDQLRAMGVFACVVEK.S + Oxidation (M)
        1933.0507  1932.0435  1931.9234    62.2     7 -  25    1   R.AMGVFACVVEKSSFSGAAR.D + Oxidation (M)
        2245.2213  2244.2140  2244.1507    28.2   232 - 250    1   K.SLCQQGHGIARILYMDIQK.E + Propionamide (C)
        2252.2275  2251.2202  2251.1557    28.7    18 -  39    1   K.SSFSGAARDLGITTSAVSQQIR.S
        2297.1105  2296.1033  2296.1600  -24.70   121 - 139    1   K.GLAIHFEADHRYIDLIEER.I
        2671.2164  2670.2091  2670.3145  -39.47    57 -  81    1   K.LSLTEAGQAFFLSCQEMLAAAERGK.I
        No match to: 805.4494, 842.5035, 909.4046, 925.4130, 931.3994, 943.5490, 1008.5232, 1017.5815, 1073.5667,
        1076.6081, 1085.6544, 1100.5430, 1117.5807, 1138.6538, 1145.6530, 1152.5748, 1168.5751, 1221.7220, 1236.7463,
        1330.7703, 1342.8198, 1358.8120, 1364.8023, 1413.8359, 1423.7457, 1528.9209, 1545.9066, 1554.7713, 1567.7853,
        1576.8616, 1597.8169, 1611.7590, 1657.0233, 1678.9891, 1687.9118, 1697.0138, 1759.8782, 1950.1483, 1956.0934,
        2003.1606, 2005.0365, 2202.1164, 2211.0972, 2224.0416, 2229.1680, 2283.1447, 2301.2929, 2429.2478, 2451.2298,
        2518.1177, 2691.1981, 2874.4195, 2898.3838, 3118.1300, 3133.1540, 3149.1353, 3519.4917, 3583.2288, 3716.2107,
        3728.4763, 3732.2097, 3748.1712, 3794.3838, 3808.3873, 3955.6468

12.     WP_005183230.1    Mass: 34482    Score: 66     Expect: 41  Matches: 10
        LysR family transcriptional regulator [Acinetobacter sp. ANC 4105]
         Observed   Mr(expt)   Mr(calc)    ppm  Start   End Miss  Peptide
        1039.5620  1038.5547  1038.5419    12.3   243 - 250    0   R.ILYMDIQK.E + Oxidation (M)
        1050.5574  1049.5501  1049.5393    10.3   132 - 139    0   R.YIDLIEER.I
        1054.6213  1053.6140  1053.5753    36.7   285 - 293    1   K.VHRCIDALK.Q
        1570.7642  1569.7569  1569.7821  -16.02    40 -  52    0   R.SLEQEMDVTLLHR.S
        1794.8836  1793.8763  1793.9168  -22.56     2 -  17    1   M.LDQLRAMGVFACVVEK.S + Oxidation (M)
        1933.0507  1932.0435  1931.9234    62.2     7 -  25    1   R.AMGVFACVVEKSSFSGAAR.D + Oxidation (M)
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```
2245.2213  2244.2140  2244.1507    28.2   232 - 250   1   K.SLCQQGHGIARILYMDIQK.E + Propionamide (C)
2252.2275  2251.2202  2251.1557    28.7    18 -  39   1   K.SSFSGAARDLGITTSAVSQQIR.S
2297.1105  2296.1033  2296.1600  -24.70   121 - 139   1   K.GLAIHFEADHRYIDLIEER.I
2671.2164  2670.2091  2670.3145  -39.47    57 -  81   1   K.LSLTEAGQAFFLSCQEMLAAAERGK.I
No match to: 805.4494, 842.5035, 909.4046, 925.4130, 931.3994, 943.5490, 1008.5232, 1017.5815, 1073.5667,
1076.6081, 1085.6544, 1100.5430, 1117.5807, 1138.6538, 1145.6530, 1152.5748, 1168.5751, 1221.7220, 1236.7463,
1330.7703, 1342.8198, 1358.8120, 1364.8023, 1413.8359, 1423.7457, 1528.9209, 1545.9066, 1554.7713, 1567.7853,
1576.8616, 1597.8169, 1611.7590, 1657.0233, 1678.9891, 1687.9118, 1697.0138, 1759.8782, 1950.1483, 1956.0934,
2003.1606, 2005.0365, 2202.1164, 2211.0972, 2224.0416, 2229.1680, 2283.1447, 2301.2929, 2429.2478, 2451.2298,
2518.1177, 2691.1981, 2874.4195, 2898.3838, 3118.1300, 3133.1540, 3149.1353, 3519.4917, 3583.2288, 3716.2107,
3728.4763, 3732.2097, 3748.1712, 3794.3838, 3808.3873, 3955.6468

13.  WP_005295489.1    Mass: 34482    Score: 66    Expect: 41  Matches: 10
     LysR family transcriptional regulator [Acinetobacter sp. NIPH 2100]
      Observed   Mr(expt)   Mr(calc)    ppm  Start   End Miss  Peptide
     1039.5620  1038.5547  1038.5419    12.3   243 - 250   0   R.ILYMDIQK.E + Oxidation (M)
     1050.5574  1049.5501  1049.5393    10.3   132 - 139   0   R.YIDLIEER.I
     1054.6213  1053.6140  1053.5753    36.7   285 - 293   1   K.VHRCIDALK.Q
     1570.7642  1569.7569  1569.7821  -16.02    40 -  52   0   R.SLEQEMDVTLLHR.S
     1794.8836  1793.8763  1793.9168  -22.56     2 -  17   1   M.LDQLRAMGVFACVVEK.S + Oxidation (M)
     1933.0507  1932.0435  1931.9234    62.2     7 -  25   1   R.AMGVFACVVEKSSFSGAAR.D + Oxidation (M)
     2245.2213  2244.2140  2244.1507    28.2   232 - 250   1   K.SLCQQGHGIARILYMDIQK.E + Propionamide (C)
     2252.2275  2251.2202  2251.1557    28.7    18 -  39   1   K.SSFSGAARDLGITTSAVSQQIR.S
     2297.1105  2296.1033  2296.1600  -24.70   121 - 139   1   K.GLAIHFEADHRYIDLIEER.I
     2671.2164  2670.2091  2670.3145  -39.47    57 -  81   1   K.LSLTEAGQAFFLSCQEMLAAAERGK.I
     No match to: 805.4494, 842.5035, 909.4046, 925.4130, 931.3994, 943.5490, 1008.5232, 1017.5815, 1073.5667,
     1076.6081, 1085.6544, 1100.5430, 1117.5807, 1138.6538, 1145.6530, 1152.5748, 1168.5751, 1221.7220, 1236.7463,
     1330.7703, 1342.8198, 1358.8120, 1364.8023, 1413.8359, 1423.7457, 1528.9209, 1545.9066, 1554.7713, 1567.7853,
     1576.8616, 1597.8169, 1611.7590, 1657.0233, 1678.9891, 1687.9118, 1697.0138, 1759.8782, 1950.1483, 1956.0934,
     2003.1606, 2005.0365, 2202.1164, 2211.0972, 2224.0416, 2229.1680, 2283.1447, 2301.2929, 2429.2478, 2451.2298,
     2518.1177, 2691.1981, 2874.4195, 2898.3838, 3118.1300, 3133.1540, 3149.1353, 3519.4917, 3583.2288, 3716.2107,
     3728.4763, 3732.2097, 3748.1712, 3794.3838, 3808.3873, 3955.6468

14.  WP_005213279.1    Mass: 34512    Score: 66    Expect: 41  Matches: 10
     LysR family transcriptional regulator [Acinetobacter sp. NIPH 1867]
      Observed   Mr(expt)   Mr(calc)    ppm  Start   End Miss  Peptide
```

1039.5620	1038.5547	1038.5419	12.3	243	250	0	R.ILYMDIQK.E + Oxidation (M)
1050.5574	1049.5501	1049.5393	10.3	132	139	0	R.YIDLIEER.I
1054.6213	1053.6140	1053.5753	36.7	285	293	1	K.VHRCIDALK.Q
1570.7642	1569.7569	1569.7821	-16.02	40	52	0	R.SLEQEMDVTLLHR.S
1794.8836	1793.8763	1793.9168	-22.56	2	17	1	M.LDQLRAMGVFACVVEK.S + Oxidation (M)
1933.0507	1932.0435	1931.9234	62.2	7	25	1	R.AMGVFACVVEKSSFSGAAR.D + Oxidation (M)
2245.2213	2244.2140	2244.1507	28.2	232	250	1	K.SLCQQGHGIARILYMDIQK.E + Propionamide (C)
2252.2275	2251.2202	2251.1557	28.7	18	39	1	K.SSFSGAARDLGITTSAVSQQIR.S
2297.1105	2296.1033	2296.1600	-24.70	121	139	1	K.GLAIHFEADHRYIDLIEER.I
2671.2164	2670.2091	2670.3145	-39.47	57	81	1	K.LSLTEAGQAFFLSCQEMLAAAERGK.I

No match to: 805.4494, 842.5035, 909.4046, 925.4130, 931.3994, 943.5490, 1008.5232, 1017.5815, 1073.5667, 1076.6081, 1085.6544, 1100.5430, 1117.5807, 1138.6538, 1145.6530, 1152.5748, 1168.5751, 1221.7220, 1236.7463, 1330.7703, 1342.8198, 1358.8120, 1364.8023, 1413.8359, 1423.7457, 1528.9209, 1545.9066, 1554.7713, 1567.7853, 1576.8616, 1597.8169, 1611.7590, 1657.0233, 1678.9891, 1687.9118, 1697.0138, 1759.8782, 1950.1483, 1956.0934, 2003.1606, 2005.0365, 2202.1164, 2211.0972, 2224.0416, 2229.1680, 2283.1447, 2301.2929, 2429.2478, 2451.2298, 2518.1177, 2691.1981, 2874.4195, 2898.3838, 3118.1300, 3133.1540, 3149.1353, 3519.4917, 3583.2288, 3716.2107, 3728.4763, 3732.2097, 3748.1712, 3794.3838, 3808.3873, 3955.6468

15. WP_107654896.1 **Mass:** 46639 **Score:** 65 **Expect:** 47 **Matches:** 12

DUF3558 domain-containing protein [Nocardia suismassiliense]

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
1073.5667	1072.5594	1072.5335	24.1	119	128	0	R.ATDPCALLNR.E
1152.5748	1151.5676	1151.6299	-54.10	79	89	0	K.VRPSAEPTAPK.A
1342.8198	1341.8125	1341.7187	69.9	117	128	1	R.IRATDPCALLNR.E
1413.8359	1412.8287	1412.7558	51.6	117	128	1	R.IRATDPCALLNR.E + Propionamide (C)
1545.9066	1544.8993	1544.7947	67.7	341	355	0	R.LPSGLDGGQAIQYAR.H
1611.7590	1610.7517	1610.7834	-19.71	378	390	1	R.ENSTCAITLNYRR.A + Propionamide (C)
1759.8782	1758.8709	1758.9199	-27.86	303	318	1	K.AYKCAITLVQTGGAHR.A + Propionamide (C)
2202.1164	2201.1091	2201.1189	-4.44	335	355	1	K.TGEVNRLPSGLDGGQAIQYAR.H

2252.2275	2251.2202	2251.1420	34.8	214	-	235	1	R.IPAGDTGFAHHLSVAKMTGPTK.T + Oxidation (M)
2297.1105	2296.1033	2296.1481	-19.53	93	-	116	0	K.AQAGTPGSQELAAIAPGTADLMAR.I
2671.2164	2670.2091	2670.2889	-29.88	53	-	78	0	R.GWAAMAALATVVLMVCACGTISTEAK.V + 2 Oxidation (M); Propionamide (C)
2898.3838	2897.3766	2897.4271	-17.46	52	-	78	1	R.RGWAAMAALATVVLMVCACGTISTEAK.V + 2 Oxidation (M); 2 Propionamide (C)

No match to: 805.4494, 842.5035, 909.4046, 925.4130, 931.3994, 943.5490, 1008.5232, 1017.5815, 1039.5620, 1050.5574, 1054.6213, 1076.6081, 1085.6544, 1100.5430, 1117.5807, 1138.6538, 1145.6530, 1168.5751, 1221.7220, 1236.7463, 1330.7703, 1358.8120, 1364.8023, 1423.7457, 1528.9209, 1554.7713, 1567.7853, 1570.7642, 1576.8616, 1597.8169, 1657.0233, 1678.9891, 1687.9118, 1697.0138, 1794.8836, 1933.0507, 1950.1483, 1956.0934, 2003.1606, 2005.0365, 2211.0972, 2224.0416, 2229.1680, 2245.2213, 2283.1447, 2301.2929, 2429.2478, 2451.2298, 2518.1177, 2691.1981, 2874.4195, 3118.1300, 3133.1540, 3149.1353, 3519.4917, 3583.2288, 3716.2107, 3728.4763, 3732.2097, 3748.1712, 3794.3838, 3808.3873, 3955.6468

16. XP_004363930.1 **Mass:** 63588 **Score:** 65 **Expect:** 52 **Matches:** 14

hypothetical protein CAOG_03091 [Capsaspora owczarzaki ATCC 30864]

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**		**End**	**Miss**	**Peptide**
842.5035	841.4962	841.5385	-50.27	515	-	522	0	K.AVIATIVR.R
1168.5751	1167.5679	1167.5859	-15.44	139	-	148	0	R.MLTPAFHHSK.L
1358.8120	1357.8047	1357.7388	48.6	329	-	339	1	K.RDLLDLLMDVR.D
1364.8023	1363.7951	1363.7936	1.09	119	-	131	1	K.RVIGHALLTAEGK.E
1423.7457	1422.7385	1422.6627	53.3	474	-	487	0	R.FLSEEQGGTGEAAK.V
1528.9209	1527.9136	1527.9249	-7.36	107	-	119	1	R.YARPLLATNLLKR.V
1554.7713	1553.7640	1553.7912	-17.52	236	-	249	0	R.AMFDLFSDLLAVGR.F
1570.7642	1569.7569	1569.7861	-18.59	236	-	249	0	R.AMFDLFSDLLAVGR.F + Oxidation (M)
1597.8169	1596.8096	1596.7285	50.8	502	-	514	1	R.MCIGHKFATMEMK.A + Propionamide (C)
1611.7590	1610.7517	1610.8450	-57.91	408	-	421	1	K.LSYLSAVISEAMRR.Y + Oxidation (M)
1687.9118	1686.9045	1686.8723	19.1	431	-	445	1	R.VAMQDDVIGNVQVRK.G + Oxidation (M)
1697.0138	1696.0066	1695.9052	59.8	508	-	522	1	K.FATMEMKAVIATIVR.R + Oxidation (M)
1759.8782	1758.8709	1758.9377	-37.95	120	-	135	1	R.VIGHALLTAEGKEHER.M
2224.0416	2223.0343	2222.9678	29.9	390	-	407	0	R.SELEDFDVEHMTWESLEK.L

No match to: 805.4494, 909.4046, 925.4130, 931.3994, 943.5490, 1008.5232, 1017.5815, 1039.5620, 1050.5574, 1054.6213, 1073.5667, 1076.6081, 1085.6544, 1100.5430, 1117.5807, 1138.6538, 1145.6530, 1152.5748, 1221.7220, 1236.7463, 1330.7703, 1342.8198, 1413.8359, 1545.9066, 1567.7853, 1576.8616, 1657.0233, 1678.9891, 1794.8836, 1933.0507, 1950.1483, 1956.0934, 2003.1606, 2005.0365, 2202.1164, 2211.0972, 2229.1680, 2245.2213, 2252.2275,

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          2283.1447, 2297.1105, 2301.2929, 2429.2478, 2451.2298, 2518.1177, 2671.2164, 2691.1981, 2874.4195, 2898.3838,
          3118.1300, 3133.1540, 3149.1353, 3519.4917, 3583.2288, 3716.2107, 3728.4763, 3732.2097, 3748.1712, 3794.3838,
          3808.3873, 3955.6468

17.       WP_004880504.1     Mass: 34674     Score: 64     Expect: 58  Matches: 10
          MULTISPECIES: LysR family transcriptional regulator [Acinetobacter]
           Observed   Mr(expt)   Mr(calc)     ppm  Start    End Miss   Peptide
          1039.5620  1038.5547  1038.5419    12.3    243 -  250    0   R.ILYMDIQK.E + Oxidation (M)
          1050.5574  1049.5501  1049.5393    10.3    132 -  139    0   R.YIDLIEER.I
          1054.6213  1053.6140  1053.5753    36.7    285 -  293    1   K.VHRCIDALK.Q
          1145.6530  1144.6457  1144.6638  -15.80    140 -  149    1   R.IDIAVRMSLK.M
          1570.7642  1569.7569  1569.7821  -16.02     40 -   52    0   R.SLEQEMDVTLLHR.S
          1794.8836  1793.8763  1793.9168  -22.56      2 -   17    1   M.LDQLRAMGVFACVVEK.S + Oxidation (M)
          1933.0507  1932.0435  1931.9234    62.2      7 -   25    1   R.AMGVFACVVEKSSFSGAAR.E + Oxidation (M)
          2245.2213  2244.2140  2244.1507    28.2    232 -  250    1   K.SLCQQGHGIARILYMDIQK.E + Propionamide (C)
          2297.1105  2296.1033  2296.1600  -24.70    121 -  139    1   K.GLAIHFEADHRYIDLIEER.I
          2671.2164  2670.2091  2670.3145  -39.47     57 -   81    1   K.LSLTEAGQAFFLSCQEMLAAAERGK.I
          No match to: 805.4494, 842.5035, 909.4046, 925.4130, 931.3994, 943.5490, 1008.5232, 1017.5815, 1073.5667,
          1076.6081, 1085.6544, 1100.5430, 1117.5807, 1138.6538, 1152.5748, 1168.5751, 1221.7220, 1236.7463, 1330.7703,
          1342.8198, 1358.8120, 1364.8023, 1413.8359, 1423.7457, 1528.9209, 1545.9066, 1554.7713, 1567.7853, 1576.8616,
          1597.8169, 1611.7590, 1657.0233, 1678.9891, 1687.9118, 1697.0138, 1759.8782, 1950.1483, 1956.0934, 2003.1606,
          2005.0365, 2202.1164, 2211.0972, 2224.0416, 2229.1680, 2252.2275, 2283.1447, 2301.2929, 2429.2478, 2451.2298,
          2518.1177, 2691.1981, 2874.4195, 2898.3838, 3118.1300, 3133.1540, 3149.1353, 3519.4917, 3583.2288, 3716.2107,
          3728.4763, 3732.2097, 3748.1712, 3794.3838, 3808.3873, 3955.6468

18.       AJY18677.1     Mass: 34526     Score: 64     Expect: 59  Matches: 11
          bacterial regulatory helix-turn-helix, lysR family protein [Burkholderia multivorans ATCC BAA-247]
           Observed   Mr(expt)   Mr(calc)     ppm  Start    End Miss   Peptide
           943.5490   942.5417   942.5498   -8.60     93 -  101    0   R.VTAPVSLTR.R
          1017.5815  1016.5742  1016.6230  -47.98     23 -   32    1   R.LGLSKSVVSK.R
          1221.7220  1220.7148  1220.6475    55.1    161 -  171    0   R.VIVCSPEYIAK.H
          1364.8023  1363.7951  1363.7459    36.0    172 -  183    1   K.HGEPKSIDQLLK.H
          1423.7457  1422.7385  1422.7143    17.0      2 -   13    0   M.DDIQAFLFAVER.Q
          1554.7713  1553.7640  1553.7548    5.90      1 -   13    0   -.MDDIQAFLFAVER.Q
          1570.7642  1569.7569  1569.7497    4.59      1 -   13    0   -.MDDIQAFLFAVER.Q + Oxidation (M)
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     1759.8782  1758.8709  1758.9662  -54.18    34 -  48    1   R.ISDLERTLGVQLLMR.S + Oxidation (M)
     2252.2275  2251.2202  2251.1379    36.6    72 -  92    1   R.QLVDVSEAIAERAHGVCGELR.V
     2429.2478  2428.2405  2428.1693    29.3     1 -  21    1   -.MDDIQAFLFAVERQSITDSAR.R + Oxidation (M)
     2898.3838  2897.3766  2897.3780   -0.48   184 - 210    1   K.HRCLNYSTAAPSATWSFAAPDGHGKPR.A
     No match to: 805.4494, 842.5035, 909.4046, 925.4130, 931.3994, 1008.5232, 1039.5620, 1050.5574, 1054.6213,
     1073.5667, 1076.6081, 1085.6544, 1100.5430, 1117.5807, 1138.6538, 1145.6530, 1152.5748, 1168.5751, 1236.7463,
     1330.7703, 1342.8198, 1358.8120, 1413.8359, 1528.9209, 1545.9066, 1567.7853, 1576.8616, 1597.8169, 1611.7590,
     1657.0233, 1678.9891, 1687.9118, 1697.0138, 1794.8836, 1933.0507, 1950.1483, 1956.0934, 2003.1606, 2005.0365,
     2202.1164, 2211.0972, 2224.0416, 2229.1680, 2245.2213, 2283.1447, 2297.1105, 2301.2929, 2451.2298, 2518.1177,
     2671.2164, 2691.1981, 2874.4195, 3118.1300, 3133.1540, 3149.1353, 3519.4917, 3583.2288, 3716.2107, 3728.4763,
     3732.2097, 3748.1712, 3794.3838, 3808.3873, 3955.6468

19.  WP_066550229.1     Mass: 13748     Score: 63     Expect: 70  Matches: 7
     MULTISPECIES: nitrite reductase (NAD(P)H) small subunit [Sphingomonadales]
      Observed   Mr(expt)   Mr(calc)    ppm  Start   End Miss   Peptide
     1145.6530  1144.6457  1144.6717  -22.69    99 - 108    1   K.VDGGRLFLLR.E
     1413.8359  1412.8287  1412.7446    59.5    90 - 103    1   R.GCTPTIPLKVDGGR.L
     1576.8616  1575.8544  1575.7868    42.9    42 -  54    1   R.GEYFALVNKCPHK.H + Propionamide (C)
     1759.8782  1758.8709  1758.9516  -45.88    25 -  41    0   R.TLPVAGGEEIAVFLTSR.G
     2202.1164  2201.1091  2201.1804  -32.40    20 -  41    1   K.AGSARTLPVAGGEEIAVFLTSR.G
     2429.2478  2428.2405  2428.1165    51.1    55 -  76    0   K.HGPLSEGMVHGDSVTCPLHNWR.I
     2898.3838  2897.3766  2897.4177  -14.21    55 -  80    1   K.HGPLSEGMVHGDSVTCPLHNWRISLR.T
     No match to: 805.4494, 842.5035, 909.4046, 925.4130, 931.3994, 943.5490, 1008.5232, 1017.5815, 1039.5620,
     1050.5574, 1054.6213, 1073.5667, 1076.6081, 1085.6544, 1100.5430, 1117.5807, 1138.6538, 1152.5748, 1168.5751,
     1221.7220, 1236.7463, 1330.7703, 1342.8198, 1358.8120, 1364.8023, 1423.7457, 1528.9209, 1545.9066, 1554.7713,
     1567.7853, 1570.7642, 1597.8169, 1611.7590, 1657.0233, 1678.9891, 1687.9118, 1697.0138, 1794.8836, 1933.0507,
     1950.1483, 1956.0934, 2003.1606, 2005.0365, 2211.0972, 2224.0416, 2229.1680, 2245.2213, 2252.2275, 2283.1447,
     2297.1105, 2301.2929, 2451.2298, 2518.1177, 2671.2164, 2691.1981, 2874.4195, 3118.1300, 3133.1540, 3149.1353,
     3519.4917, 3583.2288, 3716.2107, 3728.4763, 3732.2097, 3748.1712, 3794.3838, 3808.3873, 3955.6468

20.  WP_069623671.1     Mass: 27359     Score: 63     Expect: 76  Matches: 9
     alpha/beta hydrolase [Methyloceanibacter marginalis]
      Observed   Mr(expt)   Mr(calc)    ppm  Start   End Miss   Peptide
     1050.5574  1049.5501  1049.5182    30.5   219 - 226    0   K.QAEFWELK.D
     1085.6544  1084.6471  1084.6029    40.8   241 - 250    1   K.IAARIADWLG.-
     1576.8616  1575.8544  1575.7715    52.6   227 - 240    0   K.DHAHMLLIEPGAEK.I + Oxidation (M)
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1794.8836  1793.8763  1793.8593   9.50   118 - 132   0   K.QLCQDLMSIGPFWTR.A
2202.1164  2201.1091  2201.1184  -4.23   192 - 211   0   R.CPVLCLSGAQDNIVSLQTAK.E + 2 Propionamide (C)
2229.1680  2228.1607  2228.1299   13.8   133 - 151   0   R.ALDPNFDLACHYTLNLLPK.D + Propionamide (C)
2283.1447  2282.1374  2282.0183   52.2     4 -  23   1   K.NIVMVHGANCGGWCFDEFRK.V
2297.1105  2296.1033  2295.9976   46.0     4 -  22   0   K.NIVMVHGANCGGWCFDEFR.K + 2 Propionamide (C)
2451.2298  2450.2225  2450.1082   46.6     2 -  22   1   M.PKNIVMVHGANCGGWCFDEFR.K + Propionamide (C)
No match to: 805.4494, 842.5035, 909.4046, 925.4130, 931.3994, 943.5490, 1008.5232, 1017.5815, 1039.5620,
1054.6213, 1073.5667, 1076.6081, 1100.5430, 1117.5807, 1138.6538, 1145.6530, 1152.5748, 1168.5751, 1221.7220,
1236.7463, 1330.7703, 1342.8198, 1358.8120, 1364.8023, 1413.8359, 1423.7457, 1528.9209, 1545.9066, 1554.7713,
1567.7853, 1570.7642, 1597.8169, 1611.7590, 1657.0233, 1678.9891, 1687.9118, 1697.0138, 1759.8782, 1933.0507,
1950.1483, 1956.0934, 2003.1606, 2005.0365, 2211.0972, 2224.0416, 2245.2213, 2252.2275, 2301.2929, 2429.2478,
2518.1177, 2671.2164, 2691.1981, 2874.4195, 2898.3838, 3118.1300, 3133.1540, 3149.1353, 3519.4917, 3583.2288,
3716.2107, 3728.4763, 3732.2097, 3748.1712, 3794.3838, 3808.3873, 3955.6468
```

Search Parameters

```
Type of search         : Peptide Mass Fingerprint
Enzyme                 : Trypsin
Variable modifications : Oxidation (M),Propionamide (C)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Peptide Charge State   : 1+
Max Missed Cleavages   : 1
Number of queries      : 75
```

4. The protein band of approx. 24 kDa, obtained from the crude extract of *R. rhodochrous* M33 cells, grown on the medium with nickel.

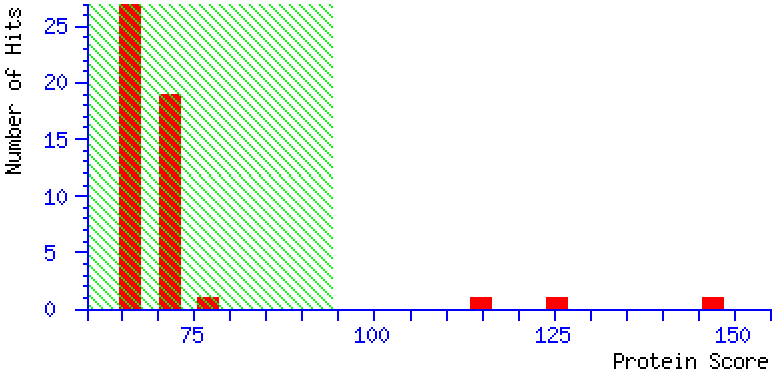
MATRIX SCIENCE

Mascot Search Results

```
User             : toropygin
Email            : toropygin@rambler.ru
Search title     : 04
Database         : NCBIprot 20180429 (152462470 sequences; 55858910152 residues)
Timestamp        : 1 Sep 2018 at 16:34:52 GMT
Top Score        : 147 for WP_006940500.1, MULTISPECIES: nitrile hydratase subunit alpha [Rhodococcus]
```

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 94 are significant (p<0.05).



Protein Summary Report

Format As	Protein Summary ▾	Help
	Significance threshold p< 0.05	Max. number of hits 20
	Preferred taxonomy All entries ▾	

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.

Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-

-Accession- -Sequence-

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
☑ 842.4989 **(1+)**				●				●				●		●						●
☑ 870.5361 **(1+)**																				
☑ 889.5177 **(1+)**												●								
☑ 908.4707 **(1+)**												●								
☑ 931.4287 **(1+)**	●	●	●				●						●							
☑ 1012.6027 **(1+)**	●	●	●		●															●
☑ 1051.5157 **(1+)**	●	●	●					●		●	●		●					●	●	●
☑ 1055.4616 **(1+)**																				
☑ 1069.4193 **(1+)**																				
☑ 1078.5508 **(1+)**	●	●	●		●	●	●		●	●	●	●						●	●	
☑ 1100.5360 **(1+)**																				
☑ 1107.6437 **(1+)**	●	●				●			●											
☑ 1129.6270 **(1+)**																				
☑ 1179.6156 **(1+)**	●	●	●					●			●				●	●			●	●
☑ 1188.7038 **(1+)**										●	●	●								
☑ 1201.5984 **(1+)**																				

☑	**1438.1686** **(1+)**																				
☑	**1522.7159** **(1+)**																				
☑	**1537.7339** **(1+)**	●	●	●	●									●	●	●				●	
☑	**1546.2266** **(1+)**																				
☑	**1550.7359** **(1+)**																				
☑	**1559.7652** **(1+)**				●	●	●	●		●			●	●				●			
☑	**1565.7838** **(1+)**					●		●			●	●	●				●	●	●		
☑	**1574.8472** **(1+)**																				
☑	**1625.7921** **(1+)**	●	●	●									●	●	●				●	●	
☑	**1673.7669** **(1+)**																				
☑	**1678.9113** **(1+)**												●								
☑	**1693.8516** **(1+)**	●	●	●	●									●	●	●	●	●	●	●	●
☑	**1713.8370** **(1+)**	●	●	●			●		●	●								●	●		
☑	**1729.8293** **(1+)**	●	●	●														●	●		
☑	**1735.8209** **(1+)**										●		●	●		●	●	●		●	
☑	**1772.9007** **(1+)**	●	●	●																	
☑	**1781.9871** **(1+)**						●			●		●	●	●	●				●	●	
☑	**1794.8987** **(1+)**					●	●			●		●									
☑	**1954.6746** **(1+)**																				

☑	2005.0908 (1+)						●		●	●								●			●
☑	2211.0929 (1+)																				
☑	2234.5867 (1+)																				
☑	2284.1530 (1+)																●				
☑	2297.0154 (1+)										●										
☑	2302.1281 (1+)																				
☑	2328.1102 (1+)																				
☑	2331.1766 (1+)				●		●	●		●	●	●							●		
☑	2346.1572 (1+)	●				●	●		●	●							●	●			●
☑	2362.1863 (1+)					●	●			●							●	●			●
☑	2368.1527 (1+)				●	●			●		●						●				●
☑	2374.2028 (1+)					●										●					
☑	2378.1596 (1+)																				
☑	2482.1949 (1+)										●										

Search Selected

Index

Accession	Mass	Score	Description

1.	**WP_006940500.1**	22776	147	MULTISPECIES: nitrile hydratase subunit alpha [Rhodococcus]
2.	**P21219.3**	22820	128	RecName: Full=High-molecular weight cobalt-containing nitrile hydratase subunit alpha; Short=H-NHase; Short=H-nitrilase
3.	**CAC83635.1**	20309	112	nitrile hydratase alpha chain, partial [uncultured bacterium SP1]
4.	**WP_019563598.1**	15157	77	MULTISPECIES: hypothetical protein [Thioalkalivibrio]
5.	**WP_034679054.1**	48801	74	diaminobutyrate--2-oxoglutarate transaminase [Acinetobacter sp. WC-141]
6.	**KOF78604.1**	64850	74	hypothetical protein OCBIM_22030533mg [Octopus bimaculoides]
7.	**WP_104689207.1**	7824	73	hypothetical protein [Lactobacillus pontis]
8.	**SFE83046.1**	27116	73	ABC transporter [Thermoanaerobacter thermohydrosulfuricus]
9.	**XP_014779384.1**	68715	73	PREDICTED: LOW QUALITY PROTEIN: very long-chain specific acyl-CoA dehydrogenase, mitochondrial-like [Octopus bimaculoides]
10.	**WP_004376243.1**	29769	73	GTP cyclohydrolase I FolE2 [Thauera phenylacetica]
11.	**OUU50395.1**	47634	73	hypothetical protein CBC14_05930 [Alphaproteobacteria bacterium TMED54]
12.	**EPR18237.1**	34566	72	integrase [Sphingobium chinhatense IP26]
13.	**WP_081588065.1**	47007	72	glycosyltransferase [Gloeocapsa sp. PCC 7428]
14.	**WP_083469462.1**	7938	72	hypothetical protein [Methylobacterium variabile]
15.	**EIE87316.1**	6498	71	hypothetical protein RO3G_12027 [Rhizopus delemar RA 99-880]
16.	**WP_047381104.1**	24434	71	peptidase [Chryseobacterium sp. YR485]
17.	**WP_076866932.1**	34360	71	AraC family transcriptional regulator [Bradyrhizobium mercantei]
18.	**WP_089684046.1**	40561	70	hypothetical protein [Halomonas gudaonensis]
19.	**ART89119.1**	29503	70	coat protein [Tomato leaf curl Joydebpur virus]
20.	**WP_100163559.1**	75038	70	3-hydroxyacyl-CoA dehydrogenase [Pseudooceanicola lipolyticus]

Results List

```
1.      WP_006940500.1     Mass: 22776     Score: 147     Expect: 3e-07  Matches: 13
        MULTISPECIES: nitrile hydratase subunit alpha [Rhodococcus]
         Observed    Mr(expt)    Mr(calc)    ppm  Start    End Miss  Peptide
          931.4287    930.4214    930.4083   14.1      8 -   14    0   K.YTEYEAR.T
         1012.6027   1011.5954   1011.5713   23.9     26 -   35    0   R.GLITPAAVDR.V
         1051.5157   1050.5084   1050.4771   29.8     56 -   63    0   K.SWVDPEYR.K
         1078.5508   1077.5435   1077.5091   32.0    153 -  161    0   R.VWDSSSEIR.Y
         1107.6437   1106.6365   1106.5971   35.5     17 -   25    0   K.AIETLLYER.G
         1179.6156   1178.6083   1178.5720   30.8     56 -   64    1   K.SWVDPEYRK.W
         1537.7339   1536.7266   1536.7097   11.0    140 -  152    0   R.DFGFDIPDEVEVR.V
         1625.7921   1624.7849   1624.7481   22.6      2 -   14    1   M.SEHVNKYTEYEAR.T
         1693.8516   1692.8443   1692.8108   19.8    139 -  152    1   K.RDFGFDIPDEVEVR.V
         1713.8370   1712.8297   1712.8080   12.7     36 -   51    0   R.VVSYYENEIGPMGGAK.V
         1729.8293   1728.8220   1728.8029   11.1     36 -   51    0   R.VVSYYENEIGPMGGAK.V + Oxidation (M)
         1772.9007   1771.8934   1771.9026  -5.18    187 -  203    0   R.DSMIGVSNALTPQEVIV.-
         2346.1572   2345.1499   2345.1539  -1.70    162 -  182    0   R.YIVIPERPAGTDGWSEDELAK.L
        No match to: 842.4989, 870.5361, 889.5177, 908.4707, 1055.4616, 1069.4193, 1100.5360, 1129.6270, 1188.7038,
        1201.5984, 1438.1686, 1522.7159, 1546.2266, 1550.7359, 1559.7652, 1565.7838, 1574.8472, 1673.7669, 1678.9113,
        1735.8209, 1781.9871, 1794.8987, 1954.6746, 2005.0908, 2211.0929, 2234.5867, 2284.1530, 2297.0154, 2302.1281,
        2328.1102, 2331.1766, 2362.1863, 2368.1527, 2374.2028, 2378.1596, 2482.1949

2.
        P21219.3     Mass: 22820     Score: 128     Expect: 2.4e-05  Matches: 12

        RecName: Full=High-molecular weight cobalt-containing nitrile hydratase subunit alpha; Short=H-NHase; Short=H-
        nitrilase
         Observed    Mr(expt)    Mr(calc)    ppm  Start    End Miss  Peptide
          931.4287    930.4214    930.4083   14.1      8 -   14    0   K.YTEYEAR.T
         1012.6027   1011.5954   1011.5713   23.9     26 -   35    0   R.GLITPAAVDR.V
         1051.5157   1050.5084   1050.4771   29.8     56 -   63    0   K.SWVDPEYR.K
         1078.5508   1077.5435   1077.5091   32.0    153 -  161    0   R.VWDSSSEIR.Y
         1107.6437   1106.6365   1106.5971   35.5     17 -   25    0   K.AIETLLYER.G
         1179.6156   1178.6083   1178.5720   30.8     56 -   64    1   K.SWVDPEYRK.W
         1537.7339   1536.7266   1536.7097   11.0    140 -  152    0   R.DFGFDIPDEVEVR.V
```

```
1625.7921  1624.7849  1624.7481   22.6     2 -  14   1   M.SEHVNKYTEYEAR.T
1693.8516  1692.8443  1692.8108   19.8   139 - 152   1   K.RDFGFDIPDEVEVR.V
1713.8370  1712.8297  1712.8080   12.7    36 -  51   0   R.VVSYYENEIGPMGGAK.V
1729.8293  1728.8220  1728.8029   11.1    36 -  51   0   R.VVSYYENEIGPMGGAK.V + Oxidation (M)
1772.9007  1771.8934  1771.9026  -5.18   187 - 203   0   R.DSMIGVSNALTPQEVIV.-
No match to: 842.4989, 870.5361, 889.5177, 908.4707, 1055.4616, 1069.4193, 1100.5360, 1129.6270, 1188.7038,
1201.5984, 1438.1686, 1522.7159, 1546.2266, 1550.7359, 1559.7652, 1565.7838, 1574.8472, 1673.7669, 1678.9113,
1735.8209, 1781.9871, 1794.8987, 1954.6746, 2005.0908, 2211.0929, 2234.5867, 2284.1530, 2297.0154, 2302.1281,
2328.1102, 2331.1766, 2346.1572, 2362.1863, 2368.1527, 2374.2028, 2378.1596, 2482.1949
```

```
3.   CAC83635.1    Mass: 20309    Score: 112    Expect: 0.00096  Matches: 11
     nitrile hydratase alpha chain, partial [uncultured bacterium SP1]
      Observed    Mr(expt)    Mr(calc)    ppm   Start    End Miss    Peptide
      931.4287    930.4214    930.4083   14.1      8 -  14    0    K.YTEYEAR.T
     1012.6027   1011.5954   1011.5713   23.9     26 -  35    0    R.GLITPAAVDR.V
     1051.5157   1050.5084   1050.4771   29.8     56 -  63    0    K.SWVDPEYR.K
     1078.5508   1077.5435   1077.5091   32.0    141 - 149    0    R.VWDSSSEIR.Y
     1179.6156   1178.6083   1178.5720   30.8     56 -  64    1    K.SWVDPEYRK.W
     1537.7339   1536.7266   1536.7097   11.0    128 - 140    0    R.DFGFDIPDEVEVR.V
     1625.7921   1624.7849   1624.7481   22.6      2 -  14    1    M.SEHVNKYTEYEAR.T
     1693.8516   1692.8443   1692.8108   19.8    127 - 140    1    K.RDFGFDIPDEVEVR.V
     1713.8370   1712.8297   1712.8080   12.7     36 -  51    0    R.VVSYYENEIGPMGGAK.V
     1729.8293   1728.8220   1728.8029   11.1     36 -  51    0    R.VVSYYENEIGPMGGAK.V + Oxidation (M)
     1772.9007   1771.8934   1771.7835   62.0      1 -  14    1    -.MSEHVNKYTEYEAR.T + Oxidation (M)
     No match to: 842.4989, 870.5361, 889.5177, 908.4707, 1055.4616, 1069.4193, 1100.5360, 1107.6437, 1129.6270,
     1188.7038, 1201.5984, 1438.1686, 1522.7159, 1546.2266, 1550.7359, 1559.7652, 1565.7838, 1574.8472, 1673.7669,
     1678.9113, 1735.8209, 1781.9871, 1794.8987, 1954.6746, 2005.0908, 2211.0929, 2234.5867, 2284.1530, 2297.0154,
     2302.1281, 2328.1102, 2331.1766, 2346.1572, 2362.1863, 2368.1527, 2374.2028, 2378.1596, 2482.1949
```

```
4.   WP_019563598.1    Mass: 15157    Score: 77    Expect: 2.9  Matches: 6
     MULTISPECIES: hypothetical protein [Thioalkalivibrio]
      Observed    Mr(expt)    Mr(calc)     ppm   Start    End Miss    Peptide
      842.4989    841.4917    841.5021  -12.46    137 - 143    1    R.RELNVVI.-
     1537.7339   1536.7266   1536.8147  -57.36    122 - 136    0    R.VELAVSLAGPAEEPR.R
     1559.7652   1558.7579   1558.7488    5.84     62 -  75    1    R.RGDAEQDQGLAFPR.S
```

1693.8516	1692.8443	1692.9158	-42.28	122	137	1	R.VELAVSLAGPAEEPRR.E
2331.1766	2330.1694	2330.0445	53.6	95	119	0	R.SGNDSAEAMPADGGPLSGGGVEALR.R + Oxidation (M)
2368.1527	2367.1454	2367.1853	-16.84	1	23	0	-.MEVPVSNPSAAIPIGTRPTGSDR.L + Oxidation (M)

No match to: 870.5361, 889.5177, 908.4707, 931.4287, 1012.6027, 1051.5157, 1055.4616, 1069.4193, 1078.5508, 1100.5360, 1107.6437, 1129.6270, 1179.6156, 1188.7038, 1201.5984, 1438.1686, 1522.7159, 1546.2266, 1550.7359, 1565.7838, 1574.8472, 1625.7921, 1673.7669, 1678.9113, 1713.8370, 1729.8293, 1735.8209, 1772.9007, 1781.9871, 1794.8987, 1954.6746, 2005.0908, 2211.0929, 2234.5867, 2284.1530, 2297.0154, 2302.1281, 2328.1102, 2346.1572, 2362.1863, 2374.2028, 2378.1596, 2482.1949

5. WP_034679054.1 **Mass:** 48801 **Score:** 74 **Expect:** 6.2 **Matches:** 9

diaminobutyrate--2-oxoglutarate transaminase [Acinetobacter sp. WC-141]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1012.6027	1011.5954	1011.6077	-12.08	446	455	0	K.AIAEALVAVR.G
1078.5508	1077.5435	1077.4873	52.2	21	29	0	R.QSQMESNVR.S
1559.7652	1558.7579	1558.8038	-29.45	358	371	1	K.LAQEFPCIGNVRGR.G
1565.7838	1564.7765	1564.8137	-23.75	99	113	0	K.DAFTEALLAYLPGGK.E
1794.8987	1793.8914	1793.9788	-48.72	253	268	0	K.HNIVLILDEVQAGFAR.S
2346.1572	2345.1499	2345.0892	25.9	389	410	0	R.MGSHPADSQLAAAIQTACFNNK.L + Propionamide (C)
2362.1863	2361.1790	2361.0841	40.2	389	410	0	R.MGSHPADSQLAAAIQTACFNNK.L + Oxidation (M); Propionamide (C)
2368.1527	2367.1454	2367.0776	28.6	170	189	0	K.NSVNGLMPGVQFMPYPHEYR.C + 2 Oxidation (M)
2374.2028	2373.1955	2373.2800	-35.60	425	444	1	R.LLCPLIITQEECVEVVARFK.K + Propionamide (C)

No match to: 842.4989, 870.5361, 889.5177, 908.4707, 931.4287, 1051.5157, 1055.4616, 1069.4193, 1100.5360, 1107.6437, 1129.6270, 1179.6156, 1188.7038, 1201.5984, 1438.1686, 1522.7159, 1537.7339, 1546.2266, 1550.7359, 1574.8472, 1625.7921, 1673.7669, 1678.9113, 1693.8516, 1713.8370, 1729.8293, 1735.8209, 1772.9007, 1781.9871, 1954.6746, 2005.0908, 2211.0929, 2234.5867, 2284.1530, 2297.0154, 2302.1281, 2328.1102, 2331.1766, 2378.1596, 2482.1949

6. KOF78604.1 **Mass:** 64850 **Score:** 74 **Expect:** 6.4 **Matches:** 10

```
     hypothetical protein OCBIM_22030533mg [Octopus bimaculoides]
      Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
     1078.5508   1077.5435   1077.5706  -25.11    177 -  186    0   K.YLPSLATGEK.L
     1107.6437   1106.6365   1106.5695    60.5      1 -    9    0   -.MFLLGHFAR.Q + Oxidation (M)
     1559.7652   1558.7579   1558.8555  -62.57      1 -   13    1   -.MFLLGHFARQALR.R
     1713.8370   1712.8297   1712.8556  -15.09    577 -  592    1   R.DIVESGCVAAKHPLGF.- + Propionamide (C)
     1781.9871   1780.9798   1780.8996    45.1    242 -  257    1   K.ASNTAEVYFDNVKVPK.E
     1794.8987   1793.8914   1793.9015   -5.64    571 -  587    1   K.MSLISRDIVESGCVAAK.H + Oxidation (M)
     2005.0908   2004.0836   2004.0132    35.1     20 -   37    1   K.TQTPCLVPVTSVNTSKCR.A + Propionamide (C)
     2331.1766   2330.1694   2330.1003    29.6    270 -  291    1   K.VAMNILNNGRFGMAACLSGTMK.T + 2 Oxidation (M)
     2346.1572   2345.1499   2345.1797  -12.71    258 -  279    1   K.ENLLGEAGEGFKVAMNILNNGR.F
     2362.1863   2361.1790   2361.1747    1.83    258 -  279    1   K.ENLLGEAGEGFKVAMNILNNGR.F + Oxidation (M)
     No match to: 842.4989, 870.5361, 889.5177, 908.4707, 931.4287, 1012.6027, 1051.5157, 1055.4616, 1069.4193,
     1100.5360, 1129.6270, 1179.6156, 1188.7038, 1201.5984, 1438.1686, 1522.7159, 1537.7339, 1546.2266, 1550.7359,
     1565.7838, 1574.8472, 1625.7921, 1673.7669, 1678.9113, 1693.8516, 1729.8293, 1735.8209, 1772.9007, 1954.6746,
     2211.0929, 2234.5867, 2284.1530, 2297.0154, 2302.1281, 2328.1102, 2368.1527, 2374.2028, 2378.1596, 2482.1949

7.   WP 104689207.1    Mass: 7824     Score: 73     Expect: 7.5  Matches: 5
     hypothetical protein [Lactobacillus pontis]
      Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
      931.4287    930.4214    930.4658  -47.67      2 -    9    0   M.EINEDALK.N
     1078.5508   1077.5435   1077.5012    39.3      1 -    9    0   -.MEINEDALK.N + Oxidation (M)
     1559.7652   1558.7579   1558.7416    10.5     10 -   22    1   K.NFQNSKFDFVDAK.G
     1565.7838   1564.7765   1564.7369    25.3     52 -   65    0   K.AQDVVDTINNEYGK.T
     2331.1766   2330.1694   2330.0663    44.2     23 -   43    1   K.GNDVDFSNLSDDVTYTLRDGK.T
     No match to: 842.4989, 870.5361, 889.5177, 908.4707, 1012.6027, 1051.5157, 1055.4616, 1069.4193, 1100.5360,
     1107.6437, 1129.6270, 1179.6156, 1188.7038, 1201.5984, 1438.1686, 1522.7159, 1537.7339, 1546.2266, 1550.7359,
     1574.8472, 1625.7921, 1673.7669, 1678.9113, 1693.8516, 1713.8370, 1729.8293, 1735.8209, 1772.9007, 1781.9871,
     1794.8987, 1954.6746, 2005.0908, 2211.0929, 2234.5867, 2284.1530, 2297.0154, 2302.1281, 2328.1102, 2346.1572,
     2362.1863, 2368.1527, 2374.2028, 2378.1596, 2482.1949

8.   SFE83046.1     Mass: 27116     Score: 73     Expect: 7.6  Matches: 7
     ABC transporter [Thermoanaerobacter thermohydrosulfuricus]
      Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
      842.4989    841.4917    841.4698    26.0    153 -  159    0   K.WLALDPK.V
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1051.5157  1050.5084  1050.5346  -24.94    73 -  81   0    R.GLVYVTEDR.K
1179.6156  1178.6083  1178.6295  -18.00    73 -  82   1    R.GLVYVTEDRK.N
1713.8370  1712.8297  1712.7927    21.6   225 - 239   0    K.EANEELIMQYATGTK.K + Oxidation (M)
2005.0908  2004.0836  2004.0310    26.2   130 - 147   1    K.CKTIEQSVITLSGGNQQK.V + Propionamide (C)
2346.1572  2345.1499  2345.0766    31.3   220 - 239   1    R.ELMDKEANEELIMQYATGTK.K + 2 Oxidation (M)
2368.1527  2367.1454  2367.2256  -33.91    20 -  41   1    K.LYEGEILGIFGLMGAGRTEVAR.G + Oxidation (M)
No match to: 870.5361, 889.5177, 908.4707, 931.4287, 1012.6027, 1055.4616, 1069.4193, 1078.5508, 1100.5360,
1107.6437, 1129.6270, 1188.7038, 1201.5984, 1438.1686, 1522.7159, 1537.7339, 1546.2266, 1550.7359, 1559.7652,
1565.7838, 1574.8472, 1625.7921, 1673.7669, 1678.9113, 1693.8516, 1729.8293, 1735.8209, 1772.9007, 1781.9871,
1794.8987, 1954.6746, 2211.0929, 2234.5867, 2284.1530, 2297.0154, 2302.1281, 2328.1102, 2331.1766, 2362.1863,
2374.2028, 2378.1596, 2482.1949

9.    XP_014779384.1     Mass: 68715     Score: 73     Expect: 8  Matches: 10

      PREDICTED: LOW QUALITY PROTEIN: very long-chain specific acyl-CoA dehydrogenase, mitochondrial-like [Octopus
      bimaculoides]
       Observed  Mr(expt)   Mr(calc)     ppm  Start    End Miss  Peptide
      1078.5508  1077.5435  1077.5706  -25.11   177 - 186   0    K.YLPSLATGEK.L
      1107.6437  1106.6365  1106.5695    60.5     1 -   9   0    -.MFLLGHFAR.Q + Oxidation (M)
      1559.7652  1558.7579  1558.8555  -62.57     1 -  13   1    -.MFLLGHFARQALR.R
      1713.8370  1712.8297  1712.8556  -15.09   611 - 626   1    R.DIVESGCVAAKHPLGF.- + Propionamide (C)
      1781.9871  1780.9798  1780.8996    45.1   276 - 291   1    K.ASNTAEVYFDNVKVPK.E
      1794.8987  1793.8914  1793.9015   -5.64   605 - 621   1    K.MSLISRDIVESGCVAAK.H + Oxidation (M)
      2005.0908  2004.0836  2004.0132    35.1    20 -  37   1    K.TQTPCLVPVTSVNTSKCR.A + Propionamide (C)
      2331.1766  2330.1694  2330.1003    29.6   304 - 325   1    K.VAMNILNNGRFGMAACLSGTMK.T + 2 Oxidation (M)
      2346.1572  2345.1499  2345.1797  -12.71   292 - 313   1    K.ENLLGEAGEGFKVAMNILNNGR.F
      2362.1863  2361.1790  2361.1747    1.83   292 - 313   1    K.ENLLGEAGEGFKVAMNILNNGR.F + Oxidation (M)
      No match to: 842.4989, 870.5361, 889.5177, 908.4707, 931.4287, 1012.6027, 1051.5157, 1055.4616, 1069.4193,
      1100.5360, 1129.6270, 1179.6156, 1188.7038, 1201.5984, 1438.1686, 1522.7159, 1537.7339, 1546.2266, 1550.7359,
      1565.7838, 1574.8472, 1625.7921, 1673.7669, 1678.9113, 1693.8516, 1729.8293, 1735.8209, 1772.9007, 1954.6746,
      2211.0929, 2234.5867, 2284.1530, 2297.0154, 2302.1281, 2328.1102, 2368.1527, 2374.2028, 2378.1596, 2482.1949

10.   WP_004376243.1     Mass: 29769     Score: 73     Expect: 8  Matches: 9
      GTP cyclohydrolase I FolE2 [Thauera phenylacetica]

       Observed  Mr(expt)   Mr(calc)     ppm  Start    End Miss  Peptide
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1051.5157	1050.5084	1050.5532	-42.66	87	-	95	0	R.GLFADMLLR.L + Oxidation (M)
1078.5508	1077.5435	1077.5753	-29.48	30	-	38	1	R.GLRYPMAVR.D + Oxidation (M)
1188.7038	1187.6965	1187.6258	59.5	96	-	106	1	R.LEASSGRIEAR.F
1565.7838	1564.7765	1564.7885	-7.68	215	-	227	1	R.AYDNPKFVEDLVR.D
1735.8209	1734.8136	1734.9087	-54.79	87	-	102	1	R.GLFADMLLRLEASSGR.I
2297.0154	2296.0081	2296.0715	-27.61	190	-	209	1	R.MAEEEASCEVFGLLKRPDEK.W + Oxidation (M)
2331.1766	2330.1694	2330.1974	-12.03	138	-	158	1	R.GEIRSTLEAVVPVTSLCPCSK.K + 2 Propionamide (C)
2368.1527	2367.1454	2367.1086	15.5	190	-	209	1	R.MAEEEASCEVFGLLKRPDEK.W + Oxidation (M); Propionamide (C)
2482.1949	2481.1877	2481.2421	-21.96	39	-	62	0	R.DLDGGVQHTVATLEMTVGLPADVK.G + Oxidation (M)

No match to: 842.4989, 870.5361, 889.5177, 908.4707, 931.4287, 1012.6027, 1055.4616, 1069.4193, 1100.5360, 1107.6437, 1129.6270, 1179.6156, 1201.5984, 1438.1686, 1522.7159, 1537.7339, 1546.2266, 1550.7359, 1559.7652, 1574.8472, 1625.7921, 1673.7669, 1678.9113, 1693.8516, 1713.8370, 1729.8293, 1772.9007, 1781.9871, 1794.8987, 1954.6746, 2005.0908, 2211.0929, 2234.5867, 2284.1530, 2302.1281, 2328.1102, 2346.1572, 2362.1863, 2374.2028, 2378.1596

11. OUU50395.1 **Mass:** 47634 **Score:** 73 **Expect:** 8.4 **Matches:** 8

hypothetical protein CBC14_05930 [Alphaproteobacteria bacterium TMED54]

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**		**End**	**Miss**	**Peptide**
1051.5157	1050.5084	1050.5709	-59.54	50	-	58	0	K.LLLNSYSNK.D
1078.5508	1077.5435	1077.5818	-35.53	40	-	48	1	K.NNFILDSKK.K
1179.6156	1178.6083	1178.6659	-48.84	49	-	58	1	K.KLLLNSYSNK.D
1188.7038	1187.6965	1187.6947	1.47	116	-	125	1	K.ISKNELMIIK.Q
1565.7838	1564.7765	1564.8249	-30.92	261	-	273	1	K.KQVLNNYPSLDFK.F
1781.9871	1780.9798	1780.8996	45.1	96	-	111	1	K.KIFDFGVTENANDIAK.N
1794.8987	1793.8914	1793.7897	56.7	59	-	73	0	K.DWTANFTSTFTFDNK.K
2331.1766	2330.1694	2330.2291	-25.63	379	-	399	1	R.TLLDVLDSEVDVMDAEVKVLK.S

No match to: 842.4989, 870.5361, 889.5177, 908.4707, 931.4287, 1012.6027, 1055.4616, 1069.4193, 1100.5360, 1107.6437, 1129.6270, 1201.5984, 1438.1686, 1522.7159, 1537.7339, 1546.2266, 1550.7359, 1559.7652, 1574.8472, 1625.7921, 1673.7669, 1678.9113, 1693.8516, 1713.8370, 1729.8293, 1735.8209, 1772.9007, 1954.6746, 2005.0908,

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       2211.0929, 2234.5867, 2284.1530, 2297.0154, 2302.1281, 2328.1102, 2346.1572, 2362.1863, 2368.1527, 2374.2028,
       2378.1596, 2482.1949

   12. EPR18237.1     Mass: 34566    Score: 72     Expect: 8.6  Matches: 11
       integrase [Sphingobium chinhatense IP26]
        Observed   Mr(expt)   Mr(calc)    ppm  Start   End Miss  Peptide
        842.4989   841.4917   841.4559    42.5   206 - 212    0  K.GHVFLNR.L
        889.5177   888.5104   888.4963    15.9   278 - 284    1  K.SLRMVQR.Y
        908.4707   907.4634   907.4763  -14.19   119 - 125    1  R.FLTKEDR.D
       1078.5508  1077.5435  1077.5455   -1.77   213 - 221    1  R.LGEPYKDTR.L
       1188.7038  1187.6965  1187.6299    56.1   107 - 116    1  R.IKGIPFDNER.V
       1559.7652  1558.7579  1558.8580  -64.18   222 - 236    1  R.LASVPGGNPLKNQHK.T
       1565.7838  1564.7765  1564.8759  -63.50    36 -  49    1  K.AKPPCPSDILRIGK.L + Propionamide (C)
       1625.7921  1624.7849  1624.8784  -57.55    50 -  63    1  K.LNERIGELSLQEPK.Q
       1678.9113  1677.9040  1677.8079    57.2   281 - 294    1  R.MVQRYSTVGVDHMR.E
       1735.8209  1734.8136  1734.8359  -12.86   285 - 299    1  R.YSTVGVDHMRESINK.L
       1781.9871  1780.9798  1780.9770    1.59   191 - 205    1  K.AALLPIWEQRGRPMK.G + Oxidation (M)
       No match to: 870.5361, 931.4287, 1012.6027, 1051.5157, 1055.4616, 1069.4193, 1100.5360, 1107.6437, 1129.6270,
       1179.6156, 1201.5984, 1438.1686, 1522.7159, 1537.7339, 1546.2266, 1550.7359, 1574.8472, 1673.7669, 1693.8516,
       1713.8370, 1729.8293, 1772.9007, 1794.8987, 1954.6746, 2005.0908, 2211.0929, 2234.5867, 2284.1530, 2297.0154,
       2302.1281, 2328.1102, 2331.1766, 2346.1572, 2362.1863, 2368.1527, 2374.2028, 2378.1596, 2482.1949

   13. WP_081588065.1     Mass: 47007    Score: 72     Expect: 9  Matches: 8
       glycosyltransferase [Gloeocapsa sp. PCC 7428]
        Observed   Mr(expt)   Mr(calc)    ppm  Start   End Miss  Peptide
        931.4287   930.4214   930.4671  -49.13   199 - 206    0  R.HPGNELHK.S
       1051.5157  1050.5084  1050.5420  -31.97    46 -  54    0  R.MPVGLDYIK.L + Oxidation (M)
       1537.7339  1536.7266  1536.8148  -57.37    70 -  82    1  K.YLGTQTDETLKLR.A
       1559.7652  1558.7579  1558.7926  -22.26   248 - 261    0  K.STIVVGPEMPQHHK.Q
       1625.7921  1624.7849  1624.7668    11.1     1 -  14    0  -.MVYSHDTFGLGNIR.R + Oxidation (M)
       1693.8516  1692.8443  1692.8934  -29.02    66 -  80    1  K.LSPKYLGTQTDETLK.L
       1735.8209  1734.8136  1734.8368  -13.36   178 - 193    1  K.CPPAVACKVQQCGYIR.K
       1781.9871  1780.9798  1780.8679    62.9     1 -  15    1  -.MVYSHDTFGLGNIRR.M + Oxidation (M)
       No match to: 842.4989, 870.5361, 889.5177, 908.4707, 1012.6027, 1055.4616, 1069.4193, 1078.5508, 1100.5360,
       1107.6437, 1129.6270, 1179.6156, 1188.7038, 1201.5984, 1438.1686, 1522.7159, 1546.2266, 1550.7359, 1565.7838,
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1574.8472, 1673.7669, 1678.9113, 1713.8370, 1729.8293, 1772.9007, 1794.8987, 1954.6746, 2005.0908, 2211.0929,
2234.5867, 2284.1530, 2297.0154, 2302.1281, 2328.1102, 2331.1766, 2346.1572, 2362.1863, 2368.1527, 2374.2028,
2378.1596, 2482.1949

14.  WP_083469462.1    Mass: 7938     Score: 72     Expect: 9.8  Matches: 5
     hypothetical protein [Methylobacterium variabile]
      Observed   Mr(expt)   Mr(calc)    ppm  Start    End Miss  Peptide
      842.4989   841.4917   841.5134 -25.80    17 -  23    1    R.RIEGVLR.A
     1537.7339  1536.7266  1536.7276  -0.68     1 -  15    0    -.MDTCSGTPVSLTLGR.R
     1625.7921  1624.7849  1624.8209 -22.20    24 -  40    0    R.AVGEFVDLPGAPGSPGR.R
     1693.8516  1692.8443  1692.8287   9.18     1 -  16    1    -.MDTCSGTPVSLTLGRR.R
     1781.9871  1780.9798  1780.9220   32.5    24 -  41    1    R.AVGEFVDLPGAPGSPGRR.L
     No match to: 870.5361, 889.5177, 908.4707, 931.4287, 1012.6027, 1051.5157, 1055.4616, 1069.4193, 1078.5508,
     1100.5360, 1107.6437, 1129.6270, 1179.6156, 1188.7038, 1201.5984, 1438.1686, 1522.7159, 1546.2266, 1550.7359,
     1559.7652, 1565.7838, 1574.8472, 1673.7669, 1678.9113, 1713.8370, 1729.8293, 1735.8209, 1772.9007, 1794.8987,
     1954.6746, 2005.0908, 2211.0929, 2234.5867, 2284.1530, 2297.0154, 2302.1281, 2328.1102, 2331.1766, 2346.1572,
     2362.1863, 2368.1527, 2374.2028, 2378.1596, 2482.1949

15.  EIE87316.1    Mass: 6498     Score: 71     Expect: 11  Matches: 5
     hypothetical protein RO3G_12027 [Rhizopus delemar RA 99-880]
      Observed   Mr(expt)   Mr(calc)    ppm  Start    End Miss  Peptide
     1179.6156  1178.6083  1178.5819   22.4    48 -  57    0    R.TLFVQQTLDD.-
     1537.7339  1536.7266  1536.8078 -52.83     1 -  14    0    -.MVIVGMTVSVLSCK.R + Propionamide (C)
     1693.8516  1692.8443  1692.9089 -38.17     1 -  15    1    -.MVIVGMTVSVLSCKR.G + Propionamide (C)
     1735.8209  1734.8136  1734.9152 -58.58    43 -  57    1    R.ILSSRTLFVQQTLDD.-
     2374.2028  2373.1955  2373.1497   19.3    16 -  34    0    R.GYEMLCLQINVTWTQTFQK.L + Propionamide (C)
     No match to: 842.4989, 870.5361, 889.5177, 908.4707, 931.4287, 1012.6027, 1051.5157, 1055.4616, 1069.4193,
     1078.5508, 1100.5360, 1107.6437, 1129.6270, 1188.7038, 1201.5984, 1438.1686, 1522.7159, 1546.2266, 1550.7359,
     1559.7652, 1565.7838, 1574.8472, 1625.7921, 1673.7669, 1678.9113, 1713.8370, 1729.8293, 1772.9007, 1781.9871,
     1794.8987, 1954.6746, 2005.0908, 2211.0929, 2234.5867, 2284.1530, 2297.0154, 2302.1281, 2328.1102, 2331.1766,
     2346.1572, 2362.1863, 2368.1527, 2378.1596, 2482.1949

16.  WP_047381104.1    Mass: 24434    Score: 71     Expect: 12  Matches: 8
     peptidase [Chryseobacterium sp. YR485]
                                                 Start    End Miss
      Observed   Mr(expt)   Mr(calc)    ppm                         Peptide
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1179.6156	1178.6083	1178.6158	-6.34	207 -	215	0	K.KPVLMWIYN.- + Oxidation (M)
1565.7838	1564.7765	1564.7093	43.0	94 -	107	0	K.YLVGHGCGSNSWSK.D + Propionamide (C)
1693.8516	1692.8443	1692.8042	23.7	93 -	107	1	K.KYLVGHGCGSNSWSK.D + Propionamide (C)
1735.8209	1734.8136	1734.8246	-6.37	146 -	160	0	K.YLMHGLEETNSNALK.R + Oxidation (M)
2284.1530	2283.1457	2283.0129	58.2	162 -	179	0	R.FIVFHSWDMMSDHEVFPK.G + 2 Oxidation (M)
2346.1572	2345.1499	2345.1595	-4.07	3 -	20	0	K.GIYLFFIAFWLYSCFQEK.K + Propionamide (C)
2362.1863	2361.1790	2361.1205	24.8	60 -	79	0	K.NLNNDFCILIDMSLHSGVNR.F + Oxidation (M); Propionamide (C)
2368.1527	2367.1454	2367.2007	-23.35	197 -	215	1	K.EIDPMIQYSKKPVLMWIYN.-

No match to: 842.4989, 870.5361, 889.5177, 908.4707, 931.4287, 1012.6027, 1051.5157, 1055.4616, 1069.4193, 1078.5508, 1100.5360, 1107.6437, 1129.6270, 1188.7038, 1201.5984, 1438.1686, 1522.7159, 1537.7339, 1546.2266, 1550.7359, 1559.7652, 1574.8472, 1625.7921, 1673.7669, 1678.9113, 1713.8370, 1729.8293, 1772.9007, 1781.9871, 1794.8987, 1954.6746, 2005.0908, 2211.0929, 2234.5867, 2297.0154, 2302.1281, 2328.1102, 2331.1766, 2374.2028, 2378.1596, 2482.1949

17. WP_076866932.1 **Mass:** 34360 **Score:** 71 **Expect:** 12 **Matches:** 9

AraC family transcriptional regulator [Bradyrhizobium mercantei]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1559.7652	1558.7579	1558.7675	-6.13	76 -	90	0	R.HVMHDGTGATPLPAR.N
1565.7838	1564.7765	1564.7820	-3.50	17 -	28	1	R.LDIRCSYSVPWR.I + Propionamide (C)
1693.8516	1692.8443	1692.9055	-36.15	170 -	185	0	R.AMLNALSTAMFALALR.L
1713.8370	1712.8297	1712.8854	-32.51	7 -	20	1	R.LFEMMPVHGRLDIR.C
1729.8293	1728.8220	1728.8804	-33.74	7 -	20	1	R.LFEMMPVHGRLDIR.C + Oxidation (M)
1735.8209	1734.8136	1734.9120	-56.75	142 -	158	1	R.MGKGTAAQLAGLVSLMR.G + 2 Oxidation (M)
2005.0908	2004.0836	2003.9532	65.1	1 -	16	1	-.MDWLSRLFEMMPVHGR.L
2346.1572	2345.1499	2345.0958	23.1	267 -	289	0	K.GSSLSTGAVAEMVGYQSEAAFQR.A
2362.1863	2361.1790	2361.0907	37.4	267 -	289	0	K.GSSLSTGAVAEMVGYQSEAAFQR.A + Oxidation (M)

No match to: 842.4989, 870.5361, 889.5177, 908.4707, 931.4287, 1012.6027, 1051.5157, 1055.4616, 1069.4193, 1078.5508, 1100.5360, 1107.6437, 1129.6270, 1179.6156, 1188.7038, 1201.5984, 1438.1686, 1522.7159, 1537.7339, 1546.2266, 1550.7359, 1574.8472, 1625.7921, 1673.7669, 1678.9113, 1772.9007, 1781.9871, 1794.8987, 1954.6746,

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      2211.0929, 2234.5867, 2284.1530, 2297.0154, 2302.1281, 2328.1102, 2331.1766, 2368.1527, 2374.2028, 2378.1596,
      2482.1949

18.   WP_089684046.1     Mass: 40561     Score: 70     Expect: 14  Matches: 9
      hypothetical protein [Halomonas gudaonensis]
       Observed   Mr(expt)   Mr(calc)    ppm  Start   End Miss  Peptide
      1051.5157  1050.5084  1050.5458 -35.60   158 - 166    1   K.KFNLESASR.H
      1078.5508  1077.5435  1077.5454  -1.76   138 - 146    1   K.SRYAIPDEK.I
      1565.7838  1564.7765  1564.7919  -9.83   180 - 193    0   R.NECLIGLVTSGNFK.K + Propionamide (C)
      1625.7921  1624.7849  1624.7580   16.5   226 - 240    0   K.TEYLQQAESAGVSDK.F
      1693.8516  1692.8443  1692.8869 -25.16   180 - 194    1   R.NECLIGLVTSGNFKK.R + Propionamide (C)
      1713.8370  1712.8297  1712.9032 -42.87     7 -  21    0   R.IALHQAQLLSEMGFR.V
      1729.8293  1728.8220  1728.8981 -44.01     7 -  21    0   R.IALHQAQLLSEMGFR.V + Oxidation (M)
      1781.9871  1780.9798  1780.9319   26.9   104 - 119    1   R.KSPSDVATIHDEILTR.Q
      2331.1766  2330.1694  2330.1987 -12.60     1 -  21    1   -.MTGATRIALHQAQLLSEMGFR.V
      No match to: 842.4989, 870.5361, 889.5177, 908.4707, 931.4287, 1012.6027, 1055.4616, 1069.4193, 1100.5360,
      1107.6437, 1129.6270, 1179.6156, 1188.7038, 1201.5984, 1438.1686, 1522.7159, 1537.7339, 1546.2266, 1550.7359,
      1559.7652, 1574.8472, 1673.7669, 1678.9113, 1735.8209, 1772.9007, 1794.8987, 1954.6746, 2005.0908, 2211.0929,
      2234.5867, 2284.1530, 2297.0154, 2302.1281, 2328.1102, 2346.1572, 2362.1863, 2368.1527, 2374.2028, 2378.1596,
      2482.1949

19.   ART89119.1     Mass: 29503     Score: 70     Expect: 14  Matches: 8
      coat protein [Tomato leaf curl Joydebpur virus]
       Observed   Mr(expt)   Mr(calc)    ppm  Start   End Miss  Peptide
      1051.5157  1050.5084  1050.5056   2.67   120 - 127    0   K.IWMDETIK.T + Oxidation (M)
      1078.5508  1077.5435  1077.5423   1.13    89 -  97    1   K.VMCVRDVTR.G
      1179.6156  1178.6083  1178.6270 -15.88    31 -  40    1   R.VAAPMFRFPK.Q + Oxidation (M)
      1537.7339  1536.7266  1536.7653 -25.22    81 -  93    1   R.HDVQHIGKVMCVR.D + Oxidation (M)
      1625.7921  1624.7849  1624.7845   0.22   205 - 218    0   R.VNNYVVYNQQEAGK.Y
      1693.8516  1692.8443  1692.8770 -19.33   128 - 141    1   K.TKNHTNSVMFFLVR.D
      1735.8209  1734.8136  1734.8624 -28.14   130 - 143    1   K.NHTNSVMFFLVRDR.R
      1781.9871  1780.9798  1780.9433   20.5   113 - 127    1   K.SVYVLGKIWMDETIK.T
      No match to: 842.4989, 870.5361, 889.5177, 908.4707, 931.4287, 1012.6027, 1055.4616, 1069.4193, 1100.5360,
      1107.6437, 1129.6270, 1188.7038, 1201.5984, 1438.1686, 1522.7159, 1546.2266, 1550.7359, 1559.7652, 1565.7838,
      1574.8472, 1673.7669, 1678.9113, 1713.8370, 1729.8293, 1772.9007, 1794.8987, 1954.6746, 2005.0908, 2211.0929,
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      2234.5867, 2284.1530, 2297.0154, 2302.1281, 2328.1102, 2331.1766, 2346.1572, 2362.1863, 2368.1527, 2374.2028,
      2378.1596, 2482.1949

20.   WP 100163559.1     Mass: 75038     Score: 70     Expect: 15  Matches: 9
      3-hydroxyacyl-CoA dehydrogenase [Pseudooceanicola lipolyticus]
       Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
       842.4989    841.4917    841.4657    30.8    588 - 595    0    R.AELGLSPR.D
      1012.6027   1011.5954   1011.6077  -12.10    140 - 148    1    R.LPRLTGVEK.A
      1051.5157   1050.5084   1050.4982    9.70    688 - 697    1    K.TFDDLNKAAG.-
      1179.6156   1178.6083   1178.5502    49.3    468 - 478    0    R.AGVCDGFIGNR.I + Propionamide (C)
      1693.8516   1692.8443   1692.8406    2.17    263 - 277    1    R.QGMIHAFFSERAVGK.L + Oxidation (M)
      2005.0908   2004.0836   2004.0276    27.9    180 - 197    1    R.EIGLAYVQDLLDSGAERR.A
      2346.1572   2345.1499   2345.1791  -12.43    198 - 219    0    R.AVSELPAPQPIDFDAAYEATLK.K
      2362.1863   2361.1790   2361.1528    11.1    668 - 687    0    R.EDEYFWQPAPLLEQLVAEGK.T
      2368.1527   2367.1454   2367.1165    12.2    482 - 502    1    K.TYRTAADHMVLDGASPYQIDK.A + Oxidation (M)
      No match to: 870.5361, 889.5177, 908.4707, 931.4287, 1055.4616, 1069.4193, 1078.5508, 1100.5360, 1107.6437,
      1129.6270, 1188.7038, 1201.5984, 1438.1686, 1522.7159, 1537.7339, 1546.2266, 1550.7359, 1559.7652, 1565.7838,
      1574.8472, 1625.7921, 1673.7669, 1678.9113, 1713.8370, 1729.8293, 1735.8209, 1772.9007, 1781.9871, 1794.8987,
      1954.6746, 2211.0929, 2234.5867, 2284.1530, 2297.0154, 2302.1281, 2328.1102, 2331.1766, 2374.2028, 2378.1596,
      2482.1949
```

Search Parameters

```
Type of search         : Peptide Mass Fingerprint
Enzyme                 : Trypsin
Variable modifications : Oxidation (M),Propionamide (C)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Peptide Charge State   : 1+
Max Missed Cleavages   : 1
Number of queries      : 49
Selected for scoring   : 25
```

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

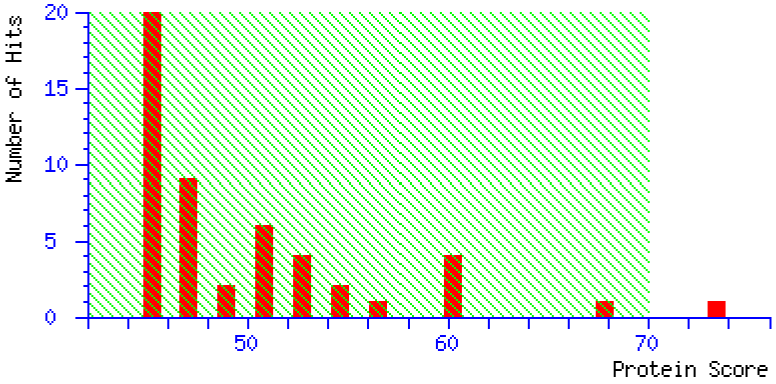
5. The protein band of approx. 27 kDa, obtained from the crude extract of *R. rhodochrous* M33 delta-const cells, grown on the medium without metals.

Mascot Search Results

```
User              : toropygin
Email             : toropygin@rambler.ru
Search title      : 01
Database          : SwissProt 2018_08 (558125 sequences; 200328830 residues)
Timestamp         : 26 Sep 2018 at 15:56:58 GMT
Top Score         : 73 for NHB1_RHORH, High-molecular weight cobalt-containing nitrile hydratase subunit beta
OS=Rhodococcus rhodochrous OX=1829 GN=nhhB PE=1 SV=2
```

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 70 are significant ($p<0.05$).



Protein Summary Report

Format As	Protein Summary ▾	Help
	Significance threshold p< 0.05	Max. number of hits 20
	Preferred taxonomy All entries ▾	

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-
-Accession- -Sequence-

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
☑ 805.4435 **(1+)**						●		●				●								
☑ 817.4339 **(1+)**			●	●	●			●				●								
☑ 891.5000 **(1+)**	●													●	●	●				
☑ 900.4889 **(1+)**								●	●											
☑ 906.5394 **(1+)**			●	●	●											●	●			
☑ 909.4223 **(1+)**												●	●		●					

☑ 943.5394 (1+)	●	●							●			●	●					●		
☑ 947.5320 (1+)	●	●	●	●	●	●	●	●				●		●		●	●	●		●
☑ 952.4985 (1+)																●				
☑ 961.5879 (1+)						●														
☑ 1044.5817 (1+)		●																●		●
☑ 1054.6305 (1+)									●										●	
☑ 1073.6009 (1+)								●			●	●		●						
☑ 1076.5738 (1+)								●			●									
☑ 1078.5780 (1+)											●									
☑ 1087.6056 (1+)						●						●				●				
☑ 1091.5907 (1+)							●				●	●								
☑ 1100.6162 (1+)								●	●								●			
☑ 1107.6426 (1+)															●					
☑ 1114.6425 (1+)		●													●					
☑ 1117.5943 (1+)							●	●	●	●					●	●				●
☑ 1131.6636 (1+)																				
☑ 1145.6759 (1+)			●	●	●						●	●								
☑ 1154.6595 (1+)							●	●	●											
☑ 1162.6289 (1+)						●	●	●												

☑	1179.6387 (1+)		●				●		●		●	●							●	●	
☑	1188.7106 (1+)								●	●	●				●						
☑	1213.6439 (1+)			●	●	●								●				●			
☑	1219.6987 (1+)			●	●	●			●						●	●		●			
☑	1221.7099 (1+)						●														
☑	1282.7596 (1+)								●												
☑	1329.7785 (1+)																				
☑	1342.8028 (1+)	●					●		●	●					●						
☑	1391.7960 (1+)		●										●						●		
☑	1423.7341 (1+)			●	●	●			●			●						●		●	
☑	1433.8679 (1+)		●					●			●			●					●		
☑	1462.7489 (1+)						●			●		●	●								
☑	1471.8574 (1+)												●							●	
☑	1486.8640 (1+)													●							
☑	1502.8443 (1+)										●										
☑	1528.9019 (1+)	●										●	●								●
☑	1537.7928 (1+)							●	●				●								
☑	1542.7750 (1+)			●	●	●			●		●		●					●			
☑	1554.7503 (1+)	●	●											●		●			●	●	

☑ 1561.8811 (1+)		●	●	●	●												●	●		
☑ 1582.8377 (1+)		●																		
☑ 1597.8184 (1+)	●							●												
☑ 1611.7719 (1+)	●							●		●	●									
☑ 1641.9273 (1+)															●					
☑ 1651.9542 (1+)							●			●										
☑ 1656.9978 (1+)								●				●		●						
☑ 1687.8846 (1+)									●			●			●	●				●
☑ 1759.9421 (1+)							●	●												
☑ 1762.9604 (1+)																			●	
☑ 1838.0268 (1+)										●			●			●				
☑ 1925.9415 (1+)			●	●	●		●										●			
☑ 1928.9792 (1+)			●	●	●	●			●				●				●			
☑ 1967.0608 (1+)		●										●						●		
☑ 2034.0174 (1+)													●							
☑ 2134.1272 (1+)																				
☑ 2202.1233 (1+)	●					●		●												
☑ 2211.0847 (1+)						●	●													
☑ 2280.2533 (1+)																				●

☑ 2318.1759 (1+)																				
☑ 2330.2339 (1+)		●				●				●							●	●		
☑ 2339.2229 (1+)		●				●	●												●
☑ 2346.1687 (1+)							●				●									
☑ 2385.2935 (1+)		●	●	●	●		●				●					●	●	●	●
☑ 2429.2638 (1+)						●							●							
☑ 2612.3789 (1+)																				
☑ 3242.5742 (1+)																		●	●
☑ 3471.5614 (1+)																				
☑ 3716.5563 (1+)	●																			

Search Selected

Index

	Accession	Mass	Score	Description
1.	NHB1_RHORH	26305	73	High-molecular weight cobalt-containing nitrile hydratase subunit beta OS=Rhodococcus rhodochrous OX=1829 GN=nhhB PE=1 SV=2
2.	THIC_STRMK	68183	68	Phosphomethylpyrimidine synthase OS=Stenotrophomonas maltophilia (strain K279a) OX=522373 GN=thiC PE=3 SV=1
3.	RBSA_SALCH	55049	61	Ribose import ATP-binding protein RbsA OS=Salmonella choleraesuis (strain SC-B67) OX=321314 GN=rbsA PE=3 SV=2
4.	RBSA_SALTI	55102	61	Ribose import ATP-binding protein RbsA OS=Salmonella typhi OX=90370 GN=rbsA PE=3 SV=1

5.	RBSA_SALTY	55058	61	Ribose import ATP-binding protein RbsA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rbsA PE=3 SV=1
6.	VP4_ROTHL	87596	60	Outer capsid protein VP4 OS=Rotavirus A (strain RVA/Human/Philippines/L26/1987/G12P1B[4]) OX=10953 PE=3 SV=1
7.	LON_UNCTG	90316	56	Lon protease OS=Uncultured termite group 1 bacterium phylotype Rs-D17 OX=471821 GN=lon PE=3 SV=1
8.	HMW2_MYCGE	216122	55	Cytadherence high molecular weight protein 2 OS=Mycoplasma genitalium (strain ATCC 33530 / G-37 / NCTC 10195) OX=243273 GN=hmw2 PE=3 SV=1
9.	TIG_BURM1	49720	54	Trigger factor OS=Burkholderia multivorans (strain ATCC 17616 / 249) OX=395019 GN=tig PE=3 SV=1
10.	MNME_ALIF1	49576	53	tRNA modification GTPase MnmE OS=Aliivibrio fischeri (strain ATCC 700601 / ES114) OX=312309 GN=mnmE PE=3 SV=1
11.	ILVD_HAEI8	65710	53	Dihydroxy-acid dehydratase OS=Haemophilus influenzae (strain 86-028NP) OX=281310 GN=ilvD PE=3 SV=1
12.	KDM3A_HUMAN	147248	53	Lysine-specific demethylase 3A OS=Homo sapiens OX=9606 GN=KDM3A PE=1 SV=4
13.	GATB_BACC4	53190	52	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B OS=Bacillus cereus (strain B4264) OX=405532 GN=gatB PE=3 SV=1
14.	COMD4_DICDI	20135	52	COMM domain-containing protein 4 OS=Dictyostelium discoideum OX=44689 GN=commd4 PE=4 SV=1
15.	GCH1_HUMAN	27885	52	GTP cyclohydrolase 1 OS=Homo sapiens OX=9606 GN=GCH1 PE=1 SV=1
16.	RK5_PYRYE	20525	52	50S ribosomal protein L5, chloroplastic OS=Pyropia yezoensis OX=2788 GN=rpl5 PE=3 SV=1
17.	RBSA_SALPA	55194	51	Ribose import ATP-binding protein RbsA OS=Salmonella paratyphi A (strain ATCC 9150 / SARB42) OX=295319 GN=rbsA PE=3 SV=1
18.	THIC_STRM5	68293	51	Phosphomethylpyrimidine synthase OS=Stenotrophomonas maltophilia (strain R551-3) OX=391008 GN=thiC PE=3 SV=1
19.	HEM1_BURP6	47530	50	Glutamyl-tRNA reductase OS=Burkholderia pseudomallei (strain 668) OX=320373 GN=hemA PE=3 SV=1
20.	ALGD_PSESM	47578	50	GDP-mannose 6-dehydrogenase OS=Pseudomonas syringae pv. tomato (strain ATCC BAA-871 / DC3000) OX=223283 GN=algD PE=2 SV=1

Results List

1. NHB1_RHORH **Mass:** 26305 **Score:** 73 **Expect:** 0.026 **Matches:** 10

High-molecular weight cobalt-containing nitrile hydratase subunit beta OS=Rhodococcus rhodochrous OX=1829 GN=nhhB PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**

891.5000	890.4927	890.4286	72.0	44	- 50	0	K.GISWWDK.S
943.5394	942.5321	942.5134	19.8	98	- 105	0	R.VQEILEGR.Y
947.5320	946.5247	946.4760	51.5	115	- 122	0	K.FDPAQIEK.A
1342.8028	1341.7955	1341.7479	35.5	33	- 43	0	R.TLSILTWMHLK.G
1528.9019	1527.8946	1527.8508	28.7	82	- 94	1	R.ILVADKIITEEER.K
1554.7503	1553.7430	1553.6780	41.8	56	- 68	0	R.ESMGNENYVNEIR.N
1597.8184	1596.8111	1596.7321	49.5	69	- 81	0	R.NSYYTHWLSAAER.I
1611.7719	1610.7646	1610.6790	53.1	21	- 32	0	K.DEPFFHYEWEGR.T
2202.1233	2201.1160	2201.1117	1.97	127	- 147	0	R.LHEPHSLALPGAEPSFSLGDK.I
3716.5563	3715.5490	3715.6137	-17.41	1	- 32	1	-.MDGIHDTGGMTGYGPVPYQKDEPFFHYEWEGR.T

No match to: 805.4435, 817.4339, 900.4889, 906.5394, 909.4223, 952.4985, 961.5879, 1044.5817, 1054.6305, 1073.6009, 1076.5738, 1078.5780, 1087.6056, 1091.5907, 1100.6162, 1107.6426, 1114.6425, 1117.5943, 1131.6636, 1145.6759, 1154.6595, 1162.6289, 1179.6387, 1188.7106, 1213.6439, 1219.6987, 1221.7099, 1282.7596, 1329.7785, 1391.7960, 1423.7341, 1433.8679, 1462.7489, 1471.8574, 1486.8640, 1502.8443, 1537.7928, 1542.7750, 1561.8811, 1582.8377, 1641.9273, 1651.9542, 1656.9978, 1687.8846, 1759.9421, 1762.9604, 1838.0268, 1925.9415, 1928.9792, 1967.0608, 2034.0174, 2134.1272, 2211.0847, 2280.2533, 2318.1759, 2330.2339, 2339.2229, 2346.1687, 2385.2935, 2429.2638, 2612.3789, 3242.5742, 3471.5614

2. THIC_STRMK **Mass:** 68183 **Score:** 68 **Expect:** 0.088 **Matches:** 14

Phosphomethylpyrimidine synthase OS=Stenotrophomonas maltophilia (strain K279a) OX=522373 GN=thiC PE=3 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
943.5394	942.5321	942.5399	-8.27	123	- 130	1	R.FPARSLPR.R
947.5320	946.5247	946.5600	-37.26	331	- 338	1	R.YVPLTAKR.V
1044.5817	1043.5744	1043.5876	-12.66	118	- 126	1	K.LDAVRFPAR.S
1114.6425	1113.6353	1113.5890	41.5	160	- 168	1	R.ENQRLDAIR.D
1179.6387	1178.6315	1178.6044	23.0	113	- 122	1	R.EHDPKLDAVR.F
1391.7960	1390.7887	1390.7602	20.5	339	- 352	1	R.VTGIVSRGGSIMAK.W + Oxidation (M)
1433.8679	1432.8606	1432.7535	74.8	491	- 502	1	K.EHLGLPNRQDVR.D
1554.7503	1553.7430	1553.7595	-10.62	346	- 359	1	R.GGSIMAKWCLAHHK.E + Oxidation (M)
1561.8811	1560.8738	1560.7579	74.3	132	- 145	1	R.ARAGANVTQMHYAR.R + Oxidation (M)
1582.8377	1581.8305	1581.7271	65.4	96	- 110	0	R.GDTEQLEGLSSSFGR.D
1967.0608	1966.0535	1965.9908	31.9	169	- 187	0	R.DAGLLQQHPGEAFGASIQK.V
2330.2339	2329.2266	2329.1961	13.1	201	- 221	1	R.GRAVLPNNINHPESEPMIIGR.N + Oxidation (M)
2339.2229	2338.2156	2338.0826	56.9	90	- 110	1	R.GWVEERGDTEQLEGLSSSFGR.D
2385.2935	2384.2862	2384.3110	-10.43	29	- 49	1	K.IHVPGSRPDLQVPMREIALTR.T

```
No match to: 805.4435, 817.4339, 891.5000, 900.4889, 906.5394, 909.4223, 952.4985, 961.5879, 1054.6305, 1073.6009,
1076.5738, 1078.5780, 1087.6056, 1091.5907, 1100.6162, 1107.6426, 1117.5943, 1131.6636, 1145.6759, 1154.6595,
1162.6289, 1188.7106, 1213.6439, 1219.6987, 1221.7099, 1282.7596, 1329.7785, 1342.8028, 1423.7341, 1462.7489,
1471.8574, 1486.8640, 1502.8443, 1528.9019, 1537.7928, 1542.7750, 1597.8184, 1611.7719, 1641.9273, 1651.9542,
1656.9978, 1687.8846, 1759.9421, 1762.9604, 1838.0268, 1925.9415, 1928.9792, 2034.0174, 2134.1272, 2202.1233,
2211.0847, 2280.2533, 2318.1759, 2346.1687, 2429.2638, 2612.3789, 3242.5742, 3471.5614, 3716.5563

3.     RBSA_SALCH     Mass: 55049     Score: 61     Expect: 0.46  Matches: 12
       Ribose import ATP-binding protein RbsA OS=Salmonella choleraesuis (strain SC-B67) OX=321314 GN=rbsA PE=3 SV=2
        Observed     Mr(expt)     Mr(calc)     ppm  Start    End Miss   Peptide
        817.4339     816.4266     816.4453  -22.92    186 - 192    1    R.ELKSQGR.G
        906.5394     905.5321     905.4793    58.4    297 - 304    0    K.VLYGAMPR.T
        947.5320     946.5247     946.5157    9.49      1 -   8    0    -.MDALLQLK.G + Oxidation (M)
       1145.6759    1144.6686    1144.5910    67.8     32 -  43    0    R.VMALVGENGAGK.S
       1213.6439    1212.6366    1212.7078  -58.70      2 -  12    1    M.DALLQLKGIDK.A
       1219.6987    1218.6914    1218.6543    30.4    193 - 202    1    R.GIVYISHRMK.E + Oxidation (M)
       1423.7341    1422.7268    1422.7871  -42.33    432 - 442    1    K.KEIYQLINQFK.A
       1542.7750    1541.7677    1541.7587    5.90    368 - 380    1    K.HKDEQQAVGDFIR.L
       1561.8811    1560.8738    1560.7817    59.0    480 - 494    0    R.EQATQEVLMAAAVGK.L + Oxidation (M)
       1925.9415    1924.9343    1924.9122    11.5    224 - 240    0    R.EVATLTEDSLIEMMVGR.K + 2 Oxidation (M)
       1928.9792    1927.9720    1928.0149  -22.28    480 - 497    1    R.EQATQEVLMAAAVGKLNR.V
       2385.2935    2384.2862    2384.2482    15.9    386 - 408    1    K.TPSMEQAIGLLSGGNQQKVAIAR.G + Oxidation (M)
       No match to: 805.4435, 891.5000, 900.4889, 909.4223, 943.5394, 952.4985, 961.5879, 1044.5817, 1054.6305,
       1073.6009, 1076.5738, 1078.5780, 1087.6056, 1091.5907, 1100.6162, 1107.6426, 1114.6425, 1117.5943, 1131.6636,
       1154.6595, 1162.6289, 1179.6387, 1188.7106, 1221.7099, 1282.7596, 1329.7785, 1342.8028, 1391.7960, 1433.8679,
       1462.7489, 1471.8574, 1486.8640, 1502.8443, 1528.9019, 1537.7928, 1554.7503, 1582.8377, 1597.8184, 1611.7719,
       1641.9273, 1651.9542, 1656.9978, 1687.8846, 1759.9421, 1762.9604, 1838.0268, 1967.0608, 2034.0174, 2134.1272,
       2202.1233, 2211.0847, 2280.2533, 2318.1759, 2330.2339, 2339.2229, 2346.1687, 2429.2638, 2612.3789, 3242.5742,
       3471.5614, 3716.5563

4.     RBSA_SALTI     Mass: 55102     Score: 61     Expect: 0.46  Matches: 12
       Ribose import ATP-binding protein RbsA OS=Salmonella typhi OX=90370 GN=rbsA PE=3 SV=1
        Observed     Mr(expt)     Mr(calc)     ppm  Start    End Miss   Peptide
        817.4339     816.4266     816.4453  -22.92    186 - 192    1    R.ELKSQGR.G
        906.5394     905.5321     905.4793    58.4    297 - 304    0    K.VLYGAMPR.T
        947.5320     946.5247     946.5157    9.49      1 -   8    0    -.MDALLQLK.G + Oxidation (M)
```

1145.6759	1144.6686	1144.5910	67.8	32	43	0	R.VMALVGENGAGK.S
1213.6439	1212.6366	1212.7078	-58.70	2	12	1	M.DALLQLKGIDK.A
1219.6987	1218.6914	1218.6543	30.4	193	202	1	R.GIVYISHRMK.E + Oxidation (M)
1423.7341	1422.7268	1422.7871	-42.33	432	442	1	K.KEIYQLINQFK.A
1542.7750	1541.7677	1541.7587	5.90	368	380	1	K.HKDEQQAVGDFIR.L
1561.8811	1560.8738	1560.7817	59.0	480	494	0	R.EQATQEVLMAAAVGK.L + Oxidation (M)
1925.9415	1924.9343	1924.9122	11.5	224	240	0	R.EVATLTEDSLIEMMVGR.K + 2 Oxidation (M)
1928.9792	1927.9720	1928.0149	-22.28	480	497	1	R.EQATQEVLMAAAVGKLNR.V
2385.2935	2384.2862	2384.2482	15.9	386	408	1	K.TPSMEQAIGLLSGGNQQKVAIAR.G + Oxidation (M)

No match to: 805.4435, 891.5000, 900.4889, 909.4223, 943.5394, 952.4985, 961.5879, 1044.5817, 1054.6305, 1073.6009, 1076.5738, 1078.5780, 1087.6056, 1091.5907, 1100.6162, 1107.6426, 1114.6425, 1117.5943, 1131.6636, 1154.6595, 1162.6289, 1179.6387, 1188.7106, 1221.7099, 1282.7596, 1329.7785, 1342.8028, 1391.7960, 1433.8679, 1462.7489, 1471.8574, 1486.8640, 1502.8443, 1528.9019, 1537.7928, 1554.7503, 1582.8377, 1597.8184, 1611.7719, 1641.9273, 1651.9542, 1656.9978, 1687.8846, 1759.9421, 1762.9604, 1838.0268, 1967.0608, 2034.0174, 2134.1272, 2202.1233, 2211.0847, 2280.2533, 2318.1759, 2330.2339, 2339.2229, 2346.1687, 2429.2638, 2612.3789, 3242.5742, 3471.5614, 3716.5563

5. RBSA_SALTY **Mass:** 55058 **Score:** 61 **Expect:** 0.46 **Matches:** 12

Ribose import ATP-binding protein RbsA OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rbsA PE=3 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
817.4339	816.4266	816.4453	-22.92	186	192	1	R.ELKSQGR.G
906.5394	905.5321	905.4793	58.4	297	304	0	K.VLYGAMPR.T
947.5320	946.5247	946.5157	9.49	1	8	0	-.MDALLQLK.G + Oxidation (M)
1145.6759	1144.6686	1144.5910	67.8	32	43	0	R.VMALVGENGAGK.S
1213.6439	1212.6366	1212.7078	-58.70	2	12	1	M.DALLQLKGIDK.A
1219.6987	1218.6914	1218.6543	30.4	193	202	1	R.GIVYISHRMK.E + Oxidation (M)
1423.7341	1422.7268	1422.7871	-42.33	432	442	1	K.KEIYQLINQFK.A
1542.7750	1541.7677	1541.7587	5.90	368	380	1	K.HKDEQQAVGDFIR.L
1561.8811	1560.8738	1560.7817	59.0	480	494	0	R.EQATQEVLMAAAVGK.L + Oxidation (M)
1925.9415	1924.9343	1924.9122	11.5	224	240	0	R.EVATLTEDSLIEMMVGR.K + 2 Oxidation (M)
1928.9792	1927.9720	1928.0149	-22.28	480	497	1	R.EQATQEVLMAAAVGKLNR.V
2385.2935	2384.2862	2384.2482	15.9	386	408	1	K.TPSMEQAIGLLSGGNQQKVAIAR.G + Oxidation (M)

```
No match to: 805.4435, 891.5000, 900.4889, 909.4223, 943.5394, 952.4985, 961.5879, 1044.5817, 1054.6305,
1073.6009, 1076.5738, 1078.5780, 1087.6056, 1091.5907, 1100.6162, 1107.6426, 1114.6425, 1117.5943, 1131.6636,
1154.6595, 1162.6289, 1179.6387, 1188.7106, 1221.7099, 1282.7596, 1329.7785, 1342.8028, 1391.7960, 1433.8679,
1462.7489, 1471.8574, 1486.8640, 1502.8443, 1528.9019, 1537.7928, 1554.7503, 1582.8377, 1597.8184, 1611.7719,
1641.9273, 1651.9542, 1656.9978, 1687.8846, 1759.9421, 1762.9604, 1838.0268, 1967.0608, 2034.0174, 2134.1272,
2202.1233, 2211.0847, 2280.2533, 2318.1759, 2330.2339, 2339.2229, 2346.1687, 2429.2638, 2612.3789, 3242.5742,
3471.5614, 3716.5563

6.     VP4_ROTHL      Mass: 87596     Score: 60     Expect: 0.57  Matches: 15
       Outer capsid protein VP4 OS=Rotavirus A (strain RVA/Human/Philippines/L26/1987/G12P1B[4]) OX=10953 PE=3 SV=1
        Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
        805.4435    804.4363    804.4090    33.9    156 -  162    0   R.TLTSNNR.L
        947.5320    946.5247    946.5157    9.51    738 -  745    0   R.MEALNLIK.S + Oxidation (M)
        961.5879    960.5806    960.5101    73.4    155 -  162    1   R.RTLTSNNR.L
       1087.6056   1086.5984   1086.6107  -11.34    766 -  774    0   R.IEQLILQCK.L
       1162.6289   1161.6216   1161.5681    46.0    137 -  144    1   K.WKFFEMFK.G
       1179.6387   1178.6315   1178.5680    53.9    728 -  737    0   K.NLNDNYGITR.M
       1221.7099   1220.7026   1220.6435    48.4    642 -  652    1   K.TKIDMSTQIGK.N
       1342.8028   1341.7955   1341.7153    59.8    753 -  763    0   R.NFINQNNPIIR.N
       1462.7489   1461.7416   1461.7973  -38.12    156 -  168    1   R.TLTSNNRLVGMLK.Y + Oxidation (M)
       1928.9792   1927.9720   1927.8523    62.1    139 -  154    1   K.FFEMFKGSSQSNFSNR.R + Oxidation (M)
       2202.1233   2201.1160   2201.0232    42.2    622 -  641    0   K.EMITQTEGMSFDDISAAVLK.T + Oxidation (M)
       2211.0847   2210.0774   2210.0914   -6.35    596 -  616    0   K.STSNITDLVNDVSTQTSTISK.K
       2330.2339   2329.2266   2329.1067    51.5    554 -  576    1   K.SKLATSISEMTNSLSDAASSASR.S + Oxidation (M)
       2339.2229   2338.2156   2338.1864    12.5    596 -  617    1   K.STSNITDLVNDVSTQTSTISKK.L
       2429.2638   2428.2565   2428.1110    59.9    341 -  359    1   R.YEVIKENSYVYIDYWDDSK.A
       No match to: 817.4339, 891.5000, 900.4889, 906.5394, 909.4223, 943.5394, 952.4985, 1044.5817, 1054.6305,
       1073.6009, 1076.5738, 1078.5780, 1091.5907, 1100.6162, 1107.6426, 1114.6425, 1117.5943, 1131.6636, 1145.6759,
       1154.6595, 1188.7106, 1213.6439, 1219.6987, 1282.7596, 1329.7785, 1391.7960, 1423.7341, 1433.8679, 1471.8574,
       1486.8640, 1502.8443, 1528.9019, 1537.7928, 1542.7750, 1554.7503, 1561.8811, 1582.8377, 1597.8184, 1611.7719,
       1641.9273, 1651.9542, 1656.9978, 1687.8846, 1759.9421, 1762.9604, 1838.0268, 1925.9415, 1967.0608, 2034.0174,
       2134.1272, 2280.2533, 2318.1759, 2346.1687, 2385.2935, 2612.3789, 3242.5742, 3471.5614, 3716.5563

7.     LON_UNCTG      Mass: 90316     Score: 56     Expect: 1.5  Matches: 14
       Lon protease OS=Uncultured termite group 1 bacterium phylotype Rs-D17 OX=471821 GN=lon PE=3 SV=1
        Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
```

947.5320	946.5247	946.5852	-63.86	59	-	66	0	R.LVFIVTQK.N
1091.5907	1090.5834	1090.5151	62.7	135	-	143	0	K.MPEVEAIMR.Q + Oxidation (M)
1117.5943	1116.5871	1116.5597	24.5	274	-	284	1	K.MPQAAKSAADK.E
1154.6595	1153.6522	1153.5979	47.1	67	-	76	0	K.NIQIEDPTPK.D
1162.6289	1161.6216	1161.6757	-46.60	345	-	354	0	R.VLEYLAVLSR.V
1433.8679	1432.8606	1432.8038	39.7	343	-	354	1	K.DRVLEYLAVLSR.V
1537.7928	1536.7856	1536.8664	-52.59	512	-	524	1	R.HIAEDFIVPKQLK.E
1651.9542	1650.9469	1650.9015	27.5	408	-	422	1	R.TYIGSMPGKIIQSIK.K + Oxidation (M)
1759.9421	1758.9348	1758.9152	11.2	423	-	438	1	K.KAGSNNPVFILDEIDK.I
1925.9415	1924.9343	1924.9638	-15.35	77	-	92	0	K.DVYNIGTICEVLQMLK.M + Oxidation (M); Propionamide (C)
2211.0847	2210.0774	2210.1439	-30.09	766	-	784	0	K.LQMIPVSHMDEVISLTIER.L
2339.2229	2338.2156	2338.2388	-9.92	765	-	784	1	K.KLQMIPVSHMDEVISLTIER.L
2346.1687	2345.1614	2345.1652	-1.59	424	-	444	1	K.AGSNNPVFILDEIDKIGSDWR.G
2385.2935	2384.2862	2384.2739	5.14	579	-	598	1	K.SITIKPENLNKYLGIAYYER.E

No match to: 805.4435, 817.4339, 891.5000, 900.4889, 906.5394, 909.4223, 943.5394, 952.4985, 961.5879, 1044.5817, 1054.6305, 1073.6009, 1076.5738, 1078.5780, 1087.6056, 1100.6162, 1107.6426, 1114.6425, 1131.6636, 1145.6759, 1179.6387, 1188.7106, 1213.6439, 1219.6987, 1221.7099, 1282.7596, 1329.7785, 1342.8028, 1391.7960, 1423.7341, 1462.7489, 1471.8574, 1486.8640, 1502.8443, 1528.9019, 1542.7750, 1554.7503, 1561.8811, 1582.8377, 1597.8184, 1611.7719, 1641.9273, 1656.9978, 1687.8846, 1762.9604, 1838.0268, 1928.9792, 1967.0608, 2034.0174, 2134.1272, 2202.1233, 2280.2533, 2318.1759, 2330.2339, 2429.2638, 2612.3789, 3242.5742, 3471.5614, 3716.5563

8. HMW2_MYCGE **Mass:** 216122 **Score:** 55 **Expect:** 1.8 **Matches:** 23

Cytadherence high molecular weight protein 2 OS=Mycoplasma genitalium (strain ATCC 33530 / G-37 / NCTC 10195) OX=243273 GN=hmw2 PE=3 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**		**End**	**Miss**	**Peptide**
805.4435	804.4363	804.4494	-16.30	1122	-	1127	0	R.QFLLER.K
817.4339	816.4266	816.4453	-22.90	1539	-	1545	1	R.ERAINSK.D
900.4889	899.4816	899.5188	-41.41	1662	-	1668	1	R.QRNLLEK.K
947.5320	946.5247	946.4971	29.2	630	-	637	0	K.ETLDQLTK.S
1073.6009	1072.5936	1072.5625	29.0	729	-	737	1	R.SELQNAKQR.I
1076.5738	1075.5665	1075.5397	24.9	693	-	701	1	K.EKEIEATEK.Q
1100.6162	1099.6089	1099.6138	-4.47	542	-	550	1	K.HALERSFIK.L
1117.5943	1116.5871	1116.5775	8.58	255	-	263	1	R.DELSQLERK.I
1154.6595	1153.6522	1153.6091	37.3	1344	-	1354	0	K.QATDAILASHK.E

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1162.6289  1161.6216  1161.6063    13.1    801 -  810    1    K.KQTMEVDAIK.Q
1179.6387  1178.6315  1178.5567    63.4   1652 - 1660    0    R.YENELNELR.R
1188.7106  1187.7034  1187.6397    53.6     49 -   58    1    K.SLEDELKNLK.G
1219.6987  1218.6914  1218.6244    55.0    352 -  361    0    K.LQQENELFAK.H
1282.7596  1281.7523  1281.7041    37.7   1343 - 1354    1    R.KQATDAILASHK.E
1342.8028  1341.7955  1341.7000    71.1    954 -  964    1    K.NNQVKLELDNR.F
1423.7341  1422.7268  1422.7354   -6.02   1416 - 1427    1    K.TKAIQEIENSYK.R
1537.7928  1536.7856  1536.8188  -21.59    509 -  520    1    K.ENELLFFEKQLK.Q
1542.7750  1541.7677  1541.8049  -24.10   1670 - 1682    0    K.LDQIQLESQLNNK.Q
1597.8184  1596.8111  1596.8147   -2.30   1328 - 1340    1    K.RAVLEDQISYFEK.Q
1611.7719  1610.7646  1610.8304  -40.85   1704 - 1716    1    R.LNDFDQKINYLTK.K
1656.9978  1655.9905  1655.9094    49.0   1360 - 1373    1    K.EGELQKLLVELETR.K
1759.9421  1758.9348  1758.9377   -1.61   1114 - 1127    1    R.DQLNSQIRQFLLER.K
2202.1233  2201.1160  2201.1076    3.80    418 -  435    1    R.REIDTLLTQASLEYEHQR.E
 No match to: 891.5000, 906.5394, 909.4223, 943.5394, 952.4985, 961.5879, 1044.5817, 1054.6305, 1078.5780,
 1087.6056, 1091.5907, 1107.6426, 1114.6425, 1131.6636, 1145.6759, 1213.6439, 1221.7099, 1329.7785, 1391.7960,
 1433.8679, 1462.7489, 1471.8574, 1486.8640, 1502.8443, 1528.9019, 1554.7503, 1561.8811, 1582.8377, 1641.9273,
 1651.9542, 1687.8846, 1762.9604, 1838.0268, 1925.9415, 1928.9792, 1967.0608, 2034.0174, 2134.1272, 2211.0847,
 2280.2533, 2318.1759, 2330.2339, 2339.2229, 2346.1687, 2385.2935, 2429.2638, 2612.3789, 3242.5742, 3471.5614,
 3716.5563

9.   TIG_BURM1    Mass: 49720    Score: 54     Expect: 2.3  Matches: 11
     Trigger factor OS=Burkholderia multivorans (strain ATCC 17616 / 249) OX=395019 GN=tig PE=3 SV=1
      Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
      900.4889    899.4816    899.4964  -16.46    308 - 315    0   K.ISELDVPK.A
      943.5394    942.5321    942.5134    19.8      2 -  10    0   M.ANVVENLGK.L
     1054.6305   1053.6232   1053.6798  -53.70    361 - 370    0   K.LGLVLAELVK.A
     1100.6162   1099.6089   1099.5622    42.5    316 - 324    0   K.ALIEQDQQR.L
     1117.5943   1116.5871   1116.5663    18.6    266 - 276    0   K.SLGIEDGDLAK.M
     1154.6595   1153.6522   1153.6165    30.9    241 - 250    1   K.TAQFTVTMKK.V
     1188.7106   1187.7034   1187.6146    74.7     22 -  31    1   K.ETVQKEIDAR.I
     1342.8028   1341.7955   1341.7868    6.50     15 -  26    1   R.VTISLPKETVQK.E
     1462.7489   1461.7416   1461.7537   -8.29    205 - 217    0   R.MLPEFEQAALGLK.A + Oxidation (M)
     1687.8846   1686.8773   1686.9338  -33.51    293 - 307    1   R.TQAIVKNQVMDALLK.I + Oxidation (M)
     1928.9792   1927.9720   1928.0288  -29.50    299 - 315    1   K.NQVMDALLKISELDVPK.A + Oxidation (M)
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      No match to: 805.4435, 817.4339, 891.5000, 906.5394, 909.4223, 947.5320, 952.4985, 961.5879, 1044.5817, 1073.6009,
      1076.5738, 1078.5780, 1087.6056, 1091.5907, 1107.6426, 1114.6425, 1131.6636, 1145.6759, 1162.6289, 1179.6387,
      1213.6439, 1219.6987, 1221.7099, 1282.7596, 1329.7785, 1391.7960, 1423.7341, 1433.8679, 1471.8574, 1486.8640,
      1502.8443, 1528.9019, 1537.7928, 1542.7750, 1554.7503, 1561.8811, 1582.8377, 1597.8184, 1611.7719, 1641.9273,
      1651.9542, 1656.9978, 1759.9421, 1762.9604, 1838.0268, 1925.9415, 1967.0608, 2034.0174, 2134.1272, 2202.1233,
      2211.0847, 2280.2533, 2318.1759, 2330.2339, 2339.2229, 2346.1687, 2385.2935, 2429.2638, 2612.3789, 3242.5742,
      3471.5614, 3716.5563

10.   MNME_ALIF1     Mass: 49576     Score: 53      Expect: 2.6  Matches: 10
      tRNA modification GTPase MnmE OS=Aliivibrio fischeri (strain ATCC 700601 / ES114) OX=312309 GN=mnmE PE=3 SV=1
       Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
      1117.5943   1116.5871   1116.5709    14.4   206 - 215    1    R.KEANQGAIMR.E
      1179.6387   1178.6315   1178.5900    35.2   328 - 337    1    K.NMGMTVIRNK.A + Oxidation (M)
      1188.7106   1187.7034   1187.6339    58.5   316 - 324    0    K.LIWPEFLDR.L
      1433.8679   1432.8606   1432.8289    22.1   157 - 168    0    K.INTLVESLIYLR.I
      1502.8443   1501.8370   1501.7372    66.4   277 - 289    1    R.EASDEVERIGIER.A
      1542.7750   1541.7677   1541.8348  -43.48   216 - 230    1    R.EGMKVVIAGRPNAGK.S + Oxidation (M)
      1611.7719   1610.7646   1610.8456  -50.30    41 -  53    1    K.ELKPRYAEYAPFK.D
      1651.9542   1650.9469   1650.8689    47.2     2 -  17    0    M.TLHTDTIVAQATAPGR.G
      1838.0268   1837.0195   1836.9118    58.6   106 - 121    1    R.TARPGEFSERAFLNDK.M
      2330.2339   2329.2266   2329.1550    30.7   426 - 446    0    R.IAQQHLSEITGEFTSDDLLGR.I
      No match to: 805.4435, 817.4339, 891.5000, 900.4889, 906.5394, 909.4223, 943.5394, 947.5320, 952.4985, 961.5879,
      1044.5817, 1054.6305, 1073.6009, 1076.5738, 1078.5780, 1087.6056, 1091.5907, 1100.6162, 1107.6426, 1114.6425,
      1131.6636, 1145.6759, 1154.6595, 1162.6289, 1213.6439, 1219.6987, 1221.7099, 1282.7596, 1329.7785, 1342.8028,
      1391.7960, 1423.7341, 1462.7489, 1471.8574, 1486.8640, 1528.9019, 1537.7928, 1554.7503, 1561.8811, 1582.8377,
      1597.8184, 1641.9273, 1656.9978, 1687.8846, 1759.9421, 1762.9604, 1925.9415, 1928.9792, 1967.0608, 2034.0174,
      2134.1272, 2202.1233, 2211.0847, 2280.2533, 2318.1759, 2339.2229, 2346.1687, 2385.2935, 2429.2638, 2612.3789,
      3242.5742, 3471.5614, 3716.5563

11.   ILVD_HAEI8     Mass: 65710     Score: 53      Expect: 2.9  Matches: 12
      Dihydroxy-acid dehydratase OS=Haemophilus influenzae (strain 86-028NP) OX=281310 GN=ilvD PE=3 SV=1
       Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
      1073.6009   1072.5936   1072.6240  -28.39   153 - 161    1    K.TKLSDQLIR.L
      1076.5738   1075.5665   1075.5734   -6.45     4 -  13    1    K.LRSATSTQGR.N
      1078.5780   1077.5707   1077.5818  -10.34   583 - 591    1    R.EREVSFALK.V
      1091.5907   1090.5834   1090.6036  -18.51   377 - 386    1    K.FFRAGPAGIR.T
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     1145.6759  1144.6686  1144.5923    66.6    14 -   23   1    R.NMAGARALWR.A
     1179.6387  1178.6315  1178.5720    50.4   592 -  602   0    K.VFGHFATSADK.G
     1423.7341  1422.7268  1422.6634    44.6     6 -   19   1    R.SATSTQGRNMAGAR.A + Oxidation (M)
     1462.7489  1461.7416  1461.7001    28.4   369 -  379   1    R.NQDEELHKFFR.A
     1528.9019  1527.8946  1527.7892    69.0   555 -  568   0    R.AINLEISNDELAAR.R
     1611.7719  1610.7646  1610.7689   -2.64   245 -  257   1    K.RYYEQDDASVLPR.S
     2346.1687  2345.1614  2345.1072    23.1   480 -  500   1    R.YEGPKGGPGMQEMLYPTSYLK.S
     2385.2935  2384.2862  2384.1365    62.8   321 -  341   1    K.YHMEDVHRAGGIMGLLGELDR.A + Oxidation (M)
     No match to: 805.4435, 817.4339, 891.5000, 900.4889, 906.5394, 909.4223, 943.5394, 947.5320, 952.4985, 961.5879,
     1044.5817, 1054.6305, 1087.6056, 1100.6162, 1107.6426, 1114.6425, 1117.5943, 1131.6636, 1154.6595, 1162.6289,
     1188.7106, 1213.6439, 1219.6987, 1221.7099, 1282.7596, 1329.7785, 1342.8028, 1391.7960, 1433.8679, 1471.8574,
     1486.8640, 1502.8443, 1537.7928, 1542.7750, 1554.7503, 1561.8811, 1582.8377, 1597.8184, 1641.9273, 1651.9542,
     1656.9978, 1687.8846, 1759.9421, 1762.9604, 1838.0268, 1925.9415, 1928.9792, 1967.0608, 2034.0174, 2134.1272,
     2202.1233, 2211.0847, 2280.2533, 2318.1759, 2330.2339, 2339.2229, 2429.2638, 2612.3789, 3242.5742, 3471.5614,
     3716.5563

12.  KDM3A_HUMAN    Mass: 147248   Score: 53    Expect: 3  Matches: 18
     Lysine-specific demethylase 3A OS=Homo sapiens OX=9606 GN=KDM3A PE=1 SV=4
      Observed    Mr(expt)    Mr(calc)    ppm  Start    End Miss   Peptide
      805.4435    804.4363    804.4606 -30.26   575 -  580    1    R.RLQFNK.H
      817.4339    816.4266    816.3977   35.4   101 -  107    0    K.SPEISER.I
      909.4223    908.4151    908.4239  -9.79  1313 - 1321    0    K.ASESSFGKP.-
      943.5394    942.5321    942.5287   3.65  1298 - 1305    0    K.NVIYHAVK.D
      947.5320    946.5247    946.5488 -25.40   169 -  176    0    K.EFQALIVK.H
     1073.6009   1072.5936   1072.5699   22.1   471 -  480    1    K.KVEPSALACR.S
     1087.6056   1086.5984   1086.5743   22.1  1036 - 1044    1    K.NEKEPMVLK.L
     1091.5907   1090.5834   1090.5771   5.79   177 -  185    0    K.HLDESHLLK.G
     1145.6759   1144.6686   1144.6088   52.2   186 -  196    1    K.GDKNLVGSEVK.I
     1391.7960   1390.7887   1390.7205   49.1   177 -  188    1    K.HLDESHLLKGDK.N
     1462.7489   1461.7416   1461.7423  -0.48   264 -  277    1    K.SSENNGTLVSKQAK.S
     1471.8574   1470.8501   1470.7752   50.9   299 -  312    0    K.EILLGCTAATPPSK.D + Propionamide (C)
     1528.9019   1527.8946   1527.7966   64.1   220 -  232    0    K.TLQVNCEEIPALK.I + Propionamide (C)
     1537.7928   1536.7856   1536.6879   63.6   998 - 1010    0    K.EFGEQEVDLVNCR.T
     1542.7750   1541.7677   1541.7184   32.0  1100 - 1112    0    K.MYNAYGLITPEDR.K
     1656.9978   1655.9905   1655.9069   50.5     1 -   15    0    -.MVLTLGESWPVLVGR.R
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1687.8846	1686.8773	1686.9127	-20.98	1298	-	1312	1	K.NVIYHAVKDAVAMLK.A + Oxidation (M)
1967.0608	1966.0535	1965.9618	46.6	1062	-	1077	1	R.FDDLMANIPLPEYTRR.D + Oxidation (M)

No match to: 891.5000, 900.4889, 906.5394, 952.4985, 961.5879, 1044.5817, 1054.6305, 1076.5738, 1078.5780, 1100.6162, 1107.6426, 1114.6425, 1117.5943, 1131.6636, 1154.6595, 1162.6289, 1179.6387, 1188.7106, 1213.6439, 1219.6987, 1221.7099, 1282.7596, 1329.7785, 1342.8028, 1423.7341, 1433.8679, 1486.8640, 1502.8443, 1554.7503, 1561.8811, 1582.8377, 1597.8184, 1611.7719, 1641.9273, 1651.9542, 1759.9421, 1762.9604, 1838.0268, 1925.9415, 1928.9792, 2034.0174, 2134.1272, 2202.1233, 2211.0847, 2280.2533, 2318.1759, 2330.2339, 2339.2229, 2346.1687, 2385.2935, 2429.2638, 2612.3789, 3242.5742, 3471.5614, 3716.5563

13. GATB_BACC4 **Mass:** 53190 **Score:** 52 **Expect:** 3.1 **Matches:** 10

Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B OS=Bacillus cereus (strain B4264) OX=405532 GN=gatB PE=3 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**		**End**	**Miss**	**Peptide**
909.4223	908.4151	908.4426	-30.28	54	-	61	0	K.EAVNFAMK.A
943.5394	942.5321	942.4658	70.4	397	-	405	0	K.GGDPEEIVK.A
1213.6439	1212.6366	1212.6139	18.7	213	-	222	0	K.NLNSFTYVQK.G
1433.8679	1432.8606	1432.7959	45.2	372	-	384	1	K.MVQLIEKGTISSK.I
1486.8640	1485.8567	1485.8151	28.0	406	-	419	1	K.AKGLVQISDEGTLR.K
1554.7503	1553.7430	1553.7977	-35.18	159	-	171	1	R.TPEEAYAYLEKLK.S
1838.0268	1837.0195	1837.0019	9.59	1	-	16	0	-.MNLETIIGLEVHVELK.T
1928.9792	1927.9720	1928.0652	-48.38	361	-	378	1	K.DVALTPAGLSKMVQLIEK.G + Oxidation (M)
2034.0174	2033.0101	2033.0364	-12.94	191	-	208	1	R.CDANISLRPVGQEKFGTK.A + Propionamide (C)
2429.2638	2428.2565	2428.1436	46.5	54	-	75	1	K.EAVNFAMKAAMALNCDIATETK.F + Oxidation (M); Propionamide (C)

No match to: 805.4435, 817.4339, 891.5000, 900.4889, 906.5394, 947.5320, 952.4985, 961.5879, 1044.5817, 1054.6305, 1073.6009, 1076.5738, 1078.5780, 1087.6056, 1091.5907, 1100.6162, 1107.6426, 1114.6425, 1117.5943, 1131.6636, 1145.6759, 1154.6595, 1162.6289, 1179.6387, 1188.7106, 1219.6987, 1221.7099, 1282.7596, 1329.7785, 1342.8028, 1391.7960, 1423.7341, 1462.7489, 1471.8574, 1502.8443, 1528.9019, 1537.7928, 1542.7750, 1561.8811, 1582.8377, 1597.8184, 1611.7719, 1641.9273, 1651.9542, 1656.9978, 1687.8846, 1759.9421, 1762.9604, 1925.9415, 1967.0608,

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      2134.1272, 2202.1233, 2211.0847, 2280.2533, 2318.1759, 2330.2339, 2339.2229, 2346.1687, 2385.2935, 2612.3789,
      3242.5742, 3471.5614, 3716.5563

14.   COMD4_DICDI     Mass: 20135     Score: 52     Expect: 3.8  Matches: 7
      COMM domain-containing protein 4 OS=Dictyostelium discoideum OX=44689 GN=commd4 PE=4 SV=1
       Observed    Mr(expt)    Mr(calc)    ppm  Start   End Miss   Peptide
        891.5000    890.4927    890.5007  -8.99      1 -    7    1    -.MTNIRIK.L + Oxidation (M)
        947.5320    946.5247    946.4794   47.9    170 - 177    0    K.LLMETVNQ.-
       1073.6009   1072.5936   1072.5665   25.2     96 - 104    0    R.SIFHNNTLK.L
       1188.7106   1187.7034   1187.6226   68.0    158 - 166    0    K.FNVLYYELK.G
       1219.6987   1218.6914   1218.6278   52.2    167 - 177    1    K.GAKLLMETVNQ.- + Oxidation (M)
       1342.8028   1341.7955   1341.7517   32.6     94 - 104    1    K.LRSIFHNNTLK.L
       1656.9978   1655.9905   1655.9763   8.60     44 -  58    0    K.ALIAAIHFIIFNSVK.N
      No match to: 805.4435, 817.4339, 900.4889, 906.5394, 909.4223, 943.5394, 952.4985, 961.5879, 1044.5817, 1054.6305,
      1076.5738, 1078.5780, 1087.6056, 1091.5907, 1100.6162, 1107.6426, 1114.6425, 1117.5943, 1131.6636, 1145.6759,
      1154.6595, 1162.6289, 1179.6387, 1213.6439, 1221.7099, 1282.7596, 1329.7785, 1391.7960, 1423.7341, 1433.8679,
      1462.7489, 1471.8574, 1486.8640, 1502.8443, 1528.9019, 1537.7928, 1542.7750, 1554.7503, 1561.8811, 1582.8377,
      1597.8184, 1611.7719, 1641.9273, 1651.9542, 1687.8846, 1759.9421, 1762.9604, 1838.0268, 1925.9415, 1928.9792,
      1967.0608, 2034.0174, 2134.1272, 2202.1233, 2211.0847, 2280.2533, 2318.1759, 2330.2339, 2339.2229, 2346.1687,
      2385.2935, 2429.2638, 2612.3789, 3242.5742, 3471.5614, 3716.5563

15.   GCH1_HUMAN     Mass: 27885     Score: 52     Expect: 3.9  Matches: 9
      GTP cyclohydrolase 1 OS=Homo sapiens OX=9606 GN=GCH1 PE=1 SV=1
       Observed    Mr(expt)    Mr(calc)     ppm  Start   End Miss   Peptide
        891.5000    890.4927    890.4644    31.9    217 - 224    1    R.GVQKMNSK.T
        909.4223    908.4151    908.3810    37.4     18 -  25    0    R.CSNGFPER.D
       1107.6426   1106.6353   1106.5972    34.5    242 - 250    1    R.EEFLTLIRS.-
       1114.6425   1113.6353   1113.6506  -13.77    179 - 187    1    R.LQVQERLTK.Q
       1117.5943   1116.5871   1116.5274    53.4     98 - 107    0    R.AASAMQFFTK.G + Oxidation (M)
       1219.6987   1218.6914   1218.7084  -13.98    168 - 177    1    K.LARIVEIYSR.R
       1554.7503   1553.7430   1553.7699  -17.29     46 -  59    1    K.SAQPADGWKGERPR.S
       1641.9273   1640.9200   1640.8133    65.0     94 - 107    1    K.TPWRAASAMQFFTK.G
       1687.8846   1686.8773   1686.8433    20.1    221 - 235    1    K.MNSKTVTSTMLGVFR.E + Oxidation (M)
      No match to: 805.4435, 817.4339, 900.4889, 906.5394, 943.5394, 947.5320, 952.4985, 961.5879, 1044.5817, 1054.6305,
      1073.6009, 1076.5738, 1078.5780, 1087.6056, 1091.5907, 1100.6162, 1131.6636, 1145.6759, 1154.6595, 1162.6289,
      1179.6387, 1188.7106, 1213.6439, 1221.7099, 1282.7596, 1329.7785, 1342.8028, 1391.7960, 1423.7341, 1433.8679,
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1462.7489, 1471.8574, 1486.8640, 1502.8443, 1528.9019, 1537.7928, 1542.7750, 1561.8811, 1582.8377, 1597.8184, 1611.7719, 1651.9542, 1656.9978, 1759.9421, 1762.9604, 1838.0268, 1925.9415, 1928.9792, 1967.0608, 2034.0174, 2134.1272, 2202.1233, 2211.0847, 2280.2533, 2318.1759, 2330.2339, 2339.2229, 2346.1687, 2385.2935, 2429.2638, 2612.3789, 3242.5742, 3471.5614, 3716.5563

16. RK5_PYRYE **Mass:** 20525 **Score:** 52 **Expect:** 3.9 **Matches:** 8

50S ribosomal protein L5, chloroplastic OS=Pyropia yezoensis OX=2788 GN=rpl5 PE=3 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
891.5000	890.4927	890.5338	-46.07	74 -	81	1	K.SIAGFKIR.E
906.5394	905.5321	905.4719	66.5	127 -	134	0	K.GNYNLGLR.E
947.5320	946.5247	946.4985	27.7	114 -	121	1	R.DFRGISPR.S
952.4985	951.4912	951.4484	45.0	174 -	181	1	K.LGMPFRES.- + Oxidation (M)
1087.6056	1086.5984	1086.5921	5.79	163 -	172	0	K.TDQEGLALLK.K
1117.5943	1116.5871	1116.6390	-46.56	152 -	162	0	R.GLDISIVTTAK.T
1687.8846	1686.8773	1686.8465	18.3	11 -	24	1	K.TTVTQSLKDEFQYK.N
1838.0268	1837.0195	1837.0171	1.29	97 -	111	1	K.MYSFLEKLINLTLPR.I

No match to: 805.4435, 817.4339, 900.4889, 909.4223, 943.5394, 961.5879, 1044.5817, 1054.6305, 1073.6009, 1076.5738, 1078.5780, 1091.5907, 1100.6162, 1107.6426, 1114.6425, 1131.6636, 1145.6759, 1154.6595, 1162.6289, 1179.6387, 1188.7106, 1213.6439, 1219.6987, 1221.7099, 1282.7596, 1329.7785, 1342.8028, 1391.7960, 1423.7341, 1433.8679, 1462.7489, 1471.8574, 1486.8640, 1502.8443, 1528.9019, 1537.7928, 1542.7750, 1554.7503, 1561.8811, 1582.8377, 1597.8184, 1611.7719, 1641.9273, 1651.9542, 1656.9978, 1759.9421, 1762.9604, 1925.9415, 1928.9792, 1967.0608, 2034.0174, 2134.1272, 2202.1233, 2211.0847, 2280.2533, 2318.1759, 2330.2339, 2339.2229, 2346.1687, 2385.2935, 2429.2638, 2612.3789, 3242.5742, 3471.5614, 3716.5563

17. RBSA_SALPA **Mass:** 55194 **Score:** 51 **Expect:** 4.1 **Matches:** 11

Ribose import ATP-binding protein RbsA OS=Salmonella paratyphi A (strain ATCC 9150 / SARB42) OX=295319 GN=rbsA PE=3 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
906.5394	905.5321	905.4793	58.4	297 -	304	0	K.VLYGAMPR.T
947.5320	946.5247	946.5157	9.49	1 -	8	0	-.MDALLQLK.G + Oxidation (M)
1100.6162	1099.6089	1099.6250	-14.69	192 -	200	1	R.RGIVYISHR.M
1213.6439	1212.6366	1212.7078	-58.70	2 -	12	1	M.DALLQLKGIDK.A
1219.6987	1218.6914	1218.6543	30.4	193 -	202	1	R.GIVYISHRMK.E + Oxidation (M)
1423.7341	1422.7268	1422.7871	-42.33	432 -	442	1	K.KEIYQLINQFK.A
1542.7750	1541.7677	1541.7587	5.90	368 -	380	1	K.HKDEQQAVGDFIR.L

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   1561.8811  1560.8738  1560.7817    59.0   480 - 494   0   R.EQATQEVLMAAAVGK.L + Oxidation (M)
   1925.9415  1924.9343  1924.9122    11.5   224 - 240   0   R.EVATLTEDSLIEMMVGR.K + 2 Oxidation (M)
   1928.9792  1927.9720  1928.0149  -22.28   480 - 497   1   R.EQATQEVLMAAAVGKLNR.V
   2385.2935  2384.2862  2384.2482    15.9   386 - 408   1   K.TPSMEQAIGLLSGGNQQKVAIAR.G + Oxidation (M)
   No match to: 805.4435, 817.4339, 891.5000, 900.4889, 909.4223, 943.5394, 952.4985, 961.5879, 1044.5817, 1054.6305,
   1073.6009, 1076.5738, 1078.5780, 1087.6056, 1091.5907, 1107.6426, 1114.6425, 1117.5943, 1131.6636, 1145.6759,
   1154.6595, 1162.6289, 1179.6387, 1188.7106, 1221.7099, 1282.7596, 1329.7785, 1342.8028, 1391.7960, 1433.8679,
   1462.7489, 1471.8574, 1486.8640, 1502.8443, 1528.9019, 1537.7928, 1554.7503, 1582.8377, 1597.8184, 1611.7719,
   1641.9273, 1651.9542, 1656.9978, 1687.8846, 1759.9421, 1762.9604, 1838.0268, 1967.0608, 2034.0174, 2134.1272,
   2202.1233, 2211.0847, 2280.2533, 2318.1759, 2330.2339, 2339.2229, 2346.1687, 2429.2638, 2612.3789, 3242.5742,
   3471.5614, 3716.5563

18.  THIC_STRM5     Mass: 68293     Score: 51     Expect: 4.4  Matches: 11
     Phosphomethylpyrimidine synthase OS=Stenotrophomonas maltophilia (strain R551-3) OX=391008 GN=thiC PE=3 SV=1
      Observed    Mr(expt)    Mr(calc)     ppm  Start   End Miss   Peptide
       943.5394   942.5321   942.5399   -8.27   123 - 130   1   R.FPARSLPR.R
       947.5320   946.5247   946.5600  -37.26   331 - 338   1   R.YVPLTAKR.V
      1044.5817  1043.5744  1043.5876  -12.66   118 - 126   1   K.LDAVRFPAR.S
      1179.6387  1178.6315  1178.6044    23.0   113 - 122   1   R.EHDPKLDAVR.F
      1391.7960  1390.7887  1390.7602    20.5   339 - 352   1   R.VTGIVSRGGSIMAK.W + Oxidation (M)
      1433.8679  1432.8606  1432.7535    74.8   491 - 502   1   K.EHLGLPNRQDVR.D
      1554.7503  1553.7430  1553.7595  -10.62   346 - 359   1   R.GGSIMAKWCLAHHK.E + Oxidation (M)
      1561.8811  1560.8738  1560.7579    74.3   132 - 145   1   R.ARAGANVTQMHYAR.R + Oxidation (M)
      1967.0608  1966.0535  1965.9908    31.9   169 - 187   0   R.DAGLLQQHPGEAFGASIQK.I
      2330.2339  2329.2266  2329.1961    13.1   201 - 221   1   R.GRAVLPNNINHPESEPMIIGR.N + Oxidation (M)
      2385.2935  2384.2862  2384.3110  -10.43    29 -  49   1   K.IHVPGSRPDLQVPMREIALTR.T
     No match to: 805.4435, 817.4339, 891.5000, 900.4889, 906.5394, 909.4223, 952.4985, 961.5879, 1054.6305, 1073.6009,
     1076.5738, 1078.5780, 1087.6056, 1091.5907, 1100.6162, 1107.6426, 1114.6425, 1117.5943, 1131.6636, 1145.6759,
     1154.6595, 1162.6289, 1188.7106, 1213.6439, 1219.6987, 1221.7099, 1282.7596, 1329.7785, 1342.8028, 1423.7341,
     1462.7489, 1471.8574, 1486.8640, 1502.8443, 1528.9019, 1537.7928, 1542.7750, 1582.8377, 1597.8184, 1611.7719,
     1641.9273, 1651.9542, 1656.9978, 1687.8846, 1759.9421, 1762.9604, 1838.0268, 1925.9415, 1928.9792, 2034.0174,
     2134.1272, 2202.1233, 2211.0847, 2280.2533, 2318.1759, 2339.2229, 2346.1687, 2429.2638, 2612.3789, 3242.5742,
     3471.5614, 3716.5563

19.  HEM1_BURP6     Mass: 47530     Score: 50     Expect: 5.5  Matches: 9
     Glutamyl-tRNA reductase OS=Burkholderia pseudomallei (strain 668) OX=320373 GN=hemA PE=3 SV=1
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 Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss  Peptide
1054.6305   1053.6232   1053.5641    56.1   237 - 246    0    R.AMPLADLPAR.M
1179.6387   1178.6315   1178.5615    59.4   354 - 363    0    R.HMHTQADALR.R
1423.7341   1422.7268   1422.6714    39.0   336 - 346    0    R.VQNFMQWLDAR.S + Oxidation (M)
1471.8574   1470.8501   1470.7765    50.0   233 - 246    1    R.FGGRAMPLADLPAR.M
1554.7503   1553.7430   1553.7256    11.2    61 -  73    1    R.TELYCATNDRAAR.D + Propionamide (C)
1762.9604   1761.9531   1761.9234    16.8   395 - 411    1    K.LIHGPTSALNRANGADR.D
2330.2339   2329.2266   2329.1584    29.3   373 - 394    1    K.MLARGDDPDAVLDALSQALTNK.L + Oxidation (M)
2385.2935   2384.2862   2384.2747    4.84     2 -  22    1    M.DMQLLTIGINHHTAPVALRER.V
3242.5742   3241.5669   3241.6740  -33.03   192 - 221    1    R.VLFIGAGEMIELCATHFAAQGPRELIVANR.T + Oxidation (M)
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No match to: 805.4435, 817.4339, 891.5000, 900.4889, 906.5394, 909.4223, 943.5394, 947.5320, 952.4985, 961.5879, 1044.5817, 1073.6009, 1076.5738, 1078.5780, 1087.6056, 1091.5907, 1100.6162, 1107.6426, 1114.6425, 1117.5943, 1131.6636, 1145.6759, 1154.6595, 1162.6289, 1188.7106, 1213.6439, 1219.6987, 1221.7099, 1282.7596, 1329.7785, 1342.8028, 1391.7960, 1433.8679, 1462.7489, 1486.8640, 1502.8443, 1528.9019, 1537.7928, 1542.7750, 1561.8811, 1582.8377, 1597.8184, 1611.7719, 1641.9273, 1651.9542, 1656.9978, 1687.8846, 1759.9421, 1838.0268, 1925.9415, 1928.9792, 1967.0608, 2034.0174, 2134.1272, 2202.1233, 2211.0847, 2280.2533, 2318.1759, 2339.2229, 2346.1687, 2429.2638, 2612.3789, 3471.5614, 3716.5563

20. ALGD_PSESM **Mass:** 47578 **Score:** 50 **Expect:** 5.7 **Matches:** 9

GDP-mannose 6-dehydrogenase OS=Pseudomonas syringae pv. tomato (strain ATCC BAA-871 / DC3000) OX=223283 GN=algD PE=2 SV=1

```
 Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss  Peptide
 947.5320    946.5247    946.5851  -63.84   316 - 324    0    K.VALLGLSFK.A
1044.5817   1043.5744   1043.5611    12.7   405 - 414    1    R.SLANKTPEGK.R
1117.5943   1116.5871   1116.6212  -30.62   201 - 210    1    R.KDIAVAEMIK.Y
1528.9019   1527.8946   1527.8218    47.7   332 - 345    0    R.ESPLVELAEMLIGK.G
1687.8846   1686.8773   1686.8611    9.63   280 - 295    0    R.AGSLDVDAPLLNSLMR.S + Oxidation (M)
2280.2533   2279.2460   2279.1078    60.6   202 - 220    1    K.DIAVAEMIKYTCNVWHATK.V + Oxidation (M); Propionamide (C)
2339.2229   2338.2156   2338.1342    34.8   346 - 366    1    K.GFDLSIFDSNVEYARVHGANK.D
2385.2935   2384.2862   2384.1457    58.9   161 - 181    1    R.ESTAIKDYDLPPMTVIGEFDK.A + Oxidation (M)
3242.5742   3241.5669   3241.6216  -16.89   332 - 360    1    R.ESPLVELAEMLIGKGFDLSIFDSNVEYAR.V
```

No match to: 805.4435, 817.4339, 891.5000, 900.4889, 906.5394, 909.4223, 943.5394, 952.4985, 961.5879, 1054.6305, 1073.6009, 1076.5738, 1078.5780, 1087.6056, 1091.5907, 1100.6162, 1107.6426, 1114.6425, 1131.6636, 1145.6759, 1154.6595, 1162.6289, 1179.6387, 1188.7106, 1213.6439, 1219.6987, 1221.7099, 1282.7596, 1329.7785, 1342.8028, 1391.7960, 1423.7341, 1433.8679, 1462.7489, 1471.8574, 1486.8640, 1502.8443, 1537.7928, 1542.7750, 1554.7503,

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1561.8811, 1582.8377, 1597.8184, 1611.7719, 1641.9273, 1651.9542, 1656.9978, 1759.9421, 1762.9604, 1838.0268,
1925.9415, 1928.9792, 1967.0608, 2034.0174, 2134.1272, 2202.1233, 2211.0847, 2318.1759, 2330.2339, 2346.1687,
2429.2638, 2612.3789, 3471.5614, 3716.5563
```

Search Parameters

```
Type of search         : Peptide Mass Fingerprint
Enzyme                 : Trypsin
Variable modifications : Oxidation (M),Propionamide (C)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 75 ppm
Peptide Charge State   : 1+
Max Missed Cleavages   : 1
Number of queries      : 73
Selected for scoring   : 66
```

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

6. The protein band of approx. 24 kDa, obtained from the crude extract of *R. rhodochrous* M33 delta-const cells, grown on the medium without metals.

MATRIX SCIENCE

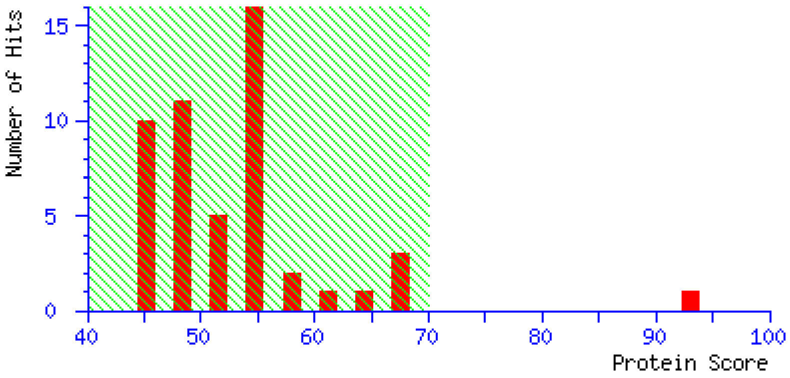
Mascot Search Results

```
User             : toropygin
Email            : toropygin@rambler.ru
Search title     : 02
Database         : SwissProt 2018_08 (558125 sequences; 200328830 residues)
```

```
Timestamp        : 26 Sep 2018 at 16:22:58 GMT
Top Score        : 93 for NHA1_RHORH, High-molecular weight cobalt-containing nitrile hydratase subunit alpha
OS=Rhodococcus rhodochrous OX=1829 GN=nhhA PE=1 SV=3
```

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 70 are significant (p<0.05).



Protein Summary Report

Format As	Protein Summary ▾	Help	
	Significance threshold p< 0.05	Max. number of hits 20	
	Preferred taxonomy All entries ▾		

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-
-Accession- -Sequence-

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
☑ 842.4703 (1+)																				
☑ 878.4498 (1+)		●	●	●					●	●										
☑ 885.4250 (1+)														●	●	●	●	●	●	●
☑ 908.4522 (1+)						●		●	●		●	●	●	●	●	●	●	●	●	●
☑ 931.4136 (1+)	●																			
☑ 935.4949 (1+)									●					●	●	●	●	●	●	●
☑ 947.5199 (1+)												●								
☑ 960.4585 (1+)					●									●	●	●	●	●	●	●
☑ 977.5319 (1+)		●	●	●	●	●	●		●				●							
☑ 996.4665 (1+)					●															
☑ 1006.5727 (1+)																				
☑ 1010.5343 (1+)									●		●									
☑ 1012.5818 (1+)	●																			

☑ **1051.5006** **(1+)**	●								●		●									
☑ **1053.4752** **(1+)**																				
☑ **1063.5487** **(1+)**																				
☑ **1078.5362** **(1+)**	●				●				●											
☑ **1090.6464** **(1+)**																				
☑ **1100.5575** **(1+)**												●								
☑ **1107.6262** **(1+)**	●								●	●		●	●							
☑ **1114.6152** **(1+)**						●							●	●	●	●	●	●	●	●
☑ **1123.5815** **(1+)**												●								
☑ **1129.6237** **(1+)**							●		●											
☑ **1154.6160** **(1+)**									●											
☑ **1164.6225** **(1+)**									●			●								
☑ **1179.6122** **(1+)**	●								●				●	●	●	●	●	●	●	●
☑ **1188.7008** **(1+)**							●	●				●								
☑ **1197.6333** **(1+)**																				
☑ **1201.6073** **(1+)**												●		●	●	●	●	●	●	●
☑ **1207.6699** **(1+)**																				
☑ **1219.6165** **(1+)**												●								
☑ **1240.6412** **(1+)**																				

☑	1246.6110 (1+)					●															
☑	1265.6549 (1+)									●											
☑	1282.7205 (1+)																				
☑	1305.6865 (1+)						●								●	●	●	●	●	●	●
☑	1328.8027 (1+)										●			●	●	●	●	●	●	●	●
☑	1341.7621 (1+)						●	●	●	●					●	●	●	●	●	●	●
☑	1343.7755 (1+)												●								
☑	1351.7809 (1+)		●	●	●	●			●	●				●							
☑	1361.7892 (1+)												●								
☑	1372.8147 (1+)																				
☑	1396.7120 (1+)																				
☑	1404.7940 (1+)												●								
☑	1418.7847 (1+)										●	●									
☑	1435.8008 (1+)							●	●				●								
☑	1522.7677 (1+)									●											
☑	1526.8482 (1+)														●	●	●	●	●	●	●
☑	1537.7531 (1+)	●	●	●	●	●					●				●	●	●	●	●	●	●
☑	1553.7815 (1+)									●											
☑	1559.7485 (1+)																				

☑ 1565.7961 (1+)																				
☑ 1574.8543 (1+)																				
☑ 1576.7603 (1+)									●											
☑ 1583.9072 (1+)																				
☑ 1614.8781 (1+)									●					●	●	●	●	●	●	●
☑ 1625.7939 (1+)	●										●									
☑ 1667.9279 (1+)									●											
☑ 1689.8869 (1+)		●	●	●		●	●													
☑ 1693.8670 (1+)	●						●			●										
☑ 1713.8417 (1+)	●													●	●	●	●	●	●	●
☑ 1716.8831 (1+)																				
☑ 1735.8501 (1+)									●											
☑ 1739.9128 (1+)																				
☑ 1759.9378 (1+)								●	●											
☑ 1772.8773 (1+)	●	●	●	●																
☑ 1781.9821 (1+)					●				●	●										
☑ 1788.8333 (1+)	●																			
☑ 1794.9051 (1+)							●							●	●	●	●	●	●	●
☑ 1797.9274 (1+)					●									●	●	●	●	●	●	●

☑ **1884.9716 (1+)**						●			●		●									
☑ **1916.9853 (1+)**																				
☑ **1947.0249 (1+)**								●	●											
☑ **1965.9832 (1+)**		●	●	●					●	●										
☑ **2005.0675 (1+)**					●	●			●											
☑ **2009.0185 (1+)**																				
☑ **2033.9909 (1+)**														●	●	●	●	●	●	●
☑ **2066.0437 (1+)**																				
☑ **2126.1346 (1+)**																				
☑ **2150.0903 (1+)**																				
☑ **2209.1040 (1+)**		●	●	●				●	●											
☑ **2250.1013 (1+)**					●	●	●		●			●								
☑ **2297.0103 (1+)**						●			●											
☑ **2331.1459 (1+)**																				
☑ **2346.1352 (1+)**																				
☑ **2362.1254 (1+)**									●											
☑ **2368.1271 (1+)**																				
☑ **2374.1534 (1+)**														●	●	●	●	●	●	●
☑ **2477.1729 (1+)**																				

☑ 2544.3770 (1+)						●														
☑ 2604.3569 (1+)								●												
☑ 2714.3223 (1+)								●												
☑ 2789.4134 (1+)				●				●		●										
☑ 2817.2664 (1+)		●	●	●			●													
☑ 2872.4328 (1+)				●				●	●		●									
☑ 2968.2772 (1+)		●	●	●					●											
☑ 2989.3711 (1+)																				
☑ 3042.4416 (1+)									●											
☑ 3242.5664 (1+)																				
☑ 3802.7447 (1+)																				
☑ 3926.7627 (1+)									●	●	●			●	●	●	●	●	●	●

Search Selected

Index

	Accession	Mass	Score	Description
1.	NHA1_RHORH	22820	93	High-molecular weight cobalt-containing nitrile hydratase subunit alpha OS=Rhodococcus rhodochrous OX=1829 GN=nhhA PE=1 SV=3
2.	DDL_STRA1	39043	66	D-alanine--D-alanine ligase OS=Streptococcus agalactiae serotype Ia (strain ATCC 27591 / A909 / CDC SS700) OX=205921 GN=ddl PE=3 SV=1

3.	DDL_STRA3	39043	66	D-alanine--D-alanine ligase OS=Streptococcus agalactiae serotype III (strain NEM316) OX=211110 GN=ddl PE=3 SV=1
4.	DDL_STRA5	39043	66	D-alanine--D-alanine ligase OS=Streptococcus agalactiae serotype V (strain ATCC BAA-611 / 2603 V/R) OX=208435 GN=ddl PE=3 SV=1
5.	REM12_ARATH	50177	64	B3 domain-containing protein REM12 OS=Arabidopsis thaliana OX=3702 GN=REM12 PE=2 SV=1
6.	HUTH_CITK8	53955	61	Histidine ammonia-lyase OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) OX=290338 GN=hutH PE=3 SV=1
7.	CYSI_SHEON	63023	59	Sulfite reductase [NADPH] hemoprotein beta-component OS=Shewanella oneidensis (strain MR-1) OX=211586 GN=cysI PE=3 SV=1
8.	BIOB_CALBD	38226	58	Biotin synthase OS=Caldicellulosiruptor bescii (strain ATCC BAA-1888 / DSM 6725 / Z-1320) OX=521460 GN=bioB PE=3 SV=1
9.	DYH1_HUMAN	487166	56	Dynein heavy chain 1, axonemal OS=Homo sapiens OX=9606 GN=DNAH1 PE=1 SV=5
10.	DER_SHELP	54588	55	GTPase Der OS=Shewanella loihica (strain ATCC BAA-1088 / PV-4) OX=323850 GN=der PE=3 SV=1
11.	LIPA_DEIGD	36739	55	Lipoyl synthase OS=Deinococcus geothermalis (strain DSM 11300) OX=319795 GN=lipA PE=3 SV=1
12.	K2C78_HUMAN	56830	54	Keratin, type II cytoskeletal 78 OS=Homo sapiens OX=9606 GN=KRT78 PE=1 SV=2
13.	AZOR8_BURL3	22928	54	FMN-dependent NADH-azoreductase 8 OS=Burkholderia lata (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB 9086 / R18194 / 383) OX=482957 GN=azoR8 PE=3 SV=1
14.	TF212_SCHPO	154819	54	Transposon Tf2-12 polyprotein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=Tf2-12 PE=3 SV=1
15.	TF21_SCHPO	154835	54	Transposon Tf2-1 polyprotein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=Tf2-1 PE=3 SV=1
16.	TF22_SCHPO	154835	54	Transposon Tf2-2 polyprotein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=Tf2-2 PE=3 SV=1
17.	TF23_SCHPO	154819	54	Transposon Tf2-3 polyprotein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=Tf2-3 PE=1 SV=1
18.	TF24_SCHPO	154835	54	Transposon Tf2-4 polyprotein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=Tf2-4 PE=3 SV=1

19.	TF25_SCHPO	154819	54	Transposon Tf2-5 polyprotein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=Tf2-5 PE=3 SV=1
20.	TF26_SCHPO	154819	54	Transposon Tf2-6 polyprotein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=Tf2-6 PE=3 SV=1

Results List

```
1.    NHA1_RHORH    Mass: 22820    Score: 93    Expect: 0.00027  Matches: 12

      High-molecular weight cobalt-containing nitrile hydratase subunit alpha OS=Rhodococcus rhodochrous OX=1829 GN=nhhA
      PE=1 SV=3
       Observed    Mr(expt)    Mr(calc)     ppm  Start   End Miss   Peptide
       931.4136    930.4063    930.4083   -2.13      8 -  14    0   K.YTEYEAR.T
      1012.5818   1011.5745   1011.5713    3.22     26 -  35    0   R.GLITPAAVDR.V
      1051.5006   1050.4933   1050.4771    15.5     56 -  63    0   K.SWVDPEYR.K
      1078.5362   1077.5289   1077.5091    18.4    153 - 161    0   R.VWDSSSEIR.Y
      1107.6262   1106.6190   1106.5971    19.7     17 -  25    0   K.AIETLLYER.G
      1179.6122   1178.6049   1178.5720    27.9     56 -  64    1   K.SWVDPEYRK.W
      1537.7531   1536.7458   1536.7097    23.5    140 - 152    0   R.DFGFDIPDEVEVR.V
      1625.7939   1624.7866   1624.7481    23.7      2 -  14    1   M.SEHVNKYTEYEAR.T
      1693.8670   1692.8598   1692.8108    28.9    139 - 152    1   K.RDFGFDIPDEVEVR.V
      1713.8417   1712.8344   1712.8080    15.5     36 -  51    0   R.VVSYYENEIGPMGGAK.V
      1772.8773   1771.8700   1771.9026  -18.37    187 - 203    0   R.DSMIGVSNALTPQEVIV.-
      1788.8333   1787.8260   1787.8975  -40.01    187 - 203    0   R.DSMIGVSNALTPQEVIV.- + Oxidation (M)
       No match to: 842.4703, 878.4498, 885.4250, 908.4522, 935.4949, 947.5199, 960.4585, 977.5319, 996.4665, 1006.5727,
       1010.5343, 1053.4752, 1063.5487, 1090.6464, 1100.5575, 1114.6152, 1123.5815, 1129.6237, 1154.6160, 1164.6225,
       1188.7008, 1197.6333, 1201.6073, 1207.6699, 1219.6165, 1240.6412, 1246.6110, 1265.6549, 1282.7205, 1305.6865,
       1328.8027, 1341.7621, 1343.7755, 1351.7809, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1418.7847, 1435.8008,
       1522.7677, 1526.8482, 1553.7815, 1559.7485, 1565.7961, 1574.8543, 1576.7603, 1583.9072, 1614.8781, 1667.9279,
       1689.8869, 1716.8831, 1735.8501, 1739.9128, 1759.9378, 1781.9821, 1794.9051, 1797.9274, 1884.9716, 1916.9853,
       1947.0249, 1965.9832, 2005.0675, 2009.0185, 2033.9909, 2066.0437, 2126.1346, 2150.0903, 2209.1040, 2250.1013,
       2297.0103, 2331.1459, 2346.1352, 2362.1254, 2368.1271, 2374.1534, 2477.1729, 2544.3770, 2604.3569, 2714.3223,
       2789.4134, 2817.2664, 2872.4328, 2968.2772, 2989.3711, 3042.4416, 3242.5664, 3802.7447, 3926.7627
```

```
2.   DDL_STRA1     Mass: 39043     Score: 66     Expect: 0.14  Matches: 10

     D-alanine--D-alanine ligase OS=Streptococcus agalactiae serotype Ia (strain ATCC 27591 / A909 / CDC SS700)
     OX=205921 GN=ddl PE=3 SV=1
      Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
      878.4498    877.4425    877.4141    32.4   185 - 192    0    K.ATDESSLR.S
      977.5319    976.5246    976.5230    1.68   228 - 236    0    K.TTFPGEVVK.D
     1351.7809   1350.7737   1350.7143    44.0   193 - 204    1    R.SAIDLALKYDSR.I
     1537.7531   1536.7458   1536.7858  -26.00   247 - 259    1    K.YIDNKITMDIPAK.V + Oxidation (M)
     1689.8869   1688.8796   1688.8944   -8.78   185 - 200    1    K.ATDESSLRSAIDLALK.Y
     1772.8773   1771.8700   1771.8749   -2.76   278 - 293    1    K.AIGACGLSRCDFFLTK.D + Propionamide (C)
     1965.9832   1964.9759   1965.0764  -51.14    36 -  51    1    K.FFVKTYFITQVGQFIK.T
     2209.1040   2208.0967   2208.0263    31.9   228 - 246    1    K.TTFPGEVVKDVDFYDYDAK.Y
     2817.2664   2816.2592   2816.2368    7.94    52 -  75    1    K.TQEFDEMPSSDEKLMTNQTVDLDK.M + Oxidation (M)
     2968.2772   2967.2700   2967.3848  -38.70    40 -  64    1    K.TYFITQVGQFIKTQEFDEMPSSDEK.L
      No match to: 842.4703, 885.4250, 908.4522, 931.4136, 935.4949, 947.5199, 960.4585, 996.4665, 1006.5727, 1010.5343,
      1012.5818, 1051.5006, 1053.4752, 1063.5487, 1078.5362, 1090.6464, 1100.5575, 1107.6262, 1114.6152, 1123.5815,
      1129.6237, 1154.6160, 1164.6225, 1179.6122, 1188.7008, 1197.6333, 1201.6073, 1207.6699, 1219.6165, 1240.6412,
      1246.6110, 1265.6549, 1282.7205, 1305.6865, 1328.8027, 1341.7621, 1343.7755, 1361.7892, 1372.8147, 1396.7120,
      1404.7940, 1418.7847, 1435.8008, 1522.7677, 1526.8482, 1553.7815, 1559.7485, 1565.7961, 1574.8543, 1576.7603,
      1583.9072, 1614.8781, 1625.7939, 1667.9279, 1693.8670, 1713.8417, 1716.8831, 1735.8501, 1739.9128, 1759.9378,
      1781.9821, 1788.8333, 1794.9051, 1797.9274, 1884.9716, 1916.9853, 1947.0249, 2005.0675, 2009.0185, 2033.9909,
      2066.0437, 2126.1346, 2150.0903, 2250.1013, 2297.0103, 2331.1459, 2346.1352, 2362.1254, 2368.1271, 2374.1534,
      2477.1729, 2544.3770, 2604.3569, 2714.3223, 2789.4134, 2872.4328, 2989.3711, 3042.4416, 3242.5664, 3802.7447,
      3926.7627

3.    DDL_STRA3     Mass: 39043     Score: 66     Expect: 0.14  Matches: 10
      D-alanine--D-alanine ligase OS=Streptococcus agalactiae serotype III (strain NEM316) OX=211110 GN=ddl PE=3 SV=1
      Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
      878.4498    877.4425    877.4141    32.4   185 - 192    0    K.ATDESSLR.S
      977.5319    976.5246    976.5230    1.68   228 - 236    0    K.TTFPGEVVK.D
     1351.7809   1350.7737   1350.7143    44.0   193 - 204    1    R.SAIDLALKYDSR.I
     1537.7531   1536.7458   1536.7858  -26.00   247 - 259    1    K.YIDNKITMDIPAK.V + Oxidation (M)
     1689.8869   1688.8796   1688.8944   -8.78   185 - 200    1    K.ATDESSLRSAIDLALK.Y
     1772.8773   1771.8700   1771.8749   -2.76   278 - 293    1    K.AIGACGLSRCDFFLTK.D + Propionamide (C)
     1965.9832   1964.9759   1965.0764  -51.14    36 -  51    1    K.FFVKTYFITQVGQFIK.T
```

```
2209.1040  2208.0967  2208.0263    31.9   228 - 246   1   K.TTFPGEVVKDVDFYDYDAK.Y
2817.2664  2816.2592  2816.2368    7.94    52 -  75   1   K.TQEFDEMPSSDEKLMTNQTVDLDK.M + Oxidation (M)
2968.2772  2967.2700  2967.3848  -38.70    40 -  64   1   K.TYFITQVGQFIKTQEFDEMPSSDEK.L
```

No match to: 842.4703, 885.4250, 908.4522, 931.4136, 935.4949, 947.5199, 960.4585, 996.4665, 1006.5727, 1010.5343, 1012.5818, 1051.5006, 1053.4752, 1063.5487, 1078.5362, 1090.6464, 1100.5575, 1107.6262, 1114.6152, 1123.5815, 1129.6237, 1154.6160, 1164.6225, 1179.6122, 1188.7008, 1197.6333, 1201.6073, 1207.6699, 1219.6165, 1240.6412, 1246.6110, 1265.6549, 1282.7205, 1305.6865, 1328.8027, 1341.7621, 1343.7755, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1418.7847, 1435.8008, 1522.7677, 1526.8482, 1553.7815, 1559.7485, 1565.7961, 1574.8543, 1576.7603, 1583.9072, 1614.8781, 1625.7939, 1667.9279, 1693.8670, 1713.8417, 1716.8831, 1735.8501, 1739.9128, 1759.9378, 1781.9821, 1788.8333, 1794.9051, 1797.9274, 1884.9716, 1916.9853, 1947.0249, 2005.0675, 2009.0185, 2033.9909, 2066.0437, 2126.1346, 2150.0903, 2250.1013, 2297.0103, 2331.1459, 2346.1352, 2362.1254, 2368.1271, 2374.1534, 2477.1729, 2544.3770, 2604.3569, 2714.3223, 2789.4134, 2872.4328, 2989.3711, 3042.4416, 3242.5664, 3802.7447, 3926.7627

4. DDL_STRA5 **Mass:** 39043 **Score:** 66 **Expect:** 0.14 **Matches:** 10

D-alanine--D-alanine ligase OS=Streptococcus agalactiae serotype V (strain ATCC BAA-611 / 2603 V/R) OX=208435 GN=ddl PE=3 SV=1

```
 Observed    Mr(expt)    Mr(calc)     ppm  Start   End Miss  Peptide
  878.4498   877.4425   877.4141    32.4   185 - 192   0   K.ATDESSLR.S
  977.5319   976.5246   976.5230    1.68   228 - 236   0   K.TTFPGEVVK.D
1351.7809  1350.7737  1350.7143    44.0   193 - 204   1   R.SAIDLALKYDSR.I
1537.7531  1536.7458  1536.7858  -26.00   247 - 259   1   K.YIDNKITMDIPAK.V + Oxidation (M)
1689.8869  1688.8796  1688.8944   -8.78   185 - 200   1   K.ATDESSLRSAIDLALK.Y
1772.8773  1771.8700  1771.8749   -2.76   278 - 293   1   K.AIGACGLSRCDFFLTK.D + Propionamide (C)
1965.9832  1964.9759  1965.0764  -51.14    36 -  51   1   K.FFVKTYFITQVGQFIK.T
2209.1040  2208.0967  2208.0263    31.9   228 - 246   1   K.TTFPGEVVKDVDFYDYDAK.Y
2817.2664  2816.2592  2816.2368    7.94    52 -  75   1   K.TQEFDEMPSSDEKLMTNQTVDLDK.M + Oxidation (M)
2968.2772  2967.2700  2967.3848  -38.70    40 -  64   1   K.TYFITQVGQFIKTQEFDEMPSSDEK.L
```

No match to: 842.4703, 885.4250, 908.4522, 931.4136, 935.4949, 947.5199, 960.4585, 996.4665, 1006.5727, 1010.5343, 1012.5818, 1051.5006, 1053.4752, 1063.5487, 1078.5362, 1090.6464, 1100.5575, 1107.6262, 1114.6152, 1123.5815, 1129.6237, 1154.6160, 1164.6225, 1179.6122, 1188.7008, 1197.6333, 1201.6073, 1207.6699, 1219.6165, 1240.6412, 1246.6110, 1265.6549, 1282.7205, 1305.6865, 1328.8027, 1341.7621, 1343.7755, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1418.7847, 1435.8008, 1522.7677, 1526.8482, 1553.7815, 1559.7485, 1565.7961, 1574.8543, 1576.7603, 1583.9072, 1614.8781, 1625.7939, 1667.9279, 1693.8670, 1713.8417, 1716.8831, 1735.8501, 1739.9128, 1759.9378, 1781.9821, 1788.8333, 1794.9051, 1797.9274, 1884.9716, 1916.9853, 1947.0249, 2005.0675, 2009.0185, 2033.9909, 2066.0437, 2126.1346, 2150.0903, 2250.1013, 2297.0103, 2331.1459, 2346.1352, 2362.1254, 2368.1271, 2374.1534, 2477.1729, 2544.3770, 2604.3569, 2714.3223, 2789.4134, 2872.4328, 2989.3711, 3042.4416, 3242.5664, 3802.7447, 3926.7627

5. REM12_ARATH **Mass:** 50177 **Score:** 64 **Expect:** 0.21 **Matches:** 13

B3 domain-containing protein REM12 OS=Arabidopsis thaliana OX=3702 GN=REM12 PE=2 SV=1

```
 Observed   Mr(expt)   Mr(calc)    ppm  Start    End Miss   Peptide
 960.4585   959.4512   959.4924 -42.87    89 -   96    0    R.EIVVTDER.E
 977.5319   976.5246   976.4574   68.9   332 - 340    0    R.DSSSAIQNR.Y
 996.4665   995.4592   995.4746 -15.44   257 - 265    0    K.EFAMANGLK.S + Oxidation (M)
1078.5362  1077.5289  1077.4760   49.1   307 - 316    0    K.ESSICAEPSR.G
1246.6110  1245.6037  1245.5700   27.1   432 - 441    0    K.FCSNSVEYVK.F + Propionamide (C)
1351.7809  1350.7737  1350.7039   51.6   353 - 364    0    R.ACTLILPSQFMK.A
1537.7531  1536.7458  1536.6726   47.7   303 - 316    1    R.DSEKESSICAEPSR.G
1781.9821  1780.9748  1780.8778   54.5   279 - 294    0    K.GTPMLSLVNTQSTNYR.S
1797.9274  1796.9201  1796.8727   26.4   279 - 294    0    K.GTPMLSLVNTQSTNYR.S + Oxidation (M)
2005.0675  2004.0602  2004.0528   3.70    69 -   86    1    K.DALYLPQDLTSSVGLERK.Y
2250.1013  2249.0941  2249.0270   29.8   144 - 164    0    R.ETPVLSFCSTESINDGTQGHK.N
2789.4134  2788.4061  2788.3450   21.9   139 - 164    1    K.LVGNRETPVLSFCSTESINDGTQGHK.N
2872.4328  2871.4255  2871.3192   37.0    41 -   67    0    R.SNTEIEADASSSDNSCFVALVTASNLR.K + Propionamide (C)
```

No match to: 842.4703, 878.4498, 885.4250, 908.4522, 931.4136, 935.4949, 947.5199, 1006.5727, 1010.5343, 1012.5818, 1051.5006, 1053.4752, 1063.5487, 1090.6464, 1100.5575, 1107.6262, 1114.6152, 1123.5815, 1129.6237, 1154.6160, 1164.6225, 1179.6122, 1188.7008, 1197.6333, 1201.6073, 1207.6699, 1219.6165, 1240.6412, 1265.6549, 1282.7205, 1305.6865, 1328.8027, 1341.7621, 1343.7755, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1418.7847, 1435.8008, 1522.7677, 1526.8482, 1553.7815, 1559.7485, 1565.7961, 1574.8543, 1576.7603, 1583.9072, 1614.8781, 1625.7939, 1667.9279, 1689.8869, 1693.8670, 1713.8417, 1716.8831, 1735.8501, 1739.9128, 1759.9378, 1772.8773, 1788.8333, 1794.9051, 1884.9716, 1916.9853, 1947.0249, 1965.9832, 2009.0185, 2033.9909, 2066.0437, 2126.1346, 2150.0903, 2209.1040, 2297.0103, 2331.1459, 2346.1352, 2362.1254, 2368.1271, 2374.1534, 2477.1729, 2544.3770, 2604.3569, 2714.3223, 2817.2664, 2968.2772, 2989.3711, 3042.4416, 3242.5664, 3802.7447, 3926.7627

6. HUTH_CITK8 **Mass:** 53955 **Score:** 61 **Expect:** 0.4 **Matches:** 10

Histidine ammonia-lyase OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) OX=290338 GN=hutH PE=3 SV=1

```
 Observed   Mr(expt)   Mr(calc)    ppm  Start    End Miss   Peptide
 908.4522   907.4449   907.5100 -71.76   241 - 248    1    R.IHAARGQR.G
 977.5319   976.5246   976.5198   4.96   356 - 363    1    R.RIALMMDK.H
```

1114.6152	1113.6079	1113.5607	42.4	165	173	0	R.WQGEWLPAK.E
1305.6865	1304.6792	1304.7129	-25.82	496	506	1	R.GDLFRLLPDFL.-
1341.7621	1340.7549	1340.6989	41.7	163	173	1	K.ARWQGEWLPAK.E
1689.8869	1688.8796	1688.8160	37.6	285	298	0	R.CQPQVMGACLTQLR.Q + 2 Propionamide (C)
1884.9716	1883.9644	1883.9927	-15.06	437	453	0	R.GVIAVEWLAACQGIDLR.E + Propionamide (C)
2005.0675	2004.0602	2003.9483	55.8	259	276	0	R.HVLTETSAIAQSHHNCEK.V
2250.1013	2249.0941	2249.1110	-7.54	375	397	0	K.NGGVNSGFMIAQVTAAALASENK.A
2297.0103	2296.0031	2296.1733	-74.14	139	162	0	K.GSVGASGDLAPLAHMSLTLLGEGK.A + Oxidation (M)

No match to: 842.4703, 878.4498, 885.4250, 931.4136, 935.4949, 947.5199, 960.4585, 996.4665, 1006.5727, 1010.5343, 1012.5818, 1051.5006, 1053.4752, 1063.5487, 1078.5362, 1090.6464, 1100.5575, 1107.6262, 1123.5815, 1129.6237, 1154.6160, 1164.6225, 1179.6122, 1188.7008, 1197.6333, 1201.6073, 1207.6699, 1219.6165, 1240.6412, 1246.6110, 1265.6549, 1282.7205, 1328.8027, 1343.7755, 1351.7809, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1418.7847, 1435.8008, 1522.7677, 1526.8482, 1537.7531, 1553.7815, 1559.7485, 1565.7961, 1574.8543, 1576.7603, 1583.9072, 1614.8781, 1625.7939, 1667.9279, 1693.8670, 1713.8417, 1716.8831, 1735.8501, 1739.9128, 1759.9378, 1772.8773, 1781.9821, 1788.8333, 1794.9051, 1797.9274, 1916.9853, 1947.0249, 1965.9832, 2009.0185, 2033.9909, 2066.0437, 2126.1346, 2150.0903, 2209.1040, 2331.1459, 2346.1352, 2362.1254, 2368.1271, 2374.1534, 2477.1729, 2544.3770, 2604.3569, 2714.3223, 2789.4134, 2817.2664, 2872.4328, 2968.2772, 2989.3711, 3042.4416, 3242.5664, 3802.7447, 3926.7627

7.

CYSI_SHEON **Mass:** 63023 **Score:** 59 **Expect:** 0.7 **Matches:** 11

Sulfite reductase [NADPH] hemoprotein beta-component OS=Shewanella oneidensis (strain MR-1) OX=211586 GN=cysI PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
977.5319	976.5246	976.5342	-9.79	313	320	1	K.FKAEVEVR.A
1129.6237	1128.6164	1128.5927	21.0	157	166	0	K.LHAQAYEVAK.K
1188.7008	1187.6936	1187.6411	44.2	168	177	0	K.LSDHLLPHTR.A
1341.7621	1340.7549	1340.7888	-25.33	412	423	1	K.RGLLGQVLTQTR.G
1435.8008	1434.7935	1434.7718	15.2	2	13	1	M.SEQKLALNEYLK.T
1689.8869	1688.8796	1688.8998	-11.98	105	118	1	R.LTTRQTFQYHGIPK.R

1693.8670	1692.8598	1692.8458	8.25	189	- 203	0	K.LLTTEDETVEPVYGK.T
1794.9051	1793.8978	1793.9425	-24.89	538	- 554	1	R.NAGETFGNFTVRVGVVK.A
2250.1013	2249.0941	2249.0755	8.25	471	- 491	0	R.MTGCPNGCARPFAAEIGLVGK.A + Oxidation (M); 2 Propionamide (C)
2544.3770	2543.3698	2543.2559	44.8	471	- 495	1	R.MTGCPNGCARPFAAEIGLVGKAPGR.Y + Propionamide (C)
2817.2664	2816.2592	2816.2891	-10.63	131	- 156	1	R.EALDSIAACGDVNRNVMCNPNPVESK.L + Propionamide (C)

No match to: 842.4703, 878.4498, 885.4250, 908.4522, 931.4136, 935.4949, 947.5199, 960.4585, 996.4665, 1006.5727, 1010.5343, 1012.5818, 1051.5006, 1053.4752, 1063.5487, 1078.5362, 1090.6464, 1100.5575, 1107.6262, 1114.6152, 1123.5815, 1154.6160, 1164.6225, 1179.6122, 1197.6333, 1201.6073, 1207.6699, 1219.6165, 1240.6412, 1246.6110, 1265.6549, 1282.7205, 1305.6865, 1328.8027, 1343.7755, 1351.7809, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1418.7847, 1522.7677, 1526.8482, 1537.7531, 1553.7815, 1559.7485, 1565.7961, 1574.8543, 1576.7603, 1583.9072, 1614.8781, 1625.7939, 1667.9279, 1713.8417, 1716.8831, 1735.8501, 1739.9128, 1759.9378, 1772.8773, 1781.9821, 1788.8333, 1797.9274, 1884.9716, 1916.9853, 1947.0249, 1965.9832, 2005.0675, 2009.0185, 2033.9909, 2066.0437, 2126.1346, 2150.0903, 2209.1040, 2297.0103, 2331.1459, 2346.1352, 2362.1254, 2368.1271, 2374.1534, 2477.1729, 2604.3569, 2714.3223, 2789.4134, 2872.4328, 2968.2772, 2989.3711, 3042.4416, 3242.5664, 3802.7447, 3926.7627

8. BIOB CALBD **Mass:** 38226 **Score:** 58 **Expect:** 0.93 **Matches:** 9

Biotin synthase OS=Caldicellulosiruptor bescii (strain ATCC BAA-1888 / DSM 6725 / Z-1320) OX=521460 GN=bioB PE=3 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
908.4522	907.4449	907.5014	-62.32	17 -	23	1	K.KIIEYDK.D
1188.7008	1187.6936	1187.6550	32.5	133 -	142	0	K.ILDIYSHISK.N
1341.7621	1340.7549	1340.7551	-0.18	248 -	259	1	K.GTPLEDIKIIDK.N
1351.7809	1350.7737	1350.6853	65.4	58 -	69	0	K.NTIELCSIYPAK.V
1435.8008	1434.7935	1434.7255	47.4	46 -	57	0	K.NLASTINQHYFK.N
1759.9378	1758.9306	1758.9185	6.83	277 -	293	1	K.TILLAGGKENALGDMEK.M
1947.0249	1946.0176	1945.8979	61.5	116 -	132	1	R.FCLVTSGEKLDDSEFEK.I
2209.1040	2208.0967	2208.0224	33.6	203 -	223	0	K.EAGLQICSGGIISMGEDMIER.I
2872.4328	2871.4255	2871.3246	35.2	171 -	194	1	K.YHNNLETSSTYFKNICSTHTQQQK.I

No match to: 842.4703, 878.4498, 885.4250, 931.4136, 935.4949, 947.5199, 960.4585, 977.5319, 996.4665, 1006.5727, 1010.5343, 1012.5818, 1051.5006, 1053.4752, 1063.5487, 1078.5362, 1090.6464, 1100.5575, 1107.6262, 1114.6152, 1123.5815, 1129.6237, 1154.6160, 1164.6225, 1179.6122, 1197.6333, 1201.6073, 1207.6699, 1219.6165, 1240.6412, 1246.6110, 1265.6549, 1282.7205, 1305.6865, 1328.8027, 1343.7755, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1418.7847, 1522.7677, 1526.8482, 1537.7531, 1553.7815, 1559.7485, 1565.7961, 1574.8543, 1576.7603, 1583.9072, 1614.8781, 1625.7939, 1667.9279, 1689.8869, 1693.8670, 1713.8417, 1716.8831, 1735.8501, 1739.9128, 1772.8773, 1781.9821, 1788.8333, 1794.9051, 1797.9274, 1884.9716, 1916.9853, 1965.9832, 2005.0675, 2009.0185, 2033.9909, 2066.0437, 2126.1346, 2150.0903, 2250.1013, 2297.0103, 2331.1459, 2346.1352, 2362.1254, 2368.1271, 2374.1534, 2477.1729, 2544.3770, 2604.3569, 2714.3223, 2789.4134, 2817.2664, 2968.2772, 2989.3711, 3042.4416, 3242.5664, 3802.7447, 3926.7627

9. DYH1_HUMAN **Mass:** 487166 **Score:** 56 **Expect:** 1.5 **Matches:** 38

Dynein heavy chain 1, axonemal OS=Homo sapiens OX=9606 GN=DNAH1 PE=1 SV=5

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
878.4498	877.4425	877.4327	11.2	1400	- 1406	1	R.EVERSMK.A
908.4522	907.4449	907.4651	-22.27	1837	- 1844	0	K.DVEGFLTK.C
935.4949	934.4876	934.4760	12.4	559	- 566	0	K.DSWISSLK.V
977.5319	976.5246	976.4825	43.1	1933	- 1942	0	R.AGAITSDTNK.K
1010.5343	1009.5270	1009.4716	54.8	440	- 447	0	R.EVSLDYER.S
1051.5006	1050.4933	1050.5280	-33.05	1355	- 1362	1	R.KCFENIAR.L + Propionamide (C)
1078.5362	1077.5289	1077.5818	-49.12	3745	- 3753	0	R.LIEHINPDK.V
1107.6262	1106.6190	1106.5794	35.8	3444	- 3452	0	R.MEYIPVAIR.T + Oxidation (M)
1129.6237	1128.6164	1128.6615	-39.91	1760	- 1770	1	K.TVISAAGNLKR.E
1154.6160	1153.6087	1153.5549	46.6	1277	- 1285	1	K.IMKNAYENR.E + Oxidation (M)
1164.6225	1163.6152	1163.5822	28.4	3389	- 3397	0	K.DIEDQILYR.L
1179.6122	1178.6049	1178.5819	19.6	1155	- 1164	0	K.EYAIEQALDK.M
1265.6549	1264.6476	1264.5904	45.3	1296	- 1305	1	R.MLDSLRDCNK.I + Propionamide (C)
1341.7621	1340.7549	1340.7486	4.67	2221	- 2233	0	K.KPVLCIGPTGTGK.T + Propionamide (C)

1351.7809	1350.7737	1350.7619	8.70	1407	-	1418	1	K.ASVHDIIEKAIR.A
1522.7677	1521.7604	1521.7299	20.0	2467	-	2477	1	R.LWYHENCRVFR.D
1553.7815	1552.7742	1552.8071	-21.22	740	-	752	1	K.AMIPLQAYAKEYR.K
1576.7603	1575.7531	1575.7926	-25.11	3081	-	3094	1	R.LREVEDGIATMQAK.Y + Oxidation (M)
1614.8781	1613.8708	1613.8269	27.2	1869	-	1883	1	K.STCYRVLAAAMTSLK.G
1667.9279	1666.9206	1666.8203	60.2	280	-	294	0	K.ALLPTDDFLGHEDPK.S
1735.8501	1734.8428	1734.8181	14.2	3533	-	3546	1	R.IMMNEGKINQSEWR.Y
1759.9378	1758.9306	1758.8280	58.3	1133	-	1147	0	R.CLEMNLQDHIESISK.V
1781.9821	1780.9748	1780.9359	21.9	753	-	767	1	R.KYLELNNNDIASFLK.T
1884.9716	1883.9644	1883.8732	48.4	359	-	374	0	R.IQLLFCAEDPCMFAQR.V
1947.0249	1946.0176	1945.8768	72.4	300	-	314	1	K.YKWCEVGVLDYDEEK.K + Propionamide (C)
1965.9832	1964.9759	1964.9374	19.6	1280	-	1295	1	K.NAYENREVINVCSDLR.M + Propionamide (C)
2005.0675	2004.0602	2003.9881	36.0	3700	-	3718	1	K.LSAISLGQGQGPRAEAMMR.S + 2 Oxidation (M)
2209.1040	2208.0967	2208.1494	-23.85	2054	-	2073	1	R.SSVKEVIASTNCNLTMSLLK.L + Propionamide (C)
2250.1013	2249.0941	2249.1262	-14.31	3498	-	3515	1	R.ISNINRYLTYSLYSNVCR.S + Propionamide (C)
2297.0103	2296.0031	2296.1157	-49.07	3791	-	3810	1	R.ANLLKSYSSLGEDFLNSCHK.V + Propionamide (C)
2362.1254	2361.1181	2361.2216	-43.83	3011	-	3031	1	K.AIQPYIDNEEFQPATIAKVSK.A
2604.3569	2603.3496	2603.2835	25.4	1126	-	1147	1	K.ANLTFARCLEMNLQDHIESISK.V + Propionamide (C)
2714.3223	2713.3150	2713.3504	-13.05	2003	-	2025	1	R.CGMVYLEPSILGLMPFIECWLRK.L + Oxidation (M)
2789.4134	2788.4061	2788.2433	58.4	136	-	159	1	R.VGSFEVPEDFQERMEQQCIGSTTR.L + Oxidation (M)

2872.4328	2871.4255	2871.4195	2.09	2003	2025	1	R.CGMVYLEPSILGLMPFIECWLRK.L + 2 Oxidation (M); 2 Propionamide (C)
2968.2772	2967.2700	2967.4470	-59.66	149	174	1	R.MEQQCIGSTTRLLAQTDFPLQAYEPK.M
3042.4416	3041.4343	3041.5683	-44.05	3203	3229	1	K.IRSWQIAGLPNDTLSVENGVINQFSQR.W
3926.7627	3925.7554	3925.9457	-48.45	1664	1698	1	R.FMFEGVEIPLVPSCAVFITMNPGYAGRTELPDNLK.A + Propionamide (C)

No match to: 842.4703, 885.4250, 931.4136, 947.5199, 960.4585, 996.4665, 1006.5727, 1012.5818, 1053.4752, 1063.5487, 1090.6464, 1100.5575, 1114.6152, 1123.5815, 1188.7008, 1197.6333, 1201.6073, 1207.6699, 1219.6165, 1240.6412, 1246.6110, 1282.7205, 1305.6865, 1328.8027, 1343.7755, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1418.7847, 1435.8008, 1526.8482, 1537.7531, 1559.7485, 1565.7961, 1574.8543, 1583.9072, 1625.7939, 1689.8869, 1693.8670, 1713.8417, 1716.8831, 1739.9128, 1772.8773, 1788.8333, 1794.9051, 1797.9274, 1916.9853, 2009.0185, 2033.9909, 2066.0437, 2126.1346, 2150.0903, 2331.1459, 2346.1352, 2368.1271, 2374.1534, 2477.1729, 2544.3770, 2817.2664, 2989.3711, 3242.5664, 3802.7447

10. DER_SHELP **Mass:** 54588 **Score:** 55 **Expect:** 1.6 **Matches:** 9

GTPase Der OS=Shewanella loihica (strain ATCC BAA-1088 / PV-4) OX=323850 GN=der PE=3 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
878.4498	877.4425	877.4657	-26.47	427	433	1	K.LPDSYKR.F
1107.6262	1106.6190	1106.6196	-0.61	16	24	1	K.STLFNRLTR.T
1328.8027	1327.7954	1327.7646	23.2	442	453	1	R.SLKVMGTPIQVR.F
1418.7847	1417.7774	1417.8769	-70.16	2	15	0	M.IPVVALVGRPNVGK.S
1537.7531	1536.7458	1536.7209	16.2	454	467	0	R.FQEGGNPFEGLNTK.K
1693.8670	1692.8598	1692.8907	-18.27	93	108	1	R.AGLTAADEAIAEHLRR.R
1781.9821	1780.9748	1781.0523	-43.49	202	218	1	K.LAIIGKPNVGKSTLTNR.I
1965.9832	1964.9759	1964.9197	28.6	384	400	0	R.IMQMAQDDHQPPLVNGR.R + Oxidation (M)
3926.7627	3925.7554	3925.9731	-55.44	71	107	1	R.MAEQSLAAIEEADVVLFLTDARAGLTAADEAIAEHLR.R + Oxidation (M)

No match to: 842.4703, 885.4250, 908.4522, 931.4136, 935.4949, 947.5199, 960.4585, 977.5319, 996.4665, 1006.5727, 1010.5343, 1012.5818, 1051.5006, 1053.4752, 1063.5487, 1078.5362, 1090.6464, 1100.5575, 1114.6152, 1123.5815, 1129.6237, 1154.6160, 1164.6225, 1179.6122, 1188.7008, 1197.6333, 1201.6073, 1207.6699, 1219.6165, 1240.6412, 1246.6110, 1265.6549, 1282.7205, 1305.6865, 1341.7621, 1343.7755, 1351.7809, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1435.8008, 1522.7677, 1526.8482, 1553.7815, 1559.7485, 1565.7961, 1574.8543, 1576.7603, 1583.9072, 1614.8781, 1625.7939, 1667.9279, 1689.8869, 1713.8417, 1716.8831, 1735.8501, 1739.9128, 1759.9378, 1772.8773, 1788.8333, 1794.9051, 1797.9274, 1884.9716, 1916.9853, 1947.0249, 2005.0675, 2009.0185, 2033.9909, 2066.0437, 2126.1346, 2150.0903, 2209.1040, 2250.1013, 2297.0103, 2331.1459, 2346.1352, 2362.1254, 2368.1271, 2374.1534, 2477.1729, 2544.3770, 2604.3569, 2714.3223, 2789.4134, 2817.2664, 2872.4328, 2968.2772, 2989.3711, 3042.4416, 3242.5664, 3802.7447

11. LIPA_DEIGD **Mass:** 36739 **Score:** 55 **Expect:** 1.9 **Matches:** 9

Lipoyl synthase OS=Deinococcus geothermalis (strain DSM 11300) OX=319795 GN=lipA PE=3 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
908.4522	907.4449	907.3891	61.4	237	243	0	R.EAMLDCR.A + Propionamide (C)
1010.5343	1009.5270	1009.5709	-43.48	10	17	1	K.FIKNGIYR.K
1051.5006	1050.4933	1050.5710	-73.93	120	128	0	K.YVVLTSVDR.D
1418.7847	1417.7774	1417.7565	14.7	33	45	0	K.VTIPTGQVYGEVR.K
1625.7939	1624.7866	1624.7524	21.0	72	85	0	R.GTATFMLMGHICTR.A + Oxidation (M); Propionamide (C)
1884.9716	1883.9644	1884.0357	-37.85	279	296	0	R.EEGLSLGFLEVVAGPLVR.S
2789.4134	2788.4061	2788.4232	-6.12	244	267	0	R.AHGVDVITFGQYLRPTMHHLPVER.Y + Oxidation (M)
2872.4328	2871.4255	2871.3531	25.2	89	114	1	R.FCAVDTGNPMGKLDLEEPAHVAESVR.L + Oxidation (M); Propionamide (C)
3926.7627	3925.7554	3925.7323	5.90	53	85	1	R.LHTVCEEAMCPNIGECWSRGTATFMLMGHICTR.A + Oxidation (M); 3 Propionamide (C)

No match to: 842.4703, 878.4498, 885.4250, 931.4136, 935.4949, 947.5199, 960.4585, 977.5319, 996.4665, 1006.5727, 1012.5818, 1053.4752, 1063.5487, 1078.5362, 1090.6464, 1100.5575, 1107.6262, 1114.6152, 1123.5815, 1129.6237, 1154.6160, 1164.6225, 1179.6122, 1188.7008, 1197.6333, 1201.6073, 1207.6699, 1219.6165, 1240.6412, 1246.6110, 1265.6549, 1282.7205, 1305.6865, 1328.8027, 1341.7621, 1343.7755, 1351.7809, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1435.8008, 1522.7677, 1526.8482, 1537.7531, 1553.7815, 1559.7485, 1565.7961, 1574.8543, 1576.7603, 1583.9072, 1614.8781, 1667.9279, 1689.8869, 1693.8670, 1713.8417, 1716.8831, 1735.8501, 1739.9128, 1759.9378, 1772.8773, 1781.9821, 1788.8333, 1794.9051, 1797.9274, 1916.9853, 1947.0249, 1965.9832, 2005.0675, 2009.0185, 2033.9909, 2066.0437, 2126.1346, 2150.0903, 2209.1040, 2250.1013, 2297.0103, 2331.1459, 2346.1352, 2362.1254, 2368.1271, 2374.1534, 2477.1729, 2544.3770, 2604.3569, 2714.3223, 2817.2664, 2968.2772, 2989.3711, 3042.4416, 3242.5664, 3802.7447

12. K2C78_HUMAN **Mass:** 56830 **Score:** 54 **Expect:** 2 **Matches:** 14

Keratin, type II cytoskeletal 78 OS=Homo sapiens OX=9606 GN=KRT78 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
908.4522	907.4449	907.4294	17.1	16	23	1	R.SACSARSR.G + Propionamide (C)
947.5199	946.5126	946.5018	11.4	384	391	1	R.MAKQNLAR.L + Oxidation (M)

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 1100.5575  1099.5502  1099.5622  -10.87   172 - 180   0   K.QLEQLQGER.G
 1107.6262  1106.6190  1106.5972    19.7   220 - 229   1   K.KDVDGVFLSK.M
 1123.5815  1122.5742  1122.5557    16.5   298 - 307   0   K.AEAEALYQTK.Y
 1164.6225  1163.6152  1163.5539    52.7     1 -  10   1   -.MSLSPCRAQR.G + Oxidation (M)
 1188.7008  1187.6936  1187.6510    35.9   339 - 348   1   R.LQSQTENLKK.Q
 1201.6073  1200.6001  1200.5636    30.4    28 -  39   1   R.GGFSSRGGFSSR.S
 1219.6165  1218.6093  1218.5961    10.8     1 -  10   1   -.MSLSPCRAQR.G + Propionamide (C)
 1343.7755  1342.7683  1342.7245    32.6    98 - 108   0   K.IEIDPQFQVVR.T
 1361.7892  1360.7819  1360.7020    58.7   375 - 386   1   K.VDELEAALRMAK.Q + Oxidation (M)
 1404.7940  1403.7868  1403.7773    6.78   208 - 219   1   R.RATLENDFVVLK.K
 1435.8008  1434.7935  1434.7831    7.32   404 - 415   1   K.LSLDVEIATYRR.L
 2250.1013  2249.0941  2249.0304    28.3   485 - 507   0   K.DPVLDSCSVSGSSAGSSCHTILK.K
 No match to: 842.4703, 878.4498, 885.4250, 931.4136, 935.4949, 960.4585, 977.5319, 996.4665, 1006.5727, 1010.5343,
 1012.5818, 1051.5006, 1053.4752, 1063.5487, 1078.5362, 1090.6464, 1114.6152, 1129.6237, 1154.6160, 1179.6122,
 1197.6333, 1207.6699, 1240.6412, 1246.6110, 1265.6549, 1282.7205, 1305.6865, 1328.8027, 1341.7621, 1351.7809,
 1372.8147, 1396.7120, 1418.7847, 1522.7677, 1526.8482, 1537.7531, 1553.7815, 1559.7485, 1565.7961, 1574.8543,
 1576.7603, 1583.9072, 1614.8781, 1625.7939, 1667.9279, 1689.8869, 1693.8670, 1713.8417, 1716.8831, 1735.8501,
 1739.9128, 1759.9378, 1772.8773, 1781.9821, 1788.8333, 1794.9051, 1797.9274, 1884.9716, 1916.9853, 1947.0249,
 1965.9832, 2005.0675, 2009.0185, 2033.9909, 2066.0437, 2126.1346, 2150.0903, 2209.1040, 2297.0103, 2331.1459,
 2346.1352, 2362.1254, 2368.1271, 2374.1534, 2477.1729, 2544.3770, 2604.3569, 2714.3223, 2789.4134, 2817.2664,
 2872.4328, 2968.2772, 2989.3711, 3042.4416, 3242.5664, 3802.7447, 3926.7627

13. AZOR8_BURL3    Mass: 22928    Score: 54     Expect: 2  Matches: 7

    FMN-dependent NADH-azoreductase 8 OS=Burkholderia lata (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB 9086 /
    R18194 / 383) OX=482957 GN=azoR8 PE=3 SV=1
     Observed    Mr(expt)   Mr(calc)     ppm  Start   End Miss   Peptide
      908.4522   907.4449   907.4763  -34.63   152 - 159   0   R.DIATGYLR.L
      977.5319   976.5246   976.4648    61.3   180 - 188   0   K.AVDMGEISR.S
     1107.6262  1106.6190  1106.5972    19.7   118 - 128   0   K.TLGFSGEGLVK.G
     1114.6152  1113.6079  1113.6295  -19.37   107 - 115   1   K.AYIDHIVRK.G
     1179.6122  1178.6049  1178.6044    0.47   150 - 159   1   R.DRDIATGYLR.L
     1328.8027  1327.7954  1327.7170    59.1     1 -  12   0   -.MPTLLVVEASPR.G + Oxidation (M)
     1351.7809  1350.7737  1350.7118    45.8    20 -  30   1   R.GLTKMFVNQWK.R
     No match to: 842.4703, 878.4498, 885.4250, 931.4136, 935.4949, 947.5199, 960.4585, 996.4665, 1006.5727, 1010.5343,
     1012.5818, 1051.5006, 1053.4752, 1063.5487, 1078.5362, 1090.6464, 1100.5575, 1123.5815, 1129.6237, 1154.6160,
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1164.6225, 1188.7008, 1197.6333, 1201.6073, 1207.6699, 1219.6165, 1240.6412, 1246.6110, 1265.6549, 1282.7205, 1305.6865, 1341.7621, 1343.7755, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1418.7847, 1435.8008, 1522.7677, 1526.8482, 1537.7531, 1553.7815, 1559.7485, 1565.7961, 1574.8543, 1576.7603, 1583.9072, 1614.8781, 1625.7939, 1667.9279, 1689.8869, 1693.8670, 1713.8417, 1716.8831, 1735.8501, 1739.9128, 1759.9378, 1772.8773, 1781.9821, 1788.8333, 1794.9051, 1797.9274, 1884.9716, 1916.9853, 1947.0249, 1965.9832, 2005.0675, 2009.0185, 2033.9909, 2066.0437, 2126.1346, 2150.0903, 2209.1040, 2250.1013, 2297.0103, 2331.1459, 2346.1352, 2362.1254, 2368.1271, 2374.1534, 2477.1729, 2544.3770, 2604.3569, 2714.3223, 2789.4134, 2817.2664, 2872.4328, 2968.2772, 2989.3711, 3042.4416, 3242.5664, 3802.7447, 3926.7627

14. TF212_SCHPO **Mass:** 154819 **Score:** 54 **Expect:** 2.4 **Matches:** 19

Transposon Tf2-12 polyprotein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=Tf2-12 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Peptide
885.4250	884.4178	884.4756	-65.38	417	-	424	0	R.NYPLPPGK.M
908.4522	907.4449	907.4552	-11.36	701	-	707	1	R.HFDFSKK.I
935.4949	934.4876	934.5124	-26.52	1320	-	1327	0	K.AIVNDYIK.N
960.4585	959.4512	959.4785	-28.37	117	-	125	1	K.VQGSNKGDR.L
1114.6152	1113.6079	1113.6407	-29.46	505	-	513	1	K.SAYHLIRVR.K
1179.6122	1178.6049	1178.6044	0.47	574	-	583	1	K.SESEHVKHVK.D
1201.6073	1200.6001	1200.6826	-68.77	1088	-	1097	1	R.TNQTVEKLLR.C
1305.6865	1304.6792	1304.6621	13.1	446	-	457	0	K.AINACPVMFVPK.K + Oxidation (M)
1328.8027	1327.7954	1327.7612	25.8	501	-	511	1	K.LDLKSAYHLIR.V
1341.7621	1340.7549	1340.7412	10.2	874	-	884	1	K.LLNLLNNEDKR.V
1526.8482	1525.8409	1525.8100	20.3	901	-	913	0	K.DQILLPNDTQLTR.T
1537.7531	1536.7458	1536.8340	-57.42	1214	-	1227	0	K.LAPSFAGPFYVLQK.S
1614.8781	1613.8708	1613.8559	9.25	357	-	370	1	K.HTLSQMNKVSNIVK.E + Oxidation (M)
1713.8417	1712.8344	1712.8693	-20.34	785	-	799	1	R.NLIGRITNESEPENK.R
1794.9051	1793.8978	1793.8697	15.7	1073	-	1087	0	K.FSLPYRPQTDGQTER.T
1797.9274	1796.9201	1796.9883	-37.98	383	-	398	1	K.DITAETNTEKLPKPIK.G
2033.9909	2032.9836	2033.0034	-9.71	425	-	442	1	K.MQAMNDEINQGLKSGIIR.E + Oxidation (M)
2374.1534	2373.1462	2373.1457	0.21	417	-	437	1	R.NYPLPPGKMQAMNDEINQGLK.S + Oxidation (M)
3926.7627	3925.7554	3925.9151	-40.68	251	-	285	1	R.YEMVLQAELPDFKCSIPCLIDTGAQANIITEETVR.A + Oxidation (M)

No match to: 842.4703, 878.4498, 931.4136, 947.5199, 977.5319, 996.4665, 1006.5727, 1010.5343, 1012.5818, 1051.5006, 1053.4752, 1063.5487, 1078.5362, 1090.6464, 1100.5575, 1107.6262, 1123.5815, 1129.6237, 1154.6160, 1164.6225, 1188.7008, 1197.6333, 1207.6699, 1219.6165, 1240.6412, 1246.6110, 1265.6549, 1282.7205, 1343.7755, 1351.7809, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1418.7847, 1435.8008, 1522.7677, 1553.7815, 1559.7485, 1565.7961, 1574.8543, 1576.7603, 1583.9072, 1625.7939, 1667.9279, 1689.8869, 1693.8670, 1716.8831, 1735.8501,

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        1739.9128, 1759.9378, 1772.8773, 1781.9821, 1788.8333, 1884.9716, 1916.9853, 1947.0249, 1965.9832, 2005.0675,
        2009.0185, 2066.0437, 2126.1346, 2150.0903, 2209.1040, 2250.1013, 2297.0103, 2331.1459, 2346.1352, 2362.1254,
        2368.1271, 2477.1729, 2544.3770, 2604.3569, 2714.3223, 2789.4134, 2817.2664, 2872.4328, 2968.2772, 2989.3711,
        3042.4416, 3242.5664, 3802.7447

15.     TF21_SCHPO     Mass: 154835    Score: 54      Expect: 2.4  Matches: 19
        Transposon Tf2-1 polyprotein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=Tf2-1 PE=3 SV=1
         Observed    Mr(expt)    Mr(calc)     ppm  Start     End Miss   Peptide
         885.4250    884.4178    884.4756  -65.38    417 -   424    0   R.NYPLPPGK.M
         908.4522    907.4449    907.4552  -11.36    701 -   707    1   R.HFDFSKK.I
         935.4949    934.4876    934.5124  -26.52   1320 - 1327    0   K.AIVNDYIK.N
         960.4585    959.4512    959.4785  -28.37    117 -   125    1   K.VQGSNKGDR.L
        1114.6152   1113.6079   1113.6407  -29.46    505 -   513    1   K.SAYHLIRVR.K
        1179.6122   1178.6049   1178.6044    0.47    574 -   583    1   K.SESEHVKHVK.D
        1201.6073   1200.6001   1200.6826  -68.77   1088 - 1097    1   R.TNQTVEKLLR.C
        1305.6865   1304.6792   1304.6621    13.1    446 -   457    0   K.AINACPVMFVPK.K + Oxidation (M)
        1328.8027   1327.7954   1327.7612    25.8    501 -   511    1   K.LDLKSAYHLIR.V
        1341.7621   1340.7549   1340.7412    10.2    874 -   884    1   K.LLNLLNNEDKR.V
        1526.8482   1525.8409   1525.8100    20.3    901 -   913    0   K.DQILLPNDTQLTR.T
        1537.7531   1536.7458   1536.8340  -57.42   1214 - 1227    0   K.LAPSFAGPFYVLQK.S
        1614.8781   1613.8708   1613.8559    9.25    357 -   370    1   K.HTLSQMNKVSNIVK.E + Oxidation (M)
        1713.8417   1712.8344   1712.8693  -20.34    785 -   799    1   R.NLIGRITNESEPENK.R
        1794.9051   1793.8978   1793.8697    15.7   1073 - 1087    0   K.FSLPYRPQTDGQTER.T
        1797.9274   1796.9201   1796.9883  -37.98    383 -   398    1   K.DITAETNTEKLPKPIK.G
        2033.9909   2032.9836   2033.0034   -9.71    425 -   442    1   K.MQAMNDEINQGLKSGIIR.E + Oxidation (M)
        2374.1534   2373.1462   2373.1457    0.21    417 -   437    1   R.NYPLPPGKMQAMNDEINQGLK.S + Oxidation (M)
        3926.7627   3925.7554   3925.9151  -40.68    251 -   285    1   R.YEMVLQAELPDFKCSIPCLIDTGAQANIITEETVR.A + Oxidation (M)
        No match to: 842.4703, 878.4498, 931.4136, 947.5199, 977.5319, 996.4665, 1006.5727, 1010.5343, 1012.5818,
        1051.5006, 1053.4752, 1063.5487, 1078.5362, 1090.6464, 1100.5575, 1107.6262, 1123.5815, 1129.6237, 1154.6160,
        1164.6225, 1188.7008, 1197.6333, 1207.6699, 1219.6165, 1240.6412, 1246.6110, 1265.6549, 1282.7205, 1343.7755,
        1351.7809, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1418.7847, 1435.8008, 1522.7677, 1553.7815, 1559.7485,
        1565.7961, 1574.8543, 1576.7603, 1583.9072, 1625.7939, 1667.9279, 1689.8869, 1693.8670, 1716.8831, 1735.8501,
        1739.9128, 1759.9378, 1772.8773, 1781.9821, 1788.8333, 1884.9716, 1916.9853, 1947.0249, 1965.9832, 2005.0675,
        2009.0185, 2066.0437, 2126.1346, 2150.0903, 2209.1040, 2250.1013, 2297.0103, 2331.1459, 2346.1352, 2362.1254,
        2368.1271, 2477.1729, 2544.3770, 2604.3569, 2714.3223, 2789.4134, 2817.2664, 2872.4328, 2968.2772, 2989.3711,
        3042.4416, 3242.5664, 3802.7447
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16.   TF22_SCHPO    Mass: 154835   Score: 54     Expect: 2.4  Matches: 19
      Transposon Tf2-2 polyprotein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=Tf2-2 PE=3 SV=1
       Observed    Mr(expt)    Mr(calc)    ppm  Start    End Miss   Peptide
       885.4250    884.4178    884.4756  -65.38   417 -  424   0    R.NYPLPPGK.M
       908.4522    907.4449    907.4552  -11.36   701 -  707   1    R.HFDFSKK.I
       935.4949    934.4876    934.5124  -26.52  1320 - 1327   0    K.AIVNDYIK.N
       960.4585    959.4512    959.4785  -28.37   117 -  125   1    K.VQGSNKGDR.L
      1114.6152   1113.6079   1113.6407  -29.46   505 -  513   1    K.SAYHLIRVR.K
      1179.6122   1178.6049   1178.6044    0.47   574 -  583   1    K.SESEHVKHVK.D
      1201.6073   1200.6001   1200.6826  -68.77  1088 - 1097   1    R.TNQTVEKLLR.C
      1305.6865   1304.6792   1304.6621    13.1   446 -  457   0    K.AINACPVMFVPK.K + Oxidation (M)
      1328.8027   1327.7954   1327.7612    25.8   501 -  511   1    K.LDLKSAYHLIR.V
      1341.7621   1340.7549   1340.7412    10.2   874 -  884   1    K.LLNLLNNEDKR.V
      1526.8482   1525.8409   1525.8100    20.3   901 -  913   0    K.DQILLPNDTQLTR.T
      1537.7531   1536.7458   1536.8340  -57.42  1214 - 1227   0    K.LAPSFAGPFYVLQK.S
      1614.8781   1613.8708   1613.8559    9.25   357 -  370   1    K.HTLSQMNKVSNIVK.E + Oxidation (M)
      1713.8417   1712.8344   1712.8693  -20.34   785 -  799   1    R.NLIGRITNESEPENK.R
      1794.9051   1793.8978   1793.8697    15.7  1073 - 1087   0    K.FSLPYRPQTDGQTER.T
      1797.9274   1796.9201   1796.9883  -37.98   383 -  398   1    K.DITAETNTEKLPKPIK.G
      2033.9909   2032.9836   2033.0034   -9.71   425 -  442   1    K.MQAMNDEINQGLKSGIIR.E + Oxidation (M)
      2374.1534   2373.1462   2373.1457    0.21   417 -  437   1    R.NYPLPPGKMQAMNDEINQGLK.S + Oxidation (M)
      3926.7627   3925.7554   3925.9151  -40.68   251 -  285   1    R.YEMVLQAELPDFKCSIPCLIDTGAQANIITEETVR.A + Oxidation (M)
      No match to: 842.4703, 878.4498, 931.4136, 947.5199, 977.5319, 996.4665, 1006.5727, 1010.5343, 1012.5818,
      1051.5006, 1053.4752, 1063.5487, 1078.5362, 1090.6464, 1100.5575, 1107.6262, 1123.5815, 1129.6237, 1154.6160,
      1164.6225, 1188.7008, 1197.6333, 1207.6699, 1219.6165, 1240.6412, 1246.6110, 1265.6549, 1282.7205, 1343.7755,
      1351.7809, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1418.7847, 1435.8008, 1522.7677, 1553.7815, 1559.7485,
      1565.7961, 1574.8543, 1576.7603, 1583.9072, 1625.7939, 1667.9279, 1689.8869, 1693.8670, 1716.8831, 1735.8501,
      1739.9128, 1759.9378, 1772.8773, 1781.9821, 1788.8333, 1884.9716, 1916.9853, 1947.0249, 1965.9832, 2005.0675,
      2009.0185, 2066.0437, 2126.1346, 2150.0903, 2209.1040, 2250.1013, 2297.0103, 2331.1459, 2346.1352, 2362.1254,
      2368.1271, 2477.1729, 2544.3770, 2604.3569, 2714.3223, 2789.4134, 2817.2664, 2872.4328, 2968.2772, 2989.3711,
      3042.4416, 3242.5664, 3802.7447

17.   TF23_SCHPO    Mass: 154819   Score: 54     Expect: 2.4  Matches: 19
      Transposon Tf2-3 polyprotein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=Tf2-3 PE=1 SV=1
```

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Peptide
885.4250	884.4178	884.4756	-65.38	417	-	424	0	R.NYPLPPGK.M
908.4522	907.4449	907.4552	-11.36	701	-	707	1	R.HFDFSKK.I
935.4949	934.4876	934.5124	-26.52	1320	-	1327	0	K.AIVNDYIK.N
960.4585	959.4512	959.4785	-28.37	117	-	125	1	K.VQGSNKGDR.L
1114.6152	1113.6079	1113.6407	-29.46	505	-	513	1	K.SAYHLIRVR.K
1179.6122	1178.6049	1178.6044	0.47	574	-	583	1	K.SESEHVKHVK.D
1201.6073	1200.6001	1200.6826	-68.77	1088	-	1097	1	R.TNQTVEKLLR.C
1305.6865	1304.6792	1304.6621	13.1	446	-	457	0	K.AINACPVMFVPK.K + Oxidation (M)
1328.8027	1327.7954	1327.7612	25.8	501	-	511	1	K.LDLKSAYHLIR.V
1341.7621	1340.7549	1340.7412	10.2	874	-	884	1	K.LLNLLNNEDKR.V
1526.8482	1525.8409	1525.8100	20.3	901	-	913	0	K.DQILLPNDTQLTR.T
1537.7531	1536.7458	1536.8340	-57.42	1214	-	1227	0	K.LAPSFAGPFYVLQK.S
1614.8781	1613.8708	1613.8559	9.25	357	-	370	1	K.HTLSQMNKVSNIVK.E + Oxidation (M)
1713.8417	1712.8344	1712.8693	-20.34	785	-	799	1	R.NLIGRITNESEPENK.R
1794.9051	1793.8978	1793.8697	15.7	1073	-	1087	0	K.FSLPYRPQTDGQTER.T
1797.9274	1796.9201	1796.9883	-37.98	383	-	398	1	K.DITAETNTEKLPKPIK.G
2033.9909	2032.9836	2033.0034	-9.71	425	-	442	1	K.MQAMNDEINQGLKSGIIR.E + Oxidation (M)
2374.1534	2373.1462	2373.1457	0.21	417	-	437	1	R.NYPLPPGKMQAMNDEINQGLK.S + Oxidation (M)
3926.7627	3925.7554	3925.9151	-40.68	251	-	285	1	R.YEMVLQAELPDFKCSIPCLIDTGAQANIITEETVR.A + Oxidation (M)

No match to: 842.4703, 878.4498, 931.4136, 947.5199, 977.5319, 996.4665, 1006.5727, 1010.5343, 1012.5818, 1051.5006, 1053.4752, 1063.5487, 1078.5362, 1090.6464, 1100.5575, 1107.6262, 1123.5815, 1129.6237, 1154.6160, 1164.6225, 1188.7008, 1197.6333, 1207.6699, 1219.6165, 1240.6412, 1246.6110, 1265.6549, 1282.7205, 1343.7755, 1351.7809, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1418.7847, 1435.8008, 1522.7677, 1553.7815, 1559.7485, 1565.7961, 1574.8543, 1576.7603, 1583.9072, 1625.7939, 1667.9279, 1689.8869, 1693.8670, 1716.8831, 1735.8501, 1739.9128, 1759.9378, 1772.8773, 1781.9821, 1788.8333, 1884.9716, 1916.9853, 1947.0249, 1965.9832, 2005.0675, 2009.0185, 2066.0437, 2126.1346, 2150.0903, 2209.1040, 2250.1013, 2297.0103, 2331.1459, 2346.1352, 2362.1254, 2368.1271, 2477.1729, 2544.3770, 2604.3569, 2714.3223, 2789.4134, 2817.2664, 2872.4328, 2968.2772, 2989.3711, 3042.4416, 3242.5664, 3802.7447

18. TF24_SCHPO **Mass:** 154835 **Score:** 54 **Expect:** 2.4 **Matches:** 19

Transposon Tf2-4 polyprotein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=Tf2-4 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Peptide
885.4250	884.4178	884.4756	-65.38	417	-	424	0	R.NYPLPPGK.M
908.4522	907.4449	907.4552	-11.36	701	-	707	1	R.HFDFSKK.I

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  935.4949   934.4876   934.5124  -26.52  1320 - 1327   0    K.AIVNDYIK.N
  960.4585   959.4512   959.4785  -28.37   117 -  125   1    K.VQGSNKGDR.L
 1114.6152  1113.6079  1113.6407  -29.46   505 -  513   1    K.SAYHLIRVR.K
 1179.6122  1178.6049  1178.6044    0.47   574 -  583   1    K.SESEHVKHVK.D
 1201.6073  1200.6001  1200.6826  -68.77  1088 - 1097   1    R.TNQTVEKLLR.C
 1305.6865  1304.6792  1304.6621    13.1   446 -  457   0    K.AINACPVMFVPK.K + Oxidation (M)
 1328.8027  1327.7954  1327.7612    25.8   501 -  511   1    K.LDLKSAYHLIR.V
 1341.7621  1340.7549  1340.7412    10.2   874 -  884   1    K.LLNLLNNEDKR.V
 1526.8482  1525.8409  1525.8100    20.3   901 -  913   0    K.DQILLPNDTQLTR.T
 1537.7531  1536.7458  1536.8340  -57.42  1214 - 1227   0    K.LAPSFAGPFYVLQK.S
 1614.8781  1613.8708  1613.8559    9.25   357 -  370   1    K.HTLSQMNKVSNIVK.E + Oxidation (M)
 1713.8417  1712.8344  1712.8693  -20.34   785 -  799   1    R.NLIGRITNESEPENK.R
 1794.9051  1793.8978  1793.8697    15.7  1073 - 1087   0    K.FSLPYRPQTDGQTER.T
 1797.9274  1796.9201  1796.9883  -37.98   383 -  398   1    K.DITAETNTEKLPKPIK.G
 2033.9909  2032.9836  2033.0034   -9.71   425 -  442   1    K.MQAMNDEINQGLKSGIIR.E + Oxidation (M)
 2374.1534  2373.1462  2373.1457    0.21   417 -  437   1    R.NYPLPPGKMQAMNDEINQGLK.S + Oxidation (M)
 3926.7627  3925.7554  3925.9151  -40.68   251 -  285   1    R.YEMVLQAELPDFKCSIPCLIDTGAQANIITEETVR.A + Oxidation (M)
 No match to: 842.4703, 878.4498, 931.4136, 947.5199, 977.5319, 996.4665, 1006.5727, 1010.5343, 1012.5818,
 1051.5006, 1053.4752, 1063.5487, 1078.5362, 1090.6464, 1100.5575, 1107.6262, 1123.5815, 1129.6237, 1154.6160,
 1164.6225, 1188.7008, 1197.6333, 1207.6699, 1219.6165, 1240.6412, 1246.6110, 1265.6549, 1282.7205, 1343.7755,
 1351.7809, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1418.7847, 1435.8008, 1522.7677, 1553.7815, 1559.7485,
 1565.7961, 1574.8543, 1576.7603, 1583.9072, 1625.7939, 1667.9279, 1689.8869, 1693.8670, 1716.8831, 1735.8501,
 1739.9128, 1759.9378, 1772.8773, 1781.9821, 1788.8333, 1884.9716, 1916.9853, 1947.0249, 1965.9832, 2005.0675,
 2009.0185, 2066.0437, 2126.1346, 2150.0903, 2209.1040, 2250.1013, 2297.0103, 2331.1459, 2346.1352, 2362.1254,
 2368.1271, 2477.1729, 2544.3770, 2604.3569, 2714.3223, 2789.4134, 2817.2664, 2872.4328, 2968.2772, 2989.3711,
 3042.4416, 3242.5664, 3802.7447

19.    TF25_SCHPO     Mass: 154819    Score: 54      Expect: 2.4   Matches: 19
       Transposon Tf2-5 polyprotein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=Tf2-5 PE=3 SV=1
       Observed    Mr(expt)    Mr(calc)    ppm  Start    End Miss   Peptide
  885.4250   884.4178   884.4756  -65.38   417 -  424   0    R.NYPLPPGK.M
  908.4522   907.4449   907.4552  -11.36   701 -  707   1    R.HFDFSKK.I
  935.4949   934.4876   934.5124  -26.52  1320 - 1327   0    K.AIVNDYIK.N
  960.4585   959.4512   959.4785  -28.37   117 -  125   1    K.VQGSNKGDR.L
 1114.6152  1113.6079  1113.6407  -29.46   505 -  513   1    K.SAYHLIRVR.K
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  1179.6122  1178.6049  1178.6044    0.47   574 -  583   1   K.SESEHVKHVK.D
  1201.6073  1200.6001  1200.6826  -68.77  1088 - 1097   1   R.TNQTVEKLLR.C
  1305.6865  1304.6792  1304.6621    13.1   446 -  457   0   K.AINACPVMFVPK.K + Oxidation (M)
  1328.8027  1327.7954  1327.7612    25.8   501 -  511   1   K.LDLKSAYHLIR.V
  1341.7621  1340.7549  1340.7412    10.2   874 -  884   1   K.LLNLLNNEDKR.V
  1526.8482  1525.8409  1525.8100    20.3   901 -  913   0   K.DQILLPNDTQLTR.T
  1537.7531  1536.7458  1536.8340  -57.42  1214 - 1227   0   K.LAPSFAGPFYVLQK.S
  1614.8781  1613.8708  1613.8559    9.25   357 -  370   1   K.HTLSQMNKVSNIVK.E + Oxidation (M)
  1713.8417  1712.8344  1712.8693  -20.34   785 -  799   1   R.NLIGRITNESEPENK.R
  1794.9051  1793.8978  1793.8697    15.7  1073 - 1087   0   K.FSLPYRPQTDGQTER.T
  1797.9274  1796.9201  1796.9883  -37.98   383 -  398   1   K.DITAETNTEKLPKPIK.G
  2033.9909  2032.9836  2033.0034   -9.71   425 -  442   1   K.MQAMNDEINQGLKSGIIR.E + Oxidation (M)
  2374.1534  2373.1462  2373.1457    0.21   417 -  437   1   R.NYPLPPGKMQAMNDEINQGLK.S + Oxidation (M)
  3926.7627  3925.7554  3925.9151  -40.68   251 -  285   1   R.YEMVLQAELPDFKCSIPCLIDTGAQANIITEETVR.A + Oxidation (M)
  No match to: 842.4703, 878.4498, 931.4136, 947.5199, 977.5319, 996.4665, 1006.5727, 1010.5343, 1012.5818,
  1051.5006, 1053.4752, 1063.5487, 1078.5362, 1090.6464, 1100.5575, 1107.6262, 1123.5815, 1129.6237, 1154.6160,
  1164.6225, 1188.7008, 1197.6333, 1207.6699, 1219.6165, 1240.6412, 1246.6110, 1265.6549, 1282.7205, 1343.7755,
  1351.7809, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1418.7847, 1435.8008, 1522.7677, 1553.7815, 1559.7485,
  1565.7961, 1574.8543, 1576.7603, 1583.9072, 1625.7939, 1667.9279, 1689.8869, 1693.8670, 1716.8831, 1735.8501,
  1739.9128, 1759.9378, 1772.8773, 1781.9821, 1788.8333, 1884.9716, 1916.9853, 1947.0249, 1965.9832, 2005.0675,
  2009.0185, 2066.0437, 2126.1346, 2150.0903, 2209.1040, 2250.1013, 2297.0103, 2331.1459, 2346.1352, 2362.1254,
  2368.1271, 2477.1729, 2544.3770, 2604.3569, 2714.3223, 2789.4134, 2817.2664, 2872.4328, 2968.2772, 2989.3711,
  3042.4416, 3242.5664, 3802.7447

20.  TF26_SCHPO    Mass: 154819   Score: 54     Expect: 2.4  Matches: 19
  Transposon Tf2-6 polyprotein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=Tf2-6 PE=3 SV=1
   Observed    Mr(expt)    Mr(calc)     ppm  Start    End Miss   Peptide
   885.4250    884.4178    884.4756  -65.38   417 -  424   0   R.NYPLPPGK.M
   908.4522    907.4449    907.4552  -11.36   701 -  707   1   R.HFDFSKK.I
   935.4949    934.4876    934.5124  -26.52  1320 - 1327   0   K.AIVNDYIK.N
   960.4585    959.4512    959.4785  -28.37   117 -  125   1   K.VQGSNKGDR.L
  1114.6152   1113.6079   1113.6407  -29.46   505 -  513   1   K.SAYHLIRVR.K
  1179.6122   1178.6049   1178.6044    0.47   574 -  583   1   K.SESEHVKHVK.D
  1201.6073   1200.6001   1200.6826  -68.77  1088 - 1097   1   R.TNQTVEKLLR.C
  1305.6865   1304.6792   1304.6621    13.1   446 -  457   0   K.AINACPVMFVPK.K + Oxidation (M)
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1328.8027  1327.7954  1327.7612    25.8    501 -  511   1   K.LDLKSAYHLIR.V
1341.7621  1340.7549  1340.7412    10.2    874 -  884   1   K.LLNLLNNEDKR.V
1526.8482  1525.8409  1525.8100    20.3    901 -  913   0   K.DQILLPNDTQLTR.T
1537.7531  1536.7458  1536.8340  -57.42   1214 - 1227   0   K.LAPSFAGPFYVLQK.S
1614.8781  1613.8708  1613.8559    9.25    357 -  370   1   K.HTLSQMNKVSNIVK.E + Oxidation (M)
1713.8417  1712.8344  1712.8693  -20.34    785 -  799   1   R.NLIGRITNESEPENK.R
1794.9051  1793.8978  1793.8697    15.7   1073 - 1087   0   K.FSLPYRPQTDGQTER.T
1797.9274  1796.9201  1796.9883  -37.98    383 -  398   1   K.DITAETNTEKLPKPIK.G
2033.9909  2032.9836  2033.0034   -9.71    425 -  442   1   K.MQAMNDEINQGLKSGIIR.E + Oxidation (M)
2374.1534  2373.1462  2373.1457    0.21    417 -  437   1   R.NYPLPPGKMQAMNDEINQGLK.S + Oxidation (M)
3926.7627  3925.7554  3925.9151  -40.68    251 -  285   1   R.YEMVLQAELPDFKCSIPCLIDTGAQANIITEETVR.A + Oxidation (M)
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No match to: 842.4703, 878.4498, 931.4136, 947.5199, 977.5319, 996.4665, 1006.5727, 1010.5343, 1012.5818, 1051.5006, 1053.4752, 1063.5487, 1078.5362, 1090.6464, 1100.5575, 1107.6262, 1123.5815, 1129.6237, 1154.6160, 1164.6225, 1188.7008, 1197.6333, 1207.6699, 1219.6165, 1240.6412, 1246.6110, 1265.6549, 1282.7205, 1343.7755, 1351.7809, 1361.7892, 1372.8147, 1396.7120, 1404.7940, 1418.7847, 1435.8008, 1522.7677, 1553.7815, 1559.7485, 1565.7961, 1574.8543, 1576.7603, 1583.9072, 1625.7939, 1667.9279, 1689.8869, 1693.8670, 1716.8831, 1735.8501, 1739.9128, 1759.9378, 1772.8773, 1781.9821, 1788.8333, 1884.9716, 1916.9853, 1947.0249, 1965.9832, 2005.0675, 2009.0185, 2066.0437, 2126.1346, 2150.0903, 2209.1040, 2250.1013, 2297.0103, 2331.1459, 2346.1352, 2362.1254, 2368.1271, 2477.1729, 2544.3770, 2604.3569, 2714.3223, 2789.4134, 2817.2664, 2872.4328, 2968.2772, 2989.3711, 3042.4416, 3242.5664, 3802.7447

Search Parameters

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Type of search         : Peptide Mass Fingerprint
Enzyme                 : Trypsin
Variable modifications : Oxidation (M),Propionamide (C)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 75 ppm
Peptide Charge State   : 1+
Max Missed Cleavages   : 1
Number of queries      : 101
Selected for scoring   : 51
```