

Supplementary materials

Occurrence of a functionally stable photoharvesting single peptide allophycocyanin

α -subunit (16.4 kDa) in the cyanobacterium *Nostoc* sp. R76DM

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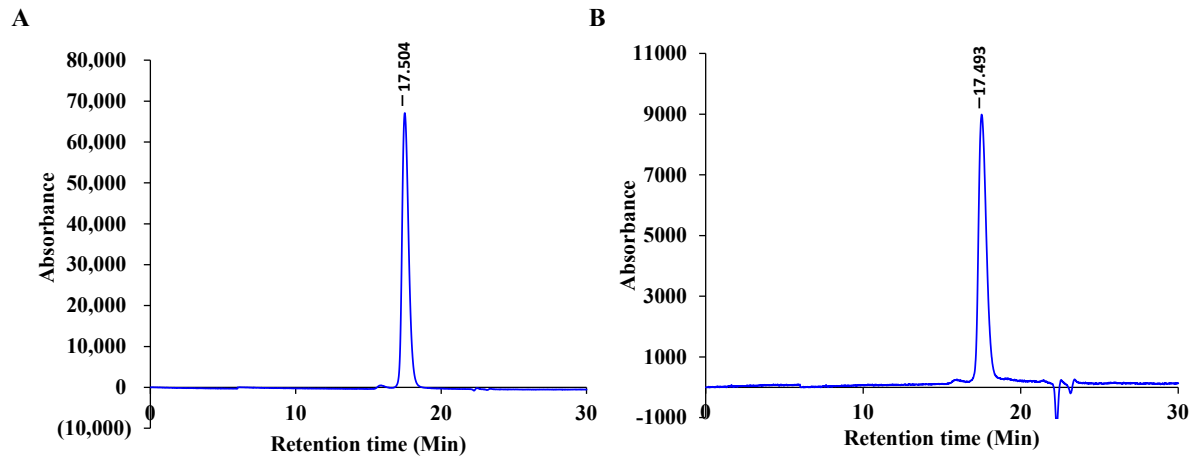
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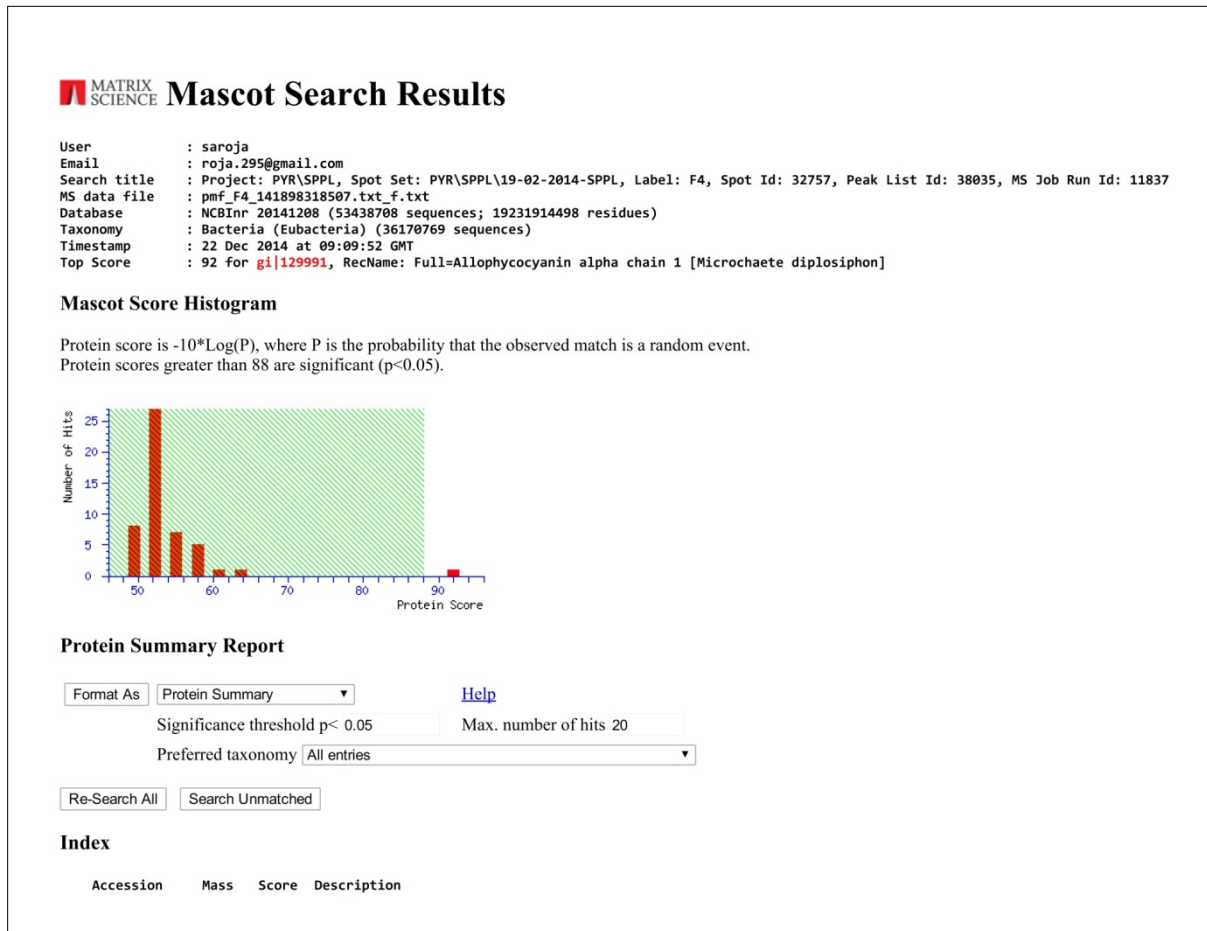
Supplementary figure 1

High performance gel permeation chromatogram of *Nostoc* APC under non-denaturing (A) and denaturing (B) conditions



Supplementary figure 2

Results of Mascot search analysis using the peptide mass fingerprint of *Nostoc* APC



Supplementary figure 2 (Contd.)

1. gi 129991	17411	92	RecName: Full=Allophycocyanin alpha chain 1 [Microchaete diplosiphon]
2. gi 631269561	25566	62	UDP-N-acetylglucosamine pyrophosphorylase [Microbacterium sp. CH12i]
3. gi 547916457	61542	61	phosphoglucosyltransferase/phosphomannosyltransferase alpha/beta/alpha domain II [Dorea sp. CAG:317]
4. gi 446245156	20910	58	hypothetical protein [Helicobacter pylori]
5. gi 684624482	27166	58	hypothetical protein JCM19239_4096 [Vibrio variabilis]
6. gi 517959773	32498	58	hypothetical protein [Bacteroidales bacterium ph8]
7. gi 506359044	34434	57	regulatory protein [Tolomonas auensis]
8. gi 658945776	36401	56	methionine synthase, partial [Vibrio parahaemolyticus]
9. gi 551200527	59166	56	hypothetical protein [Flavobacterium antarcticum]
10. gi 647607904	36999	56	rod shape-determining protein MreB [Prevotella paludivivens]
11. gi 494810447	30020	55	hypothetical protein [Sulfurihydrogenibium yellowstonense]
12. gi 507052681	15214	55	hypothetical protein [Bacillus cereus]
13. gi 654940760	7394	55	hypothetical protein [Bacillus sp. FJAT-14515]
14. gi 446059331	79522	54	tyrosine kinase [Escherichia coli]
15. gi 510898678	79508	54	tyrosine-protein kinase wzc [Escherichia coli]
16. gi 517798414	15922	54	hypothetical protein [Rubritalea marina]
17. gi 515777716	76223	53	hypothetical protein [Clostridium beijerinckii]
18. gi 657059983	17752	53	rRNA methylase [Aeromonas hydrophila]
19. gi 491449787	17688	53	MULTISPECIES: rRNA methyltransferase [Aeromonas]
20. gi 648322413	17695	53	rRNA methylase [Aeromonas hydrophila]

Results List

1.	gi 129991	Mass: 17411	Score: 92	Expect: 0.023	Matches: 6
RecName: Full=Allophycocyanin alpha chain 1 [Microchaete diplosiphon]					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Peptide
	957.3620	956.3547	956.4603	-110.41	84 - 90 0 R.DLDYLR.L
	1049.4099	1048.4026	1048.5189	-110.90	17 - 25 0 R.YLSPGELDR.I
	1290.5637	1289.5564	1289.6979	-109.71	17 - 27 1 R.YLSPGELDRK.S
	1326.5674	1325.5601	1325.7779	-164.26	37 - 47 1 R.LRIAQILTENR.E
	2010.8370	2009.8297	2009.0139	406	114 - 131 1 R.EMYKSLGTPIEGITEGIR.A + Oxidation (M)
	2358.0510	2357.0437	2357.2842	-102.03	91 - 113 0 R.LVTYGVISGDVPIEEIGVIGAR.E
No match to: 1580.6538, 1867.7657					
2.	gi 631269561	Mass: 25566	Score: 62	Expect: 22	Matches: 5
UDP-N-acetylglucosamine pyrophosphorylase [Microbacterium sp. CH12i]					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Peptide
	957.3620	956.3547	956.4087	-56.43	77 - 84 0 R.YDETNTSK.S
	1049.4099	1048.4026	1048.5600	-150.09	175 - 182 1 K.AFMRQLQR.V
	1580.6538	1579.6465	1579.8062	-101.07	1 - 15 0 -.MTLQTVILAAGMGR.L + 2 Oxidation (M)
	1867.7657	1866.7584	1866.9509	-103.11	157 - 174 1 K.GGLGEAVGINYISSMQKK.A + Oxidation (M)
	2358.0510	2357.0437	2356.1798	367	133 - 153 1 K.VSDEEVKYTVTAEGFINQLSK.S
No match to: 1290.5637, 1326.5674, 2010.8370					

Supplementary figure 2 (Contd.)

3. [gi|547916457](#) Mass: 61542 Score: 61 Expect: 28 Matches: 6
 phosphoglucomutase/phosphomannomutase alpha/beta/alpha domain II [Dorea sp. CAG:317]
- | Observed | Mr(expt) | Mr(calC) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|---------|-------|-------|------|--------------------------------|
| 957.3620 | 956.3547 | 956.5226 | -175.47 | 215 | - 222 | 0 | R.QVRPGLCK.T |
| 1049.4099 | 1048.4026 | 1048.5157 | -107.89 | 469 | - 477 | 0 | K.MAGIMQNL.R.E + Oxidation (M) |
| 1290.5637 | 1289.5564 | 1289.5598 | -2.59 | 441 | - 450 | 0 | R.MEETYTEYGR.Y |
| 1326.5674 | 1325.5601 | 1325.7415 | -136.83 | 100 | - 113 | 0 | K.TAAGVLAANGINVR.I |
| 2010.8370 | 2009.8297 | 2009.9451 | -57.42 | 130 | - 147 | 1 | R.YYKCNAGVMVTASHNPAK.Y |
| 2358.0510 | 2357.0437 | 2357.1368 | -39.50 | 395 | - 414 | 1 | R.FIFGFEEESYGLAGPYVRDK.D |
- No match to: 1580.6538, 1867.7657
4. [gi|446245156](#) Mass: 20910 Score: 58 Expect: 51 Matches: 5
 hypothetical protein [Helicobacter pylori]
- | Observed | Mr(expt) | Mr(calC) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|---------|-------|-------|------|---------------------------------|
| 957.3620 | 956.3547 | 956.4498 | -99.37 | 97 | - 103 | 1 | R.MREEQHK.Q |
| 1049.4099 | 1048.4026 | 1048.5189 | -110.90 | 73 | - 81 | 0 | R.QAEAFDLQK.R |
| 1326.5674 | 1325.5601 | 1325.6034 | -32.63 | 82 | - 92 | 1 | K.RQAEQSMDFAK.S + Oxidation (M) |
| 1580.6538 | 1579.6465 | 1579.8570 | -133.20 | 153 | - 167 | 0 | K.VPLTTQSAPITPNNK.T |
| 2010.8370 | 2009.8297 | 2009.1157 | 355 | 153 | - 171 | 1 | K.VPLTTQSAPITPNNK.TLSK.E |
- No match to: 1290.5637, 1867.7657, 2358.0510
5. [gi|684624482](#) Mass: 27166 Score: 58 Expect: 59 Matches: 5
 hypothetical protein JCM19239_4096 [Vibrio variabilis]
- | Observed | Mr(expt) | Mr(calC) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|---------|-------|-------|------|--|
| 957.3620 | 956.3547 | 956.5291 | -182.27 | 173 | - 180 | 1 | K.TPKNQIEK.W |
| 1049.4099 | 1048.4026 | 1048.5526 | -143.04 | 105 | - 113 | 1 | K.SYGRRTGR.F |
| 1867.7657 | 1866.7584 | 1866.8968 | -74.11 | 1 | - 17 | 1 | -.MSTGNKPKNLDGAMEK.K |
| 2010.8370 | 2009.8297 | 2009.1019 | 362 | 137 | - 154 | 1 | R.LQAGEKWPPIGELALLK.S + Oxidation (M) |
| 2358.0510 | 2357.0437 | 2356.1481 | 380 | 109 | - 128 | 1 | R.RPTGRFLDFADSLTESELMR.V + Oxidation (M) |
- No match to: 1290.5637, 1326.5674, 1580.6538
6. [gi|517959773](#) Mass: 32498 Score: 58 Expect: 60 Matches: 5
 hypothetical protein [Bacteroidales bacterium ph8]
- | Observed | Mr(expt) | Mr(calC) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|---------|-------|-------|------|---------------------------|
| 1290.5637 | 1289.5564 | 1289.6463 | -69.68 | 128 | - 139 | 0 | R.SLVDESLETAAR.N |
| 1326.5674 | 1325.5601 | 1325.6550 | -71.59 | 211 | - 220 | 1 | K.YILCRFSPDR.G |
| 1580.6538 | 1579.6465 | 1579.8358 | -119.83 | 55 | - 68 | 1 | K.EVVTGYPYARYAQK.F |
| 1867.7657 | 1866.7584 | 1866.0350 | 388 | 37 | - 54 | 0 | R.VEVGIPITPLAVDLTVEK.E |
| 2358.0510 | 2357.0437 | 2357.1719 | -54.39 | 3 | - 24 | 0 | K.TLVLLCCTALTIVGSASQSYR.V |
- No match to: 957.3620, 1049.4099, 2010.8370
7. [gi|506359044](#) Mass: 34434 Score: 57 Expect: 77 Matches: 5
 regulatory protein [Tolomonas auensis]

Supplementary figure 2 (Contd.)

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
1049.4099	1048.4026	1048.5553	-145.59	182	-	191	0	R.SKPVAAVDIAK.I
1290.5637	1289.5564	1289.7343	-137.92	182	-	193	1	R.SKPVAAVDIAK.K
1326.5674	1325.5601	1325.5704	-7.73	62	-	73	1	K.MSDRCGGLEASK.D + Oxidation (M)
1867.7657	1866.7584	1866.8716	-60.64	66	-	81	1	R.CGGLEASKDNKPCIYR.C
2358.0510	2357.0437	2356.1369	385	279	-	299	1	R.QTFQVTPQMYRDLTVSDGLAS.-

No match to: 957.3620, 1580.6538, 2010.8370

8. [gi|658945776](#) Mass: 36401 Score: 56 Expect: 81 Matches: 5

methionine synthase, partial [Vibrio parahaemolyticus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
957.3620	956.3547	956.5291	-182.27	7	-	14	0	R.QQIEAQLK.Q
1049.4099	1048.4026	1048.4859	-79.44	321	-	330	0	R.QMAQAVEGVV.- + Oxidation (M)
1580.6538	1579.6465	1579.6937	-29.85	140	-	153	0	R.TCSISPDVNDPGYR.N
2010.8370	2009.8297	2009.0438	391	15	-	32	1	K.QRILLIDGGMGTMIGYK.L + Oxidation (M)
2358.0510	2357.0437	2356.3366	300	170	-	191	1	R.ALIRGGADLILIEITIFDTLNAK.A

No match to: 1290.5637, 1326.5674, 1867.7657

9. [gi|551200527](#) Mass: 59166 Score: 56 Expect: 89 Matches: 6

hypothetical protein [Flavobacterium antarcticum]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
957.3620	956.3547	956.4603	-110.43	317	-	324	0	K.YLGTDFNFK.K
1049.4099	1048.4026	1048.6393	-225.70	253	-	261	1	K.LVPTHKLNK.K
1326.5674	1325.5601	1325.7303	-128.35	191	-	203	0	K.NLASISHSLSIGSK.E
1580.6538	1579.6465	1579.8253	-113.14	2	-	14	1	M.HLDLIDICRPARS.V
1867.7657	1866.7584	1866.8159	-30.81	419	-	433	0	K.EPQIFDFLNEDDEEK.N
2010.8370	2009.8297	2009.0047	411	68	-	83	1	K.ANYDFDFVRNESLFLK.N

No match to: 1290.5637, 2358.0510

10. [gi|647607904](#) Mass: 36999 Score: 56 Expect: 1e+02 Matches: 5

rod shape-determining protein MreB [Prevotella paludivivens]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
957.3620	956.3547	956.3948	-41.88	121	-	129	0	R.DSAEHADGR.D
1049.4099	1048.4026	1048.5587	-148.82	41	-	50	1	R.TDKMIAVGAK.A + Oxidation (M)
1290.5637	1289.5564	1289.7092	-118.43	285	-	297	0	K.NGIYLSGGGALLR.G
1867.7657	1866.7584	1866.9774	-117.30	324	-	340	1	K.GAGIALKNVNNFSFLMR.- + Oxidation (M)
2358.0510	2357.0437	2357.2743	-97.82	303	-	323	1	R.LTDKINIPFHIAEDPLHSVAK.G

No match to: 1326.5674, 1580.6538, 2010.8370

11. [gi|494810447](#) Mass: 30020 Score: 55 Expect: 1.1e+02 Matches: 5

hypothetical protein [Sulfurihydrogenibium yellowstonense]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide	
957.3620	956.3547	956.5542	-208.57	164	-	172	0	R.EILALVDGK.N

Supplementary figure 2 (Contd.)

1290.5637 1289.5564 1289.7594 -157.41 242 - 252 0 R.ILSVLESKPIK.Q
 1580.6538 1579.6465 1579.7803 -84.70 136 - 148 1 K.ITDPEMIFEKTEK.A
 2010.8370 2009.8297 2008.9968 415 55 - 70 1 R.SFFLYMDLDFESVLKR.D
 2358.0510 2357.0437 2357.3569 -132.86 106 - 125 1 K.YSEDIKPLINTEKLIILLSR.N
No match to: 1049.4099, 1326.5674, 1867.7657

12. [gi|507052681](#) Mass: 15214 Score: 55 Expect: 1.2e+02 Matches: 4
 hypothetical protein [Bacillus cereus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1049.4099	1048.4026	1048.5414	-132.32	121	-	128	1 K.FETRNNIR.K
1290.5637	1289.5564	1289.7343	-137.93	14	-	25	1 R.IFKGLSAQELGK.E
2010.8370	2009.8297	2010.0269	-98.12	63	-	80	1 R.LLNHKISDSVIPDDTTK.K
2358.0510	2357.0437	2357.1903	-62.19	43	-	62	1 K.EPNFEVLQKISVYFVSTDR.L

No match to: 957.3620, 1326.5674, 1580.6538, 1867.7657

13. [gi|654940760](#) Mass: 7394 Score: 55 Expect: 1.2e+02 Matches: 4
 hypothetical protein [Bacillus sp. FJAT-14515]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
957.3620	956.3547	956.4749	-125.68	13	-	20	1 K.KHVMEGEK.S
1049.4099	1048.4026	1048.4510	-46.19	1	-	7	0 -.MMVYCFK.T + Oxidation (M)
1290.5637	1289.5564	1289.6049	-37.60	1	-	9	1 -.MMVYCFKTR.M
1867.7657	1866.7584	1867.0013	-130.06	30	-	46	0 K.LTGTATMVDLYLLIDK.A

No match to: 1326.5674, 1580.6538, 2010.8370, 2358.0510

14. [gi|446059331](#) Mass: 79522 Score: 54 Expect: 1.3e+02 Matches: 6
 tyrosine kinase [Escherichia coli]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
957.3620	956.3547	956.5655	-220.32	23	-	31	0 R.LVGTVIEAR.W
1290.5637	1289.5564	1289.6584	-79.07	557	-	566	1 K.RVLLIDCDMR.K
1326.5674	1325.5601	1325.7455	-139.86	337	-	347	1 K.VHPAYRTLLEK.R
1580.6538	1579.6465	1579.7777	-83.01	138	-	150	1 K.VTTFNRPKEMADR.V + Oxidation (M)
1867.7657	1866.7584	1866.9199	-86.51	116	-	131	1 K.NTFPIFGAGWERLMGR.Q + Oxidation (M)
2358.0510	2357.0437	2356.2097	354	610	-	630	1 R.GQVPPNPSELLMSERFAELVK.W + Oxidation (M)

No match to: 1049.4099, 2010.8370

15. [gi|510898678](#) Mass: 79508 Score: 54 Expect: 1.3e+02 Matches: 6
 tyrosine-protein kinase wzc [Escherichia coli]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
957.3620	956.3547	956.5655	-220.32	23	-	31	0 R.LVGTVIEAR.W
1290.5637	1289.5564	1289.6584	-79.07	557	-	566	1 K.RVLLIDCDMR.K
1326.5674	1325.5601	1325.7455	-139.86	337	-	347	1 K.VHPAYRTLLEK.R
1580.6538	1579.6465	1579.7777	-83.01	138	-	150	1 K.VTTFNRPKEMADR.V + Oxidation (M)
1867.7657	1866.7584	1866.9199	-86.51	116	-	131	1 K.NTFPIFGAGWERLMGR.Q + Oxidation (M)

Supplementary figure 2 (Contd.)

2358.0510 2357.0437 2356.2097 354 610 - 630 1 R.GQVPPNPSELLMSERFAELVK.W + Oxidation (M)
 No match to: 1049.4099, 2010.8370

16. [gi|517798414](#) Mass: 15922 Score: 54 Expect: 1.6e+02 Matches: 4
 hypothetical protein [Rubritalea marina]
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|---|
| 1049.4099 | 1048.4026 | 1048.5050 | -97.63 | 81 | 89 | 0 | R.HLAETHDAR.F |
| 1580.6538 | 1579.6465 | 1579.6541 | -4.82 | 1 | 14 | 1 | -.MGDASQCPKCGTPE + Oxidation (M) |
| 2010.8370 | 2009.8297 | 2009.1170 | 355 | 55 | 74 | 1 | K.ALKRVIHGYGASSGVSVIAPR.A |
| 2358.0510 | 2357.0437 | 2356.2685 | 329 | 58 | 80 | 1 | R.VIHGYGASSGVSVIAPRAISLMR.H + Oxidation (M) |
- No match to: 957.3620, 1290.5637, 1326.5674, 1867.7657
17. [gi|515777716](#) Mass: 76223 Score: 53 Expect: 1.7e+02 Matches: 6
 hypothetical protein [Clostridium beijerinckii]
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|---------|-------|-----|------|-----------------------|
| 957.3620 | 956.3547 | 956.6018 | -258.32 | 202 | 209 | 1 | K.LDIKSIIR.C |
| 1290.5637 | 1289.5564 | 1289.6728 | -90.21 | 499 | 508 | 1 | K.RQLNLFNEEK.E |
| 1580.6538 | 1579.6465 | 1579.8431 | -124.40 | 559 | 574 | 1 | K.TSTSVGRAVAVPHGNK.E |
| 1867.7657 | 1866.7584 | 1866.0251 | 393 | 187 | 201 | 1 | R.LTTEIYSRIQNIFIK.L |
| 2010.8370 | 2009.8297 | 2009.9734 | -71.49 | 534 | 550 | 1 | K.YGQVLEDINVKSGYAK.S |
| 2358.0510 | 2357.0437 | 2356.2865 | 321 | 222 | 240 | 1 | K.FIENDFYTLIKLILVSR.I |
- No match to: 1049.4099, 1326.5674
18. [gi|657059983](#) Mass: 17752 Score: 53 Expect: 1.8e+02 Matches: 4
 rRNA methylase [Aeromonas hydrophila]
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|---------|-------|-----|------|------------------------------|
| 957.3620 | 956.3547 | 956.5113 | -163.72 | 122 | 129 | 0 | R.IPMLPQSR.S + Oxidation (M) |
| 1867.7657 | 1866.7584 | 1866.9628 | -109.48 | 29 | 43 | 1 | R.LHLIEPLGFWDKRV |
| 2010.8370 | 2009.8297 | 2009.1309 | 348 | 105 | 121 | 1 | R.GLPIETIESLPFQRLR.I |
| 2358.0510 | 2357.0437 | 2357.1876 | -61.05 | 82 | 104 | 1 | K.GRTAHSAVQFAAGDALLFGPESR.G |
- No match to: 1049.4099, 1290.5637, 1326.5674, 1580.6538
19. [gi|491449787](#) Mass: 17688 Score: 53 Expect: 1.8e+02 Matches: 4
 MULTISPECIES: rRNA methyltransferase [Aeromonas]
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Peptide |
|-----------|-----------|-----------|---------|-------|-----|------|------------------------------|
| 957.3620 | 956.3547 | 956.5113 | -163.72 | 122 | 129 | 0 | R.IPMLPQSR.S + Oxidation (M) |
| 1867.7657 | 1866.7584 | 1866.9628 | -109.48 | 29 | 43 | 1 | R.LHLIEPLGFWDKRV |
| 2010.8370 | 2009.8297 | 2009.1309 | 348 | 105 | 121 | 1 | R.GLPIETIESLPFQRLR.I |
| 2358.0510 | 2357.0437 | 2357.1876 | -61.05 | 82 | 104 | 1 | K.GRTAHSAVQFAAGDALLFGPESR.G |
- No match to: 1049.4099, 1290.5637, 1326.5674, 1580.6538
20. [gi|648322413](#) Mass: 17695 Score: 53 Expect: 1.8e+02 Matches: 4
 rRNA methylase [Aeromonas hydrophila]

Supplementary figure 2 (Contd.)

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
957.3620	956.3547	956.5113	-163.72	122	- 129	0	R.IPMLPQSR.S + Oxidation (M)
1867.7657	1866.7584	1866.9628	-109.48	29	- 43	1	R.LHLIEPLGFWDK.R.V
2010.8370	2009.8297	2009.1309	348	105	- 121	1	R.GLPETIIESLPFQRL.R.I
2358.0510	2357.0437	2357.1876	-61.05	82	- 104	1	K.GRTAHSVQFAAGDALLFGPESR.G

No match to: 1049.4099, 1290.5637, 1326.5674, 1580.6538

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : [Carbamidomethyl \(C\)](#)
Variable modifications : [Oxidation \(M\)](#)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 420 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 8

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