

# **Composite Sequence Proteomic Analysis of Protein Biomarkers of *Campylobacter coli*, *C. lari* and *C. concisus* for Bacterial Identification**

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## **Supplementary Information**

Amplification and gene sequencing of selected protein biomarkers whose amino acid sequence was determined by Composite Sequence Proteomic Analysis (CSPA)

### RM1051 'phnA'

**Nucleotide sequence (NCBI accession number: EF643696)**

ATGCCTAAAGATGCAAATGGAACAGAAATTAATGCTGGAGATAGCGTAAGCGTGAT  
AAAAGATTTAAAAGTTAAAGGTGCTAGCACTACTTTAAAACGCGGAACAACGATAA  
AAAATATCAAACCTTACTTCTAAAGAAAATGAAATTGAAGCTAAAGTAGATAAATTT  
GGCGTTATTGTACTAAAGACTGAATTTTTAAAGAAAATTTAG

**Amino acid sequence**

MPKDANGTELNAGDSVSVIKDLKVKGASTTLKRGTTIKNIKLTSKENEIEAKVDFKFGVIV  
LKTEFLKKI    **Average MW = 7503.8**

### RM1865 'phnA'

**Nucleotide sequence (NCBI accession number: EF643697)**

ATGCCTAAAGATGCAAATGGAACAGAAATTAATGCTGGAGATAGCGTAAGCGTGAT  
AAAAGATTTAAAAGTTAAAGGTGCTAGCACTACTTTAAAACGCGGAACAACGATAA  
AAAATATCAAACCTTACTTCTAAAGAAGGTGAAATTGAAGCCAAAGTAGATAAATTT  
GGCGTTATTGTACTAAAGACTGAATTTTTAAAGAAAATTTAG

**Amino acid sequence**

MPKDANGTELNAGDSVSVIKDLKVKGASTTLKRGTTIKNIKLTSKERGEIEAKVDFKFGVIV  
LKTEFLKKI    **Average MW = 7446.8**

RM1051 30S ribosomal S15 (*rpsO*)

**Nucleotide sequence (NCBI accession number: EF643698)**

ATGGCTTTGGATTTCGGCTAAAAAAGCAGAAATTGTTGCGAAATTCGCTAGAAAAGC  
GGGCGATACTGGCTCGACAGAAGTTCAAGTAGCACTTTTAAGTGCAAGAATTGCAG  
AACTTACAGAACATTTAAAAATCTACAAAAAAGATTTTCTTCAAGATTAGGACTTT  
TAAAACCTTGTAGGTCAAAGAAAAAGACTTTTAGCTTATCTAAAAAGAAAAGATTAC  
AATTCTTATAGTAAATTAATTACAGAATTAATCTCAGAGATAAATAA

**Amino acid sequence**

MALDSAKKAEIVAKFARKAGDTGSTEVQVALLSARIAELTEHLKIYKKDFSSRLGLLKL  
VGQRKRLAYLKRKDYNSYSKLITELNLRDK **Average MW = 10198.0**

RM1865 30S ribosomal S15 protein (*rpsO*)

**Nucleotide sequence (NCBI accession number: EF643699)**

ATGGCTTTGGATTTCGGCTAAAAAAGCAGAAATTGTTGCGAAATTCGCTAGAAAAGC  
GGGCGATACTGGCTCGACAGAAGTTCAAGTAGCACTTTTAAGTGCGAGAATTGCAG  
AACTTACAGAACATTTAAAAATCTACAAAAAAGATTTTCTTCAAGATTAGGACTTT  
TAAAACCTTGTAGGTCAAAGAAAAAGACTTTTAGCTTATCTAAAAAGAAAAGATTAC  
AATTCTTATAGTAAATTAATTACAGAATTAATCTTAGAGATAAATAA

**Amino acid sequence**

MALDSAKKAEIVAKFARKAGDTGSTEVQVALLSARIAELTEHLKIYKKDFSSRLGLLKL  
VGQRKRLAYLKRKDYNSYSKLITELNLRDK

## Proteomic Identifications

Data files of tandem mass spectrometry data were analyzed using both MASCOT and GPM software. MASCOT search engine parameters were as follows. The database was the non-redundant National Center for Biotechnology Information (NCBI nr) with a taxonomy of eubacteria. As many as five missed cleavages were allowed. Carbamidomethylation of cysteine was a fixed modification, and methionine oxidation was a variable modification. Highlight at C indicates carbamidomethyl derivative, at Q deamidation and at M oxidation. The peptide error was  $\pm 1.2$  Da and fragment ion error was 0.6 Da. The charge of the precursor ion was allowed to be: +1, +2, +3. The file format output was Mascot generic. GPM search engine parameters were as follows. The precursor ion error was  $\pm 100$  ppm, with the fragment ion mass error of 0.4 Da. Carbamidomethylation of cysteine was a fixed modification, and methionine oxidation was a

variable modification. Similarly, as many as five missed cleavages were allowed. The charge of the precursor ion was +1 to +5.

When necessary, tandem mass spectrometry data was analyzed using commercially available *de novo* sequencing software (PEAKS, Bioinformatics Solutions Inc., Version 4.0). The *de novo* analysis parameters were as follows. The parent ion mass error was  $\pm 0.2$  Da. Fragment ion error was  $\pm 0.2$  Da. A fixed modification of carbamidomethylation of cysteine and a variable modification methionine oxidation were used.

## *Campylobacter coli*

### RM2228 Protein Biomarkers

Mascot-RM2228 hplc#33 gs1

Score: 326 Queries matched: 10

Ribosomal protein L24 [*Campylobacter coli* RM2228]

1 MAVKLIKIK**KGDSVKVITGDDK**GK**TLKVLAVY**PKTLKVVVEGCKIAK**KA**IK  
51 **PSEKNPN**GGF**IN**K**EM**PMDIS**NA**KVQE

Observed Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
317.17	632.32	632.35	-0.03	1	36	2.6	1 K.KGDSVK.V
374.19	746.37	746.38	-0.01	0	49	0.11	1 K.VITGDDK.G
395.24	788.47	788.48	-0.01	0	(27)	23	1 K.VLAVYPK.T
395.68	789.34	788.48	0.86	0	38	1.6	1 K.VLAVYPK.T
450.76	899.51	899.54	-0.03	1	48	0.16	1 K.KAIKPSEK.N
466.75	931.48	931.50	-0.02	1	49	0.13	1 K.VITGDDK.GK.T
480.72	959.42	959.48	-0.06	0	44	0.35	1 K.NPNNGGFINK.E
960.49	959.48	959.48	-0.00	0	(41)	0.84	1 K.NPNNGGFINK.E
633.76	1265.51	1265.56	-0.05	0	26	16	1 K.EMPMDISNAK.V + 2 Oxidation (M)
571.97	1712.88	1712.92	-0.04	1	37	1.9	1 K.AIKPSEKNPNNGGFINK.E

GPM-RM2228 hplc#33 gs1

$\log(e) = -37.7$

RM2228 rplX [50S ribosomal protein L24]

1 MAVKLIKIKKGDSVKVITGDDK**GKTLKVLAVY**PKTLK**VVVEGCKIAKKA**IK**PSEKNPN**GGF 60  
61 **IN**K**EM**PMDIS**NA**KVQE 77

spectrum	log(e)	log(I)	m+h	delta	z	sequence
29.1	-2.6	4.59	789.488	-0.032	2	ktgk <sup>27</sup> VLAVYPK <sup>33</sup> tlkv
14.1	-1.4	4.23	790.402	-0.049	2	ktlk <sup>37</sup> VVVEGK <sup>43</sup> iakk
18.1	-1.2	3.82	900.552	-0.034	2	kiak <sup>47</sup> KAIKPSEK <sup>54</sup> npng
28.1	-2.5	3.31	1713.930	-0.048	3	iakk <sup>48</sup> AIKPSEKNPNGGFINK <sup>63</sup> empm
26.1	-2.1	3.08	846.448	-0.017	2	sekn <sup>56</sup> PNGGFINK <sup>63</sup> empm
20.1	-1.0	4.16	1266.582	-0.073	2	fink <sup>64</sup> EMPMDISNVAK <sup>74</sup> vqe]
21.1	-1.8	2.84	990.499	-0.034	2	nkem <sup>66</sup> PMDISNVAK <sup>74</sup> vqe]

Mascot-RM2228 hplc#54 gs1

Score: 314 Queries matched: 11

Probable Periplasmic Cytochrome C Cj1153 [Campylobacter coli RM2228]

1 MKKLLVVSALACLGVSFAADGATLFKKCAVCHGAK**ADKVYLNKVPALKS**

51 **ISSAERLQYMK**EYSEGKR**NAYGQGAIMKINLK**GLTEEDFK**AIEAYIETL**

Observed Mr(expt)	Mr(calc)	Delta	MissScore	Expect	Rank	Peptide
264.17	526.32	526.35	-0.03	0	24	2.3 1 K.VPALK.S
318.68	635.34	635.36	-0.02	0	19	1e+002 4 K.VYLNK.V
356.65	711.28	711.31	-0.03	0	15	1.3e+002 6 K.EYSEGK.R
375.17	748.33	748.37	-0.04	0	21	64 7 K.SISSAER.L
434.70	867.38	867.41	-0.03	1	40	0.61 1 K.EYSEGKR.N
469.72	937.42	937.44	-0.02	0	35	2.2 1 K.GLTEEDFK.A
475.75	949.49	949.52	-0.03	1	43	0.39 1 K.ADKVYLNK.V
511.75	1021.49	1021.53	-0.04	0	25	25 6 K.AIEAYIETL.-
534.75	1067.48	1067.51	-0.03	0	20	70 5 R.NAYGQGAIMK.I + Oxidation (M)
382.23	1143.66	1143.70	-0.04	1	43	0.52 1 K.VYLNKVPALK.S
486.94	1457.81	1457.86	-0.06	2	29	12 1 K.ADKVYLNKVPALK.S

GPM-RM2228 hplc#54 gs1

log(e) = -12.0

RM\_2228\_Cc1095\_[Cytochrome-  
 related\_conserved\_hypothetical\_protein,\_similar\_to\_C.\_jejunii\_CJ1153]

1 MKKLLVVSALACLGVSFAFA**ADGATLFK**KCAVCHGAK**ADKVYLNKVPALK**SISSAERLQYM 60  
 61 **KEYSEGKR**NAYGQGAIMKINLK**GLTEEDFK**AIEAYIETL 99

spectrum	log(e)	log(I)	m+h	delta	z	sequence
32.1	-2.3	3.19	822.437	-0.029	2	safa <sup>20</sup> ADGATLFK <sup>27</sup> kcaV
33.1	-2.5	2.58	1458.869	-0.051	3	hgak <sup>37</sup> ADKVYLNKVPALK <sup>49</sup> sisS
29.1	-1.8	3.36	938.448	-0.033	2	inlk <sup>83</sup> GLTEEDFK <sup>90</sup> aiea

Mascot-RM2228 hplc#69 gs1

Score: 590 Queries matched: 20

Thioredoxin [*Campylobacter coli* RM2228]

1 MGKYIELTSDNFAQAKEGVALVDFWAPWCGPCRMLAPVIDELANDFDGKA  
 51 KICKVNTDEQGDLAAEFGVRSIPTLIFFKNGEVVDQLVGAQSKQAISDKL  
 101 NSLL

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
559.29	558.28	558.34	-0.06	0	12	5.1e+002	9	K.LNSLL.-
310.17	618.32	618.35	-0.03	1	20	1e+002	8	K.AKICK.V
331.17	660.32	660.34	-0.03	0	35	3.8	1	K.QAISDK.L
533.29	1064.57	1064.63	-0.05	0	(32)	5.3	1	R.SIPTLIFFK.N
533.30	1064.59	1064.63	-0.03	0	37	1.7	1	R.SIPTLIFFK.N
533.31	1064.61	1064.63	-0.01	0	(31)	6.3	1	R.SIPTLIFFK.N
601.30	1200.58	1200.67	-0.09	1	(15)	3e+002	7	K.QAISDKLNSLL.-
1201.65	1200.64	1200.67	-0.03	1	34	3.6	2	K.QAISDKLNSLL.-
722.34	1442.67	1442.74	-0.07	0	71	0.00071	1	K.NGEVVDQLVGAQSK.Q
481.91	1442.71	1442.74	-0.03	0	(30)	8.9	1	K.NGEVVDQLVGAQSK.Q
750.32	1498.62	1498.73	-0.11	0	62	0.0055	1	K.YIELTSDNFAQAK.E
750.70	1499.39	1498.73	0.66	0	(57)	0.013	1	K.YIELTSDNFAQAK.E
562.26	1683.77	1683.85	-0.08	1	58	0.014	1	M.GKYIELTSDNFAQAK.E
860.86	1719.70	1719.81	-0.11	0	75	0.00024	1	K.VNTDEQGDLAAEFGVRS
582.94	1745.78	1746.85	-1.07	0	(53)	0.046	1	R.MLAPVIDELANDFDGK.A
882.40	1762.79	1762.84	-0.06	0	(70)	0.00082	1	R.MLAPVIDELANDFDGK.A + Oxidation (M)
588.70	1763.08	1762.84	0.23	0	(57)	0.017	1	R.MLAPVIDELANDFDGK.A + Oxidation (M)
882.90	1763.79	1762.84	0.95	0	77	0.00017	1	R.MLAPVIDELANDFDGK.A + Oxidation (M)
654.98	1961.92	1961.98	-0.06	1	49	0.098	1	R.MLAPVIDELANDFDGKAK.I + Oxidation (M)
1010.44	2018.86	2018.91	-0.05	0	61	0.0064	1	K.EGVALVDFWAPWCGPCR.M

GPM-RM2228 hplc#69 gs1

log(e) = -61.8

RM2228 trx [Thioredoxin]

1 MGKYIELTSDNFAQAKEGVALVDFWAPWCGPCRMLAPVIDELANDFDGKAKICKVNTDEQ 60  
 61 GDLAAEFGVRSIPTLIFFKNGEVVDQLVGAQSKQAISDKLNSSL 104

spectrum	log(e)	log(I)	m+h	delta	z	sequence
42.1	-1.3	3.51	1684.855	-0.079	3	[m <sup>2</sup> GKYIELTSDNFAQAK <sup>16</sup> egva
63.1	-4.8	2.81	1499.739	0.653	2	[mgk <sup>4</sup> YIELTSDNFAQAK <sup>16</sup> egva
70.1	-4.5	2.71	1499.739	0.353	2	[mgk <sup>4</sup> YIELTSDNFAQAK <sup>16</sup> egva
46.1	-2.5	3.28	1499.739	-0.040	2	[mgk <sup>4</sup> YIELTSDNFAQAK <sup>16</sup> egva
44.1	-2.4	4.31	1499.739	-0.103	2	[mgk <sup>4</sup> YIELTSDNFAQAK <sup>16</sup> egva
60.1	-4.4	3.41	2019.898	-0.032	2	aqak <sup>17</sup> EGVALVDFWAPWCGPCR <sup>33</sup> m lap
32.1	-2.1	2.39	1003.402	-0.014	2	vdw <sup>26</sup> APWCGPCR <sup>33</sup> m lap
51.1	-3.2	2.82	1962.990	-0.065	3	gpcr <sup>34</sup> MLAPVIDELANDFDGKAK <sup>51</sup> ickv
80.1	-3.6	2.74	1763.858	-0.073	3	gpcr <sup>34</sup> MLAPVIDELANDFDGK <sup>49</sup> akic
71.1	-3.3	3.07	1763.858	0.941	2	gpcr <sup>34</sup> MLAPVIDELANDFDGK <sup>49</sup> akic
58.1	-3.1	4.79	1763.858	-0.062	2	gpcr <sup>34</sup> MLAPVIDELANDFDGK <sup>49</sup> akic
45.1	-5.2	4.24	1720.815	-0.117	2	kick <sup>55</sup> VNTDEQGDLAAEFGVVR <sup>70</sup> sipt
47.1	-4.9	3.20	1720.815	-0.057	2	kick <sup>55</sup> VNTDEQGDLAAEFGVVR <sup>70</sup> sipt
61.1	-2.3	3.12	1065.635	0.470	2	fgvr <sup>71</sup> SIPTLIFFK <sup>79</sup> ngev
55.1	-2.2	4.54	1065.635	-0.055	2	fgvr <sup>71</sup> SIPTLIFFK <sup>79</sup> ngev
87.1	-2.0	2.54	1065.635	0.231	2	fgvr <sup>71</sup> SIPTLIFFK <sup>79</sup> ngev
56.1	-1.6	4.29	865.519	0.305	2	vrsi <sup>73</sup> PTLIFFK <sup>79</sup> ngev
67.1	-1.2	2.85	865.519	0.359	2	vrsi <sup>73</sup> PTLIFFK <sup>79</sup> ngev
54.1	-1.1	4.61	865.519	-0.040	2	vrsi <sup>73</sup> PTLIFFK <sup>79</sup> ngev
38.1	-2.1	4.53	1443.745	-0.069	2	iffk <sup>80</sup> NGEVVDQLVGAQSK <sup>93</sup> qais

Mascot-RM2228 hplc#70 gs1

Score: 48 Queries matched: 2

Chaperonin, 10 kDa [*Campylobacter coli* RM2228]

1 MNFQPLGKRVLVKRVEETKTTASGIIPDNAK**EKPLMGEVAVSK**EITDI  
 51 ANGDKIVFAKYGGTEIKIDNSEYLVNLDDILGILK

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
307.71	613.41	613.43	-0.01	1	24	25	1	R.VLVKR.V
468.25	1401.73	1401.75	-0.03	0	26	23	1	K.EKPLMGEVAVSK.E + Oxidation (M)

### GPM-RM2228 hplc#70 gs1

log(e) = -1.7

RM\_2228\_groES\_[10\_kD\_chaperonin\_(cpn10)\_]

1 MNFQPLGKRVLVKRVVEETKTTASGIIIPDNAK**EKPLMGEVVAVSK**EITDIANGDKIVFAK 60  
 61 YGGTEIKIDNSEYLVNLDDILGILK 86

spectrum	log(e)	log(I)	m+h	delta	z	sequence
19.1	-1.7	1.96	1402.767	-0.045	3	dnak <sup>33</sup> <b>EKPLMGEVVAVSK</b> <sup>45</sup> eidt

### Mascot-RM2228 hplc#70 gs2

Score: 1399 Queries matched: 35

Ribosomal protein L7/L12 [Campylobacter coli RM2228]

1 **MAISKEDVLEFISNLSVLELSELVKEFEKFGVSAAPVMVAGGAAAGGAA**  
 51 **AAAEKTEFDIVLVDGGAKKIEVIKIVRALTGLGLKEAKDAVEQTPSTLK**  
 101 **EGVAKADAEAAKQLEEAGAKVELK**

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
503.27	502.26	502.28	-0.01	0	35	0.77	1	K.EGVAK.A
301.18	600.35	600.38	-0.04	0	30	11	1	K.IEVIK.I
365.21	728.40	728.48	-0.08	1	(41)	0.94	1	K.KIEVIK.I
729.44	728.43	728.48	-0.05	1	46	0.28	1	K.KIEVIK.I
367.16	732.31	732.33	-0.02	0	33	5	1	K.ADAEEAK.K
386.72	771.43	771.49	-0.06	0	55	0.034	1	R.ALTGLGLK.E
423.19	844.37	844.43	-0.06	0	33	5.4	2	K.QLEEAGAK.V
431.20	860.39	860.42	-0.04	1	54	0.041	1	K.ADAEEAKK.Q
487.25	972.48	972.52	-0.04	1	66	0.0028	1	K.KLEEAGAK.V
366.57	1096.70	1096.73	-0.04	2	24	31	3	K.KIEVIKIV.RA
550.80	1099.59	1099.66	-0.07	1	64	0.0035	1	R.ALTGLGLKEAK.D
594.76	1187.50	1187.60	-0.10	0	49	0.12	1	K.DAVEQTPSTLK.E
657.84	1313.66	1313.72	-0.06	1	67	0.0019	1	K.QLEEAGAKVELK.-
438.91	1313.70	1313.72	-0.02	1	(27)	20	7	K.QLEEAGAKVELK.-
673.33	1344.64	1344.69	-0.05	2	61	0.0073	1	K.EGVAKADAEAAKQ
682.31	1362.60	1362.70	-0.10	0	(65)	0.0024	1	K.TEFDIVLVDGGAK.K
1363.66	1362.65	1362.70	-0.05	0	73	0.00047	1	K.TEFDIVLVDGGAK.K
481.59	1441.74	1441.81	-0.08	2	58	0.013	1	K.KQLEEAGAKVELK.-
497.92	1490.75	1490.80	-0.05	1	56	0.02	1	K.TEFDIVLVDGGAK.I
758.86	1515.71	1515.78	-0.06	1	68	0.0014	1	K.EAKDAVEQTPSTLK.E
558.26	1671.77	1671.87	-0.09	1	55	0.026	1	K.DAVEQTPSTLKEGVAK.A
558.29	1671.84	1671.87	-0.03	1	(26)	24	3	K.DAVEQTPSTLKEGVAK.A
563.25	1686.72	1686.84	-0.12	2	53	0.041	1	K.ADAEEAKKQLEEAGAK.V
563.27	1686.78	1686.84	-0.06	2	(37)	1.6	1	K.ADAEEAKKQLEEAGAK.V
617.72	1850.13	1850.21	-0.08	3	55	0.023	1	K.KIEVIKIVRALTGLGLK.E
667.66	1999.95	2000.04	-0.09	2	53	0.047	1	K.EAKDAVEQTPSTLKEGVAK.A
540.02	2156.04	2156.13	-0.10	3	32	5.8	1	K.ADAEEAKKQLEEAGAKVELK.-

545.58	2178.30	2178.38	-0.08	4	18	1.2e+002	6	K.KIEVIKIVRALTGLGLKEAK.D
749.68	2246.03	2246.10	-0.07	0	37	1.8	1	K.FGVSAAPVMVAGGAAAGGAAAAAEEK.T + Oxidation (M)
759.39	2275.16	2275.22	-0.06	0	35	2.7	1	K.EDVLEFISNLSVLELSELVK.E
892.47	2674.38	2674.47	-0.09	1	68	0.0016	1	M.AISKEDVLEFISNLSVLELSELVK.E
799.71	3194.83	3194.90	-0.07	4	26	21	1	K.TEFDIVLDGGAKKIEVIKIVRALTGLGLK.E
835.16	3336.59	3336.76	-0.17	2	71	0.00078	1	M.AISKEDVLEFISNLSVLELSELVKEFEK.F
1113.56	3337.67	3336.76	0.91	2	(62)	0.0058	1	M.AISKEDVLEFISNLSVLELSELVKEFEK.F
898.92	3591.66	3590.79	0.87	1	25	29	1	K.FGVSAAPVMVAGGAAAGGAAAAAEEKTEFDIVLDGGAK.K + Oxidation (M)

### GPM-RM2228 hplc#70 gs2

log(e) = -104.0 RM\_2228\_rplL\_[50S\_ribosomal\_protein\_L7/L12\_]
   
1 MAISKEDVLEFISNLSVLELSELVKEFEKFGVSAAPVMVAGGAAAGGAAAAAEEKTEFD 60
   
61 IVLVDGGAKKIEVIKIVRALTGLGLKEAKDAVEQTPSTLKEGVAKADAEAAKQLEEAGA 120
   
121 KVELK 125

spectrum	log(e)	log(I)	m+h	delta	z	sequence
60.1	-1.3	3.71	3337.767	-0.146	4	[m <sup>2</sup> AISKEDVLEFISNLSVLELSELVKEFEK <sup>30</sup> fgvs
57.1	-3.4	3.45	2675.476	-0.097	3	[m <sup>2</sup> AISKEDVLEFISNLSVLELSELVK <sup>25</sup> efee
38.1	-3.6	2.67	2247.114	-0.076	3	feek <sup>31</sup> FGVSAAPVMVAGGAAAGGAAAAAEEK <sup>56</sup> tefd
33.1	-4.2	2.96	1491.807	-0.061	3	aEEK <sup>57</sup> TEFDIVLDGGAKK <sup>70</sup> ievi
35.1	-4.4	4.33	1363.712	-0.096	2	aEEK <sup>57</sup> TEFDIVLDGGAKK <sup>69</sup> kiev
83.1	-3.2	2.75	1363.712	0.281	2	aEEK <sup>57</sup> TEFDIVLDGGAKK <sup>69</sup> kiev
46.1	-1.2	2.53	1851.217	-0.072	3	ggak <sup>70</sup> KIEVIKIVRALTGLGLK <sup>86</sup> eakd
26.1	-2.3	3.35	1100.668	-0.063	2	kiVR <sup>79</sup> ALTGLGLKEAK <sup>89</sup> dave
20.1	-2.9	3.45	2001.051	-0.094	3	lgIk <sup>87</sup> EAKDAVEQTPSTLKEGVAK <sup>105</sup> adae
14.1	-5.9	3.58	1516.786	-0.066	2	lgIk <sup>87</sup> EAKDAVEQTPSTLK <sup>100</sup> egva
16.1	-3.0	4.10	1672.876	-0.106	3	keak <sup>90</sup> DAVEQTPSTLKEGVAK <sup>105</sup> adae
13.1	-1.6	4.40	1188.612	-0.111	2	keak <sup>90</sup> DAVEQTPSTLK <sup>100</sup> egva
12.1	-1.9	3.04	1345.697	-0.054	2	stIk <sup>101</sup> EGVAKADAEAAK <sup>113</sup> qlee
18.1	-4.1	4.01	1687.851	-0.113	3	gvak <sup>106</sup> ADAEAAKQLEEAGAK <sup>121</sup> velk]
39.1	-1.2	2.37	1687.851	-0.057	3	gvak <sup>106</sup> ADAEAAKQLEEAGAK <sup>121</sup> velk]
7.1	-1.9	3.95	861.432	-0.031	2	gvak <sup>106</sup> ADAEAAK <sup>113</sup> qlee
27.1	-3.0	4.00	1297.712	-0.090	2	eakk <sup>114</sup> QLEEAGAKVELK <sup>125</sup> ]
23.1	-2.6	3.85	1314.728	-0.065	2	eakk <sup>114</sup> QLEEAGAKVELK <sup>125</sup> ]
36.1	-1.7	2.85	1297.712	-0.046	2	eakk <sup>114</sup> QLEEAGAKVELK <sup>125</sup> ]
24.1	-1.3	3.55	1297.712	-1.049	3	eakk <sup>114</sup> QLEEAGAKVELK <sup>125</sup> ]
8.1	-2.6	4.21	828.421	-1.025	2	eakk <sup>114</sup> QLEEAGAK <sup>121</sup> velk]



## RM1051 Protein Biomarkers

Mascot-RM1051 hplc#40 gs2

Score: 305 Queries matched: 6

Protein of unknown function (DUF465) family [*Campylobacter coli* RM2228]

1 MLHEYRELMSELK GKDAHFDKLFER **HNELDDQIKDAEEGRNLLSDIEISN**

51 **LKKEKLHIKDQLNQYLANYKK**

Observed Mr(expt)	Mr(calc)	DeltaMissScore	Expect	Rank	Peptide
556.29	1110.57	1110.53	0.04	0	60 0.0081 1 R.HNELDDQIK.D
679.91	1357.80	1357.75	0.05	0	46 0.24 1 R.NLLSDIEISNLK.K
685.36	1368.70	1368.67	0.03	0	42 0.59 1 K.DQLNQYLANYK.K
496.31	1485.90	1485.84	0.06	1	61 0.0077 1 R.NLLSDIEISNLK.K.E
590.29	1767.86	1767.80	0.06	1	65 0.0026 1 R.HNELDDQIKDAEEGR.N
621.02	1860.03	1859.99	0.05	1	32 6 1 K.LHIKDQLNQYLANYK.K

GPM-RM1051 hplc#40 gs2

log(e) = -31.0 RM2228 Cc0466 [Conserved hypothetical protein, similar to *C. jejuni* CJ0449]

1 MLHEYRELMSELK GKDAHFDKLFER **HNELDDQIKDAEEGRNLLSDIEISNLKKEKLHIKD** 60  
61 **QLNQYLANYKK** 71

spectrum	log(e)	log(I)	m+h	delta	z	sequence
25.1	-8.1	2.42	1768.811	0.064	3	lfer <sup>26</sup> <b>HNELDDQIKDAEEGR</b> <sup>40</sup> nlls
22.1	-3.1	2.57	1111.539	0.044	2	lfer <sup>26</sup> <b>HNELDDQIK</b> <sup>34</sup> daee
37.1	-1.2	2.29	1486.849	0.046	3	eegr <sup>41</sup> <b>NLLSDIEISNLK</b> <sup>53</sup> eklh
42.1	-1.3	2.57	1358.754	0.055	2	eegr <sup>41</sup> <b>NLLSDIEISNLK</b> <sup>52</sup> kekl
38.1	-1.7	2.23	1259.722	0.040	2	grn <sup>43</sup> <b>LSDIEISNLK</b> <sup>53</sup> eklh

Mascot-RM1051 hplc#40 gs2 060207

Score: 75 Queries matched: 3

Ribosomal protein S16 [*Campylobacter coli* RM2228]

1 **MTVIRLTRMGRTKRPFYRIVVTD**SRKRRDGGWIESIGYYNPMVEPEVVKF

51 **DSERLAYWKSVGAKLSDKVASIT**SK

ObservedMr(expt)	Mr(calc)	DeltaMissScore	Expect	Rank	Peptide
318.19	634.37	634.35	0.02	0	16 2.5e+002 2 -.MTVIR.L + Oxidation (M)

353.22 704.44 704.41 0.03 0 34 3.4 1 K.VASITSK.-  
 395.74 789.46 788.44 1.02 0 25 29 2 R.IVVTDSR.K

GPM-RM1051 hplc#40 gs3

log(e) = -60.5

RM2228 rpsS [30S ribosomal protein S19]

1 MARSLK**KGPFVDDHVMKK**VIAAK**KANDNKPIK**TWSR**RSTIIPDMIGLTFNVHNGK**SFIPV 60  
 61 **YITENHIGYKLGEFAPTR**TFKGHKGSVQKKIGK 93

spectrum	log(e)	log(I)	m+h	delta	z	sequence
24.1	-1.3	3.77	1416.737	0.041	3	rslk <sup>7</sup> <b>KGPFVDDHVM</b> <b>KK</b> <sup>18</sup> viaa
15.1	-1.9	2.77	1027.591	0.038	2	iaak <sup>24</sup> <b>KANDNKPIK</b> <sup>32</sup> twsr
17.1	-1.4	3.79	1027.591	-0.002	3	iaak <sup>24</sup> <b>KANDNKPIK</b> <sup>32</sup> twsr
13.1	-4.8	3.36	899.496	0.009	2	aakk <sup>25</sup> <b>ANDNKPIK</b> <sup>32</sup> twsr
36.1	-6.9	3.25	2129.124	0.072	3	twsr <sup>37</sup> <b>RSTIIPDM</b> <b>I</b> <b>IGLTFNVHNGK</b> <sup>55</sup> sfip
37.1	-3.4	3.64	1973.022	0.062	3	wrrr <sup>38</sup> <b>STIIPDM</b> <b>I</b> <b>IGLTFNVHNGK</b> <sup>55</sup> sfip
35.1	-5.8	2.69	1558.774	0.055	3	stii <sup>42</sup> <b>PDM</b> <b>I</b> <b>IGLTFNVHNGK</b> <sup>55</sup> sfip
38.1	-6.9	3.41	1433.743	0.047	2	ksfi <sup>59</sup> <b>PVYITENHIGYK</b> <sup>70</sup> lgef
29.1	-2.6	4.04	890.474	0.011	2	igyk <sup>71</sup> <b>LGEFAPTR</b> <sup>78</sup> tfkg
49.1	-1.4	2.30	890.474	0.034	2	igyk <sup>71</sup> <b>LGEFAPTR</b> <sup>78</sup> tfkg

Mascot-RM1051 hplc#40 gs3

Score: 492 Queries matched: 13

Ribosomal protein S19 [Campylobacter coli RM2228]

1 MARSLK**KGPFVDDHVMKK**VIAAK**KANDNKPIK**TWSR**RSTIIPDMIGLTFN**  
 51 **VHNGKSFI****PVYITENHIGYKLGEFAPTR**TFKGHK**GSVQKKIGK**

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
251.18	500.34	500.33	0.01	0	35	0.51	1	K.VIAAK.K
315.23	628.45	628.43	0.02	1	44	0.38	1	K.KVIAAK.K
323.71	645.40	645.38	0.02	1	19	1.6e+002	1	K.GSVQKK.I
445.75	889.48	889.47	0.01	0	(45)	0.27	1	K.LGEFAPTR.T
445.76	889.50	889.47	0.03	0	68	0.0016	1	K.LGEFAPTR.T
450.26	898.50	898.49	0.01	0	58	0.013	1	K.ANDNKPIK.T
343.20	1026.58	1026.58	0.00	1	(27)	18	1	K.KANDNKPIK.T
514.31	1026.61	1026.58	0.03	1	48	0.12	1	K.KANDNKPIK.T
644.85	1287.68	1287.63	0.06	1	21	70	1	K.GPFVDDHVMKK.V + Oxidation (M)
472.93	1415.78	1415.72	0.06	2	21	65	1	K.KGPFVDDHVMKK.V + Oxidation (M)
594.34	1780.00	1779.92	0.08	0	38	1.5	1	K.SFIPVYITENHIGYK.L

658.37 1972.08 1972.01 0.07 0 65 0.0026 1 R.STIIPDMIGLTFNVHNGK.S + Oxidation (M)  
 710.40 2128.19 2128.11 0.08 1 79 0.00011 1 R.RSTIIPDMIGLTFNVHNGK.S + Oxidation (M)

Mascot-RM1051 hplc#44 gs1 060207

Score: 250 Queries matched: 8

phnA protein [*Campylobacter coli* RM2228]

1 MPK DANGTELNAGDSVSM I KDLK VKGASTTLKRGTTIKNIKLTSKENEIE  
 51 AKVDFKFGVIVLKTEFLK KI

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
519.32	518.31	518.31	0.01	0	12	1.8e+002	1	R.GTTIK.N
319.18	636.34	636.35	-0.01	0	27	13	2	K.TEFLK.K
338.67	675.32	676.38	-1.06	0	30	9.1	1	K.GASTTLK.R
388.24	774.47	774.50	-0.03	0	45	0.33	1	K.FGVIVLK.T
416.70	831.39	831.40	-0.01	0	30	11	1	K.ENEIEAK.V
452.78	903.54	903.54	-0.00	1	36	2.3	1	K.VKGASTTLK.R
373.23	1116.67	1116.69	-0.02	1	38	1.4	1	K.VDKFGVIVLK.T
421.23	1260.66	1260.66	0.01	1	39	1.2	1	K.LTSKENEIEAK.V

GPM-RM1051 hplc#44 gs1 060207

log(e) = -11.1

RM\_2228\_Cc1532\_[Conserved\_hypothetical\_protein,\_PhnA-  
 like\_protein,\_similar\_to\_C.\_jejuni\_CJ0185]

1 MPK DANGTELNAGDSVSM I KDLK VVKGASTTLKRGTTIKNIKLTSKENEIE 50  
 51 AKVDFKFGVIVLKTEFLK KI 69

spectrum	log(e)	log(I)	m+h	delta	z	sequence
41.1	-2.2	3.30	1117.699	-0.013	3	ieak <sup>53</sup> VDFKFGVIVLK <sup>62</sup> tefl
44.1	-1.9	4.03	775.509	-0.032	2	kvdk <sup>56</sup> FGVIVLK <sup>62</sup> tefl
47.1	-1.2	2.77	775.509	-0.006	2	kvdk <sup>56</sup> FGVIVLK <sup>62</sup> tefl
29.1	-1.3	3.89	637.357	-0.017	2	ivlk <sup>63</sup> TEFLK <sup>67</sup> ki]

"Composite" Sequence Analysis by GPM of RM1051 hplc#44 gs1 060207

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log(e) = -18.2

Composite\_RM1051\_Cc1532\_[RM2228\_CjjHB93\_13\_Conserved\_hypothetical\_protein,  
 \_PhnA-like\_protein,\_similar\_to\_C.\_jejuni\_CJ0185]

1 MPK**DANGTELNAGDSVSVIK**DLKVKGASTTLKRGTTIKNIKLTSKENEIE 50  
 51 AK**VDKFGVIVLKTEFLK**KI 69

spectrum	log(e)	log(I)	m+h	delta	z	sequence
33.1	-2.9	3.14	1689.830	-0.012	2	[mpk <sup>4</sup> <b>DANGTELNAGDSVSVIK</b> <sup>20</sup> dlkv
41.1	-2.2	3.30	1117.699	-0.013	3	ieak <sup>53</sup> <b>VDKFGVIVLK</b> <sup>62</sup> tefl
44.1	-1.9	4.03	775.509	-0.032	2	kvdk <sup>56</sup> <b>FGVIVLK</b> <sup>62</sup> tefl
47.1	-1.2	2.77	775.509	-0.006	2	kvdk <sup>56</sup> <b>FGVIVLK</b> <sup>62</sup> tefl
29.1	-1.3	3.89	637.357	-0.017	2	ivlk <sup>63</sup> <b>TEFLK</b> <sup>67</sup> ki]

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Mascot-RM1051 hplc#44 gs1 060207

Score: 242 Queries matched: 7

Conserved Domain Protein [*Campylobacter jejuni* subsp. *jejuni* HB93-13]

1 MA**K**DANGTELNAGDSV**S**VI**K**DLK**V**KGASTTLK**R**GTT**I**KNIKLTSKE**G**EIE  
 51 AR**V**DKFGVIVLK**T**EFL**K**KI

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
519.32	518.31	518.31	0.01	0	12	1.8e+002	1	R.GTTIK.N
319.18	636.34	636.35	-0.01	0	27	13	2	K.TEFLK.K
338.67	675.32	676.38	-1.06	0	30	9.1	1	K.GASTTLK.R
388.24	774.47	774.50	-0.03	0	45	0.33	1	K.FGVIVLK.T
452.78	903.54	903.54	-0.00	1	36	2.3	1	K.VKGASTTLK.R
373.23	1116.67	1116.69	-0.02	1	38	1.4	1	R.VDKFGVIVLK.T
845.41	1688.80	1688.82	-0.02	0	58	0.013	1	K.DANGTELNAGDSVSVIK.D

Mascot-RM1051\_hplc#46\_gs2\_060207

Score: 632 Queries matched: 17

Ribosomal protein S15 [*Campylobacter coli* RM2228]

1 MALDSAKKAEIVAK**F**AR**K**AGDTG**S**TEVQ**V**ALL**S**AR**I**TELTEHLKI**Y**K**D**FD  
 51 **S**SRLGLLKL**V**GQR**K**RL**L**AYL**K**R**K**D**Y**NS**S**KL**I**TEL**N**LR**D**K

Observed Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
272.21	542.40	542.38	0.02	0	31	3	1 R.LGLLK.L
302.69	603.36	603.32	0.03	0	37	2	1 M.ALDSAK.K
315.71	629.41	629.37	0.04	0	33	6.2	1 K.AEIVAK.F
360.75	719.49	719.46	0.03	0	44	0.4	1 R.LLAYLK.R
360.76	719.51	719.46	0.05	0	(29)	10	1 R.LLAYLK.R
370.21	738.41	738.37	0.04	1	27	9.8	1 K.KDFSSR.L
379.75	757.49	757.47	0.02	1	48	0.16	1 K.KAEIVAK.F
379.77	757.52	757.47	0.05	1	(24)	43	1 K.KAEIVAK.F
438.71	875.41	875.37	0.05	0	41	0.68	1 K.DYNSYSK.L
486.31	970.60	970.58	0.02	0	61	0.007	1 K.LITELNLR.D
502.76	1003.51	1003.46	0.05	1	50	0.093	1 R.KDYNSYSK.L
548.89	1095.77	1095.71	0.06	1	58	0.0093	1 R.LGLLKLVGQR.K
387.55	1159.62	1159.56	0.06	2	21	69	1 K.RKDYNSYSK.L
448.63	1342.87	1342.78	0.08	2	46	0.22	1 M.ALDSAKKAEIVAK.F
837.98	1673.95	1673.86	0.09	0	92	5.6e-006	1 K.AGDTGSTEVQVALLSAR.I
601.68	1802.03	1801.95	0.08	1	52	0.059	1 R.KAGDTGSTEVQVALLSAR.I
601.69	1802.06	1801.95	0.11	1	(48)	0.13	1 R.KAGDTGSTEVQVALLSAR.I

GPM-RM1051\_hplc#46\_gs2\_060207

log(e) = -71.2

RM2228 rpsO [30S ribosomal protein S15]

1 MALDSAKKAEIVAKFARKAGDTGSTEVQVALLSARITELTEHLKIYKKDF 50  
 51 SSR LGLLKLVGQRKRL LAYLK R KDYNSYSK LI TELNLRDK 90

spectrum	log(e)	log(I)	m+h	delta	z	sequence
26.1	-6.5	3.12	1343.790	0.070	3	[m <sup>2</sup> ALDSAKKAEIVAK <sup>14</sup> fark
5.1	-4.0	2.77	604.331	0.029	2	[m <sup>2</sup> ALDSAK <sup>7</sup> kaei
28.1	-2.4	2.82	1159.669	0.053	2	[mal <sup>4</sup> DSAKKAEIVAK <sup>14</sup> fark
22.1	-2.1	4.32	758.478	0.022	2	dsak <sup>8</sup> KAEIVAK <sup>14</sup> fark
42.1	-4.9	3.90	1802.962	0.057	3	kfar <sup>18</sup> KAGDTGSTEVQVALLSAR <sup>35</sup> itel
92.1	-3.2	2.07	1802.962	0.108	3	kfar <sup>18</sup> KAGDTGSTEVQVALLSAR <sup>35</sup> itel
45.1	-6.3	2.53	1674.867	0.089	2	fark <sup>19</sup> AGDTGSTEVQVALLSAR <sup>35</sup> itel
47.1	-3.7	2.74	1096.721	0.055	2	fssr <sup>54</sup> LGLLKLVGQR <sup>63</sup> krll
19.1	-1.7	3.03	1160.570	0.048	3	aylk <sup>72</sup> RKDYNSYSK <sup>80</sup> lite
14.1	-2.4	2.48	1004.469	0.053	2	ylkr <sup>73</sup> KDYNSYSK <sup>80</sup> lite
50.1	-1.3	2.45	745.421	0.046	1	skli <sup>83</sup> TELNLR <sup>88</sup> dk]

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"Composite" Sequence Analysis by GPM of RM1051\_hplc#46\_gs2\_060207

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**log(e) = -87.5      "Composite" RM1051 rpsO [RM2228 & RM1221 30S ribosomal protein S15]**

1 MALDSAKKAEIVAKFARKAGDTGSTE<sup>V</sup>QVALLSARIAELTEHLK<sup>I</sup>YKKDF 50  
 51 SSR<sup>L</sup>GLLKLVGQRKRL<sup>L</sup>LAYLK<sup>R</sup>KDYNSYSK<sup>L</sup>I<sup>T</sup>ELNLRDK 90

spectrum	log(e)	log(I)	m+h	delta	z	sequence
26.1	-6.6	3.12	1343.790	0.070	3	[m <sup>2</sup> ALDSAKKAEIVAK <sup>14</sup> fark
5.1	-4.0	2.77	604.331	0.029	2	[m <sup>2</sup> ALDSAK <sup>7</sup> kaei
28.1	-2.5	2.82	1159.669	0.053	2	[mal <sup>4</sup> DSAKKAEIVAK <sup>14</sup> fark
22.1	-2.1	4.32	758.478	0.022	2	dsak <sup>8</sup> KAEIVAK <sup>14</sup> fark
42.1	-4.8	3.90	1802.962	0.057	3	kfar <sup>18</sup> KAGDTGSTE <sup>V</sup> QVALLSAR <sup>35</sup> iael
92.1	-3.3	2.07	1802.962	0.108	3	kfar <sup>18</sup> KAGDTGSTE <sup>V</sup> QVALLSAR <sup>35</sup> iael
45.1	-6.4	2.53	1674.867	0.089	2	fark <sup>19</sup> AGDTGSTE <sup>V</sup> QVALLSAR <sup>35</sup> iael
34.1	-2.0	3.53	1053.595	0.047	2	lsar <sup>36</sup> IAELTEHLK <sup>44</sup> iykk
33.1	-4.6	2.89	940.511	0.053	2	sari <sup>37</sup> AELTEHLK <sup>44</sup> iykk
47.1	-3.7	2.74	1096.721	0.055	2	fssr <sup>54</sup> LGLLKL <sup>V</sup> GQR <sup>63</sup> krll
19.1	-1.7	3.03	1160.570	0.048	3	aylk <sup>72</sup> RKDYN <sup>S</sup> YSK <sup>80</sup> lite
14.1	-2.3	2.48	1004.469	0.053	2	ylkr <sup>73</sup> KDYN <sup>S</sup> YSK <sup>80</sup> lite
50.1	-1.3	2.45	745.421	0.046	1	skl <sup>83</sup> TEL <sup>N</sup> LR <sup>88</sup> dk]

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Mascot-RM1051\_hplc#46\_gs2\_060207

Score: 516    Queries matched: 13

Ribosomal protein S15 [*Campylobacter jejuni* RM1221]

1 MALDSAKKAEIVAKFAKK<sup>P</sup>GD<sup>T</sup>GSTE<sup>V</sup>QVALL<sup>T</sup>ARIA<sup>I</sup>ELTEHLK<sup>I</sup>YKKDF  
 51 SSR<sup>L</sup>GLLKLVGQRKRL<sup>L</sup>SYLK<sup>S</sup>RKDYN<sup>S</sup>YSK<sup>L</sup>LITELNLRDK

Observed Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
272.21	542.40	542.38	0.02	0	31	3	R.LGLLK.L
302.69	603.36	603.32	0.03	0	37	2	M.ALDSAK.K
315.71	629.41	629.37	0.04	0	33	6.2	K.AEIVAK.F
370.21	738.41	738.37	0.04	1	27	9.8	K.KDFSSR.L
379.75	757.49	757.47	0.02	1	48	0.16	K.KAEIVAK.F
379.77	757.52	757.47	0.05	1	(24)	43	K.KAEIVAK.F
438.71	875.41	875.37	0.05	0	41	0.68	K.DYNSYSK.L
486.31	970.60	970.58	0.02	0	61	0.007	K.LITELNLR.D
502.76	1003.51	1003.46	0.05	1	50	0.093	R.KDYNSYSK.L
527.32	1052.63	1052.59	0.04	0	61	0.0051	R.IAELTEHLK.I

548.89 1095.77 1095.71 0.06 1 58 0.0093 1 R.LGLLKLVGQR.K  
387.55 1159.62 1159.56 0.06 2 21 69 1 K.RKDYSYSK.L  
448.63 1342.87 1342.78 0.08 2 46 0.22 1 M.ALDSAKKAEIVAK.F

GPM-RM1051\_hplc#46\_gs2\_060207

log(e) = -66.6

RM1221 rpsO [30S ribosomal protein S15]

1 MALDSAKKAEIVAKFAKKPGDTGSTEVEQVALLTARIAELTEHLKIYKKDF 50  
51 SSR LGLLKLVGQRKRLLSYLKRKDYSYSKLI TELNLRDK 90

spectrum	log(e)	log(I)	m+h	delta	z	sequence
26.1	-6.5	3.12	1343.790	0.070	3	[m <sup>2</sup> ALDSAKKAEIVAK <sup>14</sup> fakk
5.1	-4.0	2.77	604.331	0.029	2	[m <sup>2</sup> ALDSAK <sup>7</sup> kaei
28.1	-2.4	2.82	1159.669	0.053	2	[mal <sup>4</sup> DSAKKAEIVAK <sup>14</sup> fakk
22.1	-2.1	4.32	758.478	0.022	2	dsak <sup>8</sup> KAEIVAK <sup>14</sup> fakk
34.1	-2.2	3.53	1053.595	0.047	2	ltar <sup>36</sup> IAELTEHLK <sup>44</sup> iykk
33.1	-4.4	2.89	940.511	0.053	2	tari <sup>37</sup> AELTEHLK <sup>44</sup> iykk
47.1	-3.7	2.74	1096.721	0.055	2	fssr <sup>54</sup> LGLLKLVGQR <sup>63</sup> krll
19.1	-1.7	3.03	1160.570	0.048	3	sylk <sup>72</sup> RKDYSYSK <sup>80</sup> lite
14.1	-2.4	2.48	1004.469	0.053	2	ylkr <sup>73</sup> KDYSYSK <sup>80</sup> lite
50.1	-1.3	2.45	745.421	0.046	1	skli <sup>83</sup> TELNLR <sup>88</sup> dk]

Mascot-RM1051\_hplc#50\_gs1\_060207

Mass: 7030 Score: 230 Queries matched: 7

Ribosomal protein L29 [*Campylobacter coli* RM2228]

1 MKYTEIKDKTAAELATMLKEKVVLLFTLKQKLKTMQLTNPKEISEVRKDI  
51 ARINTAINALK

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
301.69	601.37	601.35	0.02	1	21	1e+002	4	R.KDIAR.I
417.29	832.57	832.54	0.03	0	36	2.7	1	K.VLLFTLK.Q
474.77	947.52	947.47	0.04	0	34	3.6	1	K.TMQLTNPKE + Oxidation (M)
479.30	956.59	956.57	0.03	0	38	1.4	1	R.INTAINALK.-
481.34	960.67	960.64	0.04	1	49	0.12	1	K.KVLLFTLK.Q
391.22	1170.62	1170.60	0.03	2	26	21	4	-.MKYTEIKDK.T + Oxidation (M)
397.24	1188.71	1188.65	0.05	1	25	26	2	K.LKTMQLTNPKE + Oxidation (M)

GPM-RM1051 hplc#50 gs1 060207

log(e) = -5.5

RM2228 rpmC [50S ribosomal protein L29]

1 MKYTEIKDKTAAELATMLKEK**KVLLFTLK**QKLKTMQLTNPKEI SEVRKDIAR**INTAINAL** 60  
 61 **K** 61

spectrum	log(e)	log(I)	m+h	delta	z	Sequence
25.1	-1.1	2.06	961.646	0.030	2	lkek <sup>22</sup> <b>KVLLFTLK</b> <sup>29</sup> qklk
18.1	-1.5	2.71	957.574	0.030	2	diar <sup>53</sup> <b>INTAINAL</b> <sup>61</sup> K

Mascot-RM1051\_hplc#53\_gs1\_060207

Score: 378 Queries matched: 10

nifU protein homolog Cj1639 [*Campylobacter coli* RM2228]

1 **MMPFSDEELINPVKASLDKSMPLERDGGGLEFLGIKNGVVYVHLIGACK**  
 51 **GCASSGTTLYGLER**QLKIDIHPEITIVNLNGGAEDFAKL

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
267.17	532.33	532.29	0.05	0	32	2.6	1	<b>K.ASLDK.S</b>
319.19	636.37	636.32	0.05	0	29	7.5	1	<b>K.YGLER.Q</b>
448.23	894.45	894.39	0.06	0	18	1.2e+002	6	<b>K.SMPMLER.D + 2 Oxidation (M)</b>
491.27	980.53	980.46	0.07	0	34	2.6	1	<b>K.GCASSGTTLY</b>
553.34	1104.66	1104.58	0.08	0	80	9.4e-005	1	<b>R.DGGGLEFLGIK.N</b>
470.60	1408.77	1408.67	0.10	1	34	3.4	1	<b>K.ASLDKSMPLER.D + 2 Oxidation (M)</b>
477.29	1428.86	1428.75	0.11	0	39	1	1	<b>K.NGVVYVHLIGACK.G</b>
841.46	1680.90	1680.77	0.12	0	45	0.25	1	<b>-.MMPFSDEELINPVK.A + 2 Oxidation (M)</b>
732.74	2195.21	2195.05	0.16	1	31	7.1	1	<b>-.MMPFSDEELINPVKASLDK.S + 2 Oxidation (M)</b>
629.88	2515.48	2515.33	0.16	1	36	2.1	1	<b>R.DGGGLEFLGIKNGVVYVHLIGACK.G</b>

GPM-RM1051\_hplc#53\_gs1\_060207

log(e) = -32.7

RM2228 Cc0124 [Cons. hypo. protein, similar to *C. jejuni* CJ1639]

1 **MMPFSDEELINPVKASLDKSMPLERDGGGLEFLGIKNGVVYVHLIGACK** 50  
 51 **GCASSGTTLY**GLERQLKIDIHPEITIVNLNGGAEDFAKL 90



spectrum	log(e)	log(I)	m+h	delta	z	sequence
27.1	-1.6	2.71	1681.792	0.110	2	[ <sup>1</sup> MMPFSDEELINPVK <sup>14</sup> asld
15.1	-1.3	2.50	1409.688	0.078	3	npvk <sup>15</sup> ASLDKSM <sup>26</sup> PMLER <sup>26</sup> dggg
10.1	-1.0	2.63	895.412	0.052	2	sldk <sup>20</sup> SMP <sup>26</sup> PMLER <sup>26</sup> dggg
34.1	-6.5	2.59	1105.590	0.071	2	m <sup>27</sup> ler <sup>27</sup> DGGGLEFLGIK <sup>37</sup> ngvv
25.1	-1.4	2.06	1429.752	0.099	3	lgik <sup>38</sup> NGVVYVHLIGACK <sup>50</sup> gcas
8.1	-1.3	2.17	981.457	0.073	2	gack <sup>51</sup> G <sup>60</sup> CASSGTTLK <sup>60</sup> ygle

Mascot-RM1051\_hplc#56\_gs1\_060210

Score: 42 Queries matched: 1

conserved hypothetical protein [*Campylobacter coli* RM2228]

1 MDKTK**VVENLNALFK**QRAEFYSYFDKNISKVGNTEVFDFSNKDLNAEEV  
 51 YKQFYHLDYAMRKLLPAIYKAYEVSDSDLNRDF

Observed Mr(expt)	Mr(calc)	Delta	MissScore	ExpectRank	Peptide
573.81	1145.61	1145.64	-0.03	0 42 0.54	1 K.VVENLNALFK.Q

Mascot-RM1051\_hplc#69\_gs1\_060210.wiff

Score: 575 Queries matched: 16

Thioredoxin [*Campylobacter jejuni* RM2228]

1 MGKYIELTSDN**FAQAK**EGVALVDFWAPWCGPCR**MLAPVIDELANDFDGKA**  
 51 **KICKVNTDEQGD**LAAEFGVRSIPTLIFFKNGEVVDQLVGAQSKQAISDKL  
 101 **NSSL**

Observed	Mr(expt)	Mr(calc)	Delta	Miss Score	Expect	Rank	Peptide
559.31	558.30	558.34	-0.04	0	11	6.2e+002	9 K.LNSLL.-
310.17	618.32	618.35	-0.03	1	20	90	9 K.AKICK.V
331.16	660.30	660.34	-0.04	0	43	0.59	1 K.QAISDK.L
533.30	1064.58	1064.63	-0.05	0	(32)	5.2	1 R.SIPTLIFFK.N
533.40	1064.79	1064.63	0.16	0	51	0.044	1 R.SIPTLIFFK.N
601.81	1201.61	1200.67	0.94	1	18	1.3e+002	5 K.QAISDKLNSLL.-
722.34	1442.67	1442.74	-0.07	0	(59)	0.011	1 K.NGEVVDQLVGAQSK.Q

722.35	1442.69	1442.74	-0.05	0	64	0.0033	1	K.NGEVVDQLVGAQSK.Q
750.34	1498.67	1498.73	-0.06	0	78	0.00013	1	K.YIELTSDNFAQAK.E
750.50	1498.99	1498.73	0.26	0	(45)	0.22	1	K.YIELTSDNFAQAK.E
562.25	1683.74	1683.85	-0.11	1	69	0.001	1	M.GKYIELTSDNFAQAK.E
860.87	1719.72	1719.81	-0.08	0	80	8.1e-005	1	K.VNTDEQGDAAEFGVR.S
582.91	1745.72	1746.85	-1.13	0	(41)	0.62	1	R.MLAPVIDELANDFDGK.A
882.37	1762.73	1762.84	-0.11	0	70	0.00075	1	R.MLAPVIDELANDFDGK.A + Oxidation (M)
588.70	1763.08	1762.84	0.23	0	(47)	0.15	1	R.MLAPVIDELANDFDGK.A + Oxidation (M)
654.96	1961.85	1961.98	-0.13	1	69	0.001	1	R.MLAPVIDELANDFDGKAK.I + Oxidation (M)

GPM-RM1051\_hplc#69\_gs1\_060210

log(e) = -51.4

RM\_2228\_trx\_[Thioredoxin]

1 MGKYIELTSDNFAQAKEGVALVDFWAPWCGPCRMLAPVIDELANDFDGKAKICKVNTDEQ 60  
 61 GDAAEFGVRSIPTLIFFKNGEVVDQLVGAQSKQAISDKLNSSL 104

spectrum	log(e)	log(I)	m+h	delta	z	sequence
28.1	-2.7	3.21	1684.855	-0.096	3	[m <sup>2</sup> GKYIELTSDNFAQAK <sup>16</sup> egva
30.1	-1.4	4.41	1499.739	-0.075	2	[mgk <sup>4</sup> YIELTSDNFAQAK <sup>16</sup> egva
40.1	-4.2	3.47	1962.990	-0.117	3	gpcr <sup>34</sup> MLAPVIDELANDFDGKAK <sup>51</sup> ickv
63.1	-6.4	2.77	1763.858	0.894	3	gpcr <sup>34</sup> MLAPVIDELANDFDGK <sup>49</sup> akic
55.1	-1.7	3.02	1763.858	0.134	2	gpcr <sup>34</sup> MLAPVIDELANDFDGK <sup>49</sup> akic
44.1	-1.6	4.33	1763.858	-0.115	2	gpcr <sup>34</sup> MLAPVIDELANDFDGK <sup>49</sup> akic
31.1	-7.3	4.22	1720.815	-0.086	2	kick <sup>55</sup> VNTDEQGDAAEFGVR <sup>70</sup> sipt
42.1	-2.2	4.48	1065.635	-0.063	2	fgvr <sup>71</sup> SIPTLIFFK <sup>79</sup> ngev
26.1	-4.6	4.30	1443.745	-0.076	2	iffk <sup>80</sup> NGEVVDQLVGAQSK <sup>93</sup> qais

Mascot-RM1051\_hplc#70\_gs2\_060210

Score: 879 Queries matched: 23

Ribosomal protein L7/L12 [*Campylobacter coli* RM2228]

1 MAISKEDVLEFISNLSVLELSELVKEFEKFGVSAAPVMVAGGAAAGGAA  
 51 AAEEKTEFDIVLDGGAKKIEVIKIVRALTGLGLKEAKDAVEQTPSTLK  
 101 EGVAKADAEAAKKQLEEAGAKVELK

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
503.27	502.26	502.28	-0.01	0	38	0.4	1	K.EGVAK.A

301.18	600.35	600.38	-0.03	0	28	19	1	K.IEVIK.I
365.22	728.42	728.48	-0.06	1	39	1.3	1	K.KIEVIK.I
367.16	732.30	732.33	-0.03	0	33	4.9	1	K.ADAEEAK.K
386.74	771.46	771.49	-0.02	0	52	0.07	1	R.ALTGLGLK.E
845.39	844.38	844.43	-0.05	0	35	3.2	1	K.QLEEAGAK.V
423.20	844.39	844.43	-0.03	0	(33)	5.7	2	K.QLEEAGAK.V
431.21	860.41	860.42	-0.02	1	52	0.059	1	K.ADAEEAKK.Q
487.24	972.46	972.52	-0.06	1	58	0.015	1	K.KQLEEAGAK.V
594.76	1187.50	1187.60	-0.10	0	(49)	0.11	1	K.DAVEQTPSTLK.E
1188.58	1187.57	1187.60	-0.03	0	51	0.066	1	K.DAVEQTPSTLK.E
682.33	1362.65	1362.70	-0.05	0	79	0.00012	1	K.TEFDIVLVDGGAK.K
617.72	1850.14	1850.21	-0.07	3	50	0.087	1	K.KIEVIKIVRALTGLGLK.E
749.67	2245.99	2246.10	-0.11	0	(37)	1.6	1	K.FGVSAAPVMVAGGAAAGGAAAAAEEK.T + Oxidation (M)
749.69	2246.06	2246.10	-0.04	0	67	0.0019	1	K.FGVSAAPVMVAGGAAAGGAAAAAEEK.T + Oxidation (M)
749.80	2246.38	2246.10	0.28	0	(25)	22	1	K.FGVSAAPVMVAGGAAAGGAAAAAEEK.T + Oxidation (M)
759.38	2275.12	2275.22	-0.10	0	70	0.00092	1	K.EDVLEFISNLSVLELSELVK.E
892.47	2674.37	2674.47	-0.09	1	68	0.0014	1	M.AISKEDVLEFISNLSVLELSELVK.E
669.70	2674.77	2674.47	0.30	1	(32)	3.9	1	M.AISKEDVLEFISNLSVLELSELVK.E
892.60	2674.78	2674.47	0.31	1	(23)	31	1	M.AISKEDVLEFISNLSVLELSELVK.E
669.85	2675.37	2674.47	0.90	1	(37)	1.7	1	M.AISKEDVLEFISNLSVLELSELVK.E
835.43	3337.67	3336.76	0.91	2	65	0.0034	1	M.AISKEDVLEFISNLSVLELSELVKEFEEK.F
898.92	3591.66	3590.79	0.87	1	94	3.3e-006	1	K.FGVSAAPVMVAGGAAAGGAAAAAEEKTEFDIVLVDGGAK.K + Oxidation (M)

GPM-RM1051\_hplc#70\_gs2\_060210

log(e) = -79.1

RM2228 rplL [50S ribosomal protein L7/L12]

1	M	AISKEDVLEFISNLSVLELSELVKEFEEKFGVSAAPVMVAGGAAAGGAAAAAEEKTEFD	60
61	I	VLVDGGAKKIEVIKIVRALTGLGLKEAKDAVEQTPSTLKEGVAKADAEAAKQLEEAGA	120
121	K	VELK	125

spectrum	log(e)	log(I)	m+h	delta	z	sequence
52.1	-2.2	3.05	3337.767	0.888	4	[m <sup>2</sup> AISKEDVLEFISNLSVLELSELVKEFEEK <sup>30</sup> fgvs
48.1	-6.1	3.58	2675.476	-0.101	3	[m <sup>2</sup> AISKEDVLEFISNLSVLELSELVK <sup>25</sup> efee
54.1	-4.1	3.67	2276.229	-0.172	3	aisk <sup>6</sup> EDVLEFISNLSVLELSELVK <sup>25</sup> efee
30.1	-1.3	3.44	3591.806	-0.113	4	feek <sup>31</sup> FGVSAAPVMVAGGAAAGGAAAAAEEKTEFDIVLVDGGAK <sup>69</sup> kiev
28.1	-1.1	3.37	3591.806	0.885	4	feek <sup>31</sup> FGVSAAPVMVAGGAAAGGAAAAAEEKTEFDIVLVDGGAK <sup>69</sup> kiev
20.1	-6.2	3.21	2247.114	-0.059	3	feek <sup>31</sup> FGVSAAPVMVAGGAAAGGAAAAAEEK <sup>56</sup> tefd
27.1	-4.1	4.67	1363.712	-0.052	2	aek <sup>57</sup> TEFDIVLVDGGAK <sup>69</sup> kiev
35.1	-3.5	2.72	1851.217	-0.061	3	ggak <sup>70</sup> KIEVIKIVRALTGLGLK <sup>86</sup> eakd
12.1	-2.1	4.37	1188.612	-0.093	2	keak <sup>90</sup> DAVEQTPSTLK <sup>100</sup> egva
14.1	-1.7	3.04	1002.548	-0.027	2	akda <sup>92</sup> VEQTPSTLK <sup>100</sup> egva
5.1	-2.6	3.96	861.432	-0.026	2	gvak <sup>106</sup> ADAEAAK <sup>113</sup> qlee
4.1	-1.6	3.29	790.395	-0.036	2	vaka <sup>107</sup> DAEAAK <sup>113</sup> qlee
10.1	-1.5	3.64	973.532	-0.070	2	eeak <sup>113</sup> KQLEEAGAK <sup>121</sup> velk]

## RM1865 Protein Biomarkers

Mascot-RM1865\_hplc#42\_gs1\_060213

Mass: 7444    Score: 227    Queries matched: 6

conserved domain protein [*Campylobacter jejuni* subsp. *jejuni* HB93-13]

1    MAK**DANGTELNAGDSVSVIK**DLKVK**GASTTLKR**GTTIKNIKLT**SK**EGEIE  
 51    AR**VDKFGVIVLKTEFLK**KI

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
519.32	518.31	518.31	0.01	0	15	90	3	R.GTTIK.N
319.18	636.34	636.35	-0.01	0	19	81	8	K.TEFLK.K
388.26	774.51	774.50	0.01	0	38	1.3	1	K.FGVIVLK.T
417.25	832.49	832.48	0.01	1	40	0.83	1	K.GASTTLKR.G
373.24	1116.70	1116.69	0.01	1	35	2.3	1	R.VDKFGVIVLK.T
845.43	1688.84	1688.82	0.01	0	80	4.8e-005	1	K.DANGTELNAGDSVSVIK.D

Mascot-RM1865\_hplc#42\_gs1\_060213

Mass: 7531    Score: 145    Queries matched: 5

phnA protein [*Campylobacter coli* RM2228]

1    MPK**DANGTELNAGDSVSVIK**DLKVK**GASTTLKR**GTTIKNIKLT**SK**ENEIE  
 51    AK**VDKFGVIVLKTEFLK**KI

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Sequence
519.3207	518.3134	518.3064	0.0070	0	15	R.GTTIK.N
319.1768	636.3391	636.3483	-0.0091	0	19	K.TEFLK.K
388.2604	774.5062	774.5003	0.0059	0	38	K.FGVIVLK.T
417.2498	832.4851	832.4766	0.0085	1	40	K.GASTTLKR.G
373.2392	1116.6959	1116.6906	0.0053	1	35	K.VDKFGVIVLK.T

### "Composite" and *de novo* sequence

\*\*\*\*\*

1    MPK**DANGTELNAGDSVSVIK**DLKVK**GASTTLKR**GTTIKNIKLT**SK**EGEIE  
 51    **AKVDKFGVIVLKTEFLK**KI

*De novo* confirms <sup>46</sup>EGEIEA<sup>52</sup>K peptide. G from *Cjj* and K from *Cc*.

"Composite" peptide.

\*\*\*\*\*

GPM Analysis of "Composite"/*de novo* Sequence RM1865\_hplc#42\_gs1\_060213

**log(e) = - 12.8 RM1865\_phnA\_[Composite\_and\_denovo\_phnA\_protein\_Cjj\_HB93\_13\_and\_RM2228]**

1 MPK**DANGTELNAGDSVSVIK**DLKVKGASTTLKRGTTIKNIKLTSKEGEIE 50  
 51 AK**VDFKFGVIVLK**TEFLKKI 69

spectrum	log(e)	log(I)	m+h	delta	z	sequence
30.1	-1.8	2.68	1689.830	0.016	2	[mpk <sup>4</sup> <b>DANGTELNAGDSVSVIK</b> <sup>20</sup> dlkv
36.1	-2.4	3.37	1117.699	-0.009	3	ieak <sup>53</sup> <b>VDFKFGVIVLK</b> <sup>62</sup> tefl
38.1	-2.4	3.62	775.509	0.009	2	kvd <sup>56</sup> <b>FGVIVLK</b> <sup>62</sup> tefl

Mascot-RM1865\_hplc#64\_gs1\_060213

Score: 712 Queries matched: 20

Ribosomal protein L7/L12 [Campylobacter coli RM2228]

1 **MAISKEDVLEFISNLSVLELSELVKEFEEKFGVSAAPVMVAGGAAAGGAA**  
 51 **AAAEKTEFDIVLDGGAKKIEVIKIVRALTGLGLKEAKDAVEQTPSTLK**  
 101 **EGVAKADAEAAKKQLEEAGAKVELK**

Observed Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
503.28	502.28	502.28	0.00	0	36	0.71	2 K.EGVAK.A
301.20	600.38	600.38	-0.00	0	30	11	1 K.IEVIK.I
365.24	728.46	728.48	-0.02	1	39	1.1	1 K.KIEVIK.I
367.17	732.33	732.33	0.00	0	37	1.7	1 K.ADAEEAK.K
386.74	771.47	771.49	-0.02	0	47	0.17	1 R.ALTGLGLK.E
423.23	844.44	844.43	0.01	0	45	0.32	1 K.QLEEAGAK.V
431.21	860.41	860.42	-0.01	1	50	0.077	1 K.ADAEEAKK.Q
487.25	972.49	972.52	-0.03	1	51	0.064	1 K.KQLEEAGAK.V
594.79	1187.56	1187.60	-0.04	0	49	0.088	1 K.DAVEQTPSTLK.E
1188.61	1187.60	1187.60	0.00	0	(41)	0.5	1 K.DAVEQTPSTLK.E
682.36	1362.70	1362.70	-0.01	0	79	7.7e-005	1 K.TEFDIVLDGGAK.K
682.50	1362.99	1362.70	0.28	0	(65)	0.0013	1 K.TEFDIVLDGGAK.K
749.71	2246.10	2246.10	0.00	0	65	0.0011	1 K.FGVSAAPVMVAGGAAAGGAAAAAEEK.T + Oxidation (M)
749.71	2246.10	2246.10	0.00	0	(59)	0.005	1 K.FGVSAAPVMVAGGAAAGGAAAAAEEK.T + Oxidation (M)
759.41	2275.20	2275.22	-0.02	0	67	0.00069	1 K.EDVLEFISNLSVLELSELVKE
759.74	2276.19	2275.22	0.97	0	(18)	61	4 K.EDVLEFISNLSVLELSELVKE
892.47	2674.39	2674.47	-0.07	1	61	0.0022	1 M.AISKEDVLEFISNLSVLELSELVKE
669.63	2674.49	2674.47	0.02	1	(50)	0.026	1 M.AISKEDVLEFISNLSVLELSELVKE
892.83	2675.47	2674.47	1.00	1	(21)	20	1 M.AISKEDVLEFISNLSVLELSELVKE
898.71	3590.83	3590.79	0.04	1	56	0.0041	1 K.FGVSAAPVMVAGGAAAGGAAAAAEEKTEFDIVLDGGAK.K + Oxidation (M)

GPM-RM1865\_hplc#64\_gs1\_060213

log(e) = -81.7

RM2228 rpL [50S ribosomal protein L7/L12]

1 MAISKEDVLEFISNLSVLELSELVKEFEKFGVSAAPVMVAGGAAAGGAAAAAEEKTEFD 60  
 61 IVLVDGGAKKIEVIKIVRALTGLGLKEAKDAVEQTPSTLKEGVAKADAEAEAKKQLEEAGA 120  
 121 KVELK 125

spectrum	log(e)	log(I)	m+h	delta	z	sequence
54.1	-1.9	3.50	3337.767	-0.040	4	[m <sup>2</sup> AISKEDVLEFISNLSVLELSELVKEFEK <sup>30</sup> fgvs
51.1	-6.7	3.79	2675.476	-0.073	3	[m <sup>2</sup> AISKEDVLEFISNLSVLELSELVK <sup>25</sup> efee
60.1	-4.6	3.51	2276.229	-0.031	3	aisk <sup>6</sup> EDVLEFISNLSVLELSELVK <sup>25</sup> efee
32.1	-1.5	3.00	3591.806	1.009	4	feek <sup>31</sup> FGVSAAPVMVAGGAAAGGAAAAAEEKTEFDIVLVDGGAK <sup>69</sup> kiev
45.1	-1.4	2.48	3591.806	0.009	4	feek <sup>31</sup> FGVSAAPVMVAGGAAAGGAAAAAEEKTEFDIVLVDGGAK <sup>69</sup> kiev
22.1	-5.3	3.29	2247.114	-0.008	3	feek <sup>31</sup> FGVSAAPVMVAGGAAAGGAAAAAEEK <sup>56</sup> tefd
29.1	-4.0	4.52	1363.712	-0.012	2	aEEK <sup>57</sup> TEFDIVLVDGGAK <sup>69</sup> kiev
40.1	-3.0	2.56	1851.217	-0.014	3	ggak <sup>70</sup> KIEVIKIVRALTGLGLK <sup>86</sup> eakd
24.1	-1.4	4.40	772.494	-0.019	2	kivr <sup>79</sup> ALTGLGLK <sup>86</sup> eakd
13.1	-1.9	4.06	1188.612	-0.042	2	keak <sup>90</sup> DAVEQTPSTLK <sup>100</sup> egva
14.1	-1.8	2.98	1002.548	-0.010	2	akda <sup>92</sup> VEQTPSTLK <sup>100</sup> egva
16.1	-1.1	2.70	1687.851	-0.004	3	gvak <sup>106</sup> ADAEAEAKKQLEEAGAK <sup>121</sup> velk]
5.1	-1.1	3.24	861.432	-0.006	2	gvak <sup>106</sup> ADAEAEAKK <sup>113</sup> qlee
4.1	-1.7	2.93	790.395	-0.005	2	vaka <sup>107</sup> DAEAEAKK <sup>113</sup> qlee

Mascot-RM1865\_hplc#65\_gs1\_060213

Score: 464 Queries matched: 10

Thioredoxin [*Campylobacter jejuni* RM2228]

1 MGKYIELTSDNFAQAKEGVALVDFWAPWCGPCRMLAPVIDELANDFDGKA  
 51 KICKVNTDEQGDAAEFGVRSIPTLIFFKNGEVVDQLVGAQSKQAISDKL  
 101 NSLL

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
331.18	660.34	660.34	-0.01	0	40	1.1	1	K.QAISDK.L
533.31	1064.61	1064.63	-0.02	0	(32)	4.3	1	R.SIPTLIFFK.N
533.32	1064.63	1064.63	0.00	0	39	0.8	1	R.SIPTLIFFK.N
533.33	1064.65	1064.63	0.02	0	(36)	1.5	1	R.SIPTLIFFK.N

722.38	1442.74	1442.74	0.00	0	63	0.003	1	K.NGEVVDQLVGAQSK.Q
750.38	1498.75	1498.73	0.02	0	81	3.8e-005	1	K.YIELTSDNFAQAK.E
562.29	1683.86	1683.85	0.01	1	58	0.0074	1	M.GKYIELTSDNFAQAK.E
860.91	1719.81	1719.81	0.01	0	66	0.0011	1	K.VNTDEQGDLAEEFGVR.S
588.62	1762.84	1762.84	-0.01	0	52	0.031	1	R.MLAPVIDELANDFDGK.A + Oxidation (M)
655.00	1961.99	1961.98	0.01	1	65	0.0015	1	R.MLAPVIDELANDFDGKAK.I + Oxidation (M)

GPM-RM1865\_hplc#65\_gs1\_060213

log(e) = -57.5

RM2228 trx [Thioredoxin]

1 MGKYIELTSDNFAQAKEGVALVDFWAPWCGPCRMLAPVIDELANDFDGKAKICKVNTDEQ 60  
 61 GDLAEEFGVRSIPTLIFFKNGEVVDQLVGAQSKQAISDKLNSLL 104

spectrum	log(e)	log(I)	m+h	delta	z	sequence
18.1	-3.2	3.00	1684.855	0.008	3	[m <sup>2</sup> GKYIELTSDNFAQAK <sup>16</sup> egva
20.1	-2.0	3.60	1499.739	0.009	2	[mgk <sup>4</sup> YIELTSDNFAQAK <sup>16</sup> egva
32.1	-4.3	3.28	1962.990	0.001	3	gpcr <sup>34</sup> MLAPVIDELANDFDGKAK <sup>51</sup> ickv
35.1	-4.8	3.44	1763.858	-0.003	3	gpcr <sup>34</sup> MLAPVIDELANDFDGK <sup>49</sup> akic
22.1	-8.0	3.49	1720.815	0.005	2	kick <sup>55</sup> VNTDEQGDLAEEFGVR <sup>70</sup> sipt
34.1	-2.1	3.88	1065.635	-0.024	2	fgvr <sup>71</sup> SIPTLIFFK <sup>79</sup> ngev
16.1	-4.3	3.31	1443.745	0.003	2	iffk <sup>80</sup> NGEVVDQLVGAQSK <sup>93</sup> qais
30.1	-2.4	2.91	1184.664	-0.007	2	aqsk <sup>94</sup> QAISDKLNSLL <sup>104</sup> ]

## *Campylobacter lari*

### RM2100 Protein Biomarkers

Mascot-RM2100\_hplc#50\_gs1\_060630

Mass: 6989 Score: 270 Queries matched: 8

Ribosomal protein L29 [*Campylobacter lari* RM2100]

1 MKYTEIKDKTAGELATMLKEKVVLLFTLRQKLKTMQLTNPKEISEVKKDI  
 51 ARINTAISALK

Observed Mr(expt)	Mr(calc)	DeltaMissScore	ExpectRank	Peptide
416.77	831.52	831.47	0.05 1 39 1.2 2	K.EISEVKK.D
431.30	860.58	860.55	0.03 0 (29) 12 1	K.VLLFTLR.Q
431.32	860.62	860.55	0.07 0 42 0.66 1	K.VLLFTLR.Q
465.82	929.63	929.55	0.07 0 44 0.43 1	R.INTAISALK.-
474.77	947.53	947.47	0.06 0 38 1.4 1	K.TMQLTNPKE + Oxidation (M)
495.35	988.69	988.64	0.04 1 41 0.73 1	K.KVLLFTLR.Q
525.82	1049.62	1049.54	0.08 0 44 0.32 1	K.TAGELATMLKE + Oxidation (M)
397.26	1188.76	1188.65	0.10 1 23 48 2	K.LKTMQLTNPKE + Oxidation (M)

Mascot-RM2100\_hplc#51\_gs1\_060630

Score: 337 Queries matched: 10

cytochrome C4, putative [*Campylobacter lari* RM2100]

1 MKKLLVLSTLACLSVSAFAADGATLYKKCAVCHGAK**ADKVYLNKVPALNT**  
 51 **LTA**ERLQYMK**DYAAGKR**NAYGQGAIMKINLK**GLTEADFK**AIEEYIESLK  
 101 **K**

Observed Mr(expt)	Mr(calc)	DeltaMissScore	ExpectRank	Peptide
318.69	635.37	635.36	0.00 0 19 90 4	K.VYLNK.V
390.71	779.41	779.39	0.02 1 31 6.2 1	K.DYAAGKR.N
440.74	879.46	879.43	0.02 0 32 4.6 1	K.GLTEADFK.A
475.77	949.53	949.52	0.01 1 (23) 38 2	K.ADKVYLNK.V
317.53	949.57	949.52	0.04 1 37 1.6 1	K.ADKVYLNK.V
534.77	1067.53	1067.51	0.02 0 20 78 3	R.NAYGQGAIMK.I + Oxidation (M)
628.37	1254.72	1254.69	0.03 0 66 0.0022 1	K.VPALNTLTAER.L
441.60	1321.77	1321.71	0.06 1 43 0.37 1	K.AIEEYIESLKK.-
625.05	1872.14	1872.05	0.09 1 59 0.011 1	K.VYLNKVPALNTLTAER.L
546.82	2183.24	2183.14	0.11 2 31 7 2	K.GLTEADFKAIEEYIESLKK.-

Mascot-RM2100\_hplc#51\_gs2\_060630

Score: 189 Queries matched: 5

Cytochrome C4, putative [*Campylobacter lari* RM2100]

1 MKKLLVLSTLACLSVSAFAADGATLYKKCAVCHGAKADK**VYLNKVPALNT**  
 51 **LTA**ERLQYMK**DYAAGKR**NAYGQGAIMKINLK**GLTEADFK**AIEEYIESLK  
 101 **K**



Observed Mr(expt)	Mr(calc)	Delta	MissScore	Expect	Rank	Peptide		
440.73	879.44	879.43	0.01	0	32	4.7	1	K.GLTEADFK.A
534.77	1067.53	1067.51	0.02	0	20	81	1	R.NAYGQGAIMK.I + Oxidation (M)
628.38	1254.74	1254.69	0.05	0	59	0.0097	1	K.VPALNTLTAAER.L
441.60	1321.77	1321.71	0.06	1	44	0.33	1	K.AIEEYIESLKK.-
625.04	1872.11	1872.05	0.06	1	34	3.3	1	K.VYLNKVPALNTLTAAER.L

Mascot-RM2100\_hplc#73\_gs1\_060630

Mass: 11545 Score: 683 Queries matched: 21

Thioredoxin [*Campylobacter lari* RM2100]

1 MGKYIDLTAE~~NF~~QA~~KE~~EGVALVDFWAPWCGPCR~~MLAPVIDELAN~~DFD~~GKA~~

51 KICKVN~~TEE~~EQ~~GD~~LAAQFGVRSIPTIFFFKDGEVVDQLVGAQSKQVLADKL

101 NSLL

Observed	Mr(expt)	Mr(calc)	Delta	MissScore	Expect	Rank	Peptide	
310.1772	618.3399	618.3523	-0.0124	1	27	27	3	K.AKICK.V
337.2009	672.3873	672.3806	0.0067	0	33	7.4	1	K.QVLADK.L
550.2948	1098.5751	1098.6113	-0.0362	0	45	0.37	1	R.SIPTIFFFK.D
722.8297	1443.6449	1443.7205	-0.0756	0	81	8.3e-05	1	K.DGEVVDQLVGAQSK.Q
482.2617	1443.7633	1443.7205	0.0428	0	(51)	0.096	1	K.DGEVVDQLVGAQSK.Q
742.3284	1482.6422	1482.7354	-0.0932	0	57	0.019	1	K.YIDLTAE <del>NF</del> QA <del>KE</del>
495.2712	1482.7918	1482.7354	0.0564	0	(33)	5.6	1	K.YIDLTAE <del>NF</del> QA <del>KE</del>
556.9556	1667.8450	1667.8518	-0.0068	1	66	0.0029	1	M.GKYIDLTAE <del>NF</del> QA <del>KE</del>
556.9872	1667.9397	1667.8518	0.0879	1	(32)	6.5	1	M.GKYIDLTAE <del>NF</del> QA <del>KE</del>
578.6144	1732.8215	1732.8380	-0.0165	0	62	0.0065	1	K.VN <del>TEE</del> EQ <del>GD</del> LAAQFGVRS
578.6359	1732.8858	1732.8380	0.0479	0	(36)	2.8	1	K.VN <del>TEE</del> EQ <del>GD</del> LAAQFGVRS
578.6573	1732.9502	1732.8380	0.1122	0	(35)	3.6	1	K.VN <del>TEE</del> EQ <del>GD</del> LAAQFGVRS
588.6087	1762.8043	1762.8447	-0.0404	0	64	0.0043	1	R.MLAPVIDELAN <del>DFD</del> GK.A + Oxidation (M)
588.6520	1762.9341	1762.8447	0.0894	0	(40)	1.2	1	R.MLAPVIDELAN <del>DFD</del> GK.A + Oxidation (M)
654.9613	1961.8620	1961.9768	-0.1147	1	66	0.0024	1	R.MLAPVIDELAN <del>DFD</del> GKAK.I + Oxidation (M)
491.4984	1961.9645	1961.9768	-0.0122	1	(49)	0.13	1	R.MLAPVIDELAN <del>DFD</del> GKAK.I + Oxidation (M)
712.3565	2134.0476	2134.0476	0.0000	1	116	2.7e-08	1	K.ICKVN <del>TEE</del> EQ <del>GD</del> LAAQFGVRS
534.5446	2134.1493	2134.0476	0.1017	1	(33)	6.1	1	K.ICKVN <del>TEE</del> EQ <del>GD</del> LAAQFGVRS
842.3938	2524.1596	2524.3212	-0.1616	1	65	0.0033	1	R.SIPTIFFFKDGEVVDQLVGAQSK.Q
632.0727	2524.2618	2524.3212	-0.0595	1	(33)	6.3	2	R.SIPTIFFFKDGEVVDQLVGAQSK.Q
842.4715	2524.3925	2524.3212	0.0713	1	(18)	1.7e+02	2	R.SIPTIFFFKDGEVVDQLVGAQSK.Q

## RM1890 Protein Biomarkers

Mascot-RM1890\_hplc#50\_gs1\_060702

Mass: 11142 Score: 319 Queries matched: 10

Cytochrome C4, putative [*Campylobacter lari* RM2100]

1 MKKLLVLSTLACLSVSAFAADGATLYKKCAVCHGAK**ADKVYLNKVPALNT**  
51 **LTA**AERLQYMK**DYAAGK**R**NAYGQGAIMK**INLK**GLTEADFK**AIEEYIESLK  
101 **K**

Observed Mr(expt)	Mr(calc)	Delta	MissScore	Expect	Rank	Peptide
312.67	623.33	623.29	0.03	0	21 42	1 K.DYAAGK.R
318.71	635.40	635.36	0.03	0	21 59	1 K.VYLNK.V
440.74	879.47	879.43	0.03	0	40 0.72	1 K.GLTEADFK.A
475.80	949.58	949.52	0.06	1	37 1.8	1 K.ADKVYLNK.V
534.80	1067.59	1067.51	0.08	0	19 82	1 R.NAYGQGAIMK.I + Oxidation (M)
597.86	1193.71	1193.62	0.09	0	44 0.31	1 K.AIEEYIESLK.K
628.38	1254.75	1254.69	0.06	0	68 0.0013	1 K.VPALNTLTAER.L
419.28	1254.81	1254.69	0.11	0	(24) 32	1 K.VPALNTLTAER.L
441.62	1321.84	1321.71	0.13	1	43 0.36	1 K.AIEEYIESLKK.-
546.85	2183.36	2183.14	0.23	2	26 19	1 K.GLTEADFKAIEEYIESLKK.-

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Mascot-RM1890\_hplc#50\_gs2\_060702

Mass: 10262 Score: 309 Queries matched: 9

Ribosomal protein S15 [*Campylobacter lari* RM2100]

1 **MALDSAKKAEIVAK**FAR**KEGDTGSPEVQIALLSAR**ISDLTEHLKIYKK**DF**  
51 **SSRLG**LLKLVGQRKRLLSYLKRKDYQAYSK**LISELNLR**DK

Observed Mr(expt)	Mr(calc)	Delta	MissScore	Expect	Rank	Peptide
272.2040	542.3935	542.3791	0.0144	0	34 1.9	1 R.LGLLK.L
302.6923	603.3700	603.3228	0.0473	0	33 6.6	1 M.ALDSAK.K
306.1694	610.3242	610.2711	0.0531	0	16 91	10 K.DFSSR.L
379.7588	757.5031	757.4697	0.0334	1	46 0.39	5 K.KAEIVAK.F

479.3061 956.5977 956.5654 0.0322 0 61 0.01 1 K.LISELNLR.D  
479.3354 956.6563 956.5654 0.0908 0 (35) 3.8 2 K.LISELNLR.D  
872.0211 1742.0276 1741.8846 0.1430 0 77 0.0002 1 K.EGDTGSPEVQIALLSAR.I  
624.3871 1870.1395 1869.9795 0.1599 1 42 0.59 1 R.KEGDTGSPEVQIALLSAR.I  
624.4094 1870.2063 1869.9795 0.2268 1 (32) 5.7 2 R.KEGDTGSPEVQIALLSAR.I

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Mascot-RM1890\_hplc#70\_gs1\_060702

Mass: 11545 Score: 555 Queries matched: 15

Thioredoxin [*Campylobacter lari* RM2100]

1 MGKYIDLTAE~~N~~FAQAKEGVALVDFWAPWCGPCRMLAPVIDELANDFDGKA  
51 KICKVNTEEQGD~~L~~AAQFGVRSIPTIFFFKDGEVVDQLVGAQSKQVLADKL  
101 NSLL

Observed	Mr(expt)	Mr(calc)	Delta	Miss Score	Expect	Rank	Peptide
337.2217	672.4288	672.3806	0.0482	0	31	12	1 K.QVLADK.L
550.3015	1098.5884	1098.6113	-0.0229	0	(42)	0.75	1 R.SIPTIFFFK.D
550.3538	1098.6930	1098.6113	0.0817	0	45	0.31	1 R.SIPTIFFFK.D
607.8962	1213.7778	1212.7077	1.0700	1	21	89	1 K.QVLADKLN <del>S</del> L.L-
722.8941	1443.7737	1443.7205	0.0533	0	80	0.00012	1 K.DGEVVDQLVGAQSK.Q
482.2745	1443.8018	1443.7205	0.0813	0	(69)	0.0015	1 K.DGEVVDQLVGAQSK.Q
742.3703	1482.7260	1482.7354	-0.0094	0	65	0.0038	1 K.YIDLTAE <del>N</del> FAQAK.E
495.2650	1482.7732	1482.7354	0.0378	0	(58)	0.017	1 K.YIDLTAE <del>N</del> FAQAK.E
556.9942	1667.9607	1667.8518	0.1089	1	51	0.097	1 M.GKYIDLTAE <del>N</del> FAQAK.E
578.6548	1732.9426	1732.8380	0.1046	0	72	0.00079	1 K.VNTEEQGD <del>L</del> AAQFGVRS
578.6655	1732.9747	1732.8380	0.1368	0	(23)	56	2 K.VNTEEQGD <del>L</del> AAQFGVRS
588.6607	1762.9603	1762.8447	0.1156	0	62	0.007	1 R.MLAPVIDELANDFDGK.A + Oxidation (M)
588.6823	1763.0252	1762.8447	0.1805	0	(59)	0.013	1 R.MLAPVIDELANDFDGK.A + Oxidation (M)
655.0422	1962.1049	1961.9768	0.1281	1	61	0.008	1 R.MLAPVIDELANDFDGKAK.I + Oxidation (M)
842.4952	2524.4638	2524.3212	0.1425	1	67	0.0019	1 R.SIPTIFFFKDGEVVDQLVGAQSK.Q

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Mascot-RM1890\_hplc#70\_gs3\_060702

Mass: 13091 Score: 1230 Queries matched: 30

Ribosomal protein L7/L12 [*Campylobacter lari* RM2100]

1 MAITKEDVLEFISNLSVLELSELVKEFEKFGVSAAPVMVAGAAVAGAAG  
51 GAAEEKTEFDIVLQDGGDKKINVIKVVRRALTGLGLKEAKDAVEQTPSVLK  
101 EGVSKAEAEAAKKQLEEAGAKVELK

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
260.1626	518.3107	518.2700	0.0408	0	44	0.14	1	K.EGVSK.A
293.7193	585.4241	585.3850	0.0391	0	30	10	1	K.INVIK.V
293.7270	585.4394	585.3850	0.0544	0	(25)	27	1	K.INVIK.V
374.2150	746.4155	746.3446	0.0709	0	31	11	1	K.AEAEAAK.K
386.7547	771.4948	771.4854	0.0094	0	54	0.058	1	R.ALTGLGLK.E
423.2439	844.4732	844.4290	0.0442	0	46	0.33	1	K.QLEEAGAK.V
438.2702	874.5258	874.4396	0.0862	1	50	0.13	1	K.AEAEAAK.Q
487.2807	972.5469	972.5240	0.0229	1	62	0.0088	1	K.KQLEEAGAK.V
593.8099	1185.6053	1185.6241	-0.0188	0	51	0.088	1	K.DAVEQTPSVLK.E
593.8642	1185.7139	1185.6241	0.0898	0	(34)	4.5	1	K.DAVEQTPSVLK.E
593.8860	1185.7574	1185.6241	0.1333	0	(45)	0.36	1	K.DAVEQTPSVLK.E
657.8979	1313.7813	1313.7190	0.0623	1	67	0.0023	1	K.QLEEAGAKVELK.-
688.4099	1374.8053	1374.6990	0.1063	2	85	3.3e-05	1	K.EGVSKAEAEAAKK.Q
481.6481	1441.9226	1441.8140	0.1087	2	53	0.053	3	K.KQLEEAGAKVELK.-
757.9510	1513.8875	1513.7987	0.0888	1	75	0.00038	1	K.EAKDAVEQTPSVLK.E
782.9224	1563.8302	1563.7780	0.0522	1	70	0.001	1	K.TEFDIVLQDGGDKK.I
522.3037	1563.8892	1563.7780	0.1112	1	(49)	0.12	1	K.TEFDIVLQDGGDKK.I
522.3139	1563.9198	1563.7780	0.1418	1	(46)	0.24	1	K.TEFDIVLQDGGDKK.I
522.3444	1564.0115	1563.7780	0.2335	1	(52)	0.057	1	K.TEFDIVLQDGGDKK.I
565.4223	1693.2449	1693.0977	0.1472	2	32	4.4	1	K.INVIKVVRRALTGLGLK.E
568.0119	1701.0138	1700.8580	0.1558	2	65	0.0039	1	K.AEAEAAKKQLEEAGAK.V
759.0684	2274.1833	2274.1313	0.0521	0	83	5.7e-05	1	K.FGVSAAPVMVAGAAVAGAAGGAAEEK.T + Oxidation (M)
569.6068	2274.3982	2274.1313	0.2669	0	(24)	39	3	K.FGVSAAPVMVAGAAVAGAAGGAAEEK.T + Oxidation (M)
759.3000	2274.8782	2274.1313	0.7469	0	(39)	1.1	1	K.FGVSAAPVMVAGAAVAGAAGGAAEEK.T + Oxidation (M)
759.4369	2275.2889	2275.2198	0.0691	0	(68)	0.0017	1	K.EDVLEFISNLSVLELSELVK.E
1138.6845	2275.3544	2275.2198	0.1346	0	100	1.1e-06	1	K.EDVLEFISNLSVLELSELVK.E
897.2275	2688.6607	2688.4836	0.1771	1	69	0.0011	1	M.AITKEDVLEFISNLSVLELSELVK.E
673.1947	2688.7498	2688.4836	0.2662	1	(45)	0.29	1	M.AITKEDVLEFISNLSVLELSELVK.E
709.9470	2835.7587	2835.5190	0.2397	1	69	0.001	1	-.MAITKEDVLEFISNLSVLELSELVK.E + Oxidation (M)
980.2579	2937.7518	2937.5109	0.2408	1	98	1.6e-06	1	K.EDVLEFISNLSVLELSELVKEFEK.F

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## *Campylobacter concisus* RM3806 Protein Biomarkers

Mascot-RM3806\_try\_p\_hplc#64\_gel#9\_041016

[gi|109673896](#) Mass: 10608 Score: 745 Queries matched: 47

Hypothetical protein Ccur5\_01001212 [*Campylobacter curvus* 525.92]

1 MKKAEFIQAVADKAGLSKKDSLKVVDTLETIQAVLEKSDSI[**S**]FIGFGTF

51 [S]TADRAARKARVPGTKKVIDVPASKAVKFKVGGKLLKEAVAAGAH[**H**]KKGKKK

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
414.7603	827.5060	827.4752	0.0307	0	(23)	55	5	K.VIDVPASK.A
414.7603	827.5060	827.4752	0.0307	0	(24)	48	10	K.VIDVPASK.A
414.7693	827.5241	827.4752	0.0489	0	48	0.19	1	K.VIDVPASK.A
414.7693	827.5241	827.4752	0.0489	0	(34)	4.4	1	K.VIDVPASK.A
428.8009	855.5873	855.5290	0.0583	2	17	2.4e+02	4	K.ARVPGTKK.V
478.8219	955.6293	955.5702	0.0591	1	63	0.0051	1	K.KVIDVPASK.A
546.3140	1090.6135	1090.5658	0.0477	0	65	0.0034	1	K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(22)	75	1	K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(57)	0.024	1	K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(51)	0.097	1	K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(56)	0.029	1	K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(39)	1.4	1	K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(61)	0.0091	1	K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(63)	0.0053	1	K.AEFIQAVADK.A
546.3245	1090.6344	1090.5658	0.0685	0	(44)	0.49	1	K.AEFIQAVADK.A
546.3245	1090.6344	1090.5658	0.0685	0	(55)	0.033	1	K.AEFIQAVADK.A
546.3245	1090.6344	1090.5658	0.0685	0	(58)	0.016	1	K.AEFIQAVADK.A
546.3245	1090.6344	1090.5658	0.0685	0	(57)	0.022	1	K.AEFIQAVADK.A
546.8145	1091.6145	1090.5658	1.0486	0	(50)	0.096	1	K.AEFIQAVADK.A
407.2469	1218.7188	1218.6608	0.0580	1	(59)	0.016	1	K.KAEFIQAVADK.A
610.3731	1218.7317	1218.6608	0.0709	1	90	1.2e-05	1	K.KAEFIQAVADK.A
498.9571	1493.8494	1493.7911	0.0583	2	(64)	0.0044	1	-.MKKAEFIQAVADK.A + Oxidation (M)
747.9468	1493.8790	1493.7911	0.0879	2	82	6.3e-05	1	-.MKKAEFIQAVADK.A + Oxidation (M)
774.4622	1546.9098	1546.8354	0.0744	1	77	0.00024	1	K.AEFIQAVADKAGLSK.K
516.6443	1546.9110	1546.8354	0.0756	1	(53)	0.058	1	K.AEFIQAVADKAGLSK.K
543.6591	1627.9555	1627.9032	0.0523	0	(23)	54	1	K.VVDTLETIQAVLEK.S
543.6591	1627.9555	1627.9032	0.0523	0	(40)	1.1	1	K.VVDTLETIQAVLEK.S
543.6591	1627.9555	1627.9032	0.0523	0	(23)	54	2	K.VVDTLETIQAVLEK.S

543.6591	1627.9555	1627.9032	0.0523	0	(20)	1.1e+02	2	K.VVDATLETIQAVLEK.S
543.6591	1627.9555	1627.9032	0.0523	0	(39)	1.6	1	K.VVDATLETIQAVLEK.S
543.6591	1627.9555	1627.9032	0.0523	0	(27)	21	1	K.VVDATLETIQAVLEK.S
814.9930	1627.9714	1627.9032	0.0683	0	111	9.2e-08	1	K.VVDATLETIQAVLEK.S
814.9930	1627.9714	1627.9032	0.0683	0	(96)	2.7e-06	1	K.VVDATLETIQAVLEK.S
814.9930	1627.9714	1627.9032	0.0683	0	(97)	2.2e-06	1	K.VVDATLETIQAVLEK.S
814.9930	1627.9714	1627.9032	0.0683	0	(100)	1.1e-06	1	K.VVDATLETIQAVLEK.S
814.9930	1627.9714	1627.9032	0.0683	0	(103)	5.6e-07	1	K.VVDATLETIQAVLEK.S
814.9930	1627.9714	1627.9032	0.0683	0	(103)	5.4e-07	1	K.VVDATLETIQAVLEK.S
814.9930	1627.9714	1627.9032	0.0683	0	(106)	2.7e-07	1	K.VVDATLETIQAVLEK.S
814.9930	1627.9714	1627.9032	0.0683	0	(92)	6.8e-06	1	K.VVDATLETIQAVLEK.S
814.9930	1627.9714	1627.9032	0.0683	0	(90)	1.2e-05	1	K.VVDATLETIQAVLEK.S
543.6695	1627.9867	1627.9032	0.0835	0	(69)	0.0016	1	K.VVDATLETIQAVLEK.S
543.6695	1627.9867	1627.9032	0.0835	0	(68)	0.0016	1	K.VVDATLETIQAVLEK.S
543.6695	1627.9867	1627.9032	0.0835	0	(20)	1e+02	3	K.VVDATLETIQAVLEK.S
543.6695	1627.9867	1627.9032	0.0835	0	(38)	2	1	K.VVDATLETIQAVLEK.S
559.3480	1675.0222	1674.9304	0.0918	2	46	0.29	1	K.KAEFIQAVADKAGLSK.K
838.5235	1675.0324	1674.9304	0.1020	2	64	0.0043	1	K.AEFIQAVADKAGLSK.K
651.0589	1950.1548	1950.0607	0.0941	3	88	1.5e-05	1	-.MKKAEFIQAVADKAGLSK.K + Oxidation (M)

Confirmation of composite, *de novo*  
and point mutation sequence by GPM analysis

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log(e) = -179.1

RM3806\_HU\_[HUP\_from\_Ccurvus\_Cconcisus\_composite\_denovo\_ESLK]

1 MKKAEFIQAVADKAGLSKESLKVVDATLETIQAVLEKKGSISFIFGFTFGTADRRAARKA 60  
 61 RVPGTKKVIDVPASKAVKFKVGGKLLKEAVAAGAAKKGKKK 100

spectrum	log(e)	log(I)	m+h	delta	z	sequence
84.1	-7.0	3.70	1951.074	0.086	3	[ <sup>1</sup> MKKAEFIQAVADKAGLSK <sup>18</sup> kesl
53.1	-6.3	3.83	1494.805	0.065	2	[ <sup>1</sup> MKKAEFIQAVADK <sup>13</sup> agls
52.1	-1.5	4.04	1494.805	0.055	3	[ <sup>1</sup> MKKAEFIQAVADK <sup>13</sup> agls
92.1	-5.3	4.05	1676.939	-0.929	3	[mk <sup>3</sup> KAEFIQAVADKAGLSK <sup>18</sup> kesl
59.1	-3.4	3.92	1219.669	0.061	2	[mk <sup>3</sup> KAEFIQAVADK <sup>13</sup> agls
62.1	-1.9	4.67	1219.669	0.051	3	[mk <sup>3</sup> KAEFIQAVADK <sup>13</sup> agls
93.1	-2.9	2.91	1675.939	0.081	2	[mkk <sup>4</sup> AEFIQAVADKAGLSK <sup>19</sup> eslk
98.1	-3.6	4.51	1547.844	0.066	3	[mkk <sup>4</sup> AEFIQAVADKAGLSK <sup>18</sup> kesl
99.1	-3.2	3.79	1547.844	0.066	2	[mkk <sup>4</sup> AEFIQAVADKAGLSK <sup>18</sup> kesl
219.1	-2.0	3.40	1091.574	0.046	2	[mkk <sup>4</sup> AEFIQAVADK <sup>13</sup> agls
65.1	-1.6	4.92	1091.574	0.046	2	[mkk <sup>4</sup> AEFIQAVADK <sup>13</sup> agls

263.1	-1.6	3.88	1091.574	0.176	2	[mkk <sup>4</sup> AEFIQAVADK <sup>13</sup> agls
119.1	-1.5	3.63	1091.574	0.046	2	[mkk <sup>4</sup> AEFIQAVADK <sup>13</sup> agls
243.1	-1.4	3.51	1091.574	0.046	2	[mkk <sup>4</sup> AEFIQAVADK <sup>13</sup> agls
257.1	-1.3	3.50	1091.574	0.066	2	[mkk <sup>4</sup> AEFIQAVADK <sup>13</sup> agls
95.1	-1.3	3.80	1091.574	0.046	2	[mkk <sup>4</sup> AEFIQAVADK <sup>13</sup> agls
195.1	-1.2	3.37	1091.574	0.046	2	[mkk <sup>4</sup> AEFIQAVADK <sup>13</sup> agls
238.1	-3.8	3.24	3828.044	1.156	3	lskk <sup>20</sup> ESLKVV DATLETIQAVLEKKG SISFIGFTFGTADR <sup>55</sup> aark
208.1	-3.1	3.97	2086.166	0.084	3	lskk <sup>20</sup> ESLKVV DATLETIQAVLEK <sup>38</sup> kgsi
212.1	-3.1	3.13	2128.165	-0.875	3	lskk <sup>20</sup> ESLKVV DATLETIQAVLEK <sup>38</sup> kgsi
192.1	-2.4	3.95	3370.790	1.090	3	eslk <sup>24</sup> VVDATLETIQAVLEKKG SISFIGFTFGTADR <sup>55</sup> aark
222.1	-2.1	2.97	3370.790	2.100	3	eslk <sup>24</sup> VVDATLETIQAVLEKKG SISFIGFTFGTADR <sup>55</sup> aark
128.1	-3.7	3.56	1757.006	0.063	3	eslk <sup>24</sup> VVDATLETIQAVLEK <sup>39</sup> gsgis
279.1	-5.5	2.98	1628.911	0.058	2	eslk <sup>24</sup> VVDATLETIQAVLEK <sup>38</sup> kgsi
185.1	-5.3	3.40	1628.911	0.058	2	eslk <sup>24</sup> VVDATLETIQAVLEK <sup>38</sup> kgsi
137.1	-5.0	5.18	1628.911	0.058	2	eslk <sup>24</sup> VVDATLETIQAVLEK <sup>38</sup> kgsi
161.1	-4.8	3.95	1628.911	0.058	2	eslk <sup>24</sup> VVDATLETIQAVLEK <sup>38</sup> kgsi
291.1	-4.8	2.93	1628.911	0.058	2	eslk <sup>24</sup> VVDATLETIQAVLEK <sup>38</sup> kgsi
253.1	-4.6	3.19	1628.911	0.068	2	eslk <sup>24</sup> VVDATLETIQAVLEK <sup>38</sup> kgsi
209.1	-4.5	3.30	1628.911	0.068	2	eslk <sup>24</sup> VVDATLETIQAVLEK <sup>38</sup> kgsi
267.1	-4.0	3.01	1628.911	0.058	2	eslk <sup>24</sup> VVDATLETIQAVLEK <sup>38</sup> kgsi
233.1	-3.9	3.32	1628.911	0.068	2	eslk <sup>24</sup> VVDATLETIQAVLEK <sup>38</sup> kgsi
206.1	-3.1	3.68	1628.911	0.068	3	eslk <sup>24</sup> VVDATLETIQAVLEK <sup>38</sup> kgsi
136.1	-3.0	4.73	1628.911	0.058	3	eslk <sup>24</sup> VVDATLETIQAVLEK <sup>38</sup> kgsi
184.1	-2.9	3.55	1628.911	0.068	3	eslk <sup>24</sup> VVDATLETIQAVLEK <sup>38</sup> kgsi
160.1	-2.7	4.24	1628.911	0.058	3	eslk <sup>24</sup> VVDATLETIQAVLEK <sup>38</sup> kgsi
232.1	-1.6	3.67	1628.911	0.048	3	eslk <sup>24</sup> VVDATLETIQAVLEK <sup>38</sup> kgsi
304.1	-1.5	3.35	1628.911	0.058	3	eslk <sup>24</sup> VVDATLETIQAVLEK <sup>38</sup> kgsi
115.1	-5.0	3.59	1315.748	0.062	2	kvvd <sup>27</sup> ATLETIQAVLEK <sup>38</sup> kgsi
246.1	-2.9	3.90	2643.415	-1.005	3	atle <sup>31</sup> TIQAVLEKKG SISFIGFTFGTADR <sup>55</sup> aark
274.1	-2.9	3.48	2643.415	-0.985	3	atle <sup>31</sup> TIQAVLEKKG SISFIGFTFGTADR <sup>55</sup> aark
132.1	-2.8	4.62	2643.415	-1.035	3	atle <sup>31</sup> TIQAVLEKKG SISFIGFTFGTADR <sup>55</sup> aark
156.1	-2.5	4.48	2643.415	-1.045	3	atle <sup>31</sup> TIQAVLEKKG SISFIGFTFGTADR <sup>55</sup> aark
300.1	-2.5	3.21	2643.415	-1.025	3	atle <sup>31</sup> TIQAVLEKKG SISFIGFTFGTADR <sup>55</sup> aark
202.1	-2.1	4.17	2643.415	-1.045	3	atle <sup>31</sup> TIQAVLEKKG SISFIGFTFGTADR <sup>55</sup> aark
180.1	-2.1	4.38	2643.415	-1.045	3	atle <sup>31</sup> TIQAVLEKKG SISFIGFTFGTADR <sup>55</sup> aark
262.1	-2.0	3.78	2643.415	-1.045	3	atle <sup>31</sup> TIQAVLEKKG SISFIGFTFGTADR <sup>55</sup> aark
226.1	-1.7	4.08	2643.415	-1.065	3	atle <sup>31</sup> TIQAVLEKKG SISFIGFTFGTADR <sup>55</sup> aark
155.1	-6.7	4.48	1760.898	1.012	2	vlek <sup>39</sup> KG SISFIGFTFGTADR <sup>55</sup> aark
201.1	-6.6	4.17	1760.898	1.012	2	vlek <sup>39</sup> KG SISFIGFTFGTADR <sup>55</sup> aark
179.1	-6.2	4.38	1760.898	1.012	2	vlek <sup>39</sup> KG SISFIGFTFGTADR <sup>55</sup> aark
261.1	-6.1	3.78	1760.898	1.012	2	vlek <sup>39</sup> KG SISFIGFTFGTADR <sup>55</sup> aark



225.1	-5.9	4.08	1760.898	1.012	2	vlek <sup>39</sup> KGSISFIGFGTFTADR <sup>55</sup> aark
245.1	-5.7	3.90	1760.898	1.042	2	vlek <sup>39</sup> KGSISFIGFGTFTADR <sup>55</sup> aark
131.1	-5.6	4.62	1760.898	1.022	2	vlek <sup>39</sup> KGSISFIGFGTFTADR <sup>55</sup> aark
299.1	-5.5	3.21	1760.898	1.032	2	vlek <sup>39</sup> KGSISFIGFGTFTADR <sup>55</sup> aark
273.1	-5.0	3.48	1760.898	1.052	2	vlek <sup>39</sup> KGSISFIGFGTFTADR <sup>55</sup> aark
305.1	-4.0	2.69	1760.898	1.022	2	vlek <sup>39</sup> KGSISFIGFGTFTADR <sup>55</sup> aark
285.1	-3.6	3.31	1760.898	1.052	2	vlek <sup>39</sup> KGSISFIGFGTFTADR <sup>55</sup> aark
134.1	-2.6	4.50	1760.898	1.012	3	vlek <sup>39</sup> KGSISFIGFGTFTADR <sup>55</sup> aark
204.1	-1.6	3.63	1760.898	1.012	3	vlek <sup>39</sup> KGSISFIGFGTFTADR <sup>55</sup> aark
158.1	-1.4	3.99	1760.898	1.012	3	vlek <sup>39</sup> KGSISFIGFGTFTADR <sup>55</sup> aark
182.1	-1.4	3.52	1760.898	1.022	3	vlek <sup>39</sup> KGSISFIGFGTFTADR <sup>55</sup> aark
248.1	-1.4	3.41	1760.898	1.012	3	vlek <sup>39</sup> KGSISFIGFGTFTADR <sup>55</sup> aark
169.1	-2.1	3.92	1260.663	0.997	2	vlek <sup>39</sup> KGSISFIGFT <sup>50</sup> gtad
235.1	-2.3	3.56	1530.749	1.521	2	kkgs <sup>42</sup> ISFIGFGTFTADR <sup>55</sup> aark
89.1	-5.0	4.44	1141.565	0.045	2	sisf <sup>45</sup> IGFGTFTADR <sup>55</sup> aark
171.1	-2.7	2.73	1141.565	0.065	2	sisf <sup>45</sup> IGFGTFTADR <sup>55</sup> aark
165.1	-2.4	3.19	1028.481	0.069	2	isfi <sup>46</sup> GFGTFTADR <sup>55</sup> aark
31.1	-1.3	3.71	956.579	0.048	2	pgtk <sup>67</sup> KVIDVPASK <sup>75</sup> avkf
80.1	-4.5	3.33	2014.255	0.095	3	pask <sup>76</sup> AVKFKVGKLLKEAVAAGAAK <sup>95</sup> kgkk
76.1	-1.1	3.34	1716.054	0.186	3	kavk <sup>79</sup> FKVGKLLKEAVAAGAAK <sup>95</sup> kgkk
79.1	-2.0	3.31	1341.822	1.408	2	kfkv <sup>82</sup> GKLLKEAVAAGAAK <sup>95</sup> kgkk
15.1	-3.6	3.15	1156.706	-0.916	2	kvgk <sup>84</sup> KLKEAVAAGAAK <sup>95</sup> kgkk
5.1	-2.7	2.75	1156.706	0.064	2	vgkk <sup>85</sup> LKEAVAAGAAK <sup>96</sup> gkkk]
3.1	-2.0	3.43	1028.611	0.079	2	vgkk <sup>85</sup> LKEAVAAGAAK <sup>95</sup> kgkk
25.1	-1.8	2.65	1028.611	0.049	2	vgkk <sup>85</sup> LKEAVAAGAAK <sup>95</sup> kgkk

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Mascot-RM3806\_tryp\_hplc#64\_gel#9\_041016

gi|109671087 Mass: 6013 Score: 347 Queries matched: 10

Hypothetical protein Ccon1\_01002013 [*Campylobacter concisus* 13826]

1 SFIGFGTFTG TADRAARKARVPGTKKVIDVPASKAVKFKVGKLLKEAVAAG  
 51 AAKKGKKK

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
414.7603	827.5060	827.4752	0.0307	0	(23)	55	5	K.VIDVPASK.A
414.7603	827.5060	827.4752	0.0307	0	(24)	48	10	K.VIDVPASK.A
414.7693	827.5241	827.4752	0.0489	0	48	0.19	1	K.VIDVPASK.A
414.7693	827.5241	827.4752	0.0489	0	(34)	4.4	1	K.VIDVPASK.A
428.8009	855.5873	855.5290	0.0583	2	17	2.4e+02	4	K.ARVPGTKK.V



478.8219	955.6293	955.5702	0.0591	1	63	0.0051	1	K.KVIDVPASK.A
514.8415	1027.6684	1027.6025	0.0659	1	(50)	0.13	2	K.LKEAVAAGAAK.K
514.8516	1027.6886	1027.6025	0.0861	1	87	2.1e-05	1	K.LKEAVAAGAAK.K
578.8919	1155.7693	1155.6975	0.0718	2	55	0.037	1	K.KLKEAVAAGAAK.K
672.1194	2013.3365	2013.2461	0.0904	5	81	6.6e-05	1	K.AVKFKVGKLLKEAVAAGAAK.K

Mascot-RM3806\_tryplc#64\_gel#1\_041016

gi|109673896 Mass: 10608 Score: 719 Queries matched: 59

hypothetical protein Ccur5\_01001212 [*Campylobacter curvus* 525.92]

1 MKKAEFIQAVADKAGLSKKDSLKVVDATLETIQAVLEKSDSISFIGFGTF

51 STADRAARKARVPGTKKVIDVPASKAVKFKVGKLLKEAVAAGAHKKGKKK

Observed	Mr(expt)	Mr(calc)	Delta	MissScore	Expect	Rank	Peptide
414.7603	827.5060	827.4752	0.0307	0	(23)	62	3 K.VIDVPASK.A
414.7693	827.5241	827.4752	0.0489	0	46	0.3	1 K.VIDVPASK.A
414.7693	827.5241	827.4752	0.0489	0	(27)	22	4 K.VIDVPASK.A
478.8122	955.6098	955.5702	0.0396	1	(13)	6e+02	9 K.KVIDVPASK.A
478.8122	955.6098	955.5702	0.0396	1	(31)	8.6	1 K.KVIDVPASK.A
478.8122	955.6098	955.5702	0.0396	1	33	5	1 K.KVIDVPASK.A
478.8219	955.6293	955.5702	0.0591	1	(16)	2.7e+02	1 K.KVIDVPASK.A
478.8219	955.6293	955.5702	0.0591	1	(22)	72	10 K.KVIDVPASK.A
546.3140	1090.6135	1090.5658	0.0477	0	72	0.00072	1 K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(32)	6.7	1 K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(59)	0.013	1 K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(46)	0.26	1 K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(56)	0.027	1 K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(49)	0.13	1 K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(56)	0.03	1 K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(58)	0.017	1 K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(62)	0.0065	1 K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(53)	0.06	1 K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(54)	0.047	1 K.AEFIQAVADK.A
546.3140	1090.6135	1090.5658	0.0477	0	(56)	0.03	1 K.AEFIQAVADK.A
546.3245	1090.6344	1090.5658	0.0685	0	(53)	0.057	1 K.AEFIQAVADK.A
546.3245	1090.6344	1090.5658	0.0685	0	(54)	0.049	1 K.AEFIQAVADK.A
610.3621	1218.7097	1218.6608	0.0489	1	89	1.3e-05	1 K.KAEFIQAVADK.A
610.3621	1218.7097	1218.6608	0.0489	1	(67)	0.0023	1 K.KAEFIQAVADK.A

610.3621	1218.7097	1218.6608	0.0489	1	(68)	0.0018	1	K.KAEFIQAVADK.A
610.3621	1218.7097	1218.6608	0.0489	1	(59)	0.016	1	K.KAEFIQAVADK.A
407.2469	1218.7188	1218.6608	0.0580	1	(49)	0.15	1	K.KAEFIQAVADK.A
610.3731	1218.7317	1218.6608	0.0709	1	(85)	3.6e-05	1	K.KAEFIQAVADK.A
610.3731	1218.7317	1218.6608	0.0709	1	(57)	0.025	1	K.KAEFIQAVADK.A
610.3731	1218.7317	1218.6608	0.0709	1	(35)	3.3	1	K.KAEFIQAVADK.A
498.9571	1493.8494	1493.7911	0.0583	2	(82)	6.6e-05	1	-.MKKAEFIQAVADK.A + Oxidation (M)
747.9468	1493.8790	1493.7911	0.0879	2	85	3.4e-05	1	-.MKKAEFIQAVADK.A + Oxidation (M)
774.4622	1546.9098	1546.8354	0.0744	1	75	0.00039	1	K.AEFIQAVADKAGLSK.K
516.6443	1546.9110	1546.8354	0.0756	1	(48)	0.2	1	K.AEFIQAVADKAGLSK.K
814.9803	1627.9460	1627.9032	0.0428	0	111	9.1e-08	1	K.VVDATLETIQAVLEK.S
543.6591	1627.9555	1627.9032	0.0523	0	(92)	6.7e-06	1	K.VVDATLETIQAVLEK.S
814.9930	1627.9714	1627.9032	0.0683	0	(93)	6.4e-06	1	K.VVDATLETIQAVLEK.S
814.9930	1627.9714	1627.9032	0.0683	0	(98)	1.7e-06	1	K.VVDATLETIQAVLEK.S
814.9930	1627.9714	1627.9032	0.0683	0	(103)	5.3e-07	1	K.VVDATLETIQAVLEK.S
814.9930	1627.9714	1627.9032	0.0683	0	(98)	1.8e-06	1	K.VVDATLETIQAVLEK.S
814.9930	1627.9714	1627.9032	0.0683	0	(103)	5.9e-07	1	K.VVDATLETIQAVLEK.S
814.9930	1627.9714	1627.9032	0.0683	0	(101)	9.2e-07	1	K.VVDATLETIQAVLEK.S
543.6695	1627.9867	1627.9032	0.0835	0	(63)	0.0051	1	K.VVDATLETIQAVLEK.S
543.6695	1627.9867	1627.9032	0.0835	0	(61)	0.0097	1	K.VVDATLETIQAVLEK.S
543.6695	1627.9867	1627.9032	0.0835	0	(44)	0.41	1	K.VVDATLETIQAVLEK.S
543.6695	1627.9867	1627.9032	0.0835	0	(35)	3.3	1	K.VVDATLETIQAVLEK.S
543.6695	1627.9867	1627.9032	0.0835	0	(24)	47	1	K.VVDATLETIQAVLEK.S
543.6695	1627.9867	1627.9032	0.0835	0	(26)	29	1	K.VVDATLETIQAVLEK.S
543.6695	1627.9867	1627.9032	0.0835	0	(36)	2.5	1	K.VVDATLETIQAVLEK.S
543.6695	1627.9867	1627.9032	0.0835	0	(31)	8.2	1	K.VVDATLETIQAVLEK.S
543.6695	1627.9867	1627.9032	0.0835	0	(32)	6.5	1	K.VVDATLETIQAVLEK.S
815.0057	1627.9969	1627.9032	0.0937	0	(89)	1.3e-05	1	K.VVDATLETIQAVLEK.S
815.0057	1627.9969	1627.9032	0.0937	0	(97)	2e-06	1	K.VVDATLETIQAVLEK.S
543.6799	1628.0179	1627.9032	0.1147	0	(24)	43	1	K.VVDATLETIQAVLEK.S
815.0185	1628.0224	1627.9032	0.1192	0	(97)	1.9e-06	1	K.VVDATLETIQAVLEK.S
815.0185	1628.0224	1627.9032	0.1192	0	(95)	3.2e-06	1	K.VVDATLETIQAVLEK.S
559.3374	1674.9905	1674.9304	0.0601	2	54	0.045	1	K.KAEFIQAVADKAGLSK.K
838.5106	1675.0066	1674.9304	0.0762	2	84	4.3e-05	1	K.AEFIQAVADKAGLSK.D
651.0589	1950.1548	1950.0607	0.0941	3	74	0.00046	1	-.MKKAEFIQAVADKAGLSK.K + Oxidation (M)

Mascot-RM3806\_tryp\_hplc#64\_gel#1\_041016

gi|109671087 Mass: 6013 Score: 267 Queries matched: 12

hypothetical protein Ccon1\_01002013 [*Campylobacter concisus* 13826]

1 SFIGFGTGTADRAARKARVPGTK**KVIDVPASK**AVKFKVGGK**LKEAVAAG**

51 **AAKKGKKK**

Observed	Mr(expt)	Mr(calc)	Delta	MissScore	Expect	Rank	Peptide
414.7603	827.5060	827.4752	0.0307	0	(23)	62	3 K.VIDVPASK.A
414.7693	827.5241	827.4752	0.0489	0	46	0.3	1 K.VIDVPASK.A
414.7693	827.5241	827.4752	0.0489	0	(27)	22	4 K.VIDVPASK.A
458.3087	914.6028	914.5185	0.0843	1	29	17	4 K.EAVAAGAAKK.G
478.8122	955.6098	955.5702	0.0396	1	(13)	6e+02	9 K.KVIDVPASK.A
478.8122	955.6098	955.5702	0.0396	1	(31)	8.6	1 K.KVIDVPASK.A
478.8122	955.6098	955.5702	0.0396	1	33	5	1 K.KVIDVPASK.A
478.8219	955.6293	955.5702	0.0591	1	(16)	2.7e+02	1 K.KVIDVPASK.A
478.8219	955.6293	955.5702	0.0591	1	(22)	72	10 K.KVIDVPASK.A
514.8415	1027.6684	1027.6025	0.0659	1	(60)	0.013	1 K.LKEAVAAGAAK.K
514.8516	1027.6886	1027.6025	0.0861	1	77	0.00023	1 K.LKEAVAAGAAK.K
578.8919	1155.7693	1155.6975	0.0718	2	84	4.7e-05	1 K.LKEAVAAGAAKK.G

Mascot-RM3806\_hplc#72\_gs3\_060216

Mass: 13007 Score: 1061 Queries matched: 25

hypothetical protein Ccon1\_01001911 [*Campylobacter concisus* 13826]

1 MAITKEDVLEFISNLSVLELSELVKEFEFEKFGVSAAPVMVAGGAVAAGGA

51 AA~~EE~~KTEFNIVLVDSGDKKINVIKVV**RALTGLGLKEAKDAVEGTPSVLK**

101 **EGVSKDEAEAAKKELEEAGAKVELK**

Observed	Mr(expt)	Mr(calc)	Delta	MissScore	Expect	Rank	Peptide
293.6949	585.3752	585.3850	-0.0098	0	27	21	1 K.INVIK.V
386.7321	771.4497	771.4854	-0.0357	0	(49)	0.22	1 R.ALTGLGLK.E
386.7497	771.4848	771.4854	-0.0006	0	50	0.14	1 R.ALTGLGLK.E
846.3858	845.3786	845.4130	-0.0345	0	44	0.62	1 K.ELEEAGAK.V
423.7111	845.4077	845.4130	-0.0053	0	(32)	9.9	1 K.ELEEAGAK.V
431.2132	860.4119	860.4239	-0.0121	1	46	0.32	1 K.DEAEAAKK.E
487.7445	973.4745	973.5080	-0.0335	1	57	0.027	1 K.KELEEAGAK.V
558.2710	1114.5274	1114.5870	-0.0596	0	44	0.6	1 K.DAVEGTPSVLK.E

617.2822	1232.5498	1232.5884	-0.0386	1	64	0.0052	1	K.EGVSKDEAEAAK.K
658.3346	1314.6546	1314.7030	-0.0485	1	54	0.054	5	K.ELEEAGAKVELK.-
681.3155	1360.6164	1360.6834	-0.0669	2	63	0.0058	1	K.EGVSKDEAEAAKK.E
718.8548	1435.6951	1435.7194	-0.0243	0	64	0.0045	1	K.TEFNIVLVDSGDK.K
481.9240	1442.7501	1442.7980	-0.0479	2	32	8.4	1	K.KELEEAGAKVELK.-
522.2700	1563.7883	1563.8144	-0.0261	1	40	1.3	1	K.TEFNIVLVDSGDKK.I
522.2802	1563.8188	1563.8144	0.0045	1	(25)	39	2	K.TEFNIVLVDSGDKK.I
565.3607	1693.0603	1693.0977	-0.0374	2	58	0.018	1	K.INVIKVRALTGLGLK.E
608.0580	1821.1520	1821.1927	-0.0406	3	29	12	1	K.KINVIKVRALTGLGLK.E
730.3503	2188.0290	2188.0858	-0.0568	3	61	0.0096	1	K.EGVSKDEAEAAKKELEEAGAK.V
759.4018	2275.1836	2275.2198	-0.0362	0	50	0.14	1	K.EDVLEFISNLSVLELSELVK.E
665.3415	2657.3369	2657.3758	-0.0389	4	60	0.015	1	K.EGVSKDEAEAAKKELEEAGAKVELK.-
897.1587	2688.4541	2688.4836	-0.0295	1	65	0.0045	1	M.AITKEDVLEFISNLSVLELSELVK.E
735.3704	2937.4526	2937.5109	-0.0583	1	36	3.4	1	K.EDVLEFISNLSVLELSELVKEFEELK.F
810.7294	3238.8883	3238.9015	-0.0132	4	59	0.015	1	K.TEFNIVLVDSGDKKINVIKVRALTGLGLK.E
838.6870	3350.7190	3350.7747	-0.0558	2	(63)	0.0067	1	M.AITKEDVLEFISNLSVLELSELVKEFEELK.F
1118.2559	3351.7459	3350.7747	0.9712	2	66	0.0033	1	M.AITKEDVLEFISNLSVLELSELVKEFEELK.F