Supplementary Materials

Top-down proteomic identification of furin-cleaved α-subunit of Shiga toxin 2 from *Escherichia coli* O157:H7 using MALDI-TOF-TOF-MS/MS

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Running title: Top-down proteomic identification of furin-cleaved α-Stx2

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Supplementary Materials

Figure S1: MS/MS of unidentified doubly charged ion at *m/z* ~ 5250 in Figure 2.

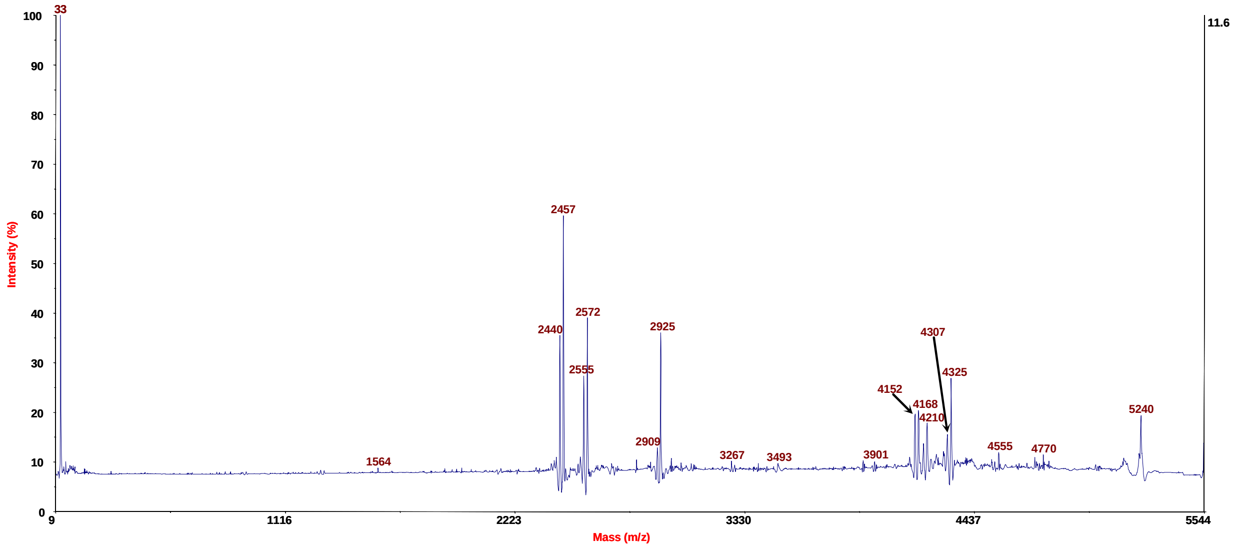

Figure S2: MS/MS of unidentified singly charged ion at *m/z* ~ 10500 in Figure 2. The doubly charged protein ion is at *m/z* ~ 5250.

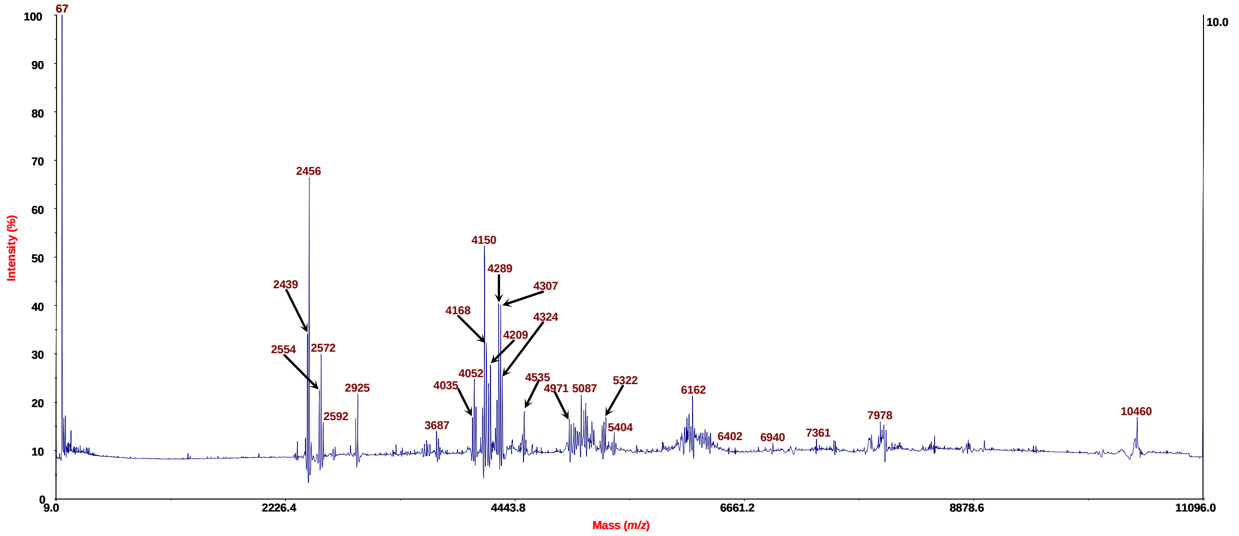

Figure S3: 1-D gel electrophoresis of ciprofloxacin-induced and ciprofloxacin-induced/furin-digested bacterial cell lysates of *E. coli* O157:H7. The gel band at ~33 kDa (#1, Lane 3) is absent from furin-digested sample (Lane 4). Gel bands at ~28 kDa and ~5-6 kDa (#3 and #9, respectively, Lane 4) are absent from non-furin-digested sample (Lane 3). Enumerated gel bands were excised, in-gel digested and analyzed by nano-LC/MS/MS and database searches. Peptide/protein identifications (below) confirmed the indicated assignments.

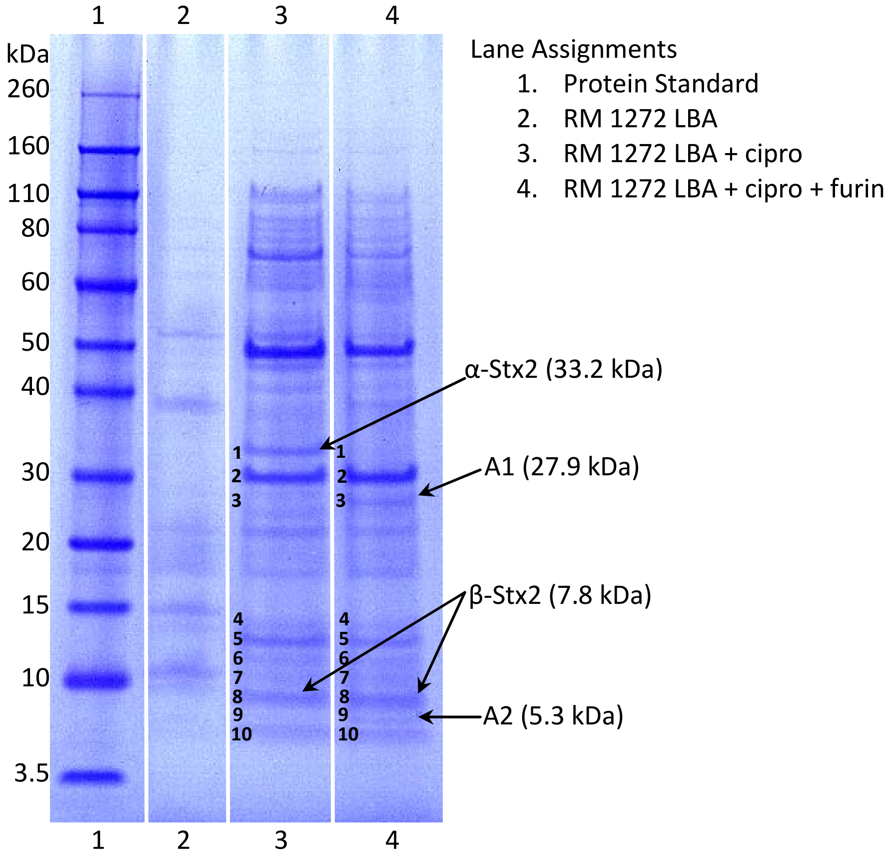

Table S1: Summary of protein identifications from bottom-up proteomics analysis of excised gel bands from lanes 3 and 4 in **Figure S3**. Shiga toxin identifications are highlighted in bold red.

Gel Lane 3

Gel band #	Name	Organism	Mass (Da)	Mascot Score	Coverage (%)	Queries Matched	Database
1	**Shiga-like toxin 2 subunit A**	**Enterobacteria phage 933W**	**35920**	**531**	**28**	**12**	**SwissProt**
	Shiga-like toxin type IIvhc	**Escherichia coli**	**35847**	**520**	**25**	**11**	**NCBI**
	Verocytotoxin 2 variant A subunit	**Escherichia coli**	**35782**	**517**	**25**	**11**	**NCBI**
	Verocytotoxin 2 variant A subunit	**Escherichia coli**	**35713**	**516**	**25**	**11**	**NCBI**
	Outer membrane protein A	Escherichia coli	37292	226	13	5	SwissProt
	Shiga toxin II A subunit	**Escherichia coli**	**35792**	**214**	**13**	**5**	**NCBI**
	Outer membrane protein A	Escherichia coli	38482	212	9	4	NCBI
	Bor protein precursor	Enterobacteria phage 933W	10642	105	25	2	NCBI
	Elongation factor Ts	Escherichia coli	30518	82	6	1	Both
	FKBP-type peptidyl-prolyl cis-trans isomerase fkpA	Escherichia coli	28864	79	7	1	Both
	Chaperone protein hchA	Escherichia coli	31276	66	3	1	Both
2	Outer membrane protein A	Escherichia coli	37292	1211	51	22	Both
	Outer membrane protein A	Escherichia coli	37291	1151	51	21	NCBI
3	50S ribosomal protein L1	Escherichia coli	24714	431	41	7	Both
	Outer membrane protein A	Escherichia coli	37292	410	19	7	Both
	30S ribosomal protein S2	Escherichia coli	26784	242	20	4	Both
	Triosephosphate isomerase	Escherichia coli	27126	54	5	1	SwissProt
4	Hypothetical protein 933Wp55	Enterobacteria phage 933W	13496	279	40	5	NCBI
	Chain A, outer membrane protein Ompx	Escherichia coli	16350	137	29	3	NCBI
	Outer membrane lipoprotein slyB	Escherichia coli	15649	132	25	2	Both
	50S ribosomal protein L24	Escherichia coli	11309	111	22	2	Both
	50S ribosomal protein L14	Escherichia coli	13646	100	27	3	SwissProt
	50S ribosomal protein L19	Escherichia coli	13125	93	20	2	SwissProt
	Outer membrane protein X	Escherichia coli	18648	89	13	2	SwissProt
	50S ribosomal protein L14	Escherichia coli	13658	83	20	2	NCBI
	50S ribosomal protein L19	Escherichia coli	13125	69	13	1	SwissProt
	Acyl carrier protein	Escherichia coli	8634	66	11	1	Both
	30S ribosomal protein S6	Escherichia coli	15177	66	8	1	Both
	Uncharacterized protein yibN	Escherichia coli	15644	61	9	1	SwissProt
5	Hypothetical protein 933Wp55	Enterobacteria phage 933W	13496	377	48	7	NCBI
	10 kDa chaperonin	Escherichia coli	10381	126	27	2	Both
	UPF0076 protein yjgF	Escherichia coli	13660	55	10	1	SwissProt
6	Hypothetical protein 933Wp55	Enterobacteria phage 933W	13496	380	48	6	NCBI
	30S ribosomal protein S10	Escherichia coli	11728	199	37	3	Both
	Major outer membrane lipoprotein	Escherichia coli	8375	153	33	2	Both
	50S ribosomal protein L7/L12	Escherichia coli	12288	133	26	3	Both
	Preprotein translocase subunit YajC	Escherichia coli	11879	105	26	2	Both
	Hypothetical protein 933Wp74	Enterobacteria phage 933W	12402	93	14	1	NCBI
	50S ribosomal protein L28	Escherichia coli	9058	70	12	1	Both
7	Major outer membrane lipoprotein	Escherichia coli	8376	293	48	5	Both
	Hypothetical protein 933Wp60	Enterobacteria phage 933W	14759	212	51	4	NCBI
	Hypothetical protein ECs1210	Escherichia coli	6914	145	45	3	NCBI
	30S ribosomal protein S16	Escherichia coli	9185	128	29	2	Both
	Bor protein precursor	Enterobacteria phage 933W	10642	91	25	2	NCBI
	Hypothetical protein 933Wp74	Enterobacteria phage 933W	12402	87	14	1	NCBI
	Transcriptional regulator HU subunit alpha	Escherichia coli	9529	82	14	1	Both
	Hypothetical protein Z4452	Escherichia coli	11045	70	9	1	Both
	30S ribosomal protein S17	Escherichia coli	9812	51	22	1	SwissProt
8	Major outer membrane lipoprotein	Escherichia coli	8375	435	62	8	SwissProt
	Shiga-like toxin 2 subunit B	**Enterobacteria phage 933W**	**9982**	**225**	**19**	**4**	**SwissProt**
	Shiga toxin II subunit B	**Escherichia coli**	**9992**	**191**	**19**	**3**	**NCBI**
	Hypothetical protein ECs1210 [Phage BP-4795]	Escherichia coli	6914	77	33	2	NCBI
	Transcriptional regulator HU subunit alpha	Escherichia coli	9529	76	14	1	Both
	Shiga-like cytotoxin subunit B	**Escherichia coli**	**9714**	**67**	**19**	**2**	**NCBI**
	Cold shock-like protein cspE	Escherichia coli	7459	56	14	1	SwissProt
	Cell division protein zapB	Escherichia coli	9397	51	13	1	SwissProt
	Lipoprotein bor homolog from lambdoid prophage DLP12	Escherichia coli	10612	47	15	1	SwissProt
9	Major outer membrane lipoprotein	Escherichia coli	8375	366	48	6	Both
	Entericidin B	Escherichia coli	4864	106	39	1	Both
10	Major outer membrane lipoprotein	Escherichia coli	8375	287	48	4	Both
	Entericidin B	Escherichia coli	4864	80	39	1	Both

Gel Lane 4

Gel band #	Name	Organism	Mass (Da)	Mascot Score	Coverage (%)	Queries Matched	Database
1	Outer membrane protein A	Escherichia coli	37292	1037	54	17	NCBI
	Outer membrane protein A	Escherichia coli	37294	958	54	18	SwissProt
	Bor protein precursor	Enterobacteria phage 933W	10642	118	25	2	NCBI
	D-ribose-binding periplasmic protein	Escherichia coli	30931	116	9	2	Both
	Shiga-like toxin 2 subunit A	**Escherichia coli**	**35924**	**54**	**3**	**1**	**SwissProt**
2	Outer membrane protein A	Escherichia coli	37292	1258	58	22	Both
	Outer membrane protein A	Escherichia coli	37291	1197	58	21	NCBI
	Chain A, outer membrane protein A (OmpA)	Escherichia coli	18864	478	46	9	NCBI
	Nucleoside-specific channel-forming protein tsx	Escherichia coli	33568	58	4	1	SwissProt
3	**Shiga-like toxin 2 subunit A**	**Enterobacteria phage 933W**	**35920**	**248**	**16**	**5**	**Both**
	Verocytotoxin 2 variant A subunit	**Escherichia coli**	**35782**	**197**	**10**	**4**	**NCBI**
4	Hypothetical protein 933Wp55	Enterobacteria phage 933W	13496	375	48	6	NCBI
	Chain A, outer membrane protein Ompx	Escherichia coli	16350	197	35	4	NCBI
	Outer membrane protein X	Escherichia coli	18648	148	18	3	SwissProt
	Outer membrane lipoprotein slyB	Escherichia coli	15649	125	29	3	SwissProt
	Putative outer membrane protein	Escherichia coli	15649	108	25	2	NCBI
	50S ribosomal protein L24	Escherichia coli	11309	73	22	2	SwissProt
5	Hypothetical protein 933Wp55	Enterobacteria phage 933W	13496	368	48	6	NCBI
	10 kDa chaperonin	Escherichia coli	10381	117	27	2	Both
	UPF0076 protein yjgF	Escherichia coli	13660	111	17	2	SwissProt
	Hypothetical protein Z5854	Escherichia coli	15273	111	15	2	NCBI
	Major outer membrane lipoprotein	Escherichia coli	8375	97	33	2	Both
	Protein tdcF	Escherichia coli	14112	55	6	1	SwissProt
6	Hypothetical protein 933Wp55	Enterobacteria phage 933W	13496	309	46	5	NCBI
	Major outer membrane lipoprotein	Escherichia coli	8375	200	48	3	Both
	UPF0092 membrane protein yajC	Escherichia coli	11879	151	26	3	Both
	Hypothetical protein 933Wp74	Enterobacteria phage 933W	12402	145	29	2	NCBI
	30S ribosomal protein S10	Escherichia coli	11728	139	24	2	Both
	Hypothetical protein Z0372	Escherichia coli	13294	120	19	2	NCBI
	50S ribosomal protein L7/L12	Escherichia coli	12288	82	17	2	Both
	30S ribosomal protein S17	Escherichia coli	9812	74	22	1	Both
7	Major outer membrane lipoprotein	Escherichia coli	8375	375	48	5	Both
	Hypothetical protein 933Wp60	Enterobacteria phage 933W	14759	228	40	4	NCBI
	Shiga-like toxin 2 subunit B	**Enterobacteria phage 933W**	**9982**	**155**	**19**	**3**	**SwissProt**
	Shiga toxin II subunit B	**Escherichia coli**	**9992**	**120**	**19**	**2**	**NCBI**
	Bor protein precursor	Enterobacteria phage 933W	10642	102	25	2	NCBI
	Hypothetical protein ECs1210	Escherichia coli	6914	94	38	2	NCBI
	Cold shock-like protein cspC	Escherichia coli	7398	59	17	1	SwissProt
	DNA-binding protein HU-alpha	Escherichia coli	9529	50	14	1	SwissProt
8	Major outer membrane lipoprotein	Escherichia coli	8375	268	48	5	Both
	Shiga-like toxin 2 subunit B	**Escherichia coli**	**9982**	**244**	**30**	**5**	**SwissProt**
	Shiga toxin II subunit B	**Escherichia coli**	**9992**	**208**	**30**	**4**	**NCBI**
	Shiga toxin 2 B subunit	**Escherichia coli**	**10011**	**200**	**30**	**4**	**NCBI**
	Variant Shiga toxin type 2 B subunit	**Escherichia coli**	**9951**	**108**	**30**	**3**	**NCBI**
9	Major outer membrane lipoprotein	Escherichia coli	8375	324	48	7	Both
	Shiga toxin 2d subunit A	**Escherichia coli**	**35873**	**110**	**11**	**2**	**NCBI**
	Shiga-like toxin 2 subunit A	**Enterobacteria phage 933W**	**35920**	**108**	**11**	**2**	**SwissProt**
	Verocytotoxin 2 variant A subunit	**Escherichia coli**	**35713**	**103**	**11**	**2**	**NCBI**
	Entericidin B	Escherichia coli	4864	78	39	1	Both
10	Major outer membrane lipoprotein	Escherichia coli	8375	141	33	2	Both

Table S2: Bottom-up peptide/protein identifications of excised gel bands from gel lanes 3 and 4 shown in **Figure S3**. Sequence coverage of α-Stx2 (boxed in red) also displayed and discussed in **Figure 4**.

Gel lane #3, gel band #1

SwissProt

Mascot Score: 531   Queries Matched: 12
Protein ID: Shiga-like toxin 2 subunit A [Enterobacteria phage 933W]
Calculated Mr = 35920; Calculated pI = 8.68

```
  1 MKCILFKWVL CLLLGFSSVS YSREFTIDFS TQQSYVSSLN SIRTEISTPL
 51 EHISQGTTSV SVINHTPPGS YFAVDIRGLD VYQARFDHLR LIIEQNNLYV
101 AGFVNTATNT FYRFSDFTHI SVPGVTTVSM TTDSSYTTLQ RVAALERSGM
151 QISRHSLVSS YLALMEFSGN TMTRDASRAV LRFVTVTAEA LRFRQIQREF
201 RQALSETAPV YTMTPGDVDL TLNWGRISNV LPEYRGEDGV RVGRISFNNI
251 SAILGTVAVI LNCHHQGARS VRAVNEESQP ECQITGDRPV IKINNTLWES
301 NTAAAFLNRK SQFLYTTGK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
461.2583  920.5020   920.4716   0.0304  0     47     0.068     1     U       R.GLDVYQAR.F
472.7600  943.5055   943.4836   0.0219  1     28     6.3       1     U       R.GEDGVRVGR.I
523.2890 1044.5634   1043.5288  1.0346  0     11     2.9e+02   9     U       K.SQFLYTTGK.-
545.8068 1089.5990   1089.5818  0.0172  0     59     0.0053    1     U       R.ISNVLPEYR.G
553.8237 1105.6328   1105.6132  0.0196  0     51     0.026     1     U       R.FVTVTAEALR.F
470.6205 1408.8395   1408.7827  0.0568  1     34     1.4       1     U       R.FVTVTAEALRFR.Q
530.6258 1588.8556   1588.8110  0.0446  1     32     2.1       1     U       R.GLDVYQARFDHLR.L
568.6395 1702.8966   1702.8638  0.0327  1     39     0.39      1     U       R.ISNVLPEYRGEDGVR.V
645.6746 1934.0019   1933.9646  0.0373  0     54     0.012     1     U       K.INNTLWESNTAAAFLNR.K
672.7059 2015.0960   2015.0548  0.0412  2     36     0.74      1     U       R.ISNVLPEYRGEDGVRVGR.I
688.3930 2062.1570   2062.0595  0.0975  1     66     0.00061   1     U       K.INNTLWESNTAAAFLNRK.S
757.3957 2269.1652   2269.1008  0.0644  0     76     6.8e-05   1     U       R.AVNEESQPECQITGDRPVIK.I
```

SwissProt

Mascot Score: 226   Queries Matched: 5
Protein ID: Outer membrane protein A [Escherichia coli O157:H7]
Calculated Mr = 37292; Calculated pI = 5.99

```
  1 MKKTAIAIAV ALAGFATVAQ AAPKDNTWYT GAKLGWSQYH DTGFINNNGP
 51 THENQLGAGA FGGYQVNPYV GFEMGYDWLG RMPYKGSVEN GAYKAQGVQL
101 TAKLGYPITD DLDIYTRLGG MVWRADTKSN VYGKNHDTGV SPVFAGGVEY
151 AITPEIATRL EYQWTNNIGD AHTIGTRPDN GMLSLGVSYR FGQGEAAPVV
201 APAPAPAPEV QTKHFTLKSD VLFNFNKATL KPEGQAALDQ LYSQLSNLDP
251 KDGSVVVLGY TDRIGSDAYN QGLSERRAQS VVDYLISKGI PADKISARGM
301 GESNPVTGNT CDNVKQRAAL IDCLAPDRRV EIEVKGIKDV VTQPQA
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
542.2925  1082.5704  1082.5397  0.0307  0     41     0.23      1     U       K.SDVLFNFNK.A
705.3258  1408.6371  1408.6582 -0.0211  0     71     0.00023   1     U       R.IGSDAYNQGLSER.R
689.9025  1377.0925  1377.7905  0.0289  1     41     0.24      1     U       R.RAQSVVDYLISK.G
611.8431  1221.6717  1221.6605  0.0112  0     58     0.0052    1     U       R.AQSVVDYLISK.G
578.3323  1154.6500  1154.6295  0.0204  1     16     86        4     U       K.GIKDVVTQPQA.-
```

SwissProt & NCBI

Mascot Score: 82   Queries Matched: 1
Protein ID: Elongation factor Ts [Escherichia coli O157:H7]
Calculated Mr = 30518; Calculated pI = 5.22

```
      1 MAEITASLVK ELRERTGAGM MDCKKALTEA NGDIELAIEN MRKSGAIKAA
     51 KKAGNVAADG VIKTKIDGNY GIILEVNCQT DFVAKDAGFQ AFADKVLDAA
    101 VAGKITDVEV LKAQFEEERV ALVAKIGENI NIRRVAALEG DVLGSYQHGA
    151 RIGVLVAAKG ADEELVKHIA MHVAASKPEF IKPEDVSAEV VEKEYQVQLD
    201 IAMQSGKPKE IAEKMVEGRM KKFTGEVSLT GQPFVMEPSK TVGQLLKEHN
    251 AEVTGFIRFE VGEGIEKVET DFAAEVAAMS KQS
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
581.6495  1741.9266  1741.8747  0.0519  0     82     2e-05     1     U       R.IGSDAYNQGLSER
```

SwissProt & NCBI

Mascot Score: 79 Queries Matched: 1

Protein ID: FKBP-type peptidyl-prolyl cis-trans isomerase fkpA [Escherichia coli O157:H7]

Calculated Mr = 28864; Calculated pI = 8.39

```
      1 MKSLFKVTLL ATTMAVALHA PITFAAEAAK PATTADSKAA FKNDDQKSAY
     51 ALGASLGRYM ENSLKEQEKL GIKLDKDQLI AGVQDAFADK SKLSDQEIEQ
    101 TLQAFEARVK SSAQAKMEKD AADNEAKGKE YREKFAKEKG VKTSSTGLVY
    151 QVVEAGKGEA PKDSDTVVVN YKGTLIDGKE FDNSYTRGEP LSFRLDGVIP
    201 GWTEGLKNIK KGGKIKLVIP PELAYGKAGV PGIPPNSTLV FDVELLDVKP
    251 APKADAKPEA DAKAADSAKK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
674.3718  2020.0937  2020.0477  0.0460  1     79     3.6e-05   1     U       K.TSSTGLVYQVVEAGKGEAPK.D
```

SwissProt & NCBI

Mascot Score: 66 Queries Matched: 1

Protein ID: Chaperone protein hchA [Escherichia coli O157:H7]

Calculated Mr = 31276; Calculated pI = 5.54

```
      1 MTVQTSKNPQ VDIAEDNAFF PSEYSLSQYT SPVSDLDGVD YPKPYRGKHK
     51 ILVIAADERY LPTDNGKLFS TGNHPIETLL PLYHLHAAGF EFEVATISGL
    101 MTKFEYWAMP QKDEKVMPFF EQHKSLFRNP KKLADVVASL NADSEYAAIF
    151 VPGGHGALIG LPESQDVAAA LQWAIKNDRF VISLCHGPAA FLALRHGDNP
    201 LNGYSICAFP DAADKQTPEI GYMPGHLTWY FGEELKKMGM NIINDDITGR
    251 VHKDRKLLTG DSPFAANALG KLAAQEMLAA YAG
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
500.3078   998.6011   998.5760  0.0250  0     66     0.00093   1     U       K.ILVIAADER.Y
```

NCBI

Mascot Score: 520 Queries Matched: 11

Protein ID: Shiga-like toxin type IIvhc [Escherichia coli]

Calculated Mr = 35847; Calculated pI = 7.74

```
      1 MKCILFKWVL CLLLGFSSVS YSREFTIDFS TQQSYVSSLN SIRTEVSTPL
     51 EHISQGTTSV SVINHTPPGS YFAVDIRGLD VYQARFDHLR LIIEQNNLYV
    101 AGFVNTATNT FYRFSDFTHI SVPGVTTVSM TTDSSYTTLQ RVAALERSGM
    151 QISRHSLVSS YLALMEFSGN TMTRDASRAV LRFVTVTAEA LRFRQIQREF
    201 RQALSETAPV YTMTPGDVDL TLNWGRISNV LPEYRGEDGV RVGRISFNNI
    251 SAILGTVAVI LNCHHQGARS VRAVNEESQP ECQITGDRPV IKINNTLWES
    301 NTAAAFLNRK SQSLYTTGE
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
461.2583  920.5020   920.4716   0.0304  0     47     1.5       1             R.GLDVYQAR.F
472.7600  943.5055   943.4836   0.0219  1     28     1.3e+02   6             R.GEDGVRVGR.I
```

545.8068	1089.5990	1089.5818	0.0172	0	59	0.11	1		R.ISNVLPEYR.G
553.8237	1105.6328	1105.6132	0.0196	0	51	0.52	2		R.FVTVTAEALR.F
470.6205	1408.8395	1408.7827	0.0568	1	34	28	1		R.FVTVTAEALRFR.Q
530.6258	1588.8556	1588.8110	0.0446	1	32	43	7		R.GLDVYQARFDHLR.L
568.6395	1702.8966	1702.8638	0.0327	1	39	7.6	1		R.ISNVLPEYRGEDGVR.V
645.6746	1934.0019	1933.9646	0.0373	0	54	0.24	1		K.INNTLWESNTAAAFLNR.K
672.7059	2015.0960	2015.0548	0.0412	2	36	15	1		R.ISNVLPEYRGEDGVRVGR.I
688.3930	2062.1570	2062.0595	0.0975	1	66	0.013	1		K.INNTLWESNTAAAFLNRK.S
757.3957	2269.1652	2269.1008	0.0644	0	76	0.0014	1		R.AVNEESQPECQITGDRPVIK.I

NCBI

Mascot Score: 517   Queries Matched: 11
Protein ID: Verocytotoxin 2 variant A subunit [Escherichia coli]
Calculated Mr = 35782; Calculated pI = 7.74

```
  1 MKCILFKWVL CLLLGFSSVS YSREFTIDFS TQQSYVSSLN SIRTEISTPL
 51 EHISQGTTSV SVINHTPPGS YFAVDIRGLD VYQARFDHLR LIIEQNNLYV
101 AGFVNTATNT FYRFSDFTHI SVPDVTTVSM TTDSSNTTLQ RVAALEXSGM
151 QISRHSXVSS XLALMEXXGN TMTRDASRAV LRFVTVTAEA LRFRQIQREF
201 RQALSETAPV YTMTPGDVDL TLNWGRLSNV LPEYRGEDGV RVGRISFNNI
251 SAILGTVAVI LNCHHQGARS VRAVNEESQP ECQITGDRPV IKINNTLWES
301 NTAAAFLNRK SQXLYTTGK
```

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
461.2583	920.5020	920.4716	0.0304	0	47	1.5	1		R.GLDVYQAR.F
472.7600	943.5055	943.4836	0.0219	1	28	1.3e+02	6		R.GEDGVRVGR.I
545.8068	1089.5990	1089.5818	0.0172	0	59	0.11	1	U	R.LSNVLPEYR.G
553.8237	1105.6328	1105.6132	0.0196	0	51	0.52	2		R.FVTVTAEALR.F
470.6205	1408.8395	1408.7827	0.0568	1	34	28	1		R.FVTVTAEALRFR.Q
530.6258	1588.8556	1588.8110	0.0446	1	32	43	7		R.GLDVYQARFDHLR.L
568.6395	1702.8966	1702.8638	0.0327	1	39	7.6	1	U	R.LSNVLPEYRGEDGVR.V
645.6746	1934.0019	1933.9646	0.0373	0	54	0.24	1		K.INNTLWESNTAAAFLNR.K
672.7059	2015.0960	2015.0548	0.0412	2	36	15	1	U	R.LSNVLPEYRGEDGVRVGR.I
688.3930	2062.1570	2062.0595	0.0975	1	66	0.013	1		K.INNTLWESNTAAAFLNRK.S
757.3957	2269.1652	2269.1008	0.0644	0	76	0.0014	1		R.AVNEESQPECQITGDRPVIK.I

NCBI

Mascot Score: 516   Queries Matched: 11
Protein ID: Verocytotoxin 2 variant A subunit [Escherichia coli]
Calculated Mr = 35713; Calculated pI = 8.35

```
  1 MKCILFKWVL CLXLGFSSVS YSREFTIDFS TQQSYVSSLN SIRTEISTPL
 51 EHISQGTTSV SVINHTPPGS YFAVDIRGLD VYQARFDHLR LIIEQNNLYV
101 AGFVNTATNT FYRFSDFTHI SVPGVTTVSM TTDSSYTTLQ RVAALERSGM
151 QISRHSLVSS YLALMEFSGN TMTRDASRAV LRFVTVTAEA LRFRQIQREF
201 RQALSETAPV YTMTPGDVDL TLNWGRISNV LPEYRGEDGV RVGRISFNNI
251 SAILGTVAVI LNCHHQGARS VRAVNEESXP ECQITGDRPV IKINNTLWES
301 NTAAAFLNRK SQSLYTTG
```

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
461.2583	920.5020	920.4716	0.0304	0	47	1.5	1		R.GLDVYQAR.F
472.7600	943.5055	943.4836	0.0219	1	28	1.3e+02	6		R.GEDGVRVGR.I
545.8068	1089.5990	1089.5818	0.0172	0	59	0.11	1		R.ISNVLPEYR.G
553.8237	1105.6328	1105.6132	0.0196	0	51	0.52	2		R.FVTVTAEALR.F
470.6205	1408.8395	1408.7827	0.0568	1	34	28	1		R.FVTVTAEALRFR.Q
530.6258	1588.8556	1588.8110	0.0446	1	32	43	7		R.GLDVYQARFDHLR.L
568.6395	1702.8966	1702.8638	0.0327	1	39	7.6	1		R.ISNVLPEYRGEDGVR.V
645.6746	1934.0019	1933.9646	0.0373	0	54	0.24	1		K.INNTLWESNTAAAFLNR.K
672.7059	2015.0960	2015.0548	0.0412	2	36	15	1		R.ISNVLPEYRGEDGVRVGR.I
688.3930	2062.1570	2062.0595	0.0975	1	66	0.013	1		K.INNTLWESNTAAAFLNRK.S
757.3957	2269.1652	2269.1372	0.0280	0	76	0.0014	1	U	R.AVNEESKPECQITGDRPVIK.I

NCBI

Mascot Score: 214 Queries Matched: 5
Protein ID: Shiga toxin II A subunit [Escherichia coli]
Calculated Mr = 35792; Calculated pI = 7.774

```
  1 MKCILLKWVL CLLLGFSSVS YSREFTIDFS TQQSYVSSLN SIRTEISTPL
 51 EHISQGTTSV SVINHTPPGS YFAVDIRGLD VYQARFDHLR LIIEQNNLYV
101 AGFVNTATNT FYRFSDFAHI SVPGVTTVSM TTDSSYTTLQ RVAALERSGM
151 QISRHSLVSS YLALMEFSGN AMTRDASRAV LRFVTVTAEA LRFRQIQREF
201 RLALSETAPV YTMTPEEVDL TLNWGRISNV LPEFRGEGGV RVGRISFNNI
251 SAILGTVAVI LNCHHQGARS VRSVNEEIQP ECQITGDRPV IRLNNTLWES
301 NTAAAFLNRR AHSLNTSGE
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
461.2583  920.5020   920.4716   0.0304  0     47     1.5      1             R.GLDVYQAR.F
553.8237 1105.6328  1105.6132   0.0196  0     51     0.52     2             R.FVTVTAEALR.F
470.6205 1408.8395  1408.7827   0.0568  1     34     28       1             R.FVTVTAEALRFR.Q
530.6258 1588.8556  1588.8110   0.0446  1     32     43       7             R.GLDVYQARFDHLR.L
645.6746 1934.0019  1933.9646   0.0373  0     54     0.24     1      U      R.LNNTLWESNTAAAFLNR.R
```

NCBI

Mascot Score: 212 Queries Matched: 4
Protein ID: Outer membrane protein A [Escherichia coli]
Calculated Mr = 38482; Calculated pI = 5.46

```
  1 LDDNEAQKMK KTAIAIAVAL AGFATVAQAA PKDNTWYTGA KLGWSQYHDT
 51 GFIPNNGPTH ENQLGAGAFG GYQVNPYVGF EMGYDWLGRM PYKGDNINGA
101 YKAQGVQLTA KLGYPITDDL DVYTRLGGMV WRADTKANVP GGASFKDHDT
151 GVSPVFAGGV EYAITPEIAT RLEYQWTNNI GDAHTIGTRP DNGMLSLGVS
201 YRFGQGEAAP VVAPAPAPAP EVQTKHFTLK SDVLFNFNKA TLKPEGQAAL
251 DQLYSQLSNL DPKDGSVVVL GYTDRIGSDA YNQGLSERRA QSVVDYLISK
301 GIPADKISAR GMGESNPVTG NTCDNVKQRA ALIDCLAPDR RVEIEVKGIK
351 DVVTQPQA
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
542.2925 1082.5704  1082.5397   0.0307  0     41     4.6      1      U      K.SDVLFNFNK.A
611.8431 1221.6717  1221.6605   0.0112  0     58     0.11     1      U      R.AQSVVDYLISK.G
689.9025 1377.7905  1377.7616   0.0289  1     41     4.9      1      U      R.RAQSVVDYLISK.G
705.3258 1408.6371  1408.6582  -0.0211  0     71     0.0046   1      U      R.IGSDAYNQGLSER.R
```

NCBI

Mascot Score: 105 Queries Matched: 2
Protein ID: Bor protein precursor [Enterobacteria phage 933W]
Calculated Mr = 10642; Calculated pI = 9.15

```
  1 MKKMLLATAL ALLITGCAQQ TFTVQNKQTA VAPKETITHH FFVSGIGQKK
 51 TVDAAKICGG TENVVKTETQ QTFVNGLLGF ITLGIYTPLE ARVYCSQ
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
538.7791 1075.5437  1075.5332   0.0105  0     57     0.15     1      U      K.ICGGTENVVK.T
567.6513 1699.9322  1699.8682   0.0639  0     47     1.1      1      U      K.ETITHHFFVSGIGQK.K
```

Gel lane #3, gel band #2

SwissProt & NCBI

Mascot Score: 1211 Queries Matched: 22
Protein ID: Outer membrane protein A [Escherichia coli O157:H7]

Calculated Mr = 37292; Calculated pI = 5.99

```
  1 MKKTAIAIAV ALAGFATVAQ AAPKDNTWYT GAKLGWSQYH DTGFINNNGP
 51 THENQLGAGA FGGYQVNPYV GFEMGYDWLG RMPYKGSVEN GAYKAQGVQL
101 TAKLGYPITD DLDIYTRLGG MVWRADTKSN VYGKNHDTGV SPVFAGGVEY
151 AITPEIATRL EYQWTNNIGD AHTIGTRPDN GMLSLGVSYR FGQGEAAPVV
201 APAPAPAPEV QTKHFTLKSD VLFNFNKATL KPEGQAALDQ LYSQLSNLDP
251 KDGSVVVLGY TDRIGSDAYN QGLSERRAQS VVDYLISKGI PADKISARGM
301 GESNPVTGNT CDNVKQRAAL IDCLAPDRRV EIEVKGIKDV VTQPQA
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
409.7268  817.4391   817.4269   0.0122  0     57     0.0081    1             R.LGGMVWR.A
417.7238  833.4330   833.4218   0.0112  0    (55)    0.013     1             R.LGGMVWR.A + Oxidation (M)
436.7678  871.5210   871.5127   0.0083  1     46     0.1       1             R.RVEIEVK.G
458.2761  914.5377   914.5185   0.0192  0     56     0.012     1     U       K.AQGVQLTAK.L
462.7338  923.4530   923.4348   0.0182  0     27     5.4       1     U       K.GSVENGAYK.A
514.3034 1026.5923   1026.5822  0.0102  1     52     0.022     1             K.GIPADKISAR.G
528.2462 1054.4779   1054.4720  0.0060  0     52     0.02      1             K.DNTWYTGAK.L
542.2821 1082.5496   1082.5397  0.0100  0     52     0.021     1             K.SDVLFNFNK.A
578.3323 1154.6500   1154.6295  0.0204  1     36     0.89      1     U       K.GIKDVVTQPQA.-
607.8252 1213.6358   1213.6125  0.0233  0     88     5.5e-06   1             R.AALIDCLAPDR.R
611.8431 1221.6717   1221.6605  0.0112  0     58     0.0055    1     U       R.AQSVVDYLISK.G
640.8358 1279.6570   1279.6409  0.0161  0     47     0.061     1     U       K.DGSVVVLGYTDR.I
457.5893 1369.7461   1369.7136  0.0325  1     36     0.94      1             R.AALIDCLAPDRR.V
689.8908 1377.7671   1377.7616  0.0055  1     75     9.8e-05   1     U       R.RAQSVVDYLISK.G
705.3377 1408.6608   1408.6582  0.0025  0    102     2.2e-07   1     U       R.IGSDAYNQGLSER.R
487.2429 1458.7069   1458.6813  0.0257  1     56     0.0085    1     U       R.MPYKGSVENGAYK.A + Oxidation (M)
827.9098 1653.8050   1653.8250 -0.0200  0     95     8.9e-07   1             K.LGYPITDDLDIYTR.L
552.2931 1653.8576   1653.8250  0.0326  0    (36)    0.71      1             K.LGYPITDDLDIYTR.L
898.3925 1794.7704   1794.7513  0.0192  0     97     5.3e-07   1     U       R.GMGESNPVTGNTCDNVK.Q + Oxidation
(M)
690.0547 2067.1424   2067.1146  0.0278  2     31     2.4       1     U       R.AALIDCLAPDRRVEIEVK.G
693.9831 2078.9274   2078.9110  0.0164  1     78     4.1e-05   1     U       R.GMGESNPVTGNTCDNVKQR.A + Oxidation
(M)
744.7395 2231.1968   2231.1586  0.0382  0     76     6.1e-05   1     U       R.FGQGEAAPVVAPAPAPAPEVQTK.H
```

<u>NCBI</u>

Mascot Score: 1151   Queries Matched: 21
Protein ID: Outer membrane protein A [Escherichia coli]
Calculated Mr = 37291; Calculated pI = 6.53

```
  1 MKKTAIAIAV ALAGFATVAQ AAPKDNTWYT GAKLGWSQYH DTGFINNNGP
 51 THENQLGAGA FGGYQVNPYV GFEMGYDWLG RMPYKGSVKN GAYKAQGVQL
101 TAKLGYPITD DLDIYTRLGG MVWRADTKSN VYGKNHDTGV SPVFAGGVEY
151 AITPEIATRL EYQWTNNIGD AHTIGTRPDN GMLSLGVSYR FGQGEAAPVV
201 APAPAPAPEV QTKHFTLKSD VLFNFNKATL KPEGQAALDQ LYSQLSNLDP
251 KDGSVVVLGY TDRIGSDAYN QGLSERRAQS VVDYLISKGI PADKISARGM
301 GESNPVTGNT CDNVKQRAAL IDCLAPDRRV EIEVKGIKDV VTQPQA
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
409.7268  817.4391   817.4269   0.0122  0     57     0.16      1             R.LGGMVWR.A
417.7238  833.4330   833.4218   0.0112  0    (55)    0.26      1             R.LGGMVWR.A + Oxidation (M)
436.7678  871.5210   871.5127   0.0083  1     46     2         2             R.RVEIEVK.G
458.2761  914.5377   914.5185   0.0192  0     56     0.24      1             K.AQGVQLTAK.L
514.3034  1026.5923  1026.5822  0.0102  1     52     0.43      1             K.GIPADKISAR.G
528.2462  1054.4779  1054.4720  0.0060  0     52     0.4       1             K.DNTWYTGAK.L
542.2821  1082.5496  1082.5397  0.0100  0     52     0.41      1             K.SDVLFNFNK.A
578.3323  1154.6500  1154.6295  0.0204  1     36     18        5             K.GIKDVVTQPQA.-
607.8252  1213.6358  1213.6125  0.0233  0     88     0.00011   1             R.AALIDCLAPDR.R
611.8431  1221.6717  1221.6605  0.0112  0     58     0.11      1             R.AQSVVDYLISK.G
640.8358  1279.6570  1279.6409  0.0161  0     47     1.3       2             K.DGSVVVLGYTDR.I
457.5893  1369.7461  1369.7136  0.0325  1     36     19        5             R.AALIDCLAPDRR.V
689.8908  1377.7671  1377.7616  0.0055  1     75     0.002     1             R.RAQSVVDYLISK.G
705.3377  1408.6608  1408.6582  0.0025  0    102     4.4e-06   1             R.IGSDAYNQGLSER.R
487.2429  1458.7069  1457.7337  0.9733  2     23     3.5e+02   6      U      R.MPYKGSVKNGAYK.A + Oxidation (M)
827.9098  1653.8050  1653.8250 -0.0200  0     95     1.8e-05   1             K.LGYPITDDLDIYTR.L
```

```
552.2931  1653.8576  1653.8250  0.0326  0     (36)   15       1            K.LGYPITDDLDIYTR.L
898.3925  1794.7704  1794.7513  0.0192  0     97     1.1e-05  1            R.GMGESNPVTGNTCDNVK.Q + Oxidation
(M)
690.0547  2067.1424  2067.1146  0.0278  2     31     49       2            R.AALIDCLAPDRRVEIEVK.G
693.9831  2078.9274  2078.9110  0.0164  1     78     0.00089  1            R.GMGESNPVTGNTCDNVKQR.A + Oxidation
(M)
744.7395  2231.1968  2231.1586  0.0382  0     76     0.0013   1            R.FGQGEAAPVVAPAPAPAPEVQTK.H
```

Gel lane #3, gel band #3

SwissProt & NCBI

Mascot Score: 431   Queries Matched: 7
Protein ID: 50S ribosomal protein L1 [Escherichia coli O157:H7]
Calculated Mr = 24714; Calculated pI = 9.64

```
  1 MAKLTKRMRV IREKVDATKQ YDINEAIALL KELATAKFVE SVDVAVNLGI
 51 DARKSDQNVR GATVLPHGTG RSVRVAVFTQ GANAEAAKAA GAELVGMEDL
101 ADQIKKGEMN FDVVIASPDA MRVVGQLGQV LGPRGLMPNP KVGTVTPNVA
151 EAVKNAKAGQ VRYRNDKNGI IHTTIGKVDF DADKLKENLE ALLVALKKAK
201 PTQAKGVYIK KVSISTTMGA GVAVDQAGLS ASVN
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
533.2997  1064.5849  1064.5727  0.0122  0     37     0.67     1             R.GATVLPHGTGR.S
611.8745  1221.7344  1221.7194  0.0151  0     75     0.00011  2     U       R.VVGQLGQVLGPR.G
642.8743  1283.7341  1283.7085  0.0256  0     70     0.00034  1             K.VGTVTPNVAEAVK.N
688.8781  1375.7416  1375.7096  0.0321  0     91     2.8e-06  1             R.VAVFTQGANAEAAK.A
695.8940  1389.7735  1389.7503  0.0231  0     63     0.0017   1     U       K.QYDINEAIALLK.E
582.9748  1745.9026  1745.8505  0.0521  0     71     0.00027  1     U       K.AAGAELVGMEDLADQIK.K + Oxidation
(M)
637.9773  1910.9101  1910.8866  0.0235  1     25     9.3      1     U       K.KGEMNFDVVIASPDAMR.V + 2 Oxidation
(M)
```

SwissProt & NCBI

Mascot Score: 410   Queries Matched: 7
Protein ID: Outer membrane protein A [Escherichia coli O157:H7]
Calculated Mr = 37292; Calculated pI = 5.99

```
  1 MKKTAIAIAV ALAGFATVAQ AAPKDNTWYT GAKLGWSQYH DTGFINNNGP
 51 THENQLGAGA FGGYQVNPYV GFEMGYDWLG RMPYKGSVEN GAYKAQGVQL
101 TAKLGYPITD DLDIYTRLGG MVWRADTKSN VYGKNHDTGV SPVFAGGVEY
151 AITPEIATRL EYQWTNNIGD AHTIGTRPDN GMLSLGVSYR FGQGEAAPVV
201 APAPAPAPEV QTKHFTLKSD VLFNFNKATL KPEGQAALDQ LYSQLSNLDP
251 KDGSVVVLGY TDRIGSDAYN QGLSERRAQS VVDYLISKGI PADKISARGM
301 GESNPVTGNT CDNVKQRAAL IDCLAPDRRV EIEVKGIKDV VTQPQA
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
458.2786  914.5426   914.5185   0.0241  0     43     0.23     1     U       K.AQGVQLTAK.L
542.2850 1082.5555  1082.5397   0.0158  0     58     0.0046   1             K.SDVLFNFNK.A
611.8524 1221.6903  1221.6605   0.0298  0     49     0.043    1     U       R.AQSVVDYLISK.G
640.8410 1279.6675  1279.6409   0.0267  0     47     0.056    1     U       K.DGSVVVLGYTDR.I
689.8966 1377.7786  1377.7616   0.0170  1     47     0.071    1     U       R.RAQSVVDYLISK.G
705.3473 1408.6800  1408.6582   0.0217  0     83     1.8e-05  1     U       R.IGSDAYNQGLSER.R
827.9379 1653.8613  1653.8250   0.0363  0     87     5.6e-06  1     U       K.LGYPITDDLDIYTR.L
```

SwissProt & NCBI

Mascot Score: 242   Queries Matched: 4
Protein ID: 30S ribosomal protein S2 [Escherichia coli O157:H7]
Calculated Mr = 26784; Calculated pI = 6.61

```
  1 MATVSMRDML KAGVHFGHQT RYWNPKMKPF IFGARNKVHI INLEKTVPMF
 51 NEALAELNKI ASRKGKILFV GTKRAASEAV KDAALSCDQF FVNHRWLGGM
101 LTNWKTVRQS IKRLKDLETQ SQDGTFDKLT KKEALMRTRE LEKLENSLGG
151 IKDMGGLPDA LFVIDADHEH IAIKEANNLG IPVFAIVDTN SDPDGVDFVI
201 PGNDDAIRAV TLYLGAVAAT VREGRSQDLA SQAEESFVEA E
```

```
Observed  Mr(expt)   Mr(calc)   Delta    Miss  Score  Expect    Rank  Unique  Peptide
483.3040  964.5935   964.5705   0.0230   0     49     0.046     1     U       K.VHIINLEK.T
541.8075 1081.6005  1081.5743   0.0262   0     43     0.16      1     U       K.MKPFIFGAR.N + Oxidation (M)
796.9173 1591.8201  1591.7916   0.0286   0     69     0.00035   1     U       K.TVPMFNEALAELNK.I + Oxidation (M)
689.6975 2066.0707  2066.0532   0.0176   2     81     2.1e-05   1     U       R.LKDLETQSQDGTFDKLTK.K
```

SwissProt

Mascot Score: 54   Queries Matched: 1
Protein ID: Triosephosphate isomerase [Escherichia coli O157:H7]
Calculated Mr = 27126; Calculated pI = 5.64

```
  1 MRHPLVMGNW KLNGSRHMVH ELVSNLRKEL AGVAGCAVAI APPEMYIDMA
 51 KREAEGSHIM LGAQNVDLNL SGAFTGETSA AMLKDIGAQY IIIGHSERRT
101 YHKESDELIA KKFAVLKEQG LTPVLCIGET EAENEAGKTE EVCARQIDAV
151 LKTQGAAAFE GAVIAYEPVW AIGTGKSATP AQAQAVHKFI RDHIAKVDAN
201 IAEQVIIQYG GSVNASNAAE LFAQPDIDGA LVGGASLKAD AFAVIVKAAE
251 AAKQA
```

```
Observed  Mr(expt)   Mr(calc)   Delta    Miss  Score  Expect    Rank  Unique  Peptide
524.6243 1570.8512  1570.8103   0.0408   0     54     0.013     1     U       K.DIGAQYIIIGHSER.R
```

Gel lane #3, gel band #4

SwissProt & NCBI

Mascot Score: 132   Queries Matched: 2
Protein ID: Outer membrane lipoprotein slyB [Escherichia coli O157:H7]
Calculated Mr = 15649; Calculated pI = 9.36

```
  1 MIKRVLVVSM VGLSLVGCVN NDTLSGDVYT ASEAKQVQNV SYGTIVNVRP
 51 VQIQGGDDSN VIGAIGGAVL GGFLGNTVGG GTGRSLATAA GAVAGGVAGQ
101 GVQSAMNKTQ GVELEIRKDD GNTIMVVQKQ GNTRFSPGQR VVLASNGSQV
151 TVSPR
```

```
Observed  Mr(expt)   Mr(calc)   Delta    Miss  Score  Expect    Rank  Unique  Peptide
757.4202 1512.8259  1512.8260  -0.0001   0     108    5.1e-08   1     U       R.VVLASNGSQVTVSPR.-
711.3764 2131.1075  2131.0692   0.0383   0     23     12        2     U       R.SLATAAGAVAGGVAGQGVQSAMNK.T +
Oxidation (M)
```

SwissProt & NCBI

Mascot Score: 111   Queries Matched: 2
Protein ID: 50S ribosomal protein L24 [Escherichia coli O157:H7]
Calculated Mr = 11309; Calculated pI = 10.21

```
  1 MAAKIRRDDE VIVLTGKDKG KRGKVKNVLS SGKVIVEGIN LVKKHQKPVP
 51 ALNQPGGIVE KEAAIQVSNV AIFNAATGKA DRVGFRFEDG KKVRFFKSNS
101 ETIK
```

```
Observed  Mr(expt)   Mr(calc)   Delta    Miss  Score  Expect    Rank  Unique  Peptide
542.3444 1082.6742  1082.6699   0.0042   0     54     0.014     1             K.VIVEGINLVK.K
```

```
505.3056 1512.8948  1512.8624   0.0325  2      58     0.0051    1     U       K.IRRDDEVIVLTGK.D
```

SwissProt

Mascot Score: 100   Queries Matched: 3
Protein ID: 50S ribosomal protein L14 [Escherichia coli O157:H7]
Calculated Mr = 13646; Calculated pI = 10.43

```
  1 MIQEQTMLNV ADNSGARRVM CIKVLGGSHR RYAGVGDIIK ITIKEAIPRG
 51 KVKKGDVLKA VVVRTKKGVR RPDGSVIRFD GNACVLLNNN SEQPIGTRIF
101 GPVTRELRSE KFMKIISLAP EVL
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
637.2973 1908.8702  1908.8669   0.0033  0      53     0.015     1     U       -.MIQEQTMLNVADNSGAR.R + 2 Oxidation
(M)
450.2670  898.5194   898.4985   0.0209  0      31     3         1             R.RPDGSVIR
477.8037  953.5928   953.5797   0.0131  0      19     38        1             K.IISLAPEVL.-
```

SwissProt

Mascot Score: 93   Queries Matched: 2
Protein ID: 50S ribosomal protein L19 [Escherichia coli O157:H7]
Calculated Mr = 13125; Calculated pI = 10.62

```
  1 MSNIIKQLEQ EQMKQDVPSF RPGDTVEVKV WVVEGSKKRL QAFEGVVIAI
 51 RNRGLHSAFT VRKISNGEGV ERVFQTHSPV VDSISVKRRG AVRKAKLYYL
101 RERTGKAARI KERLN
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
494.2739  986.5333   986.5298   0.0035  0      24     16        1     U       R.GLHSAFTVR.K
548.3090 1641.9053  1641.8727   0.0327  0      69     0.00037   1     U       R.VFQTHSPVVDSISVK.R
```

SwissProt

Mascot Score: 89   Queries Matched: 2
Protein ID: Outer membrane protein X [Escherichia coli O157:H7]
Calculated Mr = 18648; Calculated pI = 6.56

```
  1 MKKIACLSAL AAVLAFTAGT SVAATSTVTG GYAQSDAQGQ MNKMGGFNLK
 51 YRYEEDNSPL GVIGSFTYTE KSRTASSGDY NKNQYYGITA GPAYRINDWA
101 SIYGVVGVGY GKFQTTEYPT YKHDTSDYGF SYGAGLQFNP MENVALDFSY
151 EQSRIRSVDV GTWIAGVGYR F
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
639.3133 1276.6120  1276.5976   0.0144  0      35     1.1       1     U       K.FQTTEYPTYK.H
737.3617 1472.7088  1472.7048   0.0040  0      54     0.014     1     U       K.NQYYGITAGPAYR.I
```

SwissProt & NCBI

Mascot Score: 66   Queries Matched: 1
Protein ID: Acyl carrier protein [Escherichia coli (strain K12 / MC4100 / BW2952)]
Calculated Mr = 8634; Calculated pI = 3.98

```
  1 MSTIEERVKK IIGEQLGVKQ EEVTNNASFV EDLGADSLDT VELVMALEEE
 51 FDTEIPDEEA EKITTVQAAI DYINGHQA
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
478.7981  955.5816   955.5702   0.0114  0      66     0.00081   1     U       K.IIGEQLGVK.Q
```

SwissProt & NCBI

Mascot Score: 66 Queries Matched: 1
Protein ID: 30S ribosomal protein S6 [Escherichia coli O157:H7]
Calculated Mr = 15177; Calculated pI = 5.26

```
  1 MRHYEIVFMV HPDQSEQVPG MIERYTAAIT GAEGKIHRLE DWGRRQLAYP
 51 INKLHKAHYV LMNVEAPQEV IDELETTFRF NDAVIRSMVM RTKHAVTEAS
101 PMVKAKDERR ERRDDFANET ADDAEAGDSE E
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
541.2860 1080.5575  1080.5451  0.0124  0     66     0.00073   1     U       R.YTAAITGAEGK.I
```

SwissProt

Mascot Score: 61 Queries Matched: 1
Protein ID: Uncharacterized protein yibN [Escherichia coli O157:H7]
Calculated Mr = 15644; Calculated pI = 9.37

```
  1 MQEIMQFVGR HPILSIAWIA LLVAVLVTTF KSLTSKVKVI TRGEATRLIN
 51 KEDAVVVDLR QRDDFRKGHI AGSINLLPSE IKANNVGELE KHKDKPVIVV
101 DGSGMQCQEP ANALTKAGFA QVFVLKEGVA GWAGENLPLV RGK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
495.2952 1482.8638  1482.8406  0.0232  1     61     0.0027    1     U       R.LINKEDAVVVDLR.Q
```

NCBI

Mascot Score: 279 Queries Matched: 5
Protein ID: Hypothetical protein 933Wp55 [Enterobacteria phage 933W]
Calculated Mr = 13496; Calculated pI = 5.86

```
  1 MAKTILAPSL SERVYTGTHG NESVAEGVFT VNAAEADSVI HLLSLPVGIR
 51 INSLQLVSTG GLGTATVSIK SGEHALIDNS EAVSAKFARY VPVEPYTTQR
101 DGELVTVTIK TAAATGTLNV LLRYTVVGY
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
543.8195 1085.6244  1085.6080  0.0164  0     45     2.3       1     U       K.TILAPSLSER.V
643.3773 1284.7400  1284.7401 -0.0001  1     41     5.3       3     U       M.AKTILAPSLSER.V
650.8841 1299.7537  1299.7510  0.0026  0     83     0.00036   1     U       K.TAAATGTLNVLLR.Y
676.8514 1351.6882  1351.6772  0.0110  0     46     1.5       1     U       R.YVPVEPYTTQR.D
543.2791 1626.8154  1626.7849  0.0305  0     63     0.03      1     U       K.SGEHALIDNSEAVSAK.F
```

NCBI

Mascot Score: 137 Queries Matched: 3
Protein ID: Chain A, outer membrane protein Ompx [Escherichia Coli]
Calculated Mr = 16350; Calculated pI = 5.04

```
  1 ATSTVTGGYA QSDAQGQMNK MGGFNLKYRY EEDNSPLGVI GSFTYTEKSR
 51 TASSGDYNKN QYYGITAGPA YRINDWASIY GVVGVGYGKF QTTEYPTYKN
101 DTSDYGFSYG AGLQFNPMEN VALDFSYEQS RIRSVDVGTW IAGVGYRF
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
639.3133 1276.6120  1276.5976  0.0144  0     35     23        1     U       K.FQTTEYPTYK.N
737.3617 1472.7088  1472.7048  0.0040  0     54     0.29      1     U       K.NQYYGITAGPAYR.I
677.6518 2029.9336  2029.9011  0.0325  0     48     0.81      1     U       -.ATSTVTGGYAQSDAQGQMNK.M + Oxidation
(M)
```

NCBI

Mascot Score: 83 Queries Matched: 2
Protein ID: 50S ribosomal protein L14 [Escherichia Coli 536]

Calculated Mr = 13658; Calculated pI = 10.39

```
      1 MIQEQTMLNV ADNSGARRVM CIKVLGGSHR RYAGVGDIIK ITIKEAIPRG
     51 KVKKGDVLKP VVVRTNKGVR RPDGSVIRFD GNACVLLNNN SEQPIGTRIF
    101 GPVTRELRSE KFMKIISLAP EVL
```

```
Observed  Mr(expt)   Mr(calc)   Delta    Miss  Score  Expect    Rank  Unique  Peptide
637.2973 1908.8702  1908.8669  0.0033   0     53     0.32      1     U       -.MIQEQTMLNVADNSGAR.R + 2 Oxidation
(M)
```

NCBI

Mascot Score: 69   Queries Matched: 1
Protein ID: 50S ribosomal protein L19 [Escherichia coli O157:H7 EDL933]
Calculated Mr = 13125; Calculated pI = 10.62

```
      1 MSNIIKQLEQ EQMKQDVPSF RPGDTVEVKV WVVEGSKKRL QAFEGVVIAI
     51 RNRGLHSAFT VRKISNGEGV ERVFQTHSPV VDSISVKRRG AVRKAKLYYL
    101 RERTGKAARI KERLN
```

```
Observed  Mr(expt)   Mr(calc)   Delta    Miss  Score  Expect    Rank  Unique  Peptide
548.3090 1641.9053  1641.8727  0.0327   0     69     0.0074    1     U       R.VFQTHSPVVDSISVK.R
```

Gel lane #3, gel band #5

SwissProt & NCBI

Mascot Score: 126   Queries Matched: 2
Protein ID: 10 kDa chaperonin [Escherichia coli O157:H7]
Calculated Mr = 10381; Calculated pI = 5.15

```
      1 MNIRPLHDRV IVKRKEVETK SAGGIVLTGS AAAKSTRGEV LAVGNGRILE
     51 NGEVKPLDVK VGDIVIFNDG YGVKSEKIDN EEVLIMSESD ILAIVEA
```

```
Observed  Mr(expt)   Mr(calc)   Delta    Miss  Score  Expect    Rank  Unique  Peptide
485.2868 1452.8386  1452.8188  0.0198   0     40     0.33      1     U       R.ILENGEVKPLDVK.V
748.4057 1494.7968  1494.7719  0.0249   0     86     7.3e-06   1             K.VGDIVIFNDGYGVK.S
```

SwissProt

Mascot Score: 55   Queries Matched: 1
Protein ID: UPF0076 protein yjgF [Escherichia coli (strain K12)]
Calculated Mr = 13660; Calculated pI = 5.36

```
      1 MSKTIATENA PAAIGPYVQG VDLGNMIITS GQIPVNPKTG EVPADVAAQA
     51 RQSLDNVKAI VEAAGLKVGD IVKTTVFVKD LNDFATVNAT YEAFFTEHNA
    101 TFPARSCVEV ARLPKDVKIE IEAIAVRR
```

```
Observed  Mr(expt)   Mr(calc)   Delta    Miss  Score  Expect    Rank  Unique  Peptide
642.8460 1283.6773  1283.6470  0.0304   0     55     0.0098    1     U       K.TGEVPADVAAQAR.Q
```

NCBI

Mascot Score: 377   Queries Matched: 7
Protein ID: Hypothetical protein 933Wp55 [Enterobacteria phage 933W]
Calculated Mr = 13496; Calculated pI = 5.86

```
      1 MAKTILAPSL SERVYTGTHG NESVAEGVFT VNAAEADSVI HLLSLPVGIR
     51 INSLQLVSTG GLGTATVSIK SGEHALIDNS EAVSAKFARY VPVEPYTTQR
```

```
   101 DGELVTVTIK TAAATGTLNV LLRYTVVGY
```

```
Observed  Mr(expt)   Mr(calc)    Delta    Miss  Score  Expect    Rank  Unique  Peptide
537.8070 1073.5994  1073.5968   0.0026   0     61     0.06      1     U       R.DGELVTVTIK.T
543.8091 1085.6036  1085.6080  -0.0044   0     60     0.081     1     U       K.TILAPSLSER.V
642.8686 1283.7226  1284.7401  -1.0176   1    (30)    61        3     U       M.AKTILAPSLSER.V
643.3773 1284.7400  1284.7401  -0.0001   1     35     22        3     U       M.AKTILAPSLSER.V
650.8955 1299.7764  1299.7510   0.0254   0     83     0.00032   1     U       K.TAAATGTLNVLLR.Y
676.8398 1351.6650  1351.6772  -0.0122   0     60     0.068     1     U       R.YVPVEPYTTQR.D
543.2791 1626.8154  1626.7849   0.0305   0     78     0.0011    1     U       K.SGEHALIDNSEAVSAK.F
```

Gel lane #3, gel band #6

SwissProt & NCBI

Mascot Score: 199 Queries Matched: 3
Protein ID: 30S ribosomal protein S10 [Escherichia coli O157:H7]
Calculated Mr = 11728; Calculated pI = 9.68

```
     1 MQNQRIRIRL KAFDHRLIDQ ATAEIVETAK RTGAQVRGPI PLPTRKERFT
    51 VLISPHVNKD ARDQYEIRTH LRLVDIVEPT EKTVDALMRL DLAAGVDVQI
   101 SLG
```

```
Observed  Mr(expt)   Mr(calc)    Delta    Miss  Score  Expect    Rank  Unique  Peptide
571.8381 1141.6617  1141.6230   0.0386   0     58     0.0055    1     U       R.LVDIVEPTEK.T
532.9855 1595.9346  1595.8784   0.0562   1     61     0.0022    1     U       R.FTVLISPHVNKDAR.D
553.3257 1656.9552  1656.9046   0.0506   1     79     3.5e-05   1     U       R.LIDQATAEIVETAKR.T
```

SwissProt & NCBI

Mascot Score: 153 Queries Matched: 2
Protein ID: Major outer membrane lipoprotein [Escherichia coli O157:H7]
Calculated Mr = 8375; Calculated pI = 9.30

```
     1 MKATKLVLGA VILGSTLLAG CSSNAKIDQL SSDVQTLNAK VDQLSNDVNA
    51 MRSDVQAAKD DAARANQRLD NMATKYRK
```

```
Observed  Mr(expt)   Mr(calc)    Delta    Miss  Score  Expect    Rank  Unique  Peptide
689.3447 1376.6748  1376.6354   0.0394   0     72     0.00023   1     U       K.VDQLSNDVNAMR.S + Oxidation (M)
766.4178 1530.8211  1530.7889   0.0322   0     81     2.5e-05   1     U       K.IDQLSSDVQTLNAK.V
```

SwissProt & NCBI

Mascot Score: 133 Queries Matched: 3
Protein ID: 50S ribosomal protein L7/L12 [Escherichia coli O157:H7]
Calculated Mr = 12288; Calculated pI = 4.60

```
     1 MSITKDQIIE AVAAMSVMDV VELISAMEEK FGVSAAAAVA VAAGPVEAAE
    51 EKTEFDVILK AAGANKVAVI KAVRGATGLG LKEAKDLVES APAALKEGVS
   101 KDDAEALKKA LEEAGAEVEV K
```

```
Observed  Mr(expt)   Mr(calc)    Delta    Miss  Score  Expect    Rank  Unique  Peptide
482.7920  963.5694   963.5277   0.0417   0     39     0.5       1     U       K.TEFDVILK.A
557.3279 1112.6412  1112.6077   0.0335   0     41     0.25      1     U       K.DLVESAPAALK.E
463.9297 1388.7673  1388.7147   0.0527   2     53     0.019     1     U       K.EGVSKDDAEALKK.A
```

SwissProt & NCBI

Mascot Score: 105 Queries Matched: 2

Protein ID: Preprotein translocase subunit YajC [Escherichia coli O157:H7]
Calculated Mr = 11879; Calculated pI = 9.57

```
  1 MSFFISDAVA ATGAPAQGSP MSLILMLVVF GLIFYFMILR PQQKRTKEHK
 51 KLMDSIAKGD EVLTNGGLVG RVTKVAENGY IAIALNDTTE VVIKRDFVAA
101 VLPKGTMKAL
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
480.2976  958.5807   958.5488   0.0319  0     40     0.42      1     U       R.DFVAAVLPK.G
687.7072 2060.0996  2060.0572   0.0424  1     65     0.0009    1     U       K.LMDSIAKGDEVLTNGGLVGR.V + Oxidation
(M)
```

SwissProt & NCBI

Mascot Score: 70 Queries Matched: 1
Protein ID: 50S ribosomal protein L28 [Escherichia coli O157:H7]
Calculated Mr = 9058; Calculated pI = 11.42

```
  1 MSRVCQVTGK RPVTGNNRSH ALNATKRRFL PNLHSHRFWV ESEKRFVTLR
 51 VSAKGMRVID KKGIDTVLAE LRARGEKY
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
543.8146 1085.6146  1085.6081   0.0066  0     70     0.00036   1     U       K.GIDTVLAELR.A
```

NCBI

Mascot Score: 380 Queries Matched: 6
Protein ID: Hypothetical protein 933Wp55 [Enterobacteria phage 933W]
Calculated Mr = 13496; Calculated pI = 5.86

```
  1 MAKTILAPSL SERVYTGTHG NESVAEGVFT VNAAEADSVI HLLSLPVGIR
 51 INSLQLVSTG GLGTATVSIK SGEHALIDNS EAVSAKFARY VPVEPYTTQR
101 DGELVTVTIK TAAATGTLNV LLRYTVVGY
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
537.8125 1073.6105  1073.5968   0.0137  0     61     0.057     1     U       R.DGELVTVTIK.T
543.8250 1085.6354  1085.6080   0.0274  0     54     0.31      1     U       K.TILAPSLSER.V
643.3931 1284.7717  1284.7401   0.0316  1     40     7.4       2     U       M.AKTILAPSLSER.V
650.8999 1299.7853  1299.7510   0.0343  0     101    5.6e-06   1     U       K.TAAATGTLNVLLR.Y
676.8556 1351.6966  1351.6772   0.0193  0     47     1.4       1     U       R.YVPVEPYTTQR.D
543.2846 1626.8319  1626.7849   0.0470  0     77     0.0012    1     U       K.SGEHALIDNSEAVSAK.F
```

NCBI

Mascot Score: 93 Queries Matched: 1
Protein ID: Hypothetical protein 933Wp74 [Enterobacteria phage 933W]
Calculated Mr = 12402; Calculated pI = 4.86

```
  1 MKKVLIAALI SGVSFGAFAQ QGGFQGPEAE RSTVAQAKEL KDDAWVILEG
 51 SIVKKVGDER YEFRDNSGTI VTDIDDSIWA GQNVSPKDKV RIEGEIDKDL
101 SSVEVDVKAL KLLK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
625.6748 1874.0024  1873.9520   0.0504  1     93     3.1e-05   1     U       R.IEGEIDKDLSSVEVDVK.A
```

Gel lane #3, gel band #7

SwissProt & NCBI

Mascot Score: 293 Queries Matched: 5

Protein ID: Major outer membrane lipoprotein [Escherichia coli O157:H7]
Calculated Mr = 8375; Calculated pI = 9.30

```
     1 MKATKLVLGA VILGSTLLAG CSSNAKIDQL SSDVQTLNAK VDQLSNDVNA
    51 MRSDVQAAKD DAARANQRLD NMATKYRK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
416.2102 1245.6087  1245.5949   0.0138  1     57     0.0065    1     U       R.SDVQAAKDDAAR.A
689.3330 1376.6514  1376.6354   0.0160  0     67     0.00074   1     U       K.VDQLSNDVNAMR.S + Oxidation (M)
766.4055 1530.7965  1530.7889   0.0075  0     84     1.2e-05   1     U       K.IDQLSSDVQTLNAK.V
693.0128 2076.0164  2075.9906   0.0259  1     49     0.033     1     U       K.VDQLSNDVNAMRSDVQAAK.D + Oxidation
(M)
652.0718 2604.2583  2604.2198   0.0385  2     36     0.58      1      U      K.VDQLSNDVNAMRSDVQAAKDDAAR.A +
Oxidation (M)
```

SwissProt & NCBI

Mascot Score: 128   Queries Matched: 2
Protein ID: 30S ribosomal protein S16 [Escherichia coli O157:H7]
Calculated Mr = 9185; Calculated pI = 10.54

```
     1 MVTIRLARHG AKKRPFYQVV VADSRNARNG RFIERVGFFN PIASEKEEGT
    51 RLDLDRIAHW VGQGATISDR VAALIKEVNK AA
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
604.8336 1207.6526  1207.6237   0.0289  0     73     0.00015   1     U       R.VGFFNPIASEK.E
522.3060 1563.8962  1563.8522   0.0440  1     55     0.01      1     U       K.KRPFYQVVVADSR.N
```

SwissProt & NCBI

Mascot Score: 82   Queries Matched: 1
Protein ID: Transcriptional regulator HU subunit alpha [Escherichia coli O157:H7]
Calculated Mr = 9529; Calculated pI = 9.57

```
     1 MNKTQLIDVI AEKAELSKTQ AKAALESTLA AITESLKEGD AVQLVGFGTF
    51 KVNHRAERTG RNPQTGKEIK IAAANVPAFV SGKALKDAVK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
622.8570 1243.6994  1243.6925   0.0070  0     82     2.2e-05   1     U       K.IAAANVPAFVSGK.A
```

SwissProt & NCBI

Mascot Score: 70   Queries Matched: 1
Protein ID: Hypothetical protein Z4452 [Escherichia coli O157:H7]
Calculated Mr = 11045; Calculated pI = 9.05

```
     1 MSKEHTTEHL RAELKSLSDT LEEVLSSSGE KSKEELSKIR SKAEQALKQS
    51 RYRLGETGDA IAKQTRVAAA RADEYVRENP WTGVGIGAAI GVVLGVLLSR
   101 R
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
487.7607  973.5068   973.5080  -0.0012  0     70     0.00045   1     U       R.LGETGDAIAK.Q
```

SwissProt

Mascot Score: 51   Queries Matched: 1
Protein ID: 30S ribosomal protein S17 [Escherichia coli O157:H7]
Calculated Mr = 9812; Calculated pI = 9.64

```
     1 MTDKIRTLQG RVVSDKMEKS IVVAIERFVK HPIYGKFIKR TTKLHVHDEN
    51 NECGIGDVVE IRECRPLSKT KSWTLVRVVE KAVL
```

```
Observed  Mr(expt)   Mr(calc)    Delta    Miss  Score  Expect    Rank  Unique  Peptide
735.6836 2204.0291  2204.0280   0.0011   0     51     0.023     1     U       K.LHVHDENNECGIGDVVEIR.E
```

NCBI

Mascot Score: 212   Queries Matched: 4
Protein ID: Hypothetical protein 933Wp60 [Enterobacteria phage 933W]
Calculated Mr = 14759; Calculated pI = 6.71

```
      1 MPHGFRVFFS ICRSGLVTGR GRMSRGWMKW AVIQAEQEND MNILRKLMQS
     51 LCGCGKHDDC ENGQSLTAQL RLGPADILES DENGIIPEQD RVITQVVILD
    101 ADKKQIQCVV RPLQILRADG TWENIGGMK
```

```
Observed  Mr(expt)   Mr(calc)    Delta    Miss  Score  Expect    Rank  Unique  Peptide
647.7989 1293.5833  1293.5659   0.0174   0     40     5.9       1     U       R.ADGTWENIGGMK.- + Oxidation (M)
481.3044 1440.8913  1440.8552   0.0361   1     60     0.067     1     U       R.VITQVVILDADKK.Q
541.6650 1621.9730  1621.9450   0.0280   0     49     0.79      1     U       K.QIQCVVRPLQILR.A
581.9449 1742.8130  1742.7642   0.0488   0     63     0.032     1     U       K.HDDCENGQSLTAQLR.L
```

NCBI

Mascot Score: 145   Queries Matched: 3
Protein ID: hypothetical protein ECs1210 [Escherichia coli O157:H7 str. Sakai]
Calculated Mr = 6914; Calculated pI = 9.18

```
      1 MTFLNQLMLY FCTVVCVLYL LSGGYRAMRD FWRRQIDKRA AEKISASQSA
     51 GSKPEEPLI
```

```
Observed  Mr(expt)   Mr(calc)    Delta    Miss  Score  Expect    Rank  Unique  Peptide
491.2519  980.4893   980.4650   0.0243   1     35     21        8     U       R.AMRDFWR.R
807.4291 1612.8436  1612.8308   0.0128   0     65     0.02      1     U       K.ISASQSAGSKPEEPLI.-
671.6932 2012.0576  2012.0425   0.0151   1     45     1.8       1     U       R.AAEKISASQSAGSKPEEPLI.-
```

NCBI

Mascot Score: 91   Queries Matched: 2
Protein ID: Bor protein precursor [Enterobacteria phage 933W]
Calculated Mr = 10642; Calculated pI = 9.15

```
      1 MKKMLLATAL ALLITGCAQQ TFTVQNKQTA VAPKETITHH FFVSGIGQKK
     51 TVDAAKICGG TENVVKTETQ QTFVNGLLGF ITLGIYTPLE ARVYCSQ
```

```
Observed  Mr(expt)   Mr(calc)    Delta    Miss  Score  Expect    Rank  Unique  Peptide
538.7847 1075.5548  1075.5332   0.0216   0     55     0.25      1     U       K.ICGGTENVVK.T
567.6354 1699.8843  1699.8682   0.0161   0     36     17        1     U       K.ETITHHFFVSGIGQK.K
```

NCBI

Mascot Score: 87   Queries Matched: 1
Protein ID: Hypothetical protein 933Wp74 [Enterobacteria phage 933W]
Calculated Mr = 12402; Calculated pI = 4.86

```
      1 MKKVLIAALI SGVSFGAFAQ QGGFQGPEAE RSTVAQAKEL KDDAWVILEG
     51 SIVKKVGDER YEFRDNSGTI VTDIDDSIWA GQNVSPKDKV RIEGEIDKDL
    101 SSVEVDVKAL KLLK
```

```
Observed  Mr(expt)   Mr(calc)    Delta    Miss  Score  Expect    Rank  Unique  Peptide
625.6636 1873.9690  1873.9520   0.0169   1     87     0.00013   1     U       R.IEGEIDKDLSSVEVDVK.A
```

Gel lane #3, gel band #8

SwissProt & NCBI

Mascot Score: 435 Queries Matched: 8
Protein ID: Major outer membrane lipoprotein [Escherichia coli O157:H7]
Calculated Mr = 8375; Calculated pI = 9.30

```
  1 MKATKLVLGA VILGSTLLAG CSSNAKIDQL SSDVQTLNAK VDQLSNDVNA
 51 MRSDVQAAKD DAARANQRLD NMATKYRK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
623.8252 1245.6359  1245.5949  0.0410  1     75     0.00012   1     U       R.SDVQAAKDDAAR.A
639.3291 1276.6437  1276.6194  0.0243  1     54     0.015     1     U       R.ANQRLDNMATK.Y + Oxidation (M)
689.3330 1376.6514  1376.6354  0.0160  0     67     0.00065   1     U       K.VDQLSNDVNAMR.S + Oxidation (M)
766.4178 1530.8211  1530.7889  0.0322  0     95     1e-06     1     U       K.IDQLSSDVQTLNAK.V
511.2910 1530.8513  1530.7889  0.0623  0    (36)    0.87      2     U       K.IDQLSSDVQTLNAK.V
572.6272 1714.8597  1714.8346  0.0251  2     40     0.34      2     U       R.SDVQAAKDDAARANQR.L
693.0245 2076.0516  2075.9906  0.0611  1     46     0.064     1     U       K.VDQLSNDVNAMRSDVQAAK.D + Oxidation
(M)
652.1000 2604.3709  2604.2198  0.1511  2     58      0.0033   1     U       K.VDQLSNDVNAMRSDVQAAKDDAAR.A +
Oxidation (M)
```

SwissProt

Mascot Score: 225 Queries Matched: 4
Protein ID: Shiga-like toxin 2 subunit B [Enterobacteria phage 933W]
Calculated Mr = 9982; Calculated pI = 5.30

```
  1 MKKMFMAVLF ALASVNAMAA DCAKGKIEFS KYNEDDTFTV KVDGKEYWTS
 51 RWNLQPLLQS AQLTGMTVTI KSSTCESGSG FAEVQFNND
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
404.7409  807.4672   807.4490  0.0182  1     34     1.4       1     U       K.GKIEFSK.Y
616.2885 1230.5624  1230.5405  0.0220  0     60     0.0034    1     U       K.YNEDDTFTVK.V
612.6421 1834.9045  1834.8625  0.0420  1     59     0.0036    1     U       K.IEFSKYNEDDTFTVK.V
674.3529 2020.0369  2019.9789  0.0580  2     71     0.0002    1     U       K.GKIEFSKYNEDDTFTVK.V
```

SwissProt & NCBI

Mascot Score: 76 Queries Matched: 1
Protein ID: Transcriptional regulator HU subunit alpha [Escherichia coli O157:H7]
Calculated Mr = 9529; Calculated pI = 9.57

```
  1 MNKTQLIDVI AEKAELSKTQ AKAALESTLA AITESLKEGD AVQLVGFGTF
 51 KVNHRAERTG RNPQTGKEIK IAAANVPAFV SGKALKDAVK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
622.8681 1243.7217  1243.6925  0.0292  0     76     9.7e-05   1     U       K.IAAANVPAFVSGK.A
```

SwissProt

Mascot Score: 56 Queries Matched: 1
Protein ID: Cold shock-like protein cspE [Escherichia coli O157:H7]
Calculated Mr = 7459; Calculated pI = 8.09

```
  1 MSKIKGNVKW FNESKGFGFI TPEDGSKDVF VHFSAIQTNG FKTLAEGQRV
 51 EFEITNGAKG PSAANVIAL
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
554.3013 1106.5880  1106.5608  0.0272  0     56     0.0084    1     U       R.VEFEITNGAK.G
```

SwissProt

Mascot Score: 51   Queries Matched: 1

Protein ID: Cell division protein zapB [Escherichia coli O157:H7 (strain EC4115 / EHEC)]

Calculated Mr = 9397; Calculated pI = 4.69

```
  1 MSLEVFEKLE AKVQQAIDTI TLLQMEIEEL KEKNNSLSQE VQNAQHQREE
 51 LERENNHLKE QQNGWQERLQ ALLGRMEEV
```

```
Observed  Mr(expt)   Mr(calc)    Delta    Miss   Score   Expect    Rank   Unique   Peptide
646.8690 1291.7234  1291.7023   0.0210   1      51      0.026     1      U        M.SLEVFEKLEAK.V
```

SwissProt

Mascot Score: 47   Queries Matched: 1

Protein ID: Lipoprotein bor homolog from lambdoid prophage DLP12 [Escherichia coli (strain K12)]

Calculated Mr = 10612; Calculated pI = 9.33

```
  1 MKKMLLATAL ALLITGCAQQ TFTVQNKQTA VAPKETITHH FFVSGIGQKK
 51 TVDAAKICGG AENVVKTETQ QTFVNGLLGF ITLGIYTPLE ARVYCSK
```

```
Observed  Mr(expt)   Mr(calc)    Delta    Miss   Score   Expect    Rank   Unique   Peptide
567.6460 1699.9162  1699.8682   0.0479   0      47      0.063     1      U        K.ETITHHFFVSGIGQK.K
```

NCBI

Mascot Score: 191   Queries Matched: 3

Protein ID: Shiga toxin II subunit B [Escherichia coli]

Calculated Mr = 9992; Calculated pI = 5.30

```
  1 MKKMFMAVLF ALASVNAMAA DCAKGKIEFS KYNEDDTFTV KVDGKEYWTS
 51 RWNLQPLLQS AQLTGMTVXI KSSTCESGSG FAEVQFNND
```

```
Observed  Mr(expt)   Mr(calc)    Delta    Miss   Score   Expect    Rank   Unique   Peptide
616.2885 1230.5624  1230.5405   0.0220   0      60      0.069     1      U        K.YNEDDTFTVK.V
612.6421 1834.9045  1834.8625   0.0420   1      59      0.075     1      U        K.IEFSKYNEDDTFTVK.V
674.3529 2020.0369  2019.9789   0.0580   2      71      0.0044    1      U        K.GKIEFSKYNEDDTFTVK.V
```

NCBI

Mascot Score: 77   Queries Matched: 2

Protein ID: Hypothetical protein ECs1210 [Escherichia coli O157:H7 str. Sakai]

Calculated Mr = 6914; Calculated pI = 9.18

```
  1 MTFLNQLMLY FCTVVCVLYL LSGGYRAMRD FWRRQIDKRA AEKISASQSA
 51 GSKPEEPLI
```

```
Observed  Mr(expt)   Mr(calc)    Delta    Miss   Score   Expect    Rank   Unique   Peptide
807.4417 1612.8689  1612.8308   0.0381   0      44      2.3       1      U        K.ISASQSAGSKPEEPLI.-
671.6932 2012.0576  2012.0425   0.0151   1      33      31        1      U        R.AAEKISASQSAGSKPEEPLI.-
```

NCBI

Mascot Score: 67   Queries Matched: 2

Protein ID: Shiga-like cytotoxin subunit B [Escherichia coli]

Calculated Mr = 9714; Calculated pI = 9.03

```
  1 MKKIFVAALF AFVSVNAMAA DCPKGKIEFS KYNENDTFTV KVAGKEYWTN
 51 RWNLQPLLQS AQLTGMTVTI KSNTCASGSG FAEVQFN
```

```
Observed  Mr(expt)   Mr(calc)    Delta    Miss   Score   Expect    Rank   Unique   Peptide
612.6421 1834.9045  1833.8785   1.0260   1      31      50        5      U        K.IEFSKYNENDTFTVK.V
```

```
674.3529 2020.0369  2018.9949   1.0420  2     36     15       8     U       K.GKIEFSKYNENDTFTVK.V
```

Gel lane #3, gel band #9

SwissProt & NCBI

Mascot Score: 366   Queries Matched: 6
Protein ID: Major outer membrane lipoprotein [Escherichia coli O157:H7]
Calculated Mr = 8375; Calculated pI = 9.30

```
     1 MKATKLVLGA VILGSTLLAG CSSNAKIDQL SSDVQTLNAK VDQLSNDVNA
    51 MRSDVQAAKD DAARANQRLD NMATKYRK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
623.8252 1245.6359  1245.5949   0.0410  1     79     4.1e-05   1     U       R.SDVQAAKDDAAR.A
681.3394 1360.6643  1360.6405   0.0238  0     85     1.2e-05   1     U       K.VDQLSNDVNAMR.S
689.3447 1376.6748  1376.6354   0.0394  0    (72)    0.00021   1     U       K.VDQLSNDVNAMR.S + Oxidation (M)
766.4178 1530.8211  1530.7889   0.0322  0     93     1.8e-06   1     U       K.IDQLSSDVQTLNAK.V
693.0245 2076.0516  2075.9906   0.0611  1     44     0.12      1     U       K.VDQLSNDVNAMRSDVQAAK.D + Oxidation
(M)
652.0832 2604.3038  2604.2198   0.0840  2     66     0.00064   1     U       K.VDQLSNDVNAMRSDVQAAKDDAAR.A +
Oxidation (M)
```

SwissProt & NCBI

Mascot Score: 106   Queries Matched: 1
Protein ID: Entericidin B [Escherichia coli O157:H7]
Calculated Mr = 4864; Calculated pI = 7.93

```
    1 MVKKTIAAIF SVLVLSTVLT ACNTTRGVGE DISDGGNAIS GAATKAQQ
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
859.9216 1717.8287  1717.8119   0.0169  0     106     .7e-08   1     U       R.GVGEDISDGGNAISGAATK.A
```

Gel lane #3, gel band #10

SwissProt & NCBI

Mascot Score: 287   Queries Matched: 4
Protein ID: Major outer membrane lipoprotein [Escherichia coli O157:H7]
Calculated Mr = 8375; Calculated pI = 9.30

```
     1 MKATKLVLGA VILGSTLLAG CSSNAKIDQL SSDVQTLNAK VDQLSNDVNA
    51 MRSDVQAAKD DAARANQRLD NMATKYRK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
623.8141 1245.6136  1245.5949   0.0187  1     84     1.4e-05   1     U       R.SDVQAAKDDAAR.A
689.3213 1376.6280  1376.6354  -0.0074  0     70     0.00035   1     U       K.VDQLSNDVNAMR.S + Oxidation (M)
766.3932 1530.7718  1530.7889  -0.0172  0     87     7.3e-06   1     U       K.IDQLSSDVQTLNAK.V
652.1000 2604.3709  2604.2198   0.1511  2     46     0.052     1     U       K.VDQLSNDVNAMRSDVQAAKDDAAR.A +
Oxidation (M)
```

SwissProt & NCBI

Mascot Score: 80   Queries Matched: 1
Protein ID: Entericidin B [Escherichia coli O157:H7]
Calculated Mr = 4864; Calculated pI = 7.93

```
     1 MVKKTIAAIF SVLVLSTVLT ACNTTRGVGE DISDGGNAIS GAATKAQQ
```

```
Observed  Mr(expt)   Mr(calc)    Delta    Miss  Score  Expect    Rank  Unique  Peptide
859.9086 1717.8026  1717.8119  -0.0093  0     80      2.9e-05 1     U       R.GVGEDISDGGNAISGAATK.A
```

Gel lane #4, gel band #1

SwissProt

Mascot Score: 958   Queries Matched: 18

Protein ID: Outer membrane protein A [Escherichia coli O157:H7]

Calculated Mr = 37294; Calculated pI = 5.99

```
      1 MKKTAIAIAV ALAGFATVAQ AAPKDNTWYT GAKLGWSQYH DTGFINNNGP
     51 THENQLGAGA FGGYQVNPYV GFEMGYDWLG RMPYKGSVEN GAYKAQGVQL
    101 TAKLGYPITD DLDIYTRLGG MVWRADTKSN VYGKNHDTGV SPVFAGGVEY
    151 AITPEIATRL EYQWTNNIGD AHTIGTRPDN GMLSLGVSYR FGQGEAAPVV
    201 APAPAPAPEV QTKHFTLKSD VLFNFNKATL KPEGQAALDQ LYSQLSNLDP
    251 KDGSVVVLGY TDRIGSDAYN QGLSERRAQS VVDYLISKGI PADKISARGM
    301 GESNPVTGNT CDNVKQRAAL IDCLAPDRRV EIEVKGIKDV VTQPQA
```

```
Observed  Mr(expt)   Mr(calc)    Delta    Miss  Score  Expect    Rank  Unique  Peptide
409.7269   817.4392   817.4269  0.0123  0    (43)    0.22      1             R.LGGMVWR.A
417.7257   833.4369   833.4218  0.0151  0     51     0.031     1             R.LGGMVWR.A + Oxidation (M)
458.2690   914.5235   914.5185  0.0050  0     58     0.0065    1     U       K.AQGVQLTAK.L
514.2997  1026.5848  1026.5822  0.0026  1     54     0.014     1             K.GIPADKISAR.G
528.2458  1054.4770  1054.4720  0.0051  0     42     0.2       1             K.DNTWYTGAK.L
542.2746  1082.5347  1082.5397 -0.0049  0     67     0.00067   1             K.SDVLFNFNK.A
578.3227  1154.6308  1154.6295  0.0012  1     35     0.99      1     U       K.GIKDVVTQPQA.-
607.8225  1213.6305  1214.5965 -0.9660  0     19     42        3             R.AALIDCLAPDR.R
611.8414  1221.6683  1221.6605  0.0078  0     45     0.11      1             R.AQSVVDYLISK.G
640.8298  1279.6450  1279.6409  0.0041  0     49     0.042     1     U       K.DGSVVVLGYTDR.I
457.5821  1369.7244  1370.6976 -0.9732  1     34     1.4       1             R.AALIDCLAPDRR.V
689.8966  1377.7786  1377.7616  0.0170  1     59     0.0042    1             R.RAQSVVDYLISK.G
705.3473  1408.6800  1408.6582  0.0217  0     88     5.2e-06   1     U       R.IGSDAYNQGLSER.R
827.9251  1653.8357  1653.8250  0.0107  0     92     1.9e-06   1             K.LGYPITDDLDIYTR.L
570.6495  1708.9268  1708.8937  0.0331  1     55     0.0095    1             K.HFTLKSDVLFNFNK.A
898.3990  1794.7835  1795.7353 -0.9518  0     23     15        1             R.GMGESNPVTGNTCDNVK.Q + Oxidation
(M)
744.7347  2231.1821  2231.1586  0.0235  0     72     0.00017   1     U       R.FGQGEAAPVVAPAPAPAPEVQTK.H
867.7797  2600.3173  2600.2871  0.0302  0     118    3.5e-09   1     U       K.NHDTGVSPVFAGGVEYAITPEIATR.L
```

SwissProt & NCBI

Mascot Score: 116   Queries Matched: 2

Protein ID: D-ribose-binding periplasmic protein [Escherichia coli (strain K12)]

Calculated Mr = 30931; Calculated pI = 6.85

```
      1 MNMKKLATLV SAVALSATVS ANAMAKDTIA LVVSTLNNPF FVSLKDGAQK
     51 EADKLGYNLV VLDSQNNPAK ELANVQDLTV RGTKILLINP TDSDAVGNAV
    101 KMANQANIPV ITLDRQATKG EVVSHIASDN VLGGKIAGDY IAKKAGEGAK
    151 VIELQGIAGT SAARERGEGF QQAVAAHKFN VLASQPADFD RIKGLNVMQN
    201 LLTAHPDVQA VFAQNDEMAL GALRALQTAG KSDVMVVGFD GTPDGEKAVN
    251 DGKLAATIAQ LPDQIGAKGV ETADKVLKGE KVQAKYPVDL KLVVKQ
```

```
Observed  Mr(expt)   Mr(calc)    Delta    Miss  Score  Expect    Rank  Unique  Peptide
693.3909  1384.7673  1384.7674 -0.0001  0     50     0.035     1     U       K.VIELQGIAGTSAAR.E
740.3607  1478.7069  1478.7154 -0.0085  0     66     0.0008    1             K.FNVLASQPADFDR.I
```

SwissProt

Mascot Score: 54   Queries Matched: 1

Protein ID: Shiga-like toxin 2 subunit A [Enterobacteria phage 933W]

Calculated Mr = 35924; Calculated pI = 8.68

```
      1 MKCILFKWVL CLLLGFSSVS YSREFTIDFS TQQSYVSSLN SIRTEISTPL
     51 EHISQGTTSV SVINHTPPGS YFAVDIRGLD VYQARFDHLR LIIEQNNLYV
    101 AGFVNTATNT FYRFSDFTHI SVPGVTTVSM TTDSSYTTLQ RVAALERSGM
    151 QISRHSLVSS YLALMEFSGN TMTRDASRAV LRFVTVTAEA LRFRQIQREF
    201 RQALSETAPV YTMTPGDVDL TLNWGRISNV LPEYRGEDGV RVGRISFNNI
    251 SAILGTVAVI LNCHHQGARS VRAVNEESQP ECQITGDRPV IKINNTLWES
    301 NTAAAFLNRK SQFLYTTGK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
553.8189  1105.6233  1105.6132  0.0102  0     54     0.016     1     U       R.FVTVTAEALR.F
```

NCBI

Mascot Score: 1037   Queries Matched: 17

Protein ID: Outer membrane protein A [Escherichia coli O157:H7 EDL933]

Calculated Mr = 37292; Calculated pI = 5.99

```
      1 MKKTAIAIAV ALAGFATVAQ AAPKDNTWYT GAKLGWSQYH DTGFINNNGP
     51 THENQLGAGA FGGYQVNPYV GFEMGYDWLG RMPYKGSVEN GAYKAQGVQL
    101 TAKLGYPITD DLDIYTRLGG MVWRADTKSN VYGKNHDTGV SPVFAGGVEY
    151 AITPEIATRL EYQWTNNIGD AHTIGTRPDN GMLSLGVSYR FGQGEAAPVV
    201 APAPAPAPEV QTKHFTLKSD VLFNFNKATL KPEGQAALDQ LYSQLSNLDP
    251 KDGSVVVLGY TDRIGSDAYN QGLSERRAQS VVDYLISKGI PADKISARGM
    301 GESNPVTGNT CDNVKQRAAL IDCLAPDRRV EIEVKGIKDV VTQPQA
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
409.7269   817.4392   817.4269  0.0123  0     (43)   4.3       1             R.LGGMVWR.A
417.7257   833.4369   833.4218  0.0151  0      51    0.61      1             R.LGGMVWR.A + Oxidation (M)
458.2690   914.5235   914.5185  0.0050  0      58    0.13      1             K.AQGVQLTAK.L
514.2997  1026.5848  1026.5822  0.0026  1      54    0.28      1             K.GIPADKISAR.G
528.2458  1054.4770  1054.4720  0.0051  0      42    3.9       1             K.DNTWYTGAK.L
542.2746  1082.5347  1082.5397 -0.0049  0      67    0.013     1             K.SDVLFNFNK.A
578.3227  1154.6308  1154.6295  0.0012  1      35    20        2             K.GIKDVVTQPQA.-
607.8225  1213.6305  1213.6125  0.0180  0      68    0.011     1             R.AALIDCLAPDR.R
611.8414  1221.6683  1221.6605  0.0078  0      45    2.2       1             R.AQSVVDYLISK.G
640.8298  1279.6450  1279.6409  0.0041  0      49    0.91      2             K.DGSVVVLGYTDR.I
689.8966  1377.7786  1377.7616  0.0170  1      59    0.086     1             R.RAQSVVDYLISK.G
705.3473  1408.6800  1408.6582  0.0217  0      88    0.0001    1             R.IGSDAYNQGLSER.R
827.9251  1653.8357  1653.8250  0.0107  0      92    4e-05     1             K.LGYPITDDLDIYTR.L
570.6495  1708.9268  1708.8937  0.0331  1      55    0.2       1             K.HFTLKSDVLFNFNK.A
898.3990  1794.7835  1794.7513  0.0323  0      91    4.2e-05   1             R.GMGESNPVTGNTCDNVK.Q + Oxidation
(M)
744.7347  2231.1821  2231.1586  0.0235  0      72    0.0034    1             R.FGQGEAAPVVAPAPAPAPEVQTK.H
867.7797  2600.3173  2600.2871  0.0302  0      118   7.7e-08   1             K.NHDTGVSPVFAGGVEYAITPEIATR.L
```

NCBI

Mascot Score: 118   Queries Matched: 2

Protein ID: Bor protein precursor [Enterobacteria phage 933W]

Calculated Mr = 10642; Calculated pI = 9.15

```
      1 MKKMLLATAL ALLITGCAQQ TFTVQNKQTA VAPKETITHH FFVSGIGQKK
     51 TVDAAKICGG TENVVKTETQ QTFVNGLLGF ITLGIYTPLE ARVYCSQ
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
538.7812  1075.5479  1075.5332  0.0147  0      77    0.0015    1     U       K.ICGGTENVVK.T
567.6393  1699.8960  1699.8682  0.0277  0      41    5.4       1     U       K.ETITHHFFVSGIGQK.K
```

Gel lane #4, gel band #2

SwissProt & NCBI

Mascot Score: 1258 Queries Matched: 22
Protein ID: Outer membrane protein A [Escherichia coli O157:H7]
Calculated Mr = 37292; Calculated pI = 5.99

```
  1 MKKTAIAIAV ALAGFATVAQ AAPKDNTWYT GAKLGWSQYH DTGFINNNGP
 51 THENQLGAGA FGGYQVNPYV GFEMGYDWLG RMPYKGSVEN GAYKAQGVQL
101 TAKLGYPITD DLDIYTRLGG MVWRADTKSN VYGKNHDTGV SPVFAGGVEY
151 AITPEIATRL EYQWTNNIGD AHTIGTRPDN GMLSLGVSYR FGQGEAAPVV
201 APAPAPAPEV QTKHFTLKSD VLFNFNKATL KPEGQAALDQ LYSQLSNLDP
251 KDGSVVVLGY TDRIGSDAYN QGLSERRAQS VVDYLISKGI PADKISARGM
301 GESNPVTGNT CDNVKQRAAL IDCLAPDRRV EIEVKGIKDV VTQPQA
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
409.7410   817.4674   817.4269  0.0405  0     (54)   0.016     1               R.LGGMVWR.A
417.7286   833.4427   833.4218  0.0209  0      55    0.013     1               R.LGGMVWR.A + Oxidation (M)
436.7812   871.5479   871.5127  0.0352  1      49    0.061     1               R.RVEIEVK.G
458.2794   914.5443   914.5185  0.0258  0      54    0.019     1     U         K.AQGVQLTAK.L
462.7369   923.4593   923.4348  0.0245  0      28    4.6       1     U         K.GSVENGAYK.A
514.3147  1026.6148  1026.5822  0.0327  1      57    0.0066    1               K.GIPADKISAR.G
528.2571  1054.4995  1054.4720  0.0276  0      48    0.052     1               K.DNTWYTGAK.L
542.2924  1082.5703  1082.5397  0.0307  0      67    0.00064   1               K.SDVLFNFNK.A
578.3307  1154.6469  1154.6295  0.0174  1      36    0.92      1     U         K.GIKDVVTQPQA.-
607.8334  1213.6522  1213.6125  0.0397  0      89    4.9e-06   1               R.AALIDCLAPDR.R
611.8622  1221.7098  1221.6605  0.0493  0      47    0.07      1               R.AQSVVDYLISK.G
640.8428  1279.6710  1279.6409  0.0301  0      47    0.064     1     U         K.DGSVVVLGYTDR.I
685.8744  1369.7342  1369.7136  0.0206  1      49    0.04      1               R.AALIDCLAPDRR.V
689.9077  1377.8009  1377.7616  0.0393  1      71    0.00024   1               R.RAQSVVDYLISK.G
705.3423  1408.6700  1408.6582  0.0118  0      101   2.3e-07   1     U         R.IGSDAYNQGLSER.R
487.2451  1458.7136  1458.6813  0.0323  1      59    0.0044    1     U         R.MPYKGSVENGAYK.A + Oxidation (M)
827.9351  1653.8557  1653.8250  0.0307  0      101   2.7e-07   1               K.LGYPITDDLDIYTR.L
890.3909  1778.7672  1778.7564  0.0108  0     (29)   3.2       2               R.GMGESNPVTGNTCDNVK.Q
898.4026  1794.7906  1794.7513  0.0394  0      88    4.4e-06   1               R.GMGESNPVTGNTCDNVK.Q + Oxidation
(M)
690.0599  2067.1580  2067.1146  0.0434  2      38    0.46      1               R.AALIDCLAPDRRVEIEVK.G
744.7426  2231.2061  2231.1586  0.0475  0      78    4e-05     1     U         R.FGQGEAAPVVAPAPAPAPEVQTK.H
867.7917  2600.3534  2600.2871  0.0663  0      106   5.5e-08   1     U         K.NHDTGVSPVFAGGVEYAITPEIATR.L
```

SwissProt

Mascot Score: 58 Queries Matched: 1
Protein ID: Nucleoside-specific channel-forming protein tsx [Escherichia coli O157:H7]
Calculated Mr = 33568; Calculated pI = 5.07

```
  1 MKKTLLAAGA VLALSSSFTV NAAENDKPQY LSDWWHQSVN VVGSYHTRFG
 51 PQIRNDTYLE YEAFAKKDWF DFYGYADAPV FFGGNSDAKG IWNHGSPLFM
101 EIEPRFSIDK LTNTDLSFGP FKEWYFANNY IYDMGRNKDG RQSTWYMGLG
151 TDIDTGLPMS LSMNVYAKYQ WQNYGAANEN EWDGYRFKIK YFVPITDLWG
201 GQLSYIGFTN FDWGSDLGDD SGNAINGIKT RTNNSIASSH ILALNYDHWH
251 YSVVARYWHD GGQWNDDAEL NFGNGNFNVR STGWGGYLVV GYNF
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
732.3504  1462.6863  1462.6616  0.0247  0      58    0.0052    1     U         R.NDTYLEYEAFAK.K
```

NCBI

Mascot Score: 1197 Queries Matched: 21
Protein ID: Outer membrane protein A [Escherichia coli]

Calculated Mr = 37291; Calculated pI = 6.53

```
  1 MKKTAIAIAV ALAGFATVAQ AAPKDNTWYT GAKLGWSQYH DTGFINNNGP
 51 THENQLGAGA FGGYQVNPYV GFEMGYDWLG RMPYKGSVKN GAYKAQGVQL
101 TAKLGYPITD DLDIYTRLGG MVWRADTKSN VYGKNHDTGV SPVFAGGVEY
151 AITPEIATRL EYQWTNNIGD AHTIGTRPDN GMLSLGVSYR FGQGEAAPVV
201 APAPAPAPEV QTKHFTLKSD VLFNFNKATL KPEGQAALDQ LYSQLSNLDP
251 KDGSVVVLGY TDRIGSDAYN QGLSERRAQS VVDYLISKGI PADKISARGM
301 GESNPVTGNT CDNVKQRAAL IDCLAPDRRV EIEVKGIKDV VTQPQA
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
409.7410   817.4674   817.4269  0.0405  0     (54)   0.32      3             R.LGGMVWR.A
417.7286   833.4427   833.4218  0.0209  0      55    0.26      1             R.LGGMVWR.A + Oxidation (M)
436.7812   871.5479   871.5127  0.0352  1      49    1.2       1             R.RVEIEVK.G
458.2794   914.5443   914.5185  0.0258  0      54    0.39      1             K.AQGVQLTAK.L
514.3147  1026.6148  1026.5822  0.0327  1      57    0.13      1             K.GIPADKISAR.G
528.2571  1054.4995  1054.4720  0.0276  0      48    1.1       1             K.DNTWYTGAK.L
542.2924  1082.5703  1082.5397  0.0307  0      67    0.013     1             K.SDVLFNFNK.A
578.3307  1154.6469  1154.6295  0.0174  1      36    18        1             K.GIKDVVTQPQA.-
607.8334  1213.6522  1213.6125  0.0397  0      89    9.8e-05   1             R.AALIDCLAPDR.R
611.8622  1221.7098  1221.6605  0.0493  0      47    1.5       1             R.AQSVVDYLISK.G
640.8428  1279.6710  1279.6409  0.0301  0      47    1.4       1             K.DGSVVVLGYTDR.I
685.8744  1369.7342  1369.7136  0.0206  1      49    0.82      1             R.AALIDCLAPDRR.V
689.9077  1377.8009  1377.7616  0.0393  1      71    0.0049    1             R.RAQSVVDYLISK.G
705.3423  1408.6700  1408.6582  0.0118  0      101   4.6e-06   1             R.IGSDAYNQGLSER.R
487.2451  1458.7136  1457.7337  0.9799  2      26    1.7e+02   2     U       R.MPYKGSVKNGAYK.A + Oxidation (M)
827.9351  1653.8557  1653.8250  0.0307  0      101   5.5e-06   1             K.LGYPITDDLDIYTR.L
890.3909  1778.7672  1778.7564  0.0108  0     (29)   66        2             R.GMGESNPVTGNTCDNVK.Q
898.4026  1794.7906  1794.7513  0.0394  0      88    9e-05     1             R.GMGESNPVTGNTCDNVK.Q + Oxidation
(M)
690.0599  2067.1580  2067.1146  0.0434  2      38    9.4       2             R.AALIDCLAPDRRVEIEVK.G
744.7426  2231.2061  2231.1586  0.0475  0      78    0.00083   1             R.FGQGEAAPVVAPAPAPAPEVQTK.H
867.7917  2600.3534  2600.2871  0.0663  0      106   1.2e-06   1             K.NHDTGVSPVFAGGVEYAITPEIATR.L
```

NCBI

Mascot Score: 478 Queries Matched: 9
Protein ID: Chain A, outer membrane protein A (Ompa) [Escherichia coli]
Calculated Mr = 18864; Calculated pI = 5.74

```
  1 MAPKDNTWYT GAKLGWSQYH DTGLINNNGP THENKLGAGA FGGYQVNPYV
 51 GFEMGYDWLG RMPYKGSVEN GAYKAQGVQL TAKLGYPITD DLDIYTRLGG
101 MVWRADTYSN VYGKNHDTGV SPVFAGGVEY AITPEIATRL EYQWTNNIGD
151 AHTIGTRPDN GMLSLGVSYR FG
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
409.7410   817.4674   817.4269  0.0405  0     (54)   0.32      3             R.LGGMVWR.A
417.7286   833.4427   833.4218  0.0209  0      55    0.26      1             R.LGGMVWR.A + Oxidation (M)
458.2794   914.5443   914.5185  0.0258  0      54    0.39      1             K.AQGVQLTAK.L
462.7369   923.4593   923.4348  0.0245  0      28    94        1             K.GSVENGAYK.A
528.2571   1054.4995  1054.4720 0.0276  0      48    1.1       1             K.DNTWYTGAK.L
676.3469   1350.6793  1350.6568 0.0225  1      28    1.1e+02   2             M.APKDNTWYTGAK.L
487.2451   1458.7136  1458.6813 0.0323  1      59    0.089     1             R.MPYKGSVENGAYK.A + Oxidation (M)
827.9351   1653.8557  1653.8250 0.0307  0      101   5.5e-06   1             K.LGYPITDDLDIYTR.L
867.7917   2600.3534  2600.2871 0.0663  0      106   1.2e-06   1             K.NHDTGVSPVFAGGVEYAITPEIATR.L
```

Gel lane #4, gel band #3

SwissProt & NCBI

Mascot Score: 248   Queries Matched: 5
Protein ID: Shiga-like toxin 2 subunit A [Enterobacteria phage 933W]
Calculated Mr = 35920; Calculated pI = 8.68

```
  1 MKCILFKWVL CLLLGFSSVS YSREFTIDFS TQQSYVSSLN SIRTEISTPL
 51 EHISQGTTSV SVINHTPPGS YFAVDIRGLD VYQARFDHLR LIIEQNNLYV
101 AGFVNTATNT FYRFSDFTHI SVPGVTTVSM TTDSSYTTLQ RVAALERSGM
151 QISRHSLVSS YLALMEFSGN TMTRDASRAV LRFVTVTAEA LRFRQIQREF
201 RQALSETAPV YTMTPGDVDL TLNWGRISNV LPEYRGEDGV RVGRISFNNI
251 SAILGTVAVI LNCHHQGARS VRAVNEESQP ECQITGDRPV IKINNTLWES
301 NTAAAFLNRK SQFLYTTGK
```

```
Observed  Mr(expt)  Mr(calc)  Delta  Miss  Score  Expect  Rank  Unique  Peptide
461.2615   920.5084   920.4716 0.0368  0     50     0.033     1     U       R.GLDVYQAR.F
545.8066  1089.5987 1089.5818 0.0169  0     55     0.0096    1     U       R.ISNVLPEYR.G
553.8232  1105.6318 1105.6132 0.0187  0     52     0.017     1     U       R.FVTVTAEALR.F
568.6490  1702.9251 1702.8638 0.0613  1     40     0.21      1     U       R.ISNVLPEYRGEDGVR.V
759.3746  2275.1020 2275.0613 0.0407  0     51     0.012     1     U       R.HSLVSSYLALMEFSGNTMTR.D + 2
Oxidation (M)
```

NCBI

Mascot Score: 197   Queries Matched: 4
Protein ID: Verocytotoxin 2 variant A subunit [Escherichia coli]
Calculated Mr = 35782; Calculated pI = 7.74

```
  1 MKCILFKWVL CLLLGFSSVS YSREFTIDFS TQQSYVSSLN SIRTEISTPL
 51 EHISQGTTSV SVINHTPPGS YFAVDIRGLD VYQARFDHLR LIIEQNNLYV
101 AGFVNTATNT FYRFSDFTHI SVPDVTTVSM TTDSSNTTLQ RVAALEXSGM
151 QISRHSXVSS XLALMEXXGN TMTRDASRAV LRFVTVTAEA LRFRQIQREF
201 RQALSETAPV YTMTPGDVDL TLNWGRLSNV LPEYRGEDGV RVGRISFNNI
251 SAILGTVAVI LNCHHQGARS VRAVNEESQP ECQITGDRPV IKINNTLWES
301 NTAAAFLNRK SQXLYTTGK
```

```
Observed  Mr(expt)  Mr(calc)  Delta  Miss  Score  Expect  Rank  Unique  Peptide
461.2615   920.5084   920.4716 0.0368  0     50     0.88      1             R.GLDVYQAR.F
545.8066  1089.5987 1089.5818 0.0169  0     55     0.25      1     U       R.LSNVLPEYR.G
553.8232  1105.6318 1105.6132 0.0187  0     52     0.43      1             R.FVTVTAEALR.F
568.6490  1702.9251 1702.8638 0.0613  1     40     6.5       1     U       R.LSNVLPEYRGEDGVR.V
```

Gel lane #4, gel band #4

SwissProt

Mascot Score: 148   Queries Matched: 3
Protein ID: Outer membrane protein X [Escherichia coli O157:H7]
Calculated Mr = 18648; Calculated pI = 6.56

```
  1 MKKIACLSAL AAVLAFTAGT SVAATSTVTG GYAQSDAQGQ MNKMGGFNLK
```

```
   51 YRYEEDNSPL GVIGSFTYTE KSRTASSGDY NKNQYYGITA GPAYRINDWA
  101 SIYGVVGVGY GKFQTTEYPT YKHDTSDYGF SYGAGLQFNP MENVALDFSY
  151 EQSRIRSVDV GTWIAGVGYR F
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
639.3203  1276.6261  1276.5976  0.0285  0     52     0.023     1     U       K.FQTTEYPTYK.H
737.3650  1472.7155  1472.7048  0.0107  0     57     0.0065    1     U       K.NQYYGITAGPAYR.I
799.7192  2396.1357  2396.1033  0.0325  1     39     0.32      1     U       R.TASSGDYNKNQYYGITAGPAYR.I
```

SwissProt

Mascot Score: 125   Queries Matched: 3
Protein ID: Outer membrane lipoprotein slyB [Escherichia coli O157:H7]
Calculated Mr = 15649; Calculated pI = 9.36

```
    1 MIKRVLVVSM VGLSLVGCVN NDTLSGDVYT ASEAKQVQNV SYGTIVNVRP
   51 VQIQGGDDSN VIGAIGGAVL GGFLGNTVGG GTGRSLATAA GAVAGGVAGQ
  101 GVQSAMNKTQ GVELEIRKDD GNTIMVVQKQ GNTRFSPGQR VVLASNGSQV
  151 TVSPR
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
523.2999  1044.5853  1043.5611  1.0242  0     16     91        4     U       K.TQGVELEIR.K
682.3534  1362.6923  1362.6813  0.0110  1     52     0.022     1     U       R.KDDGNTIMVVQK.Q + Oxidation (M)
711.3689  2131.0850  2131.0692  0.0158  0     56     0.0062    1     U       R.SLATAAGAVAGGVAGQGVQSAMNK.T +
Oxidation (M)
```

SwissProt

Mascot Score: 73   Queries Matched: 2
Protein ID: 50S ribosomal protein L24 [Escherichia coli O157:H7]
Calculated Mr = 11309; Calculated pI = 10.21

```
    1 MAAKIRRDDE VIVLTGKDKG KRGKVKNVLS SGKVIVEGIN LVKKHQKPVP
   51 ALNQPGGIVE KEAAIQVSNV AIFNAATGKA DRVGFRFEDG KKVRFFKSNS
  101 ETIK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
542.3547  1082.6949  1082.6699  0.0250  0     48     0.052     1             K.VIVEGINLVK.K
505.3071  1512.8993  1511.8784  1.0210  2     26     8.6       8     U       K.IRRNDEVIVLTGK.D
```

NCBI

Mascot Score: 375   Queries Matched: 6
Protein ID: Hypothetical protein 933Wp55 [Enterobacteria phage 933W]
Calculated Mr = 13496; Calculated pI = 5.86

```
    1 MAKTILAPSL SERVYTGTHG NESVAEGVFT VNAAEADSVI HLLSLPVGIR
   51 INSLQLVSTG GLGTATVSIK SGEHALIDNS EAVSAKFARY VPVEPYTTQR
  101 DGELVTVTIK TAAATGTLNV LLRYTVVGY
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
537.8175  1073.6204  1073.5968  0.0236  0     55     0.23      1     U       R.DGELVTVTIK.T
543.8194  1085.6243  1085.6080  0.0162  0     51     0.62      1     U       K.TILAPSLSER.V
643.3842  1284.7538  1284.7401  0.0137  1     45     2.2       2     U       M.AKTILAPSLSER.V
650.8908  1299.7670  1299.7510  0.0159  0     95     2.2e-05   1     U       K.TAAATGTLNVLLR.Y
676.8571  1351.6996  1351.6772  0.0224  0     62     0.043     1     U       R.YVPVEPYTTQR.D
543.2790  1626.8152  1626.7849  0.0303  0     66     0.015     1     U       K.SGEHALIDNSEAVSAK.F
```

NCBI

Mascot Score: 197   Queries Matched: 4

Protein ID: Chain A, outer membrane protein Ompx [Escherichia Coli]
Calculated Mr = 16350; Calculated pI = 5.04

```
      1 ATSTVTGGYA QSDAQGQMNK MGGFNLKYRY EEDNSPLGVI GSFTYTEKSR
     51 TASSGDYNKN QYYGITAGPA YRINDWASIY GVVGVGYGKF QTTEYPTYKN
    101 DTSDYGFSYG AGLQFNPMEN VALDFSYEQS RIRSVDVGTW IAGVGYRF
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
639.3203  1276.6261  1276.5976  0.0285  0     52     0.48      1     U       K.FQTTEYPTYK.N
737.3650  1472.7155  1472.7048  0.0107  0     57     0.14      1     U       K.NQYYGITAGPAYR.I
677.6459  2029.9158  2029.9011  0.0147  0     49     0.71      1     U       -.ATSTVTGGYAQSDAQGQMNK.M + Oxidation
(M)
799.7192  2396.1357  2396.1033  0.0325  1     39     7.1       1     U       R.TASSGDYNKNQYYGITAGPAYR.I
```

NCBI

Mascot Score: 108   Queries Matched: 2
Protein ID: Putative outer membrane protein [Escherichia coli O157:H7 EDL933]
Calculated Mr = 15649; Calculated pI = 9.36

```
      1 MIKRVLVVSM VGLSLVGCVN NDTLSGDVYT ASEAKQVQNV SYGTIVNVRP
     51 VQIQGGDDSN VIGAIGGAVL GGFLGNTVGG GTGRSLATAA GAVAGGVAGQ
    101 GVQSAMNKTQ GVELEIRKDD GNTIMVVQKQ GNTRFSPGQR VVLASNGSQV
    151 TVSPR
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
682.3534  1362.6923  1362.6813  0.0110  1     52     0.45      1     U       R.KDDGNTIMVVQK.Q + Oxidation (M)
711.3689  2131.0850  2131.0692  0.0158  0     56     0.13      1     U       R.SLATAAGAVAGGVAGQGVQSAMNK.T +
Oxidation (M)
```

Gel lane #4, gel band #5

SwissProt & NCBI

Mascot Score: 117   Queries Matched: 2
Protein ID: 10 kDa chaperonin [Escherichia coli O157:H7]
Calculated Mr = 10381; Calculated pI = 5.15

```
      1 MNIRPLHDRV IVKRKEVETK SAGGIVLTGS AAAKSTRGEV LAVGNGRILE
     51 NGEVKPLDVK VGDIVIFNDG YGVKSEKIDN EEVLIMSESD ILAIVEA
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
485.2989  1452.8749  1452.8188  0.0561  0     48     0.05      1     U       R.ILENGEVKPLDVK.V
748.3964  1494.7783  1494.7719  0.0064  0     69     0.00041   1             K.VGDIVIFNDGYGVK.S
```

SwissProt

Mascot Score: 111   Queries Matched: 2
Protein ID: UPF0076 protein yjgF [Escherichia coli (strain K12)]
Calculated Mr = 13660; Calculated pI = 5.36

```
      1 MSKTIATENA PAAIGPYVQG VDLGNMIITS GQIPVNPKTG EVPADVAAQA
     51 RQSLDNVKAI VEAAGLKVGD IVKTTVFVKD LNDFATVNAT YEAFFTEHNA
    101 TFPARSCVEV ARLPKDVKIE IEAIAVRR
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
507.3130  1012.6115  1012.5917  0.0198  0     55     0.011     1     U       K.IEIEAIAVR.R
642.8416  1283.6686  1283.6470  0.0217  0     56     0.0096    1     U     K.TGEVPADVAAQAR.Q
```

SwissProt & NCBI

Mascot Score: 97 Queries Matched: 2
Protein ID: Major outer membrane lipoprotein [Escherichia coli O157:H7]
Calculated Mr = 8375; Calculated pI = 9.30

```
     1 MKATKLVLGA VILGSTLLAG CSSNAKIDQL SSDVQTLNAK VDQLSNDVNA
    51 MRSDVQAAKD DAARANQRLD NMATKYRK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
689.3459  1376.6772  1376.6354  0.0417  0     59     0.004    1     U       K.VDQLSNDVNAMR.S + Oxidation (M)
511.2764  1530.8074  1530.7889  0.0185  0     38     0.55     1     U       K.IDQLSSDVQTLNAK.V
```

SwissProt

Mascot Score: 55 Queries Matched: 1
Protein ID: Protein tdcF [Escherichia coli (strain K12)]
Calculated Mr = 14112; Calculated pI = 5.06

```
     1 MKKIIETQRA PGAIGPYVQG VDLGSMVFTS GQIPVCPQTG EIPADVQDQA
    51 RLSLENVKAI VVAAGLSVGD IIKMTVFITD LNDFATINEV YKQFFDEHQA
   101 TYPTRSCVQV ARLPKDVKLE IEAIAVRSA
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
507.3130  1012.6115  1012.5917  0.0198  0     55     0.011    1     U       K.LEIEAIAVR.S
```

NCBI

Mascot Score: 368 Queries Matched: 6
Protein ID: Hypothetical protein 933Wp55 [Enterobacteria phage 933W]
Calculated Mr = 13496; Calculated pI = 5.86

```
     1 MAKTILAPSL SERVYTGTHG NESVAEGVFT VNAAEADSVI HLLSLPVGIR
    51 INSLQLVSTG GLGTATVSIK SGEHALIDNS EAVSAKFARY VPVEPYTTQR
   101 DGELVTVTIK TAAATGTLNV LLRYTVVGY
```

```
Observed  Mr(expt)   Mr(calc)   Delta    Miss  Score  Expect   Rank  Unique  Peptide
537.8175  1073.6204  1073.5968  0.0236   0     59     0.098    1     U       R.DGELVTVTIK.T
543.8194  1085.6243  1085.6080  0.0162   0     62     0.052    1     U       K.TILAPSLSER.V
643.3842  1284.7538  1284.7401  0.0137   1     37     13       3     U       M.AKTILAPSLSER.V
650.8908  1299.7670  1299.7510  0.0159   0     97     1.3e-05  1     U       K.TAAATGTLNVLLR.Y
676.8455  1351.6764  1351.6772 -0.0008   0     63     0.034    1     U       R.YVPVEPYTTQR.D
543.2790  1626.8152  1626.7849  0.0303   0     50     0.61     1     U       K.SGEHALIDNSEAVSAK.F
```

NCBI

Mascot Score: 111 Queries Matched: 2
Protein ID: Hypothetical protein Z5854 [Escherichia coli O157:H7 EDL933]
Calculated Mr = 15273; Calculated pI = 5.82

```
     1 MSQTFYRCNK GEIMSKTIAT ENAPAAIGPY VQGVDXGNMI ITSGQIPVNP
    51 KTGEVPADVA AQARQSLDNV KAIVEAAGLK VGDIVKTTVF VKDLNDFATV
   101 NATYEAFFTE HNATFPARSC VEVARLPKDV KIEIEAIAVR R
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
507.3130  1012.6115  1012.5917  0.0198  0     55     0.21     1     U       K.IEIEAIAVR.R
642.8416  1283.6686  1283.6470  0.0217  0     56     0.19     1     U       K.TGEVPADVAAQAR.Q
```

Gel lane #4, gel band #6

SwissProt &NCBI

Mascot Score: 200 Queries Matched: 3
Protein ID: Major outer membrane lipoprotein [Escherichia coli O157:H7]
Calculated Mr = 8375; Calculated pI = 9.30

```
     1 MKATKLVLGA VILGSTLLAG CSSNAKIDQL SSDVQTLNAK VDQLSNDVNA
    51 MRSDVQAAKD DAARANQRLD NMATKYRK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
623.8058  1245.5971  1245.5949  0.0022  1     51     0.026     1     U       R.SDVQAAKDDAAR.A
689.3341  1376.6537  1376.6354  0.0183  0     72     0.00021   1     U       K.VDQLSNDVNAMR.S + Oxidation (M)
766.4046  1530.7946  1530.7889  0.0056  0     77      7e-05    1     U       K.IDQLSSDVQTLNAK.V
```

SwissProt &NCBI

Mascot Score: 151 Queries Matched: 3
Protein ID: UPF0092 membrane protein yajC [Escherichia coli O157:H7]
Calculated Mr = 11879; Calculated pI = 9.57

```
     1 MSFFISDAVA ATGAPAQGSP MSLILMLVVF GLIFYFMILR PQQKRTKEHK
    51 KLMDSIAKGD EVLTNGGLVG RVTKVAENGY IAIALNDTTE VVIKRDFVAA
   101 VLPKGTMKAL
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
480.2941   958.5736   958.5488  0.0248  0     56     0.012     1     U       R.DFVAAVLPK.G
643.8478  1285.6811  1285.6626  0.0185  0     47     0.065     1     U       K.GDEVLTNGGLVGR.V
687.6967  2060.0682  2060.0572  0.0110  1     48     0.048     1     U       K.LMDSIAKGDEVLTNGGLVGR.V + Oxidation
(M)
```

SwissProt &NCBI

Mascot Score: 139 Queries Matched: 2
Protein ID: 30S ribosomal protein S10 [Escherichia coli O157:H7]
Calculated Mr = 11728; Calculated pI = 9.68

```
     1 MQNQRIRIRL KAFDHRLIDQ ATAEIVETAK RTGAQVRGPI PLPTRKERFT
    51 VLISPHVNKD ARDQYEIRTH LRLVDIVEPT EKTVDALMRL DLAAGVDVQI
   101 SLG
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
571.8316  1141.6487  1141.6230  0.0256  0     75     0.00013   1     U       R.LVDIVEPTEK.T
553.3198  1656.9375  1656.9046  0.0329  1     64     0.0011    1     U       R.LIDQATAEIVETAKR.T
```

SwissProt &NCBI

Mascot Score: 82 Queries Matched: 2
Protein ID: 50S ribosomal protein L7/L12 [Escherichia coli O157:H7]
Calculated Mr = 12288; Calculated pI = 4.60

```
     1 MSITKDQIIE AVAAMSVMDV VELISAMEEK FGVSAAAAVA VAAGPVEAAE
    51 EKTEFDVILK AAGANKVAVI KAVRGATGLG LKEAKDLVES APAALKEGVS
   101 KDDAEALKKA LEEAGAEVEV K
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
482.7786   963.5426   963.5277  0.0149  0     42     0.22      1     U       K.TEFDVILK.A
463.9171  1388.7294  1388.7147  0.0147  2     40     0.37      1     U       K.EGVSKDDAEALKK.A
```

SwissProt &NCBI

Mascot Score: 74 Queries Matched: 1
Protein ID: 30S ribosomal protein S17 [Escherichia coli O157:H7]
Calculated Mr = 9812; Calculated pI = 9.64

```
     1 MTDKIRTLQG RVVSDKMEKS IVVAIERFVK HPIYGKFIKR TTKLHVHDEN
    51 NECGIGDVVE IRECRPLSKT KSWTLVRVVE KAVL
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
735.6836  2204.0288  2204.0280  0.0008  0     74     9.7e-05   1     U       K.LHVHDENNECGIGDVVEIR.E
```

NCBI

Mascot Score: 309 Queries Matched: 5
Protein ID: Hypothetical protein 933Wp55 [Enterobacteria phage 933W]
Calculated Mr = 13496; Calculated pI = 5.86

```
     1 MAKTILAPSL SERVYTGTHG NESVAEGVFT VNAAEADSVI HLLSLPVGIR
    51 INSLQLVSTG GLGTATVSIK SGEHALIDNS EAVSAKFARY VPVEPYTTQR
   101 DGELVTVTIK TAAATGTLNV LLRYTVVGY
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
537.8071  1073.5997  1073.5968  0.0029  0     53     0.43      1     U       R.DGELVTVTIK.T
543.8194  1085.6243  1085.6080  0.0162  0     51     0.62      1     U       K.TILAPSLSER.V
650.8908  1299.7670  1299.7510  0.0159  0     72     0.0041    1     U       K.TAAATGTLNVLLR.Y
676.8571  1351.6996  1351.6772  0.0224  0     55     0.2       1     U       R.YVPVEPYTTQR.D
543.2790  1626.8152  1626.7849  0.0303  0     78     0.00095   1     U       K.SGEHALIDNSEAVSAK.F
```

NCBI

Mascot Score: 145 Queries Matched: 2
Protein ID: Hypothetical protein 933Wp74 [Enterobacteria phage 933W]
Calculated Mr = 12402; Calculated pI = 4.86

```
     1 MKKVLIAALI SGVSFGAFAQ QGGFQGPEAE RSTVAQAKEL KDDAWVILEG
    51 SIVKKVGDER YEFRDNSGTI VTDIDDSIWA GQNVSPKDKV RIEGEIDKDL
   101 SSVEVDVKAL KLLK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
625.6553  1873.9440  1873.9520 -0.0080  1     99     7.4e-06   1     U       R.IEGEIDKDLSSVEVDVK.A
648.3686  1942.0840  1942.0775  0.0065  2     46     1.5       1     U       K.ELKDDAWVILEGSIVKK.V
```

NCBI

Mascot Score: 120 Queries Matched: 2
Protein ID: Hypothetical protein Z0372 [Escherichia coli O157:H7 EDL933]
Calculated Mr = 13294; Calculated pI = 5.03

```
     1 MNKNLILAFA LFSLPVFAEE DLGPGKYVCD IRISSLDTAT QILSKSATVL
    51 DNGNNFIVQM PNGDQLYSPD LENVDDGIKQ KATIGGVTFI RRPTFNDRFI
   101 VEDGNTGFFY KMRNCEKK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
517.8082  1033.6018  1033.5920  0.0097  0     48     1.1       1     U       K.ATIGGVTFIR.R
688.8895  1375.7645  1375.7558  0.0086  0     72     0.0046    1     U       R.ISSLDTATQILSK.S
```

Gel lane #4, gel band #7

SwissProt & NCBI

Mascot Score: 375 Queries Matched: 5
Protein ID: Major outer membrane lipoprotein [Escherichia coli O157:H7]
Calculated Mr = 8375; Calculated pI = 9.30

```
 1 MKATKLVLGA VILGSTLLAG CSSNAKIDQL SSDVQTLNAK VDQLSNDVNA
51 MRSDVQAAKD DAARANQRLD NMATKYRK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
623.8170  1245.6194  1245.5949  0.0245  1     79     4.4e-05  1     U       R.SDVQAAKDDAAR.A
689.3341  1376.6537  1376.6354  0.0183  0     87     7.2e-06  1     U       K.VDQLSNDVNAMR.S + Oxidation (M)
766.4046  1530.7946  1530.7889  0.0056  0     92     2e-06    1     U       K.IDQLSSDVQTLNAK.V
693.0138  2076.0197  2075.9906  0.0291  1     50     0.03     1     U       K.VDQLSNDVNAMRSDVQAAK.D + Oxidation
(M)
652.0740  2604.2669  2604.2198  0.0471  2     67     0.00041  1     U       K.VDQLSNDVNAMRSDVQAAKDDAAR.A +
Oxidation (M)
```

SwissProt

Mascot Score: 155 Queries Matched: 3
Protein ID: Shiga-like toxin 2 subunit B [Enterobacteria phage 933W]
Calculated Mr = 9982; Calculated pI = 5.30

```
 1 MKKMFMAVLF ALASVNAMAA DCAKGKIEFS KYNEDDTFTV KVDGKEYWTS
51 RWNLQPLLQS AQLTGMTVTI KSSTCESGSG FAEVQFNND
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
404.7486   807.4826   807.4490  0.0336  1     35     0.97     3     U       K.GKIEFSK.Y
616.2916  1230.5686  1230.5405  0.0281  0     62     0.0024   1     U       K.YNEDDTFTVK.V
674.3429  2020.0069  2019.9789  0.0280  2     58     0.0046   1     U       K.GKIEFSKYNEDDTFTVK.V
```

SwissProt

Mascot Score: 59 Queries Matched: 1
Protein ID: Cold shock-like protein cspC [Escherichia coli O157:H7]
Calculated Mr = 7398; Calculated pI = 6.54

```
 1 MAKIKGQVKW FNESKGFGFI TPADGSKDVF VHFSAIQGNG FKTLAEGQNV
51 EFEIQDGQKG PAAVNVTAI
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
598.8117  1195.6088  1195.5874  0.0215  0     59     0.0039   1     U       K.GFGFITPADGSK.D
```

SwissProt

Mascot Score: 50 Queries Matched: 1
Protein ID: DNA-binding protein HU-alpha [Escherichia coli O157:H7]
Calculated Mr = 9529; Calculated pI = 9.57

```
 1 MNKTQLIDVI AEKAELSKTQ AKAALESTLA AITESLKEGD AVQLVGFGTF
51 KVNHRAERTG RNPQTGKEIK IAAANVPAFV SGKALKDAVK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
622.8599  1243.7052  1243.6925  0.0128  0     50     0.033    1     U       K.IAAANVPAFVSGK.A
```

NCBI

Mascot Score: 228 Queries Matched: 4
Protein ID: Hypothetical protein 933Wp60 [Enterobacteria phage 933W]
Calculated Mr = 14759; Calculated pI = 6.71

```
  1 MPHGFRVFFS ICRSGLVTGR GRMSRGWMKW AVIQAEQEND MNILRKLMQS
 51 LCGCGKHDDC ENGQSLTAQL RLGPADILES DENGIIPEQD RVITQVVILD
101 ADKKQIQCVV RPLQILRADG TWENIGGMK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
647.8012  1293.5879  1293.5659  0.0219  0     66     0.016    1     U       R.ADGTWENIGGMK.- + Oxidation (M)
481.3106  1440.9099  1440.8552  0.0547  1     62     0.037    1     U       R.VITQVVILDADKK.Q
541.6698  1621.9876  1621.9450  0.0426  0     38     10       1     U       K.QIQCVVRPLQILR.A
727.7136  2180.1191  2180.0597  0.0594  0     63     0.034    1     U       R.LGPADILESDENGIIPEQDR.V
```

NCBI

Mascot Score: 120 Queries Matched: 2
Protein ID: Shiga toxin II subunit B [Escherichia coli]
Calculated Mr = 9992; Calculated pI = 5.30

```
  1 MKKMFMAVLF ALASVNAMAA DCAKGKIEFS KYNEDDTFTV KVDGKEYWTS
 51 RWNLQPLLQS AQLTGMTVXI KSSTCESGSG FAEVQFNND
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
616.2916  1230.5686  1230.5405  0.0281  0     62     0.048    1     U       K.YNEDDTFTVK.V
674.3429  2020.0069  2019.9789  0.0280  2     58     0.1      1     U       K.GKIEFSKYNEDDTFTVK.V
```

NCBI

Mascot Score: 102 Queries Matched: 2
Protein ID: Bor protein precursor [Enterobacteria phage 933W]
Calculated Mr = 10642; Calculated pI = 9.15

```
  1 MKKMLLATAL ALLITGCAQQ TFTVQNKQTA VAPKETITHH FFVSGIGQKK
 51 TVDAAKICGG TENVVKTETQ QTFVNGLLGF ITLGIYTPLE ARVYCSQ
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
538.7793  1075.5440  1075.5332  0.0108  0     56     0.19     1     U       K.ICGGTENVVK.T
567.6396  1699.8971  1699.8682  0.0288  0     46     1.7      1     U       K.ETITHHFFVSGIGQK.K
```

NCBI

Mascot Score: 94 Queries Matched: 2
Protein ID: Hypothetical protein ECs1210 [Escherichia coli O157:H7 str. Sakai]
Calculated Mr = 6914; Calculated pI = 9.18

```
  1 MTFLNQLMLY FCTVVCVLYL LSGGYRAMRD FWRRQIDKRA AEKISASQSA
 51 GSKPEEPLI
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
491.2480   980.4815   980.4650  0.0165  1     47     1.3      2     U       R.AMRDFWR.R
807.4396  1612.8647  1612.8308  0.0339  0     47     1.3      1     U       K.ISASQSAGSKPEEPLI.-
```

Gel lane #4, gel band #8

SwissProt & NCBI

Mascot Score: 268 Queries Matched: 5

Protein ID: Major outer membrane lipoprotein [Escherichia coli O157:H7]
Calculated Mr = 8375; Calculated pI = 9.30

```
 1 MKATKLVLGA VILGSTLLAG CSSNAKIDQL SSDVQTLNAK VDQLSNDVNA
51 MRSDVQAAKD DAARANQRLD NMATKYRK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
416.2095  1245.6067  1245.5949  0.0118  1     45     0.11     1     U       R.SDVQAAKDDAAR.A
689.3276  1376.6406  1376.6354  0.0052  0     69     0.00043  1     U       K.VDQLSNDVNAMR.S + Oxidation (M)
766.3956  1530.7767  1530.7889 -0.0123  0     93     1.7e-06  1     U       K.IDQLSSDVQTLNAK.V
693.0071  2075.9996  2075.9906  0.0090  1     42     0.16     1     U       K.VDQLSNDVNAMRSDVQAAK.D + Oxidation
(M)
652.1000  2604.3709  2604.2198  0.1511  2     19     30       2     U       K.VDQLSNDVNAMRSDVQAAKDDAAR.A +
Oxidation (M)
```

SwissProt

Mascot Score: 244   Queries Matched: 5
Protein ID: Shiga-like toxin 2 subunit B [Enterobacteria phage 933W]
Calculated Mr = 9982; Calculated pI = 5.30

```
 1 MKKMFMAVLF ALASVNAMAA DCAKGKIEFS KYNEDDTFTV KVDGKEYWTS
51 RWNLQPLLQS AQLTGMTVTI KSSTCESGSG FAEVQFNND
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
404.7408   807.4671   807.4490  0.0181  1     36     0.88     3     U       K.GKIEFSK.Y
616.2761  1230.5376  1230.5405 -0.0029  0     58     0.0054   1     U       K.YNEDDTFTVK.V
414.2113  1239.6122  1239.5884  0.0238  1     31     2.6      1     U       K.VDGKEYWTSR.W
612.6299  1834.8680  1834.8625  0.0054  1     59     0.0035   1     U       K.IEFSKYNEDDTFTVK.V
674.3368  2019.9885  2019.9789  0.0096  2     60     0.0029   1     U       K.GKIEFSKYNEDDTFTVK.V
```

NCBI

Mascot Score: 208   Queries Matched: 4
Protein ID: Shiga toxin II subunit B [Escherichia coli]
Calculated Mr = 9992; Calculated pI = 5.30

```
 1 MKKMFMAVLF ALASVNAMAA DCAKGKIEFS KYNEDDTFTV KVDGKEYWTS
51 RWNLQPLLQS AQLTGMTVXI KSSTCESGSG FAEVQFNND
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
616.2761  1230.5376  1230.5405 -0.0029  0     58     0.11     1             K.YNEDDTFTVK.V
414.2113  1239.6122  1239.5884  0.0238  1     31     51       1             K.VDGKEYWTSR.W
612.6299  1834.8680  1834.8625  0.0054  1     59     0.074    1             K.IEFSKYNEDDTFTVK.V
674.3368  2019.9885  2019.9789  0.0096  2     60     0.063    1             K.GKIEFSKYNEDDTFTVK.V
```

NCBI

Mascot Score: 200   Queries Matched: 4
Protein ID: Shiga toxin 2 B subunit [Escherichia coli]
Calculated Mr = 10011; Calculated pI = 4.79

```
 1 MKKMFMAVLF ALVSVNAMAA DCAKGKIEFS KYNEDDTFTV KVDGEEYWTS
51 RWNLQPLLQS AQLTGMTVTI KSSTCESGSG FAEVQFNND
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
616.2761  1230.5376  1230.5405 -0.0029  0     58     0.11     1             K.YNEDDTFTVK.V
414.2113  1239.6122  1240.5360 -0.9238  0     23     3.6e+02  6     U       K.VDGEEYWTSR.W
612.6299  1834.8680  1834.8625  0.0054  1     59     0.074    1             K.IEFSKYNEDDTFTVK.V
674.3368  2019.9885  2019.9789  0.0096  2     60     0.063    1             K.GKIEFSKYNEDDTFTVK.V
```

NCBI

Mascot Score: 108   Queries Matched: 3
Protein ID: Variant Shiga toxin type 2 B subunit [Escherichia coli]
Calculated Mr = 9951; Calculated pI = 7.74

```
  1 MKKMFMAVLF ALVSVNAMAA DCAKGKIEFS KYNENDTFTV KVDGKEYWTS
 51 RWNLQPLLQS AQLTGMTVTI KSSTCASGSG FAEVQFNND
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
414.2113  1239.6122  1239.5884  0.0238  1     31     51        1              K.VDGKEYWTSR.W
612.6299  1834.8680  1833.8785  0.9895  1     41     4.5       5       U      K.IEFSKYNENDTFTVK.V
674.3368  2019.9885  2018.9949  0.9936  2     35     18        7       U      K.GKIEFSKYNENDTFTVK.V
```

Gel lane #4, gel band #9

SwissProt & NCBI

Mascot Score: 324   Queries Matched: 7
Protein ID: Major outer membrane lipoprotein [Escherichia coli O157:H7]
Calculated Mr = 8375; Calculated pI = 9.30

```
  1 MKATKLVLGA VILGSTLLAG CSSNAKIDQL SSDVQTLNAK VDQLSNDVNA
 51 MRSDVQAAKD DAARANQRLD NMATKYRK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
416.2095  1245.6067  1245.5949  0.0118  1     52     0.022     1     U       R.SDVQAAKDDAAR.A
681.3228  1360.6311  1360.6405 -0.0094  0     84     1.3e-05   1     U       K.VDQLSNDVNAMR.S
689.3159  1376.6172  1376.6354 -0.0182  0    (76)    8.5e-05   1     U       K.VDQLSNDVNAMR.S + Oxidation (M)
766.3833  1530.7520  1530.7889 -0.0369  0     95     9.9e-07   1     U       K.IDQLSSDVQTLNAK.V
511.2749  1530.8030  1530.7889  0.0140  0    (38)    0.53      1     U       K.IDQLSSDVQTLNAK.V
692.9954  2075.9644  2075.9906 -0.0262  1     53     0.015     1     U       K.VDQLSNDVNAMRSDVQAAK.D + Oxidation
(M)
652.0571  2604.1995  2604.2198 -0.0203  2     40     0.21      1     U       K.VDQLSNDVNAMRSDVQAAKDDAAR.A +
Oxidation (M)
```

SwissProt

Mascot Score: 108   Queries Matched: 2
Protein ID: Shiga-like toxin 2 subunit A [Enterobacteria phage 933W]
Calculated Mr = 35920; Calculated pI = 8.68

```
  1 MKCILFKWVL CLLLGFSSVS YSREFTIDFS TQQSYVSSLN SIRTEISTPL
 51 EHISQGTTSV SVINHTPPGS YFAVDIRGLD VYQARFDHLR LIIEQNNLYV
101 AGFVNTATNT FYRFSDFTHI SVPGVTTVSM TTDSSYTTLQ RVAALERSGM
151 QISRHSLVSS YLALMEFSGN TMTRDASRAV LRFVTVTAEA LRFRQIQREF
201 RQALSETAPV YTMTPGDVDL TLNWGRISNV LPEYRGEDGV RVGRISFNNI
251 SAILGTVAVI LNCHHQGARS VRAVNEESQP ECQITGDRPV IKINNTLWES
301 NTAAAFLNRK SQFLYTTGK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect    Rank  Unique  Peptide
645.6535  1933.9386  1933.9646 -0.0260  0     50     0.027     1     U       K.INNTLWESNTAAAFLNR.K
757.3651  2269.0734  2269.1008 -0.0275  0     59     0.0029    1     U       R.AVNEESQPECQITGDRPVIK.I
```

SwissProt & NCBI

Mascot Score: 78   Queries Matched: 1
Protein ID: Entericidin B [Escherichia coli O157:H7]

Calculated Mr = 4864; Calculated pI = 7.93

```
      1 MVKKTIAAIF SVLVLSTVLT ACNTTRGVGE DISDGGNAIS GAATKAQQ
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
859.9061  1717.7976  1717.8119 -0.0143  0     78     5.3e-05  1     U       R.GVGEDISDGGNAISGAATK.A
```

NCBI

Mascot Score: 110   Queries Matched: 2
Protein ID: Shiga toxin 2d subunit A [Escherichia coli]
Calculated Mr = 35873; Calculated pI = 7.74

```
      1 MKCILFKWVL CLLLGFSSVS YSREFTIDFS TQQSYVSSLN SIRAEISTPL
     51 EHISQGTTSV SVINHTPPGS YFAVDIRGLD VYQARFDHLR LIIEQNNLYV
    101 AGFVNTATNT FYRFSDFTHI SVPGVTTVSM TTDSSYTTLQ RVAALERSGM
    151 QISRHSLVSS YLALMEFSGN TMTRDASRAV LRFVTVIAEA LRFRQIQREF
    201 RQALSETAPV YTMMPGDVDL TLNWGRISNV LPEYRGEDGV RVGRISFNNI
    251 SAILGTVAVI LNCHHQGARS VRAVNEESQP ECQITGDRPV IKINNTLWES
    301 NTAAAFLNRK SQSLYTTGE
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
645.6535  1933.9386  1933.9646 -0.0260  0     50     0.56     1             K.INNTLWESNTAAAFLNR.K
757.3651  2269.0734  2269.1008 -0.0275  0     59     0.06     1     U       R.AVNEESQPECQITGDRPVIK.I
```

NCBI

Mascot Score: 103   Queries Matched: 2
Protein ID: Verocytotoxin 2 variant A subunit [Escherichia coli]
Calculated Mr = 35713; Calculated pI = 8.35

```
      1 MKCILFKWVL CLXLGFSSVS YSREFTIDFS TQQSYVSSLN SIRTEISTPL
     51 EHISQGTTSV SVINHTPPGS YFAVDIRGLD VYQARFDHLR LIIEQNNLYV
    101 AGFVNTATNT FYRFSDFTHI SVPGVTTVSM TTDSSYTTLQ RVAALERSGM
    151 QISRHSLVSS YLALMEFSGN TMTRDASRAV LRFVTVTAEA LRFRQIQREF
    201 RQALSETAPV YTMTPGDVDL TLNWGRISNV LPEYRGEDGV RVGRISFNNI
    251 SAILGTVAVI LNCHHQGARS VRAVNEESXP ECQITGDRPV IKINNTLWES
    301 NTAAAFLNRK SQSLYTTG
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
645.6535  1933.9386  1933.9646 -0.0260  0     50     0.56     1             K.INNTLWESNTAAAFLNR.K
757.3651  2269.0734  2269.1372 -0.0638  0     59     0.06     1     U       R.AVNEESKPECQITGDRPVIK.I
```

Gel lane #4, gel band #10

SwissProt & NCBI

Mascot Score: 141   Queries Matched: 2
Protein ID: Major outer membrane lipoprotein [Escherichia coli O157:H7]
Calculated Mr = 8375; Calculated pI = 9.30

```
      1 MKATKLVLGA VILGSTLLAG CSSNAKIDQL SSDVQTLNAK VDQLSNDVNA
     51 MRSDVQAAKD DAARANQRLD NMATKYRK
```

```
Observed  Mr(expt)   Mr(calc)   Delta   Miss  Score  Expect   Rank  Unique  Peptide
689.3276  1376.6406  1376.6354  0.0052  0     63     0.0016   1     U       K.VDQLSNDVNAMR.S + Oxidation (M)
766.3956  1530.7767  1530.7889 -0.0123  0     78     5.8e-05  1     U       K.IDQLSSDVQTLNAK.V
```

Supplementary Materials