

# Mascot Search Results

User : r-nakagawa  
 Email :  
 Search title : SN221362\_deTOP2B\_control\_lul\_Node:2  
 MS data file : File Name: Z:\SN221362\_deTOP2B\_control\_lul.raw; File Path: : File Time: 3/1/2023 7:06:29 AM; File Size: 352609374 [Byte]  
 Database 1 : cRAP STRAV\_proteinG\_20230313 (118 sequences: 39090 residues)  
 Database 2 : Original\_21\_21\_TOP2B\_1-566\_20210618 (1 sequences: 589 residues)  
 Database 3 : Uniprot\_Proteome\_E.coli\_K12\_Proteome\_E.coli\_K12\_UP000000625\_2022\_01 (4448 sequences: 1358110 residues)  
 Timestamp : 13 Sep 2023 at 00:22:17 GMT  
 Enzyme : Trypsin  
 Fixed modifications : Carbamidomethyl (C)  
 Variable modifications : Acetyl (Protein N-term), Oxidation (M), Phospho (ST), Phospho (Y)  
 Mass values :  
 Protein Mass : Unrestricted  
 Peptide Mass Tolerance : ± 10 ppm  
 Fragment Mass Tolerance : ± 0.8 Da  
 Max Missed Cleavages : 3  
 Instrument type : Default  
 Number of queries : 14029  
 Protein hits :

2::TOP2B\_1-566  
 1::sp|TRYP\_PIG|  
 1::sp|K2C1\_HUMAN|  
 1::sp|K1C10\_HUMAN|  
 3::P0AAZ5|THIO\_EC01|  
 1::sp|ALBU\_BOVIN|  
 1::sp|K2E\_HUMAN|  
 3::P76298|FLHA\_EC01|  
 3::P0AD96|LIVJ\_EC01|  
 3::P39220|YABP\_EC01|  
 3::P0AFB5|NTRB\_EC01|  
 3::Q06065|ATOC\_EC01|  
 3::P69741|HYB0\_EC01|  
 3::P39220|YABP\_EC01|  
 3::P06149|DLDD\_EC01|  
 3::P28722|YHCA\_EC01|  
 3::Q46857|DKGA\_EC01|  
 3::P28630|HOLA\_EC01|  
 1::sp|RS27A\_HUMAN|  
 3::Q46793|YGEN\_EC01|  
 3::P0A930|YPMF\_EC01|  
 3::P15877|DHG\_EC01|  
 3::P69797|P1NAB\_EC01|  
 3::P75882|GFCD\_EC01|  
 3::P04152|UMUG\_EC01|  
 3::P20986|PTFC\_EC01|  
 3::P77739|Y13K\_EC01|  
 3::P31829|YDOL\_EC01|  
 3::P0A069|GNLQ\_EC01|  
 3::P0A8N3|SYK1\_EC01|  
 3::P76550|EUT0\_EC01|  
 3::P0A1X9|MALF\_EC01|  
 3::Q46861|YGIO\_EC01|  
 3::P0AGY1|YDJA\_EC01|  
 3::P63924|SMHA\_EC01|  
 3::V9H702|YPMF\_EC01|  
 3::P0A8H5|HSLU\_EC01|  
 3::P02943|LAMB\_EC01|  
 3::P52101|GLRK\_EC01|  
 3::P68644|Y1XG\_EC01|  
 3::P77766|RNAAM\_EC01|  
 3::P06045|SSUD\_EC01|  
 3::P75893|YDOL\_EC01|  
 3::P38035|K1CR\_EC01|  
 3::P0AEM0|FKBX\_EC01|  
 3::P0A088|GMAD\_EC01|  
 3::AOA/H2C769|AOA/H2C769\_EC01|  
 3::P0A840|SURE\_EC01|  
 3::P21893|RECQ\_EC01|  
 3::E30852|SMF\_EC01|  
 3::P38035|K1CR\_EC01|  
 3::P23871|HEMH\_EC01|  
 3::P00683|PPB\_EC01|  
 3::Q46864|MQSA\_EC01|  
 1::sp|DHE3\_BOVIN|  
 3::P0A624|SPO1\_EC01|  
 3::E37650|BCSC\_EC01|  
 3::P77293|GTRB\_EC01|  
 3::P36678|GSPM\_EC01|  
 3::P16869|FHUE\_EC01|  
 3::P76161|REO2\_EC01|  
 3::P64570|YQGC\_EC01|  
 3::P77732|RHMIR\_EC01|  
 3::P38035|K1CR\_EC01|  
 3::P75977|YMF0\_EC01|  
 3::P77658|YNA4\_EC01|  
 3::P0A7R9|RS1T\_EC01|  
 3::P00957|SYA\_EC01|  
 3::P07813|SY1\_EC01|  
 3::P0A023|CUSR\_EC01|  
 3::P24216|UXUA\_EC01|  
 3::P38134|Y1XG\_EC01|  
 3::P0ADI3|YGLM\_EC01|  
 3::P0AFA2|NARX\_EC01|  
 3::P70099|B1SG\_EC01|  
 3::P33362|YEHZ\_EC01|  
 3::P39358|YJHG\_EC01|  
 TOP2B\_1-566  
 sp|TRYP\_PIG|  
 sp|K2C1\_HUMAN|  
 sp|K1C10\_HUMAN|  
 Thioredoxin 1 OS=Escherichia coli (strain K12) OX=83333 GN=trxA PE=1 SV=2  
 sp|ALBU\_BOVIN|  
 sp|K2E\_HUMAN|  
 Flagellar biosynthesis protein FlaH OS=Escherichia coli (strain K12) OX=83333 GN=flaH PE=3 SV=1  
 Leu/Ile/Val-binding protein OS=Escherichia coli (strain K12) OX=83333 GN=livJ PE=1 SV=1  
 Protein YabP OS=Escherichia coli (strain K12) OX=83333 GN=yabP PE=4 SV=2  
 Sensory histidine kinase/phosphatase NtrB OS=Escherichia coli (strain K12) OX=83333 GN=ntrB PE=1 SV=1  
 Regulatory protein AtoC OS=Escherichia coli (strain K12) OX=83333 GN=atoC PE=1 SV=2  
 Hydrogenase-2, small chain OS=Escherichia coli (strain K12) OX=83333 GN=hyb0 PE=1 SV=1  
 Multiphosphoryl transfer protein 1 OS=Escherichia coli (strain K12) OX=83333 GN=fryA PE=1 SV=3  
 Quinone-dependent D-lactate dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=ddl PE=1 SV=3  
 Uncharacterized fimbrial chaperone YhcA OS=Escherichia coli (strain K12) OX=83333 GN=yhcA PE=3 SV=2  
 2,5-diketo-D-gluconic acid reductase A OS=Escherichia coli (strain K12) OX=83333 GN=dkgA PE=1 SV=3  
 DNA polymerase III subunit delta OS=Escherichia coli (strain K12) OX=83333 GN=hoIA PE=1 SV=1  
 sp|RS27A\_HUMAN|  
 Putative uncharacterized protein YgeN OS=Escherichia coli (strain K12) OX=83333 GN=ygeN PE=5 SV=3  
 Murein D0-endopeptidase MepM OS=Escherichia coli (strain K12) OX=83333 GN=mepM PE=1 SV=1  
 Quinoprotein glucose dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=gcd PE=1 SV=2  
 PTS system mannose-specific EIIB component OS=Escherichia coli (strain K12) OX=83333 GN=manX PE=1 SV=2  
 Uncharacterized lipoprotein Gfcd OS=Escherichia coli (strain K12) OX=83333 GN=gfcd PE=3 SV=1  
 Protein UmuC OS=Escherichia coli (strain K12) OX=83333 GN=umuC PE=1 SV=2  
 PTS system fructose-specific EIIB' BC component OS=Escherichia coli (strain K12) OX=83333 GN=fruA PE=1 SV=1  
 Probable ketonase YniA OS=Escherichia coli (strain K12) OX=83333 GN=yniA PE=3 SV=1  
 Probable zinc protease Pqol OS=Escherichia coli (strain K12) OX=83333 GN=pqol PE=1 SV=2  
 HTH-type transcriptional regulator GntR OS=Escherichia coli (strain K12) OX=83333 GN=gntR PE=1 SV=1  
 Lysine-tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=lysS PE=1 SV=2  
 Acetate kinase Eut0 OS=Escherichia coli (strain K12) OX=83333 GN=eut0 PE=1 SV=1  
 Maltose/maltodextrin-binding periplasmic protein OS=Escherichia coli (strain K12) OX=83333 GN=malE PE=1 SV=1  
 UPF013 protein Ygi0 OS=Escherichia coli (strain K12) OX=83333 GN=ygi0 PE=3 SV=3  
 Putative NAD(P)H nitroreductase YdjA OS=Escherichia coli (strain K12) OX=83333 GN=ydjA PE=1 SV=1  
 Phosphoheptose isomerase OS=Escherichia coli (strain K12) OX=83333 GN=gmaA PE=1 SV=1  
 Uncharacterized protein YpaA OS=Escherichia coli (strain K12) OX=83333 GN=yypA PE=4 SV=1  
 ATP-dependent protease ATPase subunit HslU OS=Escherichia coli (strain K12) OX=83333 GN=hslU PE=1 SV=1  
 Maltoporin OS=Escherichia coli (strain K12) OX=83333 GN=lamB PE=1 SV=1  
 Sensor histidine kinase GlrK OS=Escherichia coli (strain K12) OX=83333 GN=glrK PE=1 SV=3  
 Protein FixC OS=Escherichia coli (strain K12) OX=83333 GN=fixC PE=3 SV=1  
 5'-3' exoribonuclease OS=Escherichia coli (strain K12) OX=83333 GN=yviV PE=1 SV=1  
 Alkanesulfonate monooxygenase OS=Escherichia coli (strain K12) OX=83333 GN=ssuD PE=1 SV=3  
 Lipoprotein-releasing system transmembrane protein LolE OS=Escherichia coli (strain K12) OX=83333 GN=lolE PE=1 SV=3  
 L-methionine/branched-chain amino acid exporter YjeH OS=Escherichia coli (strain K12) OX=83333 GN=yjeH PE=1 SV=1  
 FKBP-type 16 kDa peptidyl-prolyl cis-trans isomerase OS=Escherichia coli (strain K12) OX=83333 GN=fkpB PE=1 SV=2  
 GDP-mannose 4,6-dehydratase OS=Escherichia coli (strain K12) OX=83333 GN=gmd PE=1 SV=1  
 Putative type II secretion system C-type protein YghF OS=Escherichia coli (strain K12) OX=83333 GN=yghF PE=3 SV=1  
 5'/3'-nucleotidase SurE OS=Escherichia coli (strain K12) OX=83333 GN=surE PE=1 SV=1  
 Single-stranded-DNA-specific exonuclease RecJ OS=Escherichia coli (strain K12) OX=83333 GN=recJ PE=1 SV=2  
 Protein Smf OS=Escherichia coli (strain K12) OX=83333 GN=smf PE=3 SV=1  
 Uncharacterized protein YbbC OS=Escherichia coli (strain K12) OX=83333 GN=ybbC PE=2 SV=1  
 Transcriptional regulatory protein RtrC OS=Escherichia coli (strain K12) OX=83333 GN=rtrC PE=4 SV=2  
 Ferrochelatase OS=Escherichia coli (strain K12) OX=83333 GN=hemH PE=1 SV=3  
 Alkaline phosphatase OS=Escherichia coli (strain K12) OX=83333 GN=phoA PE=1 SV=1  
 Antitoxin MqsA OS=Escherichia coli (strain K12) OX=83333 GN=mqsA PE=1 SV=1  
 sp|DHE3\_BOVIN|  
 Bifunctional (p)pppp synthase/hydrolase SpoT OS=Escherichia coli (strain K12) OX=83333 GN=spoT PE=1 SV=1  
 Cellulose synthase operon protein C OS=Escherichia coli (strain K12) OX=83333 GN=bcsc PE=1 SV=3  
 L-methionine/branched-chain amino acid exporter YjeH OS=Escherichia coli (strain K12) OX=83333 GN=yjeH PE=1 SV=1  
 Prophage bacteriophage glucosyl transferase homolog OS=Escherichia coli (strain K12) OX=83333 GN=yfdH PE=1 SV=1  
 Putative type II secretion system protein M OS=Escherichia coli (strain K12) OX=83333 GN=gspM PE=2 SV=2  
 FhuE receptor OS=Escherichia coli (strain K12) OX=83333 GN=fhuE PE=1 SV=2  
 Prophage antitermination protein Q homolog QuuQ OS=Escherichia coli (strain K12) OX=83333 GN=quuQ PE=3 SV=2  
 Protein YggC OS=Escherichia coli (strain K12) OX=83333 GN=yggC PE=1 SV=1  
 Uncharacterized HTH-type transcriptional regulator RhmR OS=Escherichia coli (strain K12) OX=83333 GN=rhmR PE=1 SV=1  
 DNA ligase B OS=Escherichia coli (strain K12) OX=83333 GN=ligB PE=1 SV=2  
 Uncharacterized protein YmfM OS=Escherichia coli (strain K12) OX=83333 GN=yfmM PE=4 SV=1  
 Protein YnaA OS=Escherichia coli (strain K12) OX=83333 GN=ynaA PE=4 SV=1  
 30S ribosomal protein S11 OS=Escherichia coli (strain K12) OX=83333 GN=rpsK PE=1 SV=2  
 Alanine-tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=alaS PE=1 SV=2  
 Leucine-tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=leuS PE=1 SV=2  
 Transcriptional regulatory protein CusR OS=Escherichia coli (strain K12) OX=83333 GN=cusR PE=1 SV=1  
 Mannonate dehydratase OS=Escherichia coli (strain K12) OX=83333 GN=uxuA PE=1 SV=2  
 Tyrosine-protein kinase etk OS=Escherichia coli (strain K12) OX=83333 GN=etk PE=1 SV=2  
 Uncharacterized protein YgiM OS=Escherichia coli (strain K12) OX=83333 GN=ygiM PE=3 SV=1  
 Nitrate/nitrite sensor protein NarX OS=Escherichia coli (strain K12) OX=83333 GN=narX PE=1 SV=1  
 Biotin sulfoxide reductase OS=Escherichia coli (strain K12) OX=83333 GN=bisC PE=1 SV=3  
 Glycine betaine-binding protein YehZ OS=Escherichia coli (strain K12) OX=83333 GN=yehZ PE=1 SV=1  
 D-xylonate dehydratase YjhG OS=Escherichia coli (strain K12) OX=83333 GN=yjhG PE=1 SV=2

## Target Decoy. False discovery rate

Peptide matches above identity threshold 462 55 11.90 %  
 Peptide matches above homology or identity threshold 463 59 12.74 %

## Select Summary Report

Format As  Select Summary (protein hits)  [Help](#) [Help](#)  
 Significance threshold p <  Max. number of hits  Show Percolator scores   
 Standard scoring  MudPIT scoring  Display non-significant matches  Show sub-sets   
 Show pop-ups  Suppress pop-ups  Require bold red   
 Preferred taxonomy

Re-Search  All queries  Unassigned  Below homology threshold  Below identity threshold

1. 2::TOP2B\_1-566 Mass: 66629 Score: 8456 Matches: 341 (341) Sequences: 49 (49) emPAI: 40.10

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
303	388	7291	775.4437	775.4439	-0.27	1	17	0.02	1	U K.TSEAKIK.H
410	401	7254	801.4362	801.4344	2.25	0	36	0.00031	1	U K.AQTQLNK.K 408
480	410	7507	819.4868	819.4854	1.71	0	32	0.00057	1	U K.IVGLQYK.K 476 477 479
521	414	7815	827.5485	827.5480	0.57	1	26	0.0024	1	U K.LIEVVKK.K
640	426	2421	850.4697	850.4701	-0.46	0	35	0.00033	1	U R.YGVFPLR.G 639 641 642 643 644 645 646 647 648
779	439	7585	877.5025	877.5022	0.38	0	28	0.002	1	U K.GIPVVEHK.V 781
988	459	7574	917.5003	917.5004	-0.11	0	42	0.00012	1	U K.DIVALMTR.R
1061	465	7719	929.5293	929.5294	-0.12	1	32	0.00081	1	U K.AQTQLNK.C 1060 1062
1093	467	7551	933.4957	933.4953	0.41	0	(32)	0.00084	1	U K.DIVALMTR.R 1088 1089 1090 1091 1092
1154	473	2665	944.5185	944.5179	0.69	0	51	1.1e-005	1	U K.LDETGVALK.V



<a href="#">2278</a>	546.7549	1091.4953	1091.4956	-0.26	0	28	0.0015	1	U	R.GSGGGSSGGSSIGGR.G
<a href="#">2578</a>	563.2767	1124.5389	1124.5349	3.50	0	40	0.00021	1	U	K.AEAESLYQSK.Y
<a href="#">3080</a>	590.3038	1178.5931	1178.5931	0.00	0	28	0.0038	1	U	K.YEELQITAGR.H
<a href="#">4086</a>	651.8613	1301.7079	1301.7078	0.09	0	49	2.6e-005	1	U	R.SLDLDSIIAEVK.A
<a href="#">4138</a>	436.8899	1307.6479	1307.6469	0.75	2	45	9e-005	1	U	R.NKYEDEINKR.T
<a href="#">4688</a>	692.3493	1382.6841	1382.6830	0.76	0	54	7.3e-006	1	U	K.SLNNQFASFDK.V

4. [1::sp|K1C10\\_HUMAN|](#) Mass: 59711 Score: 161 Matches: 5(5) Sequences: 5(5) emPAI: 0.43

sp|K1C10\_HUMAN|

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">433</a>	404.2033	806.3920	806.3923	-0.29	0	27	0.0027	1	U	R.LAADDR.L
<a href="#">441</a>	405.2239	808.4332	808.4330	0.18	0	14	0.037	1	U	R.LASYLDK.V
<a href="#">3718</a>	631.8024	1261.5902	1261.5899	0.24	0	40	0.00022	1	U	R.SLLEGEESGGGGGR.G
<a href="#">4563</a>	683.3234	1364.6322	1364.6320	0.12	0	60	1.8e-006	1	U	R.SQYEQLAEQNR.K
<a href="#">4673</a>	691.3284	1380.6422	1380.6408	1.01	0	80	2.8e-008	1	U	R.ALEESNYELEGK.I

5. [3::P0AA25|THIO\\_ECOLI](#) Mass: 11913 Score: 127 Matches: 2(2) Sequences: 2(2) emPAI: 1.01

Thioredoxin 1 OS=Escherichia coli (strain K12) OX=83333 GN=trxA PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">3771</a>	634.3357	1266.6569	1266.6568	0.10	0	67	4e-007	1	U	K.LNIDQNPGTAPK.Y
<a href="#">8495</a>	903.4535	1804.8924	1804.8917	0.42	0	77	6.6e-008	1	U	K.MIAPILDEIADEYQGK.L

6. [1::sp|ALBU\\_BOVIN|](#) Mass: 71244 Score: 125 Matches: 6(6) Sequences: 6(6) emPAI: 0.43

sp|ALBU\_BOVIN|

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">363</a>	395.2400	788.4654	788.4644	1.37	0	18	0.017	1	U	K.LVTDLTK.V
<a href="#">468</a>	409.7170	817.4195	817.4181	1.72	0	23	0.0053	1	U	K.ATEEQLK.T
<a href="#">1001</a>	461.7478	921.4810	921.4807	0.31	0	27	0.0027	1	U	K.AEFVEVTK.L
<a href="#">4116</a>	653.3620	1304.7094	1304.7088	0.47	0	47	3.2e-005	1	U	K.HLVDEPQNLK.Q
<a href="#">6450</a>	784.3763	1566.7381	1566.7354	1.70	0	45	9.6e-005	1	U	K.DAFLGSFLYEYSR.R
<a href="#">7012</a>	547.3176	1638.9310	1638.9305	0.30	1	36	0.00024	1	U	R.KVPQVSTPTLVEYSR.S

7. [1::sp|K22E\\_HUMAN|](#) Mass: 66110 Score: 102 Matches: 4(4) Sequences: 4(4) emPAI: 0.29

sp|K22E\_HUMAN|

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1324</a>	487.2693	972.5240	972.5240	0.06	0	33	0.00068	1	U	K.IEISELNR.V
<a href="#">2398</a>	554.2752	1108.5358	1106.5356	0.19	0	27	0.0023	1	U	K.AQYEEIAQR.S
<a href="#">3178</a>	398.8754	1193.6045	1193.6040	0.38	2	25	0.0046	1	U	K.KYDEEINKR.T
<a href="#">3653</a>	627.8076	1253.6007	1253.6001	0.49	0	59	3e-006	1	U	R.GFSSGSAVSVGGSR.R

8. [3::P76298|FLHA\\_ECOLI](#) Mass: 74795 Score: 95 Matches: 12(12) Sequences: 1(1) emPAI: 0.06

Flagellar biosynthesis protein FlhA OS=Escherichia coli (strain K12) OX=83333 GN=flhA PE=3 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">3743</a>	632.8199	1263.6252	1263.6159	7.37	1	26	0.0045	1	U	R.HIRMTAIGGK. - <a href="#">3726</a> <a href="#">3735</a> <a href="#">3742</a> <a href="#">3746</a> <a href="#">3753</a> <a href="#">3756</a>
<a href="#">3755</a>	632.8202	1263.6259	1263.6159	7.94	1	(26)	0.0041	1	U	R.HIRMTAIGGK. - <a href="#">3734</a> <a href="#">3744</a> <a href="#">3748</a> <a href="#">3754</a>

9. [3::P0AD96|LIVJ\\_ECOLI](#) Mass: 39223 Score: 31 Matches: 1(1) Sequences: 1(1) emPAI: 0.11

Leu/Ile/Val-binding protein OS=Escherichia coli (strain K12) OX=83333 GN=livj PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">397</a>	400.7352	799.4559	799.4552	0.85	0	31	0.00082	1	U	K.QAVAVANK.V

Proteins matching the same set of peptides:

[3::P04816|LIVK\\_ECOLI](#) Mass: 39468 Score: 31 Matches: 1(1) Sequences: 1(1)

Leucine-specific-binding protein OS=Escherichia coli (strain K12) OX=83333 GN=livk PE=1 SV=2

10. [3::P39220|YARP\\_ECOLI](#) Mass: 24946 Score: 26 Matches: 2(2) Sequences: 2(2) emPAI: 0.40

Protein YabP OS=Escherichia coli (strain K12) OX=83333 GN=yabP PE=4 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">815</a>	443.2374	884.4602	884.4603	-0.16	0	17	0.021	1	U	K.NPDELVAK.G
<a href="#">4109</a>	652.8180	1303.6214	1303.6213	0.05	0	23	0.009	1	U	K.FINSLLEFNK.L

11. [3::P0AFB5|NTRB\\_ECOLI](#) Mass: 38532 Score: 26 Matches: 1(1) Sequences: 1(1) emPAI: 0.12

Sensory histidine kinase/phosphatase NtrB OS=Escherichia coli (strain K12) OX=83333 GN=gnL PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">89</a>	363.7163	725.4180	725.4184	-0.50	0	26	0.0027	1	U	K.NPLGGLR.G

12. [3::Q06065|ATOC\\_ECOLI](#) Mass: 52428 Score: 25 Matches: 2(2) Sequences: 1(1) emPAI: 0.08

Regulatory protein AtoC OS=Escherichia coli (strain K12) OX=83333 GN=atoC PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">3733</a>	422.2154	1263.6245	1263.6203	3.32	1	20	0.017	1	U	R.MPEMDGKALK.E <a href="#">3736</a>

13. [3::P69741|NRHT\\_ECOLI](#) Mass: 40368 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.11

Hydrogenase-2 small chain OS=Escherichia coli (strain K12) OX=83333 GN=hybD PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">9983</a>	697.6294	2089.8665	2089.8689	-1.13	1	24	0.014	1	U	R.DFMKLAALAAIMGLSSK.A

14. [3::P77439|PTFX1\\_ECOLI](#) Mass: 92757 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.05

Multiphosphoryl transfer protein 1 OS=Escherichia coli (strain K12) OX=83333 GN=fryA PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">11359</a>	849.0838	2544.2297	2544.2134	6.39	0	24	0.025	1	U	R.LMTEHQHGLGAAIISNMEQVCAK.L

15. [3::P06149|DLD\\_ECOLI](#) Mass: 64914 Score: 24 Matches: 2(2) Sequences: 1(1) emPAI: 0.07

Quinone-dependent D-lactate dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=dld PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">758</a>	437.7350	873.4555	873.4556	-0.11	1	23	0.008	1	U	K.LDDDRIK.D <a href="#">759</a>

16.	<a href="#">3::P28722 YHCA_ECOLI</a>	Mass: 25323	Score: 23	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.18	
	Uncharacterized fibrial chaperone YhcA OS=Escherichia coli (strain K12) OX=83333 GN=yhcA PE=3 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide	
	<a href="#">14028</a>	999.8786	4994.3566	4994.3418	2.97	3 23 0.04 1 U	<a href="#">M_LRHIIFIVFITTSMNTLAI<del>G</del>MVPETS<del>V</del>LLVDEKRGESAINIK.N</a>
17.	<a href="#">3::Q46857 DKGA_ECOLI</a>	Mass: 31147	Score: 23	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.15	
	2,5-diketo-D-gluconic acid reductase A OS=Escherichia coli (strain K12) OX=83333 GN=dkgA PE=1 SV=3						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide	
	<a href="#">1066</a>	466.2461	930.4777	930.4844	-7.23	0 23 0.0054 1 U	<a href="#">-<del>M</del>ANPTVIK.L</a>
18.	<a href="#">3::P28630 HOLA_ECOLI</a>	Mass: 38965	Score: 23	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.12	
	DNA polymerase III subunit delta OS=Escherichia coli (strain K12) OX=83333 GN=holA PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide	
	<a href="#">1049</a>	464.7828	927.5509	927.5502	0.85	0 23 0.0059 1 U	<a href="#">R.QAVQLLR.T</a>
19.	<a href="#">1::sp RS27A_HUMAN </a>	Mass: 18296	Score: 22	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.26	
	sp RS27A_HUMAN						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide	
	<a href="#">8272</a>	894.4670	1786.9194	1786.9200	-0.32	0 22 0.022 1 U	<a href="#">K.TITLEVEPSDTIENVK.A</a>
20.	<a href="#">3::Q46793 YGEN_ECOLI</a>	Mass: 27575	Score: 21	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.17	
	Putative uncharacterized protein YgeN OS=Escherichia coli (strain K12) OX=83333 GN=ygeN PE=5 SV=3						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide	
	<a href="#">6063</a>	765.8946	1529.7746	1529.7710	2.36	3 21 0.021 1 U	<a href="#">-<del>M</del>RKKIEMSLIK.S</a>
21.	<a href="#">3::POAFS9 MEPM_ECOLI</a>	Mass: 49027	Score: 20	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.09	
	Murein DD-endopeptidase MepM OS=Escherichia coli (strain K12) OX=83333 GN=mepM PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide	
	<a href="#">8884</a>	620.6257	1858.8553	1858.8703	-8.07	2 20 0.039 1 U	<a href="#">R.EQS<del>Q</del>LLGVRLR<del>S</del>EGK.D</a>
22.	<a href="#">3::P15877 DHG_ECOLI</a>	Mass: 87091	Score: 20	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.05	
	Quinoprotein glucose dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=gcd PE=1 SV=3						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide	
	<a href="#">1603</a>	507.2217	1012.4289	1012.4284	0.54	0 20 0.0099 1 U	<a href="#">R.AYNMSNGEK.L</a>
23.	<a href="#">3::P69797 PTNAB_ECOLI</a>	Mass: 35026	Score: 20	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.13	
	PTS system mannose-specific EIIB' component OS=Escherichia coli (strain K12) OX=83333 GN=manX PE=1 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide	
	<a href="#">6062</a>	765.8940	1529.7735	1529.7598	8.98	2 20 0.028 1 U	<a href="#">K.LK<del>M</del>DLI<del>S</del>KIDK.-</a>
24.	<a href="#">3::P75882 GFCD_ECOLI</a>	Mass: 78923	Score: 20	Matches: 2(2)	Sequences: 1(1)	emPAI: 0.06	
	Uncharacterized lipoprotein GfdC OS=Escherichia coli (strain K12) OX=83333 GN=gfdC PE=3 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide	
	<a href="#">1642</a>	509.2826	1016.5505	1016.5502	0.33	1 19 0.019 1 U	<a href="#">K.DKGATIDVAK.R</a> <a href="#">1642</a>
25.	<a href="#">3::PO4152 UMUC_ECOLI</a>	Mass: 48276	Score: 20	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.09	
	Protein UmuC OS=Escherichia coli (strain K12) OX=83333 GN=umuC PE=1 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide	
	<a href="#">765</a>	437.2432	872.4719	872.4716	0.42	0 20 0.017 1 U	<a href="#">R.DIINAATR.S</a>
26.	<a href="#">3::P20966 PTFBC_ECOLI</a>	Mass: 57824	Score: 19	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.08	
	PTS system fructose-specific EIIB' BC component OS=Escherichia coli (strain K12) OX=83333 GN=fruA PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide	
	<a href="#">419</a>	402.7089	803.4032	803.4025	0.90	0 19 0.011 1 U	<a href="#">K.TAQELDK.A</a>
27.	<a href="#">3::P77739 KT3K_ECOLI</a>	Mass: 32666	Score: 19	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.14	
	Probable ketoamine kinase YniA OS=Escherichia coli (strain K12) OX=83333 GN=yniA PE=3 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide	
	<a href="#">1083</a>	467.2354	932.4562	932.4538	2.57	0 19 0.011 1 U	<a href="#">-<del>M</del>WQAI<del>S</del>R.L</a>
28.	<a href="#">3::P31828 PQQL_ECOLI</a>	Mass: 104706	Score: 19	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.04	
	Probable zinc protease PqqL OS=Escherichia coli (strain K12) OX=83333 GN=pqqL PE=1 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide	
	<a href="#">4857</a>	707.3304	1412.6462	1412.6371	6.48	0 19 0.023 1 U	<a href="#">K.QMIVENVNTAVK.Q</a>
29.	<a href="#">3::POACP5 GNTR_ECOLI</a>	Mass: 36570	Score: 19	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.12	
	HTH-type transcriptional regulator GntR OS=Escherichia coli (strain K12) OX=83333 GN=gntR PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide	
	<a href="#">664</a>	428.7663	855.5179	855.5178	0.18	0 19 0.012 1 U	<a href="#">R.LASVLT<del>P</del>R.E</a>
30.	<a href="#">3::POA8N3 SYK1_ECOLI</a>	Mass: 57624	Score: 19	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.16	
	Lysine--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=lysS PE=1 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide	
	<a href="#">2234</a>	363.2009	1086.5810	1086.5710	9.24	0 19 0.02 1 U	<a href="#">K.WDLGILGAK.G</a>
	<a href="#">2613</a>	376.8961	1127.6663	1127.6775	-9.89	1 14 0.044 2 U	<a href="#">K.VRSQILSGIR.Q</a>
31.	<a href="#">3::P76555 EUTQ_ECOLI</a>	Mass: 25516	Score: 19	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.18	
	Acetate kinase EutQ OS=Escherichia coli (strain K12) OX=83333 GN=eutQ PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide	
	<a href="#">8326</a>	896.4427	1790.8708	1790.8580	7.13	2 19 0.048 1 U	<a href="#">K.<del>S</del>VIGKGGI<del>K</del>VIDGSSVK.F</a>
32.	<a href="#">3::POAEX9 MALE_ECOLI</a>	Mass: 43360	Score: 19	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.10	
	Maltose/maltodextrin-binding periplasmic protein OS=Escherichia coli (strain K12) OX=83333 GN=malE PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide	
	<a href="#">900</a>	452.2428	902.4711	902.4709	0.19	0 19 0.026 1 U	<a href="#">R.QTVDEALK.D</a>

33.	<a href="#">3::046861 YGIQ_ECOLI</a>	Mass: 84223	Score: 19	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.05
UPF0313 protein YgiQ OS=Escherichia coli (strain K12) OX=83333 GN=ygiQ PE=3 SV=3						
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide						
	<a href="#">6614</a>	528.5888	1582.7445	1582.7449	-0.22	1 19 0.04 1 U K.TYVLLP\$FEKVK.G
34.	<a href="#">3::POACY1 YDJA_ECOLI</a>	Mass: 20217	Score: 19	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.23
Putative NAD(P)H nitroreductase YdJA OS=Escherichia coli (strain K12) OX=83333 GN=ydJA PE=1 SV=1						
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide						
	<a href="#">8068</a>	880.9706	1759.9266	1759.9362	-5.49	2 19 0.035 1 U -.M\$ALELLINRRSASR.L
35.	<a href="#">3::P63224 GMHA_ECOLI</a>	Mass: 20973	Score: 18	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.22
Phosphoheptose isomerase OS=Escherichia coli (strain K12) OX=83333 GN=gmHA PE=1 SV=1						
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide						
	<a href="#">5154</a>	725.3482	1448.6818	1448.6929	-7.71	1 18 0.033 1 U K.DGGK\$MAGTADIEIR.V
36.	<a href="#">3::Y9HVXQ YPA\$A_ECOLI</a>	Mass: 6876	Score: 18	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.80
Uncharacterized protein YpaA OS=Escherichia coli (strain K12) OX=83333 GN=ypaA PE=4 SV=1						
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide						
	<a href="#">5318</a>	732.8890	1463.7635	1463.7555	5.51	1 18 0.043 1 U K.IALR\$MLEGGFDR.D
37.	<a href="#">3::POA6H5 H\$LIU_ECOLI</a>	Mass: 49677	Score: 18	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.09
ATP-dependent protease ATPase subunit HsIU OS=Escherichia coli (strain K12) OX=83333 GN=hsIU PE=1 SV=1						
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide						
	<a href="#">535</a>	416.7247	831.4348	831.4338	1.27	0 18 0.017 1 U R.DLTDAAVK.M
38.	<a href="#">3::P02943 L\$MBR_ECOLI</a>	Mass: 49995	Score: 18	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.09
Maltoporin OS=Escherichia coli (strain K12) OX=83333 GN=lamb PE=1 SV=1						
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide						
	<a href="#">113</a>	366.2242	730.4338	730.4337	0.15	0 18 0.017 1 U K.L\$LAATR.S
39.	<a href="#">3::P52101 G\$LRK_ECOLI</a>	Mass: 53639	Score: 18	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.08
Sensor histidine kinase GlrK OS=Escherichia coli (strain K12) OX=83333 GN=glrK PE=1 SV=3						
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide						
	<a href="#">94</a>	364.1959	726.3772	726.3773	-0.04	0 18 0.017 1 U R.\$SSLHGAR.V
40.	<a href="#">3::P68644 F\$IXC_ECOLI</a>	Mass: 45902	Score: 18	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.10
Protein FixC OS=Escherichia coli (strain K12) OX=83333 GN=fixC PE=3 SV=1						
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide						
	<a href="#">8291</a>	447.9621	1787.8193	1787.8165	1.57	1 18 0.037 1 U R.DL\$FIDG\$APEL\$MRK.K
41.	<a href="#">3::P77766 R\$NAAM_ECOLI</a>	Mass: 32902	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.14
5'-3' exoribonuclease OS=Escherichia coli (strain K12) OX=83333 GN=yxiV PE=1 SV=1						
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide						
	<a href="#">397</a>	400.7352	799.4559	799.4552	0.87	0 17 0.02 2 U R.AQLIAER.L
42.	<a href="#">3::P80645 S\$SUD_ECOLI</a>	Mass: 41768	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.11
Alkanesulfonate monooxygenase OS=Escherichia coli (strain K12) OX=83333 GN=ssuD PE=1 SV=3						
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide						
	<a href="#">296</a>	387.7090	773.4034	773.4032	0.33	0 17 0.018 1 U R.GAATLDR.L
43.	<a href="#">3::P75958 L\$OLE_ECOLI</a>	Mass: 45429	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.10
Lipoprotein-releasing system transmembrane protein LoIE OS=Escherichia coli (strain K12) OX=83333 GN=loIE PE=1 SV=3						
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide						
	<a href="#">4299</a>	443.2331	1326.6775	1326.6892	-8.81	1 17 0.04 1 U R.ASNIDPARVLSGQ.-
44.	<a href="#">3::P76399 M\$DTG_ECOLI</a>	Mass: 111168	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.04
Multidrug resistance protein MdtC OS=Escherichia coli (strain K12) OX=83333 GN=mdtC PE=1 SV=1						
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide						
	<a href="#">13433</a>	1163.2966	3486.8679	3486.8455	6.41	2 17 0.043 1 U R.NAGMTNAK\$PAILL\$MIRKLP\$EANIQTVD\$SIR.A
45.	<a href="#">3::POAEM0 F\$K\$BX_ECOLI</a>	Mass: 16071	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.30
FKBP-type 16 kDa peptidyl-prolyl cis-trans isomerase OS=Escherichia coli (strain K12) OX=83333 GN=fkpB PE=1 SV=2						
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide						
	<a href="#">13461</a>	881.5934	3522.3444	3522.3506	-1.76	1 17 0.039 1 U -.M\$ESVQ\$N\$AVLVHFTLKLDDGT\$IAE\$SR.N
46.	<a href="#">3::POAC88 G\$M4D_ECOLI</a>	Mass: 42191	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.11
GDP-mannose 4,6-dehydratase OS=Escherichia coli (strain K12) OX=83333 GN=gmd PE=1 SV=1						
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide						
	<a href="#">134</a>	368.2053	734.3961	734.3963	-0.19	0 17 0.019 1 U R.SPYAVAK.L
47.	<a href="#">3::AOA7H2C769 AOA7H2C769_ECOLI</a>	Mass: 37383	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.12
Putative type II secretion system C-type protein YghF OS=Escherichia coli (strain K12) OX=83333 GN=yghF PE=3 SV=1						
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide						
	<a href="#">5116</a>	722.3780	1442.7413	1442.7323	6.28	0 17 0.046 1 U K.IFN\$YIQLTPYR.K
Proteins matching the same set of peptides:						
	<a href="#">3::046834 YGHF_ECOLI</a>	Mass: 37383	Score: 17	Matches: 1(1)	Sequences: 1(1)	
Putative type II secretion system C-type protein YghF OS=Escherichia coli (strain K12) OX=83333 GN=yghF PE=3 SV=2						
48.	<a href="#">3::POA840 S\$URE_ECOLI</a>	Mass: 27169	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.17
5'/3'-nucleotidase SurE OS=Escherichia coli (strain K12) OX=83333 GN=surE PE=1 SV=1						
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide						
	<a href="#">10700</a>	577.5629	2306.2224	2306.2052	7.45	1 17 0.05 1 U -.M\$RILLSNDDGVHAPGIQTLAK.A
49.	<a href="#">3::P21893 R\$ECJ_ECOLI</a>	Mass: 63634	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.07
Single-stranded-DNA-specific exonuclease RecJ OS=Escherichia coli (strain K12) OX=83333 GN=recJ PE=1 SV=2						

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2228	543.8046	1085.5947	1085.6015	-6.31	1	17	0.037	1	U	-_MKQQQLR.R
<hr/>										
50.	3::P30852 SMF_ECOLI Mass: 41158 Score: 17 Matches: 1(1) Sequences: 1(1) emPAI: 0.11 Protein Smf OS=Escherichia coli (strain K12) OX=83333 GN=smf PE=3 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
730	435.7076	869.4007	869.4008	-0.14	0	17	0.025	1	U	R.SGSLVIAR.C
<hr/>										
51.	3::P33668 YBBC_ECOLI Mass: 14257 Score: 17 Matches: 1(1) Sequences: 1(1) emPAI: 0.34 Uncharacterized protein Ybbc OS=Escherichia coli (strain K12) OX=83333 GN=ybbc PE=2 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1649	509.7495	1017.4845	1017.4896	-5.04	1	17	0.032	1	U	K.YSVKIVK.T
<hr/>										
52.	3::P38035 RTCRC_ECOLI Mass: 60604 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.07 Transcriptional regulatory protein RtcR OS=Escherichia coli (strain K12) OX=83333 GN=rtcR PE=4 SV=2									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1216	479.2299	956.4453	956.4386	7.03	0	16	0.035	1	U	R.MATFATSGR.I
<hr/>										
53.	3::P23871 HEMH_ECOLI Mass: 36089 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.12 Ferrochelatase OS=Escherichia coli (strain K12) OX=83333 GN=hemH PE=1 SV=3									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4465	451.9139	1352.7199	1352.7329	-9.64	2	16	0.034	1	U	R.KRSIPGIFSR.D
<hr/>										
54.	3::P00634 PPB_ECOLI Mass: 49636 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.09 Alkaline phosphatase OS=Escherichia coli (strain K12) OX=83333 GN=phoA PE=1 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3426	614.2892	1226.5638	1226.5601	2.99	1	16	0.046	1	U	R.KCYGPSATSEK.C
<hr/>										
55.	3::Q46864 MQSA_ECOLI Mass: 14922 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.32 Antitoxin MqsA OS=Escherichia coli (strain K12) OX=83333 GN=mqsA PE=1 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
862	449.2430	896.4714	896.4732	-2.03	1	16	0.025	1	U	K.KLSLTQK.E
<hr/>										
56.	1::sp DHE3_BOVIN  Mass: 61815 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.07 sp DHE3_BOVIN									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
282	386.1642	770.3139	770.3211	-9.31	0	16	0.025	1	U	R.ISGASEK.D
<hr/>										
57.	3::P0A624 SPOT_ECOLI Mass: 79748 Score: 16 Matches: 2(2) Sequences: 1(1) emPAI: 0.06 Bifunctional (p)ppGpp synthase/hydrolase SpoT OS=Escherichia coli (strain K12) OX=83333 GN=spoT PE=1 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
874	450.2146	898.4147	898.4201	-6.03	0	15	0.033	1	U	K.DYIAIPK.A 873
<hr/>										
58.	3::P37650 BCSC_ECOLI Mass: 127760 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.03 Cellulose synthase operon protein C OS=Escherichia coli (strain K12) OX=83333 GN=bcsC PE=1 SV=3									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1350	488.7422	975.4698	975.4733	-3.58	1	16	0.037	1	U	K.SNAGREGASK.I
<hr/>										
59.	3::P39277 YJEH_ECOLI Mass: 45261 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.10 L-methionine/branched-chain amino acid exporter YjeH OS=Escherichia coli (strain K12) OX=83333 GN=yjeH PE=1 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1251	480.7538	959.4929	959.4924	0.60	1	15	0.044	1	U	R.KTPENGITT.-
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60.	3::P77293 GTRB_ECOLI Mass: 34614 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.13 Prophage bactoprenol glucosyl transferase homolog OS=Escherichia coli (strain K12) OX=83333 GN=yfdH PE=1 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
457	408.7265	815.4385	815.4389	-0.42	0	15	0.031	1	U	R.DVVENIK.L
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61.	3::P36678 GSPM_ECOLI Mass: 17280 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.27 Putative type II secretion system protein M OS=Escherichia coli (strain K12) OX=83333 GN=gspM PE=2 SV=2									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2219	543.3199	1084.6252	1084.6240	1.09	1	15	0.042	1	U	K.NILLEAKR.E
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62.	3::P16869 FHUE_ECOLI Mass: 81239 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.05 FhuE receptor OS=Escherichia coli (strain K12) OX=83333 GN=fhuE PE=1 SV=2									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
662	428.6925	855.3704	855.3739	-4.08	0	15	0.033	1	U	K.AVDGIYSK.G
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63.	3::P76161 RFQ2_ECOLI Mass: 28478 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.16 Prophage antitermination protein Q homolog QuuQ OS=Escherichia coli (strain K12) OX=83333 GN=quuQ PE=3 SV=2									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1066	466.2461	930.4777	930.4844	-7.21	0	15	0.033	2	U	-_MNLEALPK.Y
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64.	3::P64570 YQGC_ECOLI Mass: 8166 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.64 Protein YqgC OS=Escherichia coli (strain K12) OX=83333 GN=yqgC PE=1 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3472	617.7462	1233.4779	1233.4883	-8.45	0	15	0.033	1	U	-_HGITSGMQSR.D
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65.	3::P77732 RHMR_ECOLI Mass: 29228 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.16 Uncharacterized HTH-type transcriptional regulator RhmR OS=Escherichia coli (strain K12) OX=83333 GN=rhmR PE=1 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
706	432.7089	863.4033	863.4025	0.89	0	15	0.034	1	U	K.SPFDLQAS.-
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66.	3::P25772 LIGB_ECOLI Mass: 63425 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.07 DNA ligase B OS=Escherichia coli (strain K12) OX=83333 GN=ligB PE=1 SV=2									

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">150</a>	372.7215	743.4285	743.4290	-0.62	0	14	0.036	1	U	R.VNIGSVR.R
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67.	<a href="#">3::P75977 YMF ECOLI</a> Mass: 12319 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.40 Uncharacterized protein YmfM OS=Escherichia coli (strain K12) OX=83333 GN=yfmf PE=4 SV=1									
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2462</a>	371.8297	1112.4672	1112.4652	1.87	0	14	0.045	1	U	M_NSLTIHYR.R
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68.	<a href="#">3::P77658 YNA ECOLI</a> Mass: 37094 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.12 Protein YnaA OS=Escherichia coli (strain K12) OX=83333 GN=ynaA PE=4 SV=1									
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1063</a>	465.7797	929.5448	929.5406	4.53	2	14	0.037	1	U	R.KIQETRR.E
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69.	<a href="#">3::POA7R9 RS11 ECOLI</a> Mass: 13950 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.35 30S ribosomal protein S11 OS=Escherichia coli (strain K12) OX=83333 GN=rpsK PE=1 SV=2									
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">350</a>	393.7395	785.4644	785.4581	7.92	1	14	0.038	1	U	--MAKAPIR.A
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70.	<a href="#">3::P00957 SYA ECOLI</a> Mass: 96315 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.05 Alanine--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=alaS PE=1 SV=2									
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">491</a>	412.2393	822.4640	822.4712	-8.69	0	14	0.039	1	U	R.VIADHIR.S
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71.	<a href="#">3::P07813 SYL ECOLI</a> Mass: 97799 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.04 Leucine--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=leuS PE=1 SV=2									
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">712</a>	433.2287	864.4428	864.4388	4.61	0	14	0.04	1	U	R.LHGHVR.N
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72.	<a href="#">3::POACZ8 CUSR ECOLI</a> Mass: 25378 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.18 Transcriptional regulatory protein CusR OS=Escherichia coli (strain K12) OX=83333 GN=cusR PE=1 SV=1									
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1357</a>	489.2346	976.4547	976.4502	4.63	0	14	0.04	1	U	K.IDNDFEPK.L
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73.	<a href="#">3::P24215 UXUA ECOLI</a> Mass: 44981 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.10 Mannanase OS=Escherichia coli (strain K12) OX=83333 GN=uxuA PE=1 SV=2									
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">818</a>	443.2834	884.5523	884.5443	9.02	1	14	0.041	1	U	R.LKGLAEVR.G
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74.	<a href="#">3::P38134 ETK ECOLI</a> Mass: 81191 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.05 Tyrosine-protein kinase etk OS=Escherichia coli (strain K12) OX=83333 GN=etk PE=1 SV=2									
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2422</a>	555.2141	1108.4135	1108.4025	9.97	0	14	0.042	1	U	K.EVSLSMQR.L
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75.	<a href="#">3::POADT8 YGIW ECOLI</a> Mass: 23062 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.20 Uncharacterized protein YgiW OS=Escherichia coli (strain K12) OX=83333 GN=ygiW PE=3 SV=1									
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2937</a>	580.7940	1159.5734	1159.5721	1.13	0	14	0.049	1	U	K.VDAASVOLDDK.Q
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76.	<a href="#">3::POAFA2 NARX ECOLI</a> Mass: 67669 Score: 13 Matches: 1(1) Sequences: 1(1) emPAI: 0.07 Nitrate/nitrite sensor protein NarX OS=Escherichia coli (strain K12) OX=83333 GN=narX PE=1 SV=1									
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">196</a>	378.2061	754.3976	754.3973	0.36	0	13	0.047	1	U	K.TAGLEHK.N
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77.	<a href="#">3::P20099 BISC ECOLI</a> Mass: 86366 Score: 13 Matches: 1(1) Sequences: 1(1) emPAI: 0.05 Biotin sulfoxide reductase OS=Escherichia coli (strain K12) OX=83333 GN=bisC PE=1 SV=3									
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">254</a>	384.6712	767.3278	767.3232	6.08	0	13	0.047	1	U	--ANSSSR.Y
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78.	<a href="#">3::P33362 YEHZ ECOLI</a> Score: 13 Matches: 1(1) Sequences: 1(1) Glycine betaine-binding protein YehZ OS=Escherichia coli (strain K12) OX=83333 GN=yehZ PE=1 SV=1									
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1066</a>	466.2461	930.4777	930.4770	0.72	1	13	0.048	3	U	R.QDVAEKNK.L
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79.	<a href="#">3::P39358 YJHG ECOLI</a> Score: 13 Matches: 1(1) Sequences: 1(1) D-xylonate dehydratase YjhG OS=Escherichia coli (strain K12) OX=83333 GN=yjhG PE=1 SV=2									
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">150</a>	372.7215	743.4285	743.4290	-0.62	0	13	0.049	2	U	K.VQTIGAR.F

Proteins matching the same set of peptides:

[3::P77596|YAGF ECOLI](#) Mass: 69926 Score: 13 Matches: 1(1) Sequences: 1(1)  
D-xylonate dehydratase YagF OS=Escherichia coli (strain K12) OX=83333 GN=yagF PE=1 SV=1