

Mascot Search Results

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User : r-nakagawa
Email :
Search title : SN221366_deTOP2B_Erk2m_lul_Node:2
MS data file : File Name: Z:\SN221366_deTOP2B_Erk2m_lul_raw\File Path: :File Time: 3/1/2023 6:25:31 PM:File Size: 352168572 [Byte]
Database 1 : cRAP STRAW_proteinG_2023031 (118 sequences: 3090 residues)
Database 2 : Original_21_TOP2B_1-566_20210618 (1 sequences: 599 residues)
Database 3 : Uniprot Proteome E.coli K12 Proteome_E.coli_K12_UP000000625_2022_01 (4448 sequences: 1358110 residues)
Timestamp : 13 Sep 2023 at 00:33:54 GMT
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Acetyl (Protein N-term), Oxidation (M), Phospho (ST), Phospho (Y)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 10 ppm
Fragment Mass Tolerance : ± 0.8 Da
Max Missed Cleavages : 3
Instrument type : Default
Number of queries : 13249
Protein hits : 2::TOP2B_1-566 TOP2B_1-566
1::sp|K2C1|HUMAN| sp|K2C1|HUMAN|
1::sp|K1C10|HUMAN| sp|K1C10|HUMAN|
1::sp|K22E|HUMAN| sp|K22E|HUMAN|
1::sp|TRYP_PIG| sp|TRYP_PIG|
1::sp|K1C9|HUMAN| sp|K1C9|HUMAN|
3::P0AA25|ALBU_BOVIN| Thioesterase 1 OS=Escherichia coli (strain K12) OX=83333 GN=trxA PE=1 SV=2
sp|ALBU_BOVIN| sp|ALBU_BOVIN|
3::P76298|FLHA_ECOLI| Flagellar biosynthesis protein FlhA OS=Escherichia coli (strain K12) OX=83333 GN=flhA PE=3 SV=1
3::Q46857|DKGA_ECOLI| 2,5-diketo-D-gluconic acid reductase A OS=Escherichia coli (strain K12) OX=83333 GN=dkgA PE=1 SV=3
3::P0AD96|LIVJ_ECOLI| Leu/Val-binding protein OS=Escherichia coli (strain K12) OX=83333 GN=livJ PE=1 SV=1
3::P75882|GFCD_ECOLI| Uncharacterized lipoprotein Gfcd OS=Escherichia coli (strain K12) OX=83333 GN=gfcd PE=3 SV=1
3::P0AAB4|UBID_ECOLI| 3-octaprenyl-4-hydroxybenzoate carboxy-lyase OS=Escherichia coli (strain K12) OX=83333 GN=ubid PE=1 SV=1
3::P13009|METH_ECOLI| Methionine synthase OS=Escherichia coli (strain K12) OX=83333 GN=meth PE=1 SV=5
3::P67601|TREF_ECOLI| Cytoplasmic trehalase OS=Escherichia coli (strain K12) OX=83333 GN=tref PE=1 SV=1
3::P0ACP5|GNTR_ECOLI| HTH-type transcriptional regulator GntR OS=Escherichia coli (strain K12) OX=83333 GN=gntR PE=1 SV=1
sp|RS27A_HUMAN| sp|RS27A_HUMAN|
1::sp|P29362|YAHG_ECOLI| Biotin synthase OS=Escherichia coli (strain K12) OX=83333 GN=yahg PE=1 SV=2
3::P77221|YAHG_ECOLI| Uncharacterized protein YahG OS=Escherichia coli (strain K12) OX=83333 GN=yahg PE=4 SV=1
3::P67660|YHAJ_ECOLI| Probable HTH-type transcriptional regulator YhaJ OS=Escherichia coli (strain K12) OX=83333 GN=yhaJ PE=3 SV=1
3::P39358|YJHG_ECOLI| D-xylonate dehydratase Yjhg OS=Escherichia coli (strain K12) OX=83333 GN=yjhg PE=1 SV=2
3::P24177|ACRD_ECOLI| Probable aminoglycoside efflux pump OS=Escherichia coli (strain K12) OX=83333 GN=acrD PE=3 SV=3
3::P38095|RTOR_ECOLI| Transcriptional regulatory protein RtcR OS=Escherichia coli (strain K12) OX=83333 GN=rtcR PE=4 SV=2
3::P71242|WCAK_ECOLI| Colanic acid biosynthesis protein WcaK OS=Escherichia coli (strain K12) OX=83333 GN=wcaK PE=3 SV=2
3::P77682|GTRA_ECOLI| Prophage bacteriophage-linked glucose translocase homolog OS=Escherichia coli (strain K12) OX=83333 GN=yfdG PE=1 SV=1
3::P0AF59|MEPM_ECOLI| Murein DD-endopeptidase MepM OS=Escherichia coli (strain K12) OX=83333 GN=mepM PE=1 SV=1
3::Q46861|YGI0_ECOLI| UFP0313 protein Ygi0 OS=Escherichia coli (strain K12) OX=83333 GN=ygi0 PE=3 SV=3
3::P25772|TUBO_ECOLI| DNA long-term factor Tu1 OS=Escherichia coli (strain K12) OX=83333 GN=tuA PE=1 SV=1
3::P0ABD5|ACCA_ECOLI| Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha OS=Escherichia coli (strain K12) OX=83333 GN=accA PE=1 SV=2
3::Q46793|YGEN_ECOLI| Putative uncharacterized protein Ygen OS=Escherichia coli (strain K12) OX=83333 GN=ygen PE=5 SV=3
3::P38134|ETK_ECOLI| Tyrosine-protein kinase etk OS=Escherichia coli (strain K12) OX=83333 GN=etk PE=1 SV=2
3::P37371|YFDC_ECOLI| Inner membrane protein Yfdc OS=Escherichia coli (strain K12) OX=83333 GN=yfdc PE=1 SV=1
3::P9VH0Y|YPAO_ECOLI| Uncharacterized protein YpaA OS=Escherichia coli (strain K12) OX=83333 GN=ypaA PE=4 SV=1
3::P16384|MIAA_ECOLI| tRNA dimethylallyltransferase OS=Escherichia coli (strain K12) OX=83333 GN=miaA PE=1 SV=2
3::P63224|GMHA_ECOLI| Phosphopentose isomerase OS=Escherichia coli (strain K12) OX=83333 GN=gmhA PE=1 SV=1
3::P0A823|YBGC_ECOLI| Acyl-CoA thioester hydrolase YbgC OS=Escherichia coli (strain K12) OX=83333 GN=ybgC PE=1 SV=1
sp|KRHB4_HUMAN| sp|KRHB4_HUMAN|
1::sp|KRHB4_HUMAN| DNA ligase B OS=Escherichia coli (strain K12) OX=83333 GN=ligB PE=1 SV=2
3::P0A759|NAGB_ECOLI| Glucosamine-6-phosphate deaminase OS=Escherichia coli (strain K12) OX=83333 GN=nagB PE=1 SV=1
3::P0AD18|YGIW_ECOLI| Uncharacterized protein YgiW OS=Escherichia coli (strain K12) OX=83333 GN=ygiW PE=3 SV=1
3::P0AGD7|SRP54_ECOLI| Signal recognition particle protein OS=Escherichia coli (strain K12) OX=83333 GN=ffh PE=1 SV=1
sp|KRHB4_HUMAN| sp|KRHB4_HUMAN|
3::P77211|CUSC_ECOLI| Cation efflux system protein CusC OS=Escherichia coli (strain K12) OX=83333 GN=cusC PE=1 SV=1
3::P69811|PTFAH_ECOLI| Multiphosphoryl transfer protein OS=Escherichia coli (strain K12) OX=83333 GN=frub PE=1 SV=1
3::P0AE15|DFGB_ECOLI| D-galactose-binding periplasmic protein OS=Escherichia coli (strain K12) OX=83333 GN=mgIB PE=1 SV=1
3::P15028|YFCC_ECOLI| Fe(3+) dicitrate-binding periplasmic protein OS=Escherichia coli (strain K12) OX=83333 GN=fecB PE=2 SV=3
3::Q08065|ATOC_ECOLI| Regulatory protein Atoc OS=Escherichia coli (strain K12) OX=83333 GN=atoc PE=1 SV=2
3::P00634|RFB ECOLI| Alkaline phosphatase OS=Escherichia coli (strain K12) OX=83333 GN=rphA PE=1 SV=1
3::P06932|RSMA_ECOLI| Ribosome RNA small subunit methyltransferase A OS=Escherichia coli (strain K12) OX=83333 GN=rsmA PE=1 SV=1
3::P71377|WZXC_ECOLI| Lipopolysaccharide biosynthesis protein WzxC OS=Escherichia coli (strain K12) OX=83333 GN=wzxC PE=1 SV=1
3::P33668|YBBC_ECOLI| Uncharacterized protein YbcC OS=Escherichia coli (strain K12) OX=83333 GN=ybcC PE=2 SV=1
3::P80645|SSUD_ECOLI| Alkanesulfonate monooxygenase OS=Escherichia coli (strain K12) OX=83333 GN=ssuD PE=1 SV=3
3::P13738|NHAO_ECOLI| Na(+)/H(+) antiporter NhaA OS=Escherichia coli (strain K12) OX=83333 GN=nhaA PE=1 SV=3
3::P31434|XYLS_ECOLI| Alpha-xylidase OS=Escherichia coli (strain K12) OX=83333 GN=yicI PE=1 SV=2
3::P21893|RECJ_ECOLI| 23S rRNA 5-hydroxytyridine C2501 synthase YecJ OS=Escherichia coli (strain K12) OX=83333 GN=rliHA PE=1 SV=2
Single-stranded-DNA-specific exonuclease RecJ OS=Escherichia coli (strain K12) OX=83333 GN=recJ PE=1 SV=2
3::P76016|DHAR_ECOLI| PTS-dependent dihydroxyacetone kinase operon regulatory protein OS=Escherichia coli (strain K12) OX=83333 GN=dhar PE=1 SV=2
3::P0AF48|NUOM_ECOLI| NADH-quinone oxidoreductase subunit M OS=Escherichia coli (strain K12) OX=83333 GN=nuoM PE=1 SV=1
3::P08172|GRPE_ECOLI| NADH-quinone oxidoreductase subunit N OS=Escherichia coli (strain K12) OX=83333 GN=grpe PE=1 SV=1
3::P28917|YDCC_ECOLI| H repeat-associated putative transposase YdcC OS=Escherichia coli (strain K12) OX=83333 GN=ydcC PE=3 SV=1
3::P37007|YAGA_ECOLI| Uncharacterized protein YagA OS=Escherichia coli (strain K12) OX=83333 GN=yagA PE=2 SV=3
3::P28912|YHHI_ECOLI| H repeat-associated putative transposase YhhI OS=Escherichia coli (strain K12) OX=83333 GN=yhhI PE=3 SV=1
3::P28630|HOLA_ECOLI| DNA polymerase III subunit delta OS=Escherichia coli (strain K12) OX=83333 GN=hoIA PE=1 SV=1
3::P0AAK7|NRFEC_ECOLI| Protein NrfC OS=Escherichia coli (strain K12) OX=83333 GN=nrfC PE=3 SV=1
3::P37650|RCSC_ECOLI| Cellulose synthase operon protein C OS=Escherichia coli (strain K12) OX=83333 GN=bcsC PE=1 SV=3
3::P0AFB8|NTRC_ECOLI| DNA-binding transcriptional regulator NtrC OS=Escherichia coli (strain K12) OX=83333 GN=glnG PE=1 SV=1
3::P0AG96|SECE_ECOLI| Protein translocase subunit SecE OS=Escherichia coli (strain K12) OX=83333 GN=secE PE=1 SV=1
3::P02925|RBSB_ECOLI| Ribose import binding protein RbsB OS=Escherichia coli (strain K12) OX=83333 GN=rbsB PE=1 SV=1
3::P0A664|DSBA_ECOLI| Thiol disulfide interchange protein DsbA OS=Escherichia coli (strain K12) OX=83333 GN=dsbA PE=1 SV=1
3::P77766|RNAAM_ECOLI| 5'-3' exoribonuclease OS=Escherichia coli (strain K12) OX=83333 GN=yciV PE=1 SV=1
3::P39374|INTB_ECOLI| Putative protein IntB OS=Escherichia coli (strain K12) OX=83333 GN=intB PE=5 SV=1
3::P00957|SYA_ECOLI| Alanine--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=alaS PE=1 SV=2
3::P18869|FHUE_ECOLI| FhuE receptor OS=Escherichia coli (strain K12) OX=83333 GN=fhuE PE=1 SV=2
3::P77658|YNAO_ECOLI| Protein YnaA OS=Escherichia coli (strain K12) OX=83333 GN=ynaA PE=4 SV=1
3::P50456|MLCC_ECOLI| Protein mlc OS=Escherichia coli (strain K12) OX=83333 GN=mlc PE=1 SV=2
3::P07943|LAMB_ECOLI| Maltoporin OS=Escherichia coli (strain K12) OX=83333 GN=lamb PE=1 SV=1
3::P0AD6|EDD_ECOLI| Phosphogluconate dehydratase OS=Escherichia coli (strain K12) OX=83333 GN=edd PE=1 SV=1
3::P37902|GLTI_ECOLI| Glutamate/aspartate import solute-binding protein OS=Escherichia coli (strain K12) OX=83333 GN=gltI PE=1 SV=2
3::P28659|METQ_ECOLI| D-methionine-binding lipoprotein MetQ OS=Escherichia coli (strain K12) OX=83333 GN=metQ PE=1 SV=2
3::P23847|PDEA_ECOLI| Probable cyclic di-GMP phosphodiesterase PdeA OS=Escherichia coli (strain K12) OX=83333 GN=pdeA PE=2 SV=2
3::P56258|WECF_ECOLI| TDP-N-acetylucosamine:lipid II N-acetylucosaminyltransferase OS=Escherichia coli (strain K12) OX=83333 GN=wecF PE=1 SV=2
3::P31224|ACRB_ECOLI| Multidrug efflux pump subunit AcrB OS=Escherichia coli (strain K12) OX=83333 GN=acrB PE=1 SV=1

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Target Decoy False discovery rate

Peptide matches above identity threshold 487 57 11.70 %
 Peptide matches above homology or identity threshold 488 60 12.30 %

Select Summary Report

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

All queries
 Unassigned
 Below homology threshold
 Below identity threshold

1. [2::TOP2B_1-566](#) Mass: 66629 Score: 7213 Matches: 298 (298) Sequences: 44 (44) emPA1: 30.81

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
377	401.7245	801.4344	801.4344	-0.07	0	32	0.00087	1	U	K.AQTQLNK.K 376
447	410.7502	819.4858	819.4854	0.51	0	38	0.00018	1	U	K.IVGLQYK.K 441 445 446
482	414.7811	827.5477	827.5480	-0.40	1	32	0.00059	1	U	K.LIEVVKK.K
596	426.2430	850.4714	850.4701	1.51	0	28	0.0014	1	U	R.YGVFPLR.G 592 594 595
730	439.7585	877.5024	877.5022	0.32	0	23	0.0057	1	U	K.GIPVVEHK.V 729

6.	1::sp K1C9_HUMAN 	Mass: 62320	Score: 174	Matches: 6(6)	Sequences: 6(6)	emPAI: 0.51
sp K1C9_HUMAN						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
405	405.2239	808.4332	808.4330	0.15	0 20	0.0095 1 R.LASYLDK.V
1870	530.7864	1059.5583	1059.5560	2.13	0 19	0.02 1 U K.TLLDIDNTR.M
1903	533.2532	1064.4919	1064.4920	-0.10	0 44	4.9e-005 1 U K.STMQELNSR.L
6188	793.8866	1585.7586	1585.7583	0.15	0 74	1.2e-007 1 U K.VOALEEANNDLENK.I
7637	896.3673	1790.7200	1790.7205	-0.29	0 64	8e-007 1 U R.GSGGGYGGGGGGGGYGGGSGR.G
12070	1088.8423	3263.5050	3263.5066	-0.48	0 31	0.0065 1 U K.DIENQYETQITQIEHVSSSGQEVQSSAK.E
7.	3::POA25 THIO_ECOLI	Mass: 11913	Score: 137	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
3557	634.3358	1266.6571	1266.6568	0.21	0 69	2.9e-007 1 U K.LNIDONPGTAPK.Y
7808	903.4531	1804.8916	1804.8917	-0.04	0 85	1.1e-008 1 U K.MIAPILDEIAEYQGK.L
8.	1::sp ALBU_BOVIN 	Mass: 71244	Score: 123	Matches: 5(5)	Sequences: 4(4)	emPAI: 0.27
sp ALBU_BOVIN						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
952	461.7476	921.4807	921.4807	-0.06	0 36	0.00036 1 U K.AEFVEYTK.L
2758	582.3191	1162.6237	1162.6234	0.31	0 30	0.0014 1 U K.LVNELTEFAK.T
3867	653.3625	1304.7105	1304.7088	1.25	0 43	7.9e-005 1 U K.HLVDEPQNLIK.Q 3866
6495	547.3181	1638.9324	1638.9305	1.20	1 35	0.00029 1 U R.KVPQVSTPTLVESR.S
9.	3::P76298 FLHA_ECOLI	Mass: 74795	Score: 92	Matches: 14(14)	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
3513	632.8193	1263.6241	1263.6159	6.55	1 (19)	0.021 1 U R.HIRMATIGGK. - 3530 3538
3525	632.8197	1263.6249	1263.6159	7.12	1 26	0.0047 1 U R.HIRMTAIGGK. - 3514 3515 3516 3519 3524 3527 3528 3534 3536 3540
10.	3::Q46857 DKGA_ECOLI	Mass: 31147	Score: 34	Matches: 2(2)	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
1011	466.2456	930.4766	930.4844	-8.41	0 25	0.0034 1 U -_MANPTVIK.L 1012
11.	3::POAD96 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
369	400.7352	799.4558	799.4552	0.75	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	
12.	3::P75882 GFCO_ECOLI	Mass: 78923	Score: 31	Matches: 3(3)	Sequences: 1(1)	emPAI: 0.06
Uncharacterized lipoprotein GfcD OS=Escherichia coli (strain K12) OX=83333 GN=gfcD PE=3 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
1552	509.2826	1016.5506	1016.5502	0.40	1 22	0.0089 1 U K.DKGATIDYAK.R 1548 1550
13.	3::POAAB4 UBID_ECOLI	Mass: 55967	Score: 28	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.08
3-octaprenyl-4-hydroxybenzoate carboxy-lyase OS=Escherichia coli (strain K12) OX=83333 GN=ubiD PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
12975	1078.2271	4308.8795	4308.8650	3.37	2 28	0.011 1 U R.MDPARDIVLVENTPIDYLDFAFPVSLGSKMGLDAINK.W
14.	3::P13009 METH_ECOLI	Mass: 136653	Score: 28	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.06
Methionine synthase OS=Escherichia coli (strain K12) OX=83333 GN=metH PE=1 SV=5						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
414	406.7352	811.4559	811.4552	0.84	0 22	0.0061 1 U R.AVEGLAPR.K
3663	427.1728	1278.4965	1278.5080	-8.99	1 19	0.017 1 U -_MSSKVEQLR.A
15.	3::P62601 TREF_ECOLI	Mass: 63828	Score: 27	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.07
Cytoplasmic trehalase OS=Escherichia coli (strain K12) OX=83333 GN=treF PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
6426	812.4229	1622.8312	1622.8280	1.98	1 27	0.0044 1 U K.LESAIANISALKGK.E
16.	3::POACP5 GNTR_ECOLI	Mass: 36570	Score: 26	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
612	428.7661	855.5176	855.5178	-0.24	0 26	0.0025 1 U R.LASVLTPE.E
17.	1::sp RS27A_HUMAN 	Mass: 18296	Score: 25	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
7607	894.4668	1786.9191	1786.9200	-0.51	0 25	0.0093 1 U K.TITLEVEPSDTIENVK.A
18.	3::P12996 BIOB_ECOLI	Mass: 39079	Score: 25	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.11
Biotin synthase OS=Escherichia coli (strain K12) OX=83333 GN=bioB PE=1 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
217	379.7296	757.4446	757.4446	0.03	1 25	0.0041 1 U K.VRDAGIK.V
19.	3::P77221 YAHG_ECOLI	Mass: 50740	Score: 24	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.09
Uncharacterized protein YahG OS=Escherichia coli (strain K12) OX=83333 GN=yahG PE=4 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide

20. [3::P67660|YHAJ_ECOLI](#) Mass: 33293 Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.14
Probable HTH-type transcriptional regulator YhaJ OS=Escherichia coli (strain K12) OX=83333 GN=yhaJ PE=3 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[11542](#) 767.8403 3067.3323 3067.3025 9.73 2 24 0.025 1 U R.LEQGRADIVIAPDMHFRSSSEINSR.K
21. [3::P39358|YJHG_ECOLI](#) Mass: 70486 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.06
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
[150](#) 372.7220 743.4294 743.4290 0.57 0 23 0.0051 1 U K.VQTIGAR.F
- Proteins matching the same set of peptides:
[3::P77596|YAGF_ECOLI](#) Mass: 69926 Score: 23 Matches: 1(1) Sequences: 1(1)
D-xylonate dehydratase YagF OS=Escherichia coli (strain K12) OX=83333 GN=yagF PE=1 SV=1
22. [3::P24177|ACRD_ECOLI](#) Mass: 113203 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.04
Probable aminoglycoside efflux pump OS=Escherichia coli (strain K12) OX=83333 GN=acrD PE=3 SV=3
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[13075](#) 1105.2711 4417.0552 4417.0516 0.80 2 22 0.05 1 U R.EAIRKSMGQIQGALVGIAMVLSAVFVPMAFFGGITGIAYR.Q
23. [3::P38035|RTCRC_ECOLI](#) Mass: 60604 Score: 22 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
[2732](#) 580.7935 1159.5725 1159.5638 7.46 1 22 0.0075 1 U R.SRSLFEILK.R
24. [3::P71242|WCAK_ECOLI](#) Mass: 47598 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.09
Colanic acid biosynthesis protein WcaK OS=Escherichia coli (strain K12) OX=83333 GN=wcaK PE=3 SV=2
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[781](#) 445.7564 889.4982 889.4981 0.16 1 22 0.012 1 U K.RSNITAK.V
25. [3::P77682|GTRA_ECOLI](#) Mass: 13388 Score: 21 Matches: 1(1) Sequences: 1(1) emPAI: 0.36
Prophage bacteriophage-linked glucose translocase homolog OS=Escherichia coli (strain K12) OX=83333 GN=yfdG PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[4860](#) 484.1993 1449.5762 1449.5765 -0.17 1 21 0.012 1 U K.FIFKASTTMR.Y
26. [3::P0AFS9|MEPM_ECOLI](#) 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
[8174](#) 620.6276 1858.8610 1858.8703 -5.02 2 20 0.037 1 U R.EQSQLLVRLRSEGK.D
27. [3::Q46861|YGIQ_ECOLI](#) Mass: 84223 Score: 20 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
[6156](#) 528.5885 1582.7436 1582.7449 -0.83 1 20 0.029 1 U K.TYVLLPSFEKVK.G
28. [3::P0CE47|EFTU1_ECOLI](#) Mass: 43427 Score: 19 Matches: 1(1) Sequences: 1(1) emPAI: 0.10
Elongation factor Tu 1 OS=Escherichia coli (strain K12) OX=83333 GN=tufA PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[2658](#) 577.2888 1152.5631 1152.5652 -1.84 1 19 0.031 1 U R.GIVVTGRVER.G
- Proteins matching the same set of peptides:
[3::P0CE48|EFTU2_ECOLI](#) Mass: 43457 Score: 19 Matches: 1(1) Sequences: 1(1)
Elongation factor Tu 2 OS=Escherichia coli (strain K12) OX=83333 GN=tufB PE=1 SV=1
29. [3::P0ARD5|ACCA_ECOLI](#) Mass: 35333 Score: 19 Matches: 1(1) Sequences: 1(1) emPAI: 0.13
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha OS=Escherichia coli (strain K12) OX=83333 GN=accA PE=1 SV=2
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[11987](#) 807.7025 3226.7809 3226.7747 1.92 3 19 0.02 1 U R.LKELKIDSIIPEPLGGAHNPEAMAASLK.A
30. [3::Q46793|YGEN_ECOLI](#) Mass: 27575 Score: 19 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
[5685](#) 765.8949 1529.7752 1529.7710 2.76 3 19 0.034 1 U -_MRKKIEMSLIK.S
31. [3::P38134|ETK_ECOLI](#) Mass: 81191 Score: 18 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
[4508](#) 467.8997 1400.6773 1400.6754 1.35 1 18 0.038 1 U K.YFPVIGRGWAR.L
32. [3::P37327|YFDC_ECOLI](#) Mass: 34538 Score: 18 Matches: 1(1) Sequences: 1(1) emPAI: 0.13
Inner membrane protein YfdC OS=Escherichia coli (strain K12) OX=83333 GN=yfdC PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1003](#) 465.7541 929.4936 929.4930 0.62 1 18 0.016 1 U K.AERAENIK.K
33. [3::V9HVX0|YPAA_ECOLI](#) Mass: 6876 Score: 18 Matches: 1(1) Sequences: 1(1) emPAI: 0.80
Uncharacterized protein YpaA OS=Escherichia coli (strain K12) OX=83333 GN=yapaA PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[5000](#) 732.8884 1463.7623 1463.7555 4.66 1 18 0.039 1 U K.IALRMLEGGFDR.D
34. [3::P16384|MIAA_ECOLI](#) Mass: 35157 Score: 18 Matches: 2(2) Sequences: 1(1) emPAI: 0.13
tRNA dimethylallyltransferase OS=Escherichia coli (strain K12) OX=83333 GN=miaA PE=1 SV=2
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[2792](#) 390.8832 1169.6278 1169.6292 -1.23 0 17 0.025 1 U R.DEVLQVVGAIAG.-

35. [3::P63224|GMHA_ECOLI](#) 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
[4854](#) 725.3482 1448.6817 1448.6929 -7.72 1 18 0.035 1 U K.DGGK**M**AGTADIEIR.V
-
36. [3::POA823|YBGC_ECOLI](#) Mass: 15609 Score: 18 Matches: 1(1) Sequences: 1(1) emPAI: 0.31
Acyl-CoA thioester hydrolase YbgC OS=Escherichia coli (strain K12) OX=83333 GN=ybgC PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[3110](#) 406.1946 1215.5620 1215.5594 2.15 0 18 0.032 1 U K.**M**TVVEYYAPAR.L
-
37. [1::sp|KRHB1_HUMAN|](#) Mass: 56875 Score: 18 Matches: 1(1) Sequences: 1(1) emPAI: 0.08
sp|KRHB1_HUMAN|
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[410](#) 406.2213 810.4280 810.4276 0.48 0 18 0.017 1 U R.FAA**F**IDK.V
- Proteins matching the same set of peptides:
[1::sp|K2M2_SHEEP|](#) Mass: 55472 Score: 18 Matches: 1(1) Sequences: 1(1)
sp|K2M2_SHEEP|
[1::sp|K2M3_SHEEP|](#) Mass: 56418 Score: 18 Matches: 1(1) Sequences: 1(1)
sp|K2M3_SHEEP|
[1::sp|KRHB3_HUMAN|](#) Mass: 56004 Score: 18 Matches: 1(1) Sequences: 1(1)
sp|KRHB3_HUMAN|
[1::sp|KRHB5_HUMAN|](#) Mass: 57306 Score: 18 Matches: 1(1) Sequences: 1(1)
sp|KRHB5_HUMAN|
[1::sp|KRHB6_HUMAN|](#) Mass: 55120 Score: 18 Matches: 1(1) Sequences: 1(1)
sp|KRHB6_HUMAN|
-
38. [3::P25772|LIGB_ECOLI](#) Mass: 63425 Score: 17 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
[150](#) 372.7220 743.4294 743.4290 0.57 0 17 0.018 2 U R.VNIGSVR.R
-
39. [3::POA759|NAGB_ECOLI](#) Mass: 29983 Score: 17 Matches: 1(1) Sequences: 1(1) emPAI: 0.15
Glucosamine-6-phosphate deaminase OS=Escherichia coli (strain K12) OX=83333 GN=nagB PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1221](#) 483.2577 964.5008 964.4978 3.20 1 17 0.039 1 U R.QYEEKIR.S
-
40. [3::POADT8|YGI_M_ECOLI](#) Mass: 23062 Score: 17 Matches: 2(2) Sequences: 2(2) emPAI: 0.44
Uncharacterized protein YgiM OS=Escherichia coli (strain K12) OX=83333 GN=ygiM PE=3 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1698](#) 521.2824 1040.5503 1040.5502 0.11 0 14 0.038 2 U R.VPDLENQVK.T
[2732](#) 580.7935 1159.5725 1159.5721 0.33 0 16 0.028 2 U K.VDAASVQLDDK.Q
-
41. [3::POAGD7|SRP54_ECOLI](#) Mass: 49812 Score: 17 Matches: 1(1) Sequences: 1(1) emPAI: 0.09
Signal recognition particle protein OS=Escherichia coli (strain K12) OX=83333 GN=ffh PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1496](#) 505.7783 1009.5421 1009.5412 0.83 3 17 0.028 1 U K.K**M**KKGG**M**AK.M
-
42. [1::sp|KRHB4_HUMAN|](#) Mass: 65938 Score: 17 Matches: 1(1) Sequences: 1(1) emPAI: 0.07
sp|KRHB4_HUMAN|
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1552](#) 509.2826 1016.5506 1016.5502 0.43 2 17 0.028 2 U K.KDEKEIQIK.T
-
43. [3::P77211|CUSC_ECOLI](#) Mass: 50410 Score: 17 Matches: 1(1) Sequences: 1(1) emPAI: 0.09
Cation efflux system protein CusC OS=Escherichia coli (strain K12) OX=83333 GN=cusC PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[9863](#) 789.7597 2366.2573 2366.2706 -5.61 1 17 0.047 2 U K.IEIPFNAGRNQANLDIAEIR.Q
-
44. [3::P69811|PTFAH_ECOLI](#) Mass: 39624 Score: 17 Matches: 1(1) Sequences: 1(1) emPAI: 0.11
Multiphosphoryl transfer protein OS=Escherichia coli (strain K12) OX=83333 GN=fruB PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[6393](#) 540.2932 1617.8577 1617.8474 6.31 1 17 0.04 1 U R.LRFTAQGADEQALK.A
-
45. [3::POAEF5|DGAL_ECOLI](#) Mass: 35690 Score: 17 Matches: 1(1) Sequences: 1(1) emPAI: 0.13
D-galactose-binding periplasmic protein OS=Escherichia coli (strain K12) OX=83333 GN=mgIB PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[839](#) 451.7506 901.4866 901.4869 -0.30 1 17 0.04 1 U R.KAIEQDAK.A
-
46. [3::P15028|FECB_ECOLI](#) Mass: 33126 Score: 17 Matches: 1(1) Sequences: 1(1) emPAI: 0.14
Fe(3+) dicitrate-binding periplasmic protein OS=Escherichia coli (strain K12) OX=83333 GN=fecB PE=2 SV=3
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[75](#) 359.2105 716.4065 716.4068 -0.44 0 17 0.021 1 U R.IAADTVK.I
-
47. [3::Q06065|ATOC_ECOLI](#) Mass: 52428 Score: 17 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
[3531](#) 422.2157 1263.6252 1263.6203 3.93 1 16 0.046 1 U R.**M**PE**M**DG**I**KALK.E [3532](#)
-
48. [3::P00634|PPB_ECOLI](#) Mass: 49636 Score: 17 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
[3209](#) 614.2891 1226.5636 1226.5601 2.86 1 17 0.042 1 U R.KCYGPSATSEK.C

49.	3::P06992 RSMA_ECOLI	Mass: 30515	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.15
Ribosomal RNA small subunit methyltransferase A OS=Escherichia coli (strain K12) OX=83333 GN=rsmA PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	156	373.2140	744.4135	744.4130	0.62	0 17 0.022 1 U K.VDSAVVR.L
50.	3::P77377 WZXC_ECOLI	Mass: 53886	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.08
Lipopolysaccharide biosynthesis protein WzxC OS=Escherichia coli (strain K12) OX=83333 GN=wzxC PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	5672	510.6170	1528.8292	1528.8395	-6.75	1 17 0.04 1 U R.SVGNPIGSLLMAKAR.V
51.	3::P33668 YBBC_ECOLI	Mass: 14257	Score: 16	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
	1556	509.7492	1017.4839	1017.4896	-5.57	1 16 0.035 1 U K.YSVKNLVK.T
52.	3::P80645 SSUD_ECOLI	Mass: 41768	Score: 16	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
	285	387.7088	773.4031	773.4032	-0.03	0 16 0.024 1 U R.QAATLDR.L
53.	3::P13738 NHAA_ECOLI	Mass: 41500	Score: 16	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.11
Na(+)/H(+) antiporter NhaA OS=Escherichia coli (strain K12) OX=83333 GN=nhaA PE=1 SV=3						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	12915	1014.3229	4053.2625	4053.2390	5.80	2 16 0.024 1 U R.RTGVYILVGVVLWIAVLKSGVHATLAGVIVGFFIPLK.E
54.	3::P31434 XYLS_ECOLI	Mass: 88764	Score: 16	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.05
Alpha-xylosidase OS=Escherichia coli (strain K12) OX=83333 GN=yicI PE=1 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	1613	514.2439	1026.4733	1026.4648	8.30	1 16 0.05 1 U R.LHGSKSYR.V
55.	3::P76104 RLHA_ECOLI	Mass: 73170	Score: 16	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.06
23S rRNA 5-hydroxycytidine C2501 synthase OS=Escherichia coli (strain K12) OX=83333 GN=rIhA PE=1 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	217	379.7296	757.4446	757.4446	0.05	1 16 0.03 2 U K.QAKGNIK.S
56.	3::P21893 RECJ_ECOLI	Mass: 63634	Score: 16	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
	2098	543.8044	1085.5943	1085.6015	-6.68	1 16 0.043 1 U -_MKQQIQLR.R
57.	3::P76016 DHAR_ECOLI	Mass: 71088	Score: 16	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.06
PTS-dependent dihydroxyacetone kinase operon regulatory protein OS=Escherichia coli (strain K12) OX=83333 GN=dhaR PE=1 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	8370	634.6957	1901.0653	1901.0638	0.79	0 16 0.036 1 U R.AIELLTLPAVLQQAIK.Q
58.	3::P0AFE8 NUOM_ECOLI	Mass: 56658	Score: 16	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.08
NADH-quinone oxidoreductase subunit M OS=Escherichia coli (strain K12) OX=83333 GN=nuoM PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	1065	471.2400	940.4654	940.4743	-9.45	1 16 0.029 1 U K.TRITAAIK.F
59.	3::P09372 GRPE_ECOLI	Mass: 21784	Score: 16	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.21
Protein GrpE OS=Escherichia coli (strain K12) OX=83333 GN=grpE PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	2088	543.3196	1084.6246	1084.6353	-9.87	2 16 0.038 1 U R.ERDGLRVK.A
60.	3::P28917 YDCC_ECOLI	Mass: 43507	Score: 15	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.10
H repeat-associated putative transposase YdcC OS=Escherichia coli (strain K12) OX=83333 GN=ydcC PE=3 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	723	439.2244	876.4342	876.4375	-3.72	0 15 0.028 1 U K.ELEMTVR.Y
61.	3::P37007 YAGA_ECOLI	Mass: 44026	Score: 15	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.10
Uncharacterized protein YagA OS=Escherichia coli (strain K12) OX=83333 GN=yagA PE=2 SV=3						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	217	379.7296	757.4446	757.4446	0.03	1 15 0.034 3 U R.GERVGLK.E
62.	3::P28912 YHHI_ECOLI	Mass: 43574	Score: 15	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.10
H repeat-associated putative transposase YhhI OS=Escherichia coli (strain K12) OX=83333 GN=yhhI PE=3 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	2081	362.4979	1084.4720	1084.4624	8.86	1 15 0.034 1 U K.KEPETLVR.Y
Proteins matching the same set of peptides:						
	3::P75741 YBFL_ECOLI	Mass: 43532	Score: 15	Matches: 1(1)	Sequences: 1(1)	
Putative protein Ybfl OS=Escherichia coli (strain K12) OX=83333 GN=ybfl PE=5 SV=3						
63.	3::P28630 HOLA_ECOLI	Mass: 38965	Score: 15	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.12
DNA polymerase III subunit delta OS=Escherichia coli (strain K12) OX=83333 GN=hoIA PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
	995	464.7822	927.5499	927.5502	-0.29	0 15 0.031 1 U R.QAVQLLTR.T
64.	3::P0AAK7 NRFC_ECOLI	Mass: 25464	Score: 15	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.18
Protein NrfC OS=Escherichia coli (strain K12) OX=83333 GN=nrfC PE=3 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide

628 430.2534 858.4923 858.4923 0.02 1 15 0.048 1 U R.KTLQAGK.L

65. [3::P37650|BCSC_ECOLI](#) Mass: 127760 Score: 15 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
[1282](#) 488.7422 975.4699 975.4733 -3.52 1 15 0.043 2 U K.SNAGREGASK.I

66. [3::POAFB8|NTRC_ECOLI](#) Mass: 52336 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.08

DNA-binding transcriptional regulator NtrC OS=Escherichia coli (strain K12) OX=83333 GN=glnG PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[681](#) 435.7076 869.4006 869.4048 -4.84 0 15 0.04 1 U R.VGGYAPVK.V

67. [3::POAG96|SECF_ECOLI](#) Mass: 13635 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.36

Protein translocase subunit SecE OS=Escherichia coli (strain K12) OX=83333 GN=secE PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1455](#) 503.3082 1004.6019 1004.6019 0.08 0 15 0.035 1 U R.LVSFITGLR.F

68. [3::P02925|RBSB_ECOLI](#) Mass: 30931 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.15

Ribose import binding protein RbsB OS=Escherichia coli (strain K12) OX=83333 GN=rbsB PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1196](#) 481.2367 960.4588 960.4512 7.90 1 14 0.037 1 U K.DGAQKADK.L

69. [3::POAEG4|DSBA_ECOLI](#) Mass: 23204 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.20

Thiol:disulfide interchange protein DsbA OS=Escherichia coli (strain K12) OX=83333 GN=dsbA PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[3068](#) 605.8174 1209.6203 1209.6192 0.92 2 14 0.05 1 U K.KLPEGVKMK.Y

70. [3::P77766|RNAAM_ECOLI](#) Score: 14 Matches: 1(1) Sequences: 1(1)

5'-3' exoribonuclease OS=Escherichia coli (strain K12) OX=83333 GN=yoiV PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[369](#) 400.7352 799.4558 799.4552 0.77 0 14 0.042 2 U R.AQLIAER.L

71. [3::P39347|INTB_ECOLI](#) Mass: 45725 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.10

Putative protein IntB OS=Escherichia coli (strain K12) OX=83333 GN=intB PE=5 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[2577](#) 381.8837 1142.6292 1142.6196 8.33 0 14 0.048 1 U M_HLLVHPNGSK.Y

72. [3::P00957|SYA_ECOLI](#) 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
[455](#) 412.2393 822.4640 822.4712 -8.74 0 14 0.04 1 U R.VIADHIR.S

73. [3::P16869|FHUE_ECOLI](#) Mass: 81239 Score: 14 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
[3632](#) 638.2583 1274.5021 1274.5114 -7.30 0 14 0.043 1 U R.LITLAIFR.I

74. [3::P77658|YNAA_ECOLI](#) 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
[1009](#) 465.7793 929.5440 929.5406 3.59 2 14 0.042 1 U R.KIOETRR.E

75. [3::P50456|MLC_ECOLI](#) Mass: 44516 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.10

Protein mlc OS=Escherichia coli (strain K12) OX=83333 GN=mlc PE=1 SV=2
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[1724](#) 522.7363 1043.4580 1043.4634 -5.19 0 14 0.045 1 U R.MPFYEDVK.E

76. [3::P02943|LAMB_ECOLI](#) Mass: 49995 Score: 14 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
[113](#) 366.2239 730.4332 730.4337 -0.75 0 14 0.043 1 U K.LSLAATR.S

77. [3::POADF6|EDD_ECOLI](#) Mass: 65054 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.07

Phosphogluconate dehydratase OS=Escherichia coli (strain K12) OX=83333 GN=edd PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[2](#) 350.1556 698.2967 698.3000 -4.78 0 14 0.043 1 U R.LSGASGK.V

78. [3::P37902|GLTI_ECOLI](#) Score: 14 Matches: 1(1) Sequences: 1(1)

Glutamate/aspartate import solute-binding protein OS=Escherichia coli (strain K12) OX=83333 GN=glti PE=1 SV=2
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[723](#) 439.2244 876.4342 876.4341 0.11 1 14 0.045 2 U R.KDDPQFK.K

79. [3::P28635|METO_ECOLI](#) Mass: 29471 Score: 13 Matches: 1(1) Sequences: 1(1) emPAI: 0.15

D-methionine-binding lipoprotein MetQ OS=Escherichia coli (strain K12) OX=83333 GN=metQ PE=1 SV=2
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[350](#) 396.2241 790.4336 790.4337 -0.17 0 13 0.046 1 U K.VFNGGAVK.G

80. [3::P23842|PDEA_ECOLI](#) Mass: 84325 Score: 13 Matches: 1(1) Sequences: 1(1) emPAI: 0.05

Probable cyclic di-GMP phosphodiesterase PdeA OS=Escherichia coli (strain K12) OX=83333 GN=pdeA PE=2 SV=2
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
[11012](#) 577.1268 2880.5974 2880.6176 -7.03 3 13 0.047 1 U R.FSVNL_MPLILLKKNIAGRIRLRFK.R

81. [3::P56258|WECF_ECOLI](#) Mass: 40899 Score: 13 Matches: 1(1) Sequences: 1(1) emPAI: 0.11
TDP-N-acetylfucosamine:lipid II N-acetylfucosaminyltransferase OS=Escherichia coli (strain K12) OX=83333 GN=wecF PE=1 SV=2
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
529 420.6980 839.3815 839.3790 2.98 0 13 0.047 1 U R.QLASVDK.N

82. [3::P31224|ACRB_ECOLI](#) Mass: 113615 Score: 13 Matches: 1(1) Sequences: 1(1) emPAI: 0.04
Multidrug efflux pump subunit AcrB OS=Escherichia coli (strain K12) OX=83333 GN=acrB PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide
632 430.7217 859.4288 859.4287 0.11 0 13 0.05 1 U K.IDIDQEK.A

