

Cambridge Centre for Proteomics Mascot Search Results

User : anja
Email : aa2030@cam.ac.uk
Search title : M291 run2 (\\prot-filesvr1\data\CORE\PARAMETERS\Mascot_search_parameters\Yagnesh\M291_Ben_Luisi_Ecoli_velos_xlink_chymo_031218.par), submitted from Daemon on CCP-PC158
MS data file : \\prot-filesvr1\data\CORE\RAW_DATA_2018_Velos\Ben_Luisi\Ben_Luisi_band2.mgf
Database 1 : cRAP FullIdentifiers (117 sequences; 38809 residues)
Database 2 : CCP Uniprot Escherichia coli
Uniprot Escherichia coli_20180613 (4324 sequences; 1357163 residues)
Timestamp : 3 Dec 2018 at 11:08:49 GMT

Protein hits	: 2::sp P02930 TOLC ECOLI	Outer membrane protein TolC OS=Escherichia coli
	: 2::sp P0A9P0 DLDH ECOLI	Dihydrolipoyl dehydrogenase OS=Escherichia coli
	: 2::sp P0ABB4 ATPB ECOLI	ATP synthase subunit beta OS=Escherichia coli
	: 2::sp P0A850 TIG ECOLI	Trigger factor OS=Escherichia coli (strain K12)
	: 2::sp P02931 OMPF ECOLI	Outer membrane protein F OS=Escherichia coli
	: 2::sp P0CE47 EFTU1 ECOLI	Elongation factor Tu 1 OS=Escherichia coli
	: 2::sp P0AE06 ACRA ECOLI	Multidrug efflux pump subunit AcrA OS=Escherichia coli
	: 1::sp cRAP022 P00766 CTRA BOVIN	Chymotrypsinogen A OS=Bos taurus PE=1 SV=1
	: 2::sp P0A6F3 GLPK ECOLI	Glycerol kinase OS=Escherichia coli (strain K12)
	: 2::sp P0ABB0 ATPA ECOLI	ATP synthase subunit alpha OS=Escherichia coli
	: 2::sp P0A6P9 ENO ECOLI	Enolase OS=Escherichia coli (strain K12)
	: 2::sp P00350 6PGD ECOLI	6-phosphogluconate dehydrogenase, decarboxylating OS=Escherichia coli
	: 2::sp P0A6H5 HSLU ECOLI	ATP-dependent protease ATPase subunit HsA OS=Escherichia coli
	: 2::sp P0A8M0 SYN ECOLI	Asparagine--tRNA ligase OS=Escherichia coli
	: 2::sp P0AFG6 ODO2 ECOLI	Dihydrolipoyllysine-residue succinyltransferase OS=Escherichia coli
	: 2::sp P0A7D4 PURA ECOLI	Adenylosuccinate synthetase OS=Escherichia coli
	: 2::sp P0A6P1 EFTS ECOLI	Elongation factor Ts OS=Escherichia coli
	: 2::sp P0A836 SUCC ECOLI	Succinate--CoA ligase [ADP-forming] subunit beta OS=Escherichia coli
	: 2::sp P0A9B2 G3P1 ECOLI	Glyceraldehyde-3-phosphate dehydrogenase OS=Escherichia coli
	: 2::sp P21165 PEPQ ECOLI	Xaa-Pro dipeptidase OS=Escherichia coli
	: 2::sp P04805 SYE ECOLI	Glutamate--tRNA ligase OS=Escherichia coli
	: 2::sp P08200 IDH ECOLI	Isocitrate dehydrogenase [NADP] OS=Escherichia coli
	: 2::sp P0A910 OMPA ECOLI	Outer membrane protein A OS=Escherichia coli
	: 2::sp P0C8J8 GATZ ECOLI	D-tagatose-1,6-bisphosphate aldolase subunit beta OS=Escherichia coli
	: 2::sp P0A6E4 ASSY ECOLI	Argininosuccinate synthase OS=Escherichia coli
	: 2::sp P0AEX9 MALE ECOLI	Maltose-binding periplasmic protein OS=Escherichia coli
	: 2::sp P0A799 PGK ECOLI	Phosphoglycerate kinase OS=Escherichia coli
	: 2::sp P0C0V0 DEGP ECOLI	Periplasmic serine endoprotease DegP OS=Escherichia coli

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Citrate synthase OS=Escherichia coli (str
Serine hydroxymethyltransferase OS=Esche
Transcription termination factor Rho OS=
Pyruvate kinase II OS=Escherichia coli (
Aspartate ammonia-lyase OS=Escherichia c
Serine--tRNA ligase OS=Escherichia coli
Ribose import binding protein RbsB OS=Es
Soluble pyridine nucleotide transhydroge
Fructose-bisphosphate aldolase class 2 O
30S ribosomal protein S1 OS=Escherichia
Cysteine--tRNA ligase OS=Escherichia col
Glutathione reductase OS=Escherichia col
DNA-directed RNA polymerase subunit alph
3-oxoacyl-[acyl-carrier-protein] synthas
Cytosol aminopeptidase OS=Escherichia co
Outer membrane protein C OS=Escherichia
Multidrug efflux pump subunit AcrB OS=Es
Transaldolase B OS=Escherichia coli (str
60 kDa chaperonin OS=Escherichia coli (s
Bifunctional protein HldE OS=Escherichia
Metalloprotease TldD OS=Escherichia coli
Biotin carboxylase OS=Escherichia coli (
ATP-dependent Clp protease ATP-binding s
Acetate kinase OS=Escherichia coli (stra
S-adenosylmethionine synthase OS=Escheri
Lactaldehyde dehydrogenase OS=Escherichi
Signal recognition particle protein OS=E
Elongation factor G OS=Escherichia coli
ATP-dependent RNA helicase SrmB OS=Esche
Maltoporin OS=Escherichia coli (strain K
Alkyl hydroperoxide reductase C OS=Esche
3-oxoacyl-[acyl-carrier-protein] synthas
Succinate--CoA ligase [ADP-forming] subu
NADH-quinone oxidoreductase subunit F OS
Peptidase B OS=Escherichia coli (strain
Histidine--tRNA ligase OS=Escherichia co
Malate dehydrogenase OS=Escherichia coli
Tol-Pal system protein TolB OS=Escherich
Argininosuccinate lyase OS=Escherichia c
Phosphoethanolamine transferase EptA OS=
Aspartate aminotransferase OS=Escherichi
50S ribosomal protein L3 OS=Escherichia
Ribosomal protein S12 methylthiotransfer
Protein-lysine deacetylase OS=Escherichi
50S ribosomal protein L2 OS=Escherichia
Uncharacterized protease YegQ OS=Escheri
30S ribosomal protein S4 OS=Escherichia
Ketol-acid reductoisomerase (NADP(+)) OS

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30S ribosomal protein S3 OS=Escherichia
UDP-N-acetylmuramoyl-L-alanyl-D-glutamat
PhoH-like protein OS=Escherichia coli (s
Triosephosphate isomerase OS=Escherichia
Enoyl-[acyl-carrier-protein] reductase [NADPH]
Superoxide dismutase [Mn] OS=Escherichia
Xaa-Pro aminopeptidase OS=Escherichia coli
50S ribosomal protein L1 OS=Escherichia
Lysine-sensitive aspartokinase 3 OS=Escherichia
50S ribosomal protein L4 OS=Escherichia
Maltodextrin phosphorylase OS=Escherichia coli
Cytoskeleton protein RodZ OS=Escherichia coli
Tyrosine--tRNA ligase OS=Escherichia coli
Thiol peroxidase OS=Escherichia coli (str
Bifunctional protein GlmU OS=Escherichia coli
50S ribosomal protein L21 OS=Escherichia coli
30S ribosomal protein S13 OS=Escherichia coli
Modulator of FtsH protease HflK OS=Escherichia coli
50S ribosomal protein L18 OS=Escherichia coli
Adenylosuccinate lyase OS=Escherichia coli
Inorganic pyrophosphatase OS=Escherichia coli
Glycine--tRNA ligase alpha subunit OS=Escherichia coli
50S ribosomal protein L10 OS=Escherichia coli
Pyruvate kinase I OS=Escherichia coli (str
UDP-N-acetylmuramate--L-alanyl-gamma-D-glutamate
FKBP-type peptidyl-prolyl cis-trans isomerase
30S ribosomal protein S2 OS=Escherichia coli
UDP-glucose 6-dehydrogenase OS=Escherichia coli
Cysteine desulfurase IscS OS=Escherichia coli
Cyclic di-GMP-binding protein OS=Escherichia coli
Pyrimidine/purine nucleotide 5'-monophosphate
Succinate dehydrogenase flavoprotein subunit
Metalloprotease PmbA OS=Escherichia coli
Aconitate hydratase B OS=Escherichia coli
Chaperone protein DnaK OS=Escherichia coli
Ribose-phosphate pyrophosphokinase OS=Escherichia coli
Oxygen-independent coproporphyrinogen III synthase
Cysteine synthase A OS=Escherichia coli
4-alpha-glucanotransferase OS=Escherichia coli
Histidine--tRNA ligase, cytoplasmic OS=Escherichia coli
33 kDa chaperonin OS=Escherichia coli (str
Chromosomal replication initiator protein
Tryptophan--tRNA ligase OS=Escherichia coli
2-amino-3-ketobutyrate coenzyme A ligase
Serum albumin OS=Bos taurus GN=ALB PE=1
Aminomethyltransferase OS=Escherichia coli
30S ribosomal protein S18 OS=Escherichia coli
Phosphoenolpyruvate-dependent phosphotransferase

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50S ribosomal protein L13 OS=Escherichia
Adenylate kinase OS=Escherichia coli (st
ADP-L-glycero-D-manno-heptose-6-epimeras
Macrolide export ATP-binding/permease pr
Multiphosphoryl transfer protein 1 OS=Es
Trk system potassium uptake protein TrkA
Bifunctional protein PaaZ OS=Escherichia
Uncharacterized protein YjgR OS=Escheric
ATP-dependent RNA helicase Rhle OS=Esche
L-arabinose isomerase OS=Escherichia col
Uncharacterized sulfatase YdeN OS=Escher
Cell division protein FtsZ OS=Escherichi
Phosphoserine aminotransferase OS=Escher
Phosphoadenosine phosphosulfate reductas
Transcriptional regulatory protein BtsR
Acid stress chaperone HdeB OS=Escherichi
Fructose-6-phosphate aldolase 1 OS=Esche
Translocation and assembly module subuni
Acetyl-coenzyme A carboxylase carboxyl t
Biotin carboxyl carrier protein of acety
Uncharacterized protein YbbN OS=Escheric
50S ribosomal protein L7/L12 OS=Escheric
Nucleoside diphosphate kinase OS=Escheri
AMP nucleosidase OS=Escherichia coli (st
Phosphoglucosamine mutase OS=Escherichia
Protein RecA OS=Escherichia coli (strain
H repeat-associated putative transposase
Fumarate hydratase class II OS=Escherich
30S ribosomal protein S9 OS=Escherichia
Ribokinase OS=Escherichia coli (strain K
Phosphopentomutase OS=Escherichia coli (
Type-1 fimbrial protein, A chain OS=Esch
tRNA-2-methylthio-N(6)-dimethylallyladen
Cellulose synthase catalytic subunit [UD
D-mannonate oxidoreductase OS=Escherichi
L-threonine 3-dehydrogenase OS=Escherich
Fe/S biogenesis protein NfuA OS=Escheric
ATP-dependent RNA helicase RhlB OS=Esche
2,3,4,5-tetrahydropyridine-2,6-dicarboxy
Uncharacterized oxidoreductase YdfI OS=E
Uncharacterized HTH-type transcriptional
D-lactate dehydrogenase OS=Escherichia c
Uncharacterized protein YebT OS=Escheric
50S ribosomal protein L6 OS=Escherichia
30S ribosomal protein S8 OS=Escherichia
Uncharacterized protein YhdP OS=Escheric
Putative alkyl/aryl-sulfatase YjcS OS=Es
Alpha-galactosidase OS=Escherichia coli

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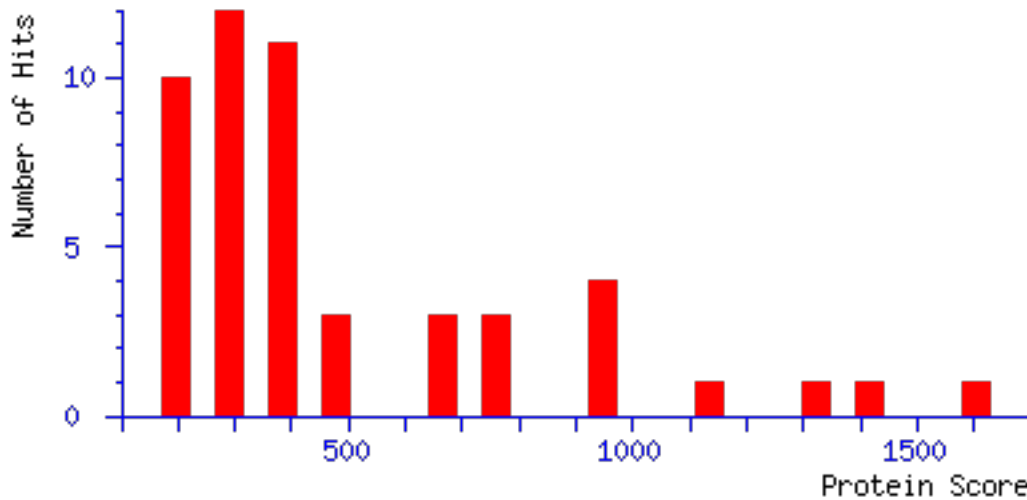
30S ribosomal protein S15 OS=Escherichia
Outer membrane protein assembly factor B
Purine nucleoside phosphorylase DeoD-ty
N-glycosidase YbiA OS=Escherichia coli (
FhuE receptor OS=Escherichia coli (strai
D-methionine-binding lipoprotein MetQ OS
Beta-barrel assembly-enhancing protease
D-malate dehydrogenase [decarboxylating]
Cytochrome bo(3) ubiquinol oxidase subun
HTH-type transcriptional repressor Cytr
Hydrogenase-2 large chain OS=Escherichia
Glucose-6-phosphate 1-dehydrogenase OS=E
Uncharacterized protein YhhZ OS=Escheric
50S ribosomal protein L5 OS=Escherichia
L-glyceraldehyde 3-phosphate reductase O
Uncharacterized protein YjiJ OS=Escheric
Uncharacterized protein YhjY OS=Escheric
Deoxyguanosinetriphosphate triphosphohyd
Motility protein B OS=Escherichia coli (
PTS system beta-glucoside-specific EIIBC
2,3-bisphosphoglycerate-dependent phosph
Uncharacterized protein YecJ OS=Escheric
HTH-type transcriptional regulator XapR
Transcriptional regulator GadE OS=Escher
Elongation factor P OS=Escherichia coli
Endoglucanase OS=Escherichia coli (strai
Cell division protein ZipA OS=Escherichi
D-serine dehydratase OS=Escherichia coli
Uncharacterized outer membrane usher pro
Galactitol 1-phosphate 5-dehydrogenase O
Cytidine deaminase OS=Escherichia coli (
Trypsin OS=Sus scrofa PE=1 SV=1
Inner membrane protein YeeA OS=Escherich
Murein hydrolase activator NlpD OS=Esche
Uncharacterized protein YgeY OS=Escheric
Spermidine/putrescine-binding periplasmi
Glutamate 5-kinase OS=Escherichia coli (
Peptidyl-prolyl cis-trans isomerase C OS
High-affinity branched-chain amino acid
Beta-galactosidase OS=Escherichia coli (
Protein HemX OS=Escherichia coli (strain
2,3-diketo-L-gulonate TRAP transporter 1
Putative type II secretion system protei
Potassium-transporting ATPase potassium-
sn-glycerol-3-phosphate transport system
Enterobactin synthase component E OS=Esc
Alpha-D-ribose 1-methylphosphonate 5-tri
Flagellar hook-associated protein 1 OS=E

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[2::sp|P75906|PGAB ECOLI](#)

Probable outer membrane usher protein El
 Ethanolamine utilization protein EutA OS
 Glutamyl-tRNA reductase OS=Escherichia c
 Multidrug export protein AcrF OS=Escheri
 Putative uncharacterized protein YaiT OS
 Lysine--tRNA ligase OS=Escherichia coli
 Hydrogenase-4 component B OS=Escherichia
 Cytochrome bd-I ubiquinol oxidase subuni
 Uncharacterized HTH-type transcriptional
 Phosphoglycerol transferase I OS=Escheri
 Carbamoyl-phosphate synthase small chain
 Chaperone SurA OS=Escherichia coli (stra
 Uncharacterized J domain-containing prot
 Putative uncharacterized protein YjgW OS
 Chaperone protein ClpB OS=Escherichia co
 Poly-beta-1,6-N-acetyl-D-glucosamine N-d

Mascot Score Histogram

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 24 indicate identity or extensive homology ($p < 0.05$). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Protein Family Summary	Peptide Summary	Select Summary (protein hits)	Select Summary (unassigned)	Exp
Significance threshold $p <$				
Standard scoring MudPIT scoring				

Show pop-ups Suppress pop-ups

Preferred taxonomy All entries . . Archaea (Archaeobacteria) . . Eukaryota (eucaryotes) Alveolata (alveolates and relatives) bony vertebrates lobe-finned fish and tetrapod clade Mammalia (mammals) Mus musculus (house mouse) Rattus norvegicus (brown rat) Other Mammals (mammals) Takifugu rubripes (Japanese Pufferfish) Danio rerio (zebra fish) Schizosaccharomyces pombe (fission yeast) Pneumocystis carinii Other Fungi Viridiplantae (green algae and plants) Mycobacterium tuberculosis complex Other Actinobacteria (class) Firmicutes (gram-positive bacteria) Agrobacterium tumefaciens Campylobacter jejuni Escherichia coli Neisseria meningitidis (meningococcus) Species information unavailable

Error tolerant

1. [2::sp|P02930|TOLC_ECOLI](#) Mass: 53708 Score: 1604 Matches: 95(90) Sequences: 95
Outer membrane protein TolC OS=Escherichia coli (strain K12) OX=83333 GN=tolC PE=1 SF=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
596	418.7290	835.4435	835.4440	-0.55	1	28	0.02	1	U	L.QLTQS
598	418.7293	835.4441	835.4440	0.12	1	(20)	0.1	3	U	L.QLTQS
739	426.2215	850.4285	850.4297	-1.41	0	(21)	0.12	1	U	L.RQITG
740	426.2219	850.4293	850.4297	-0.49	0	29	0.019	1	U	L.RQITG
1170	458.7767	915.5388	915.5389	-0.07	1	31	0.0073	1	U	L.NIKSA
1171	458.7771	915.5396	915.5389	0.81	1	(23)	0.045	1	U	L.NIKSA
1439	474.7351	947.4557	947.4560	-0.25	1	38	0.003	1	U	F.SLSQ
1597	482.7406	963.4667	963.4662	0.57	1	(43)	0.00088	1	U	Y.NFVGA
1598	482.7408	963.4671	963.4662	1.01	1	46	0.00043	1	U	Y.NFVGA
2040	501.7590	1001.5034	1001.5029	0.52	2	32	0.01	1	U	L.GTLNE
2041	501.7593	1001.5040	1001.5029	1.08	2	(26)	0.046	1	U	L.GTLNE
2133	507.2694	1012.5243	1012.5229	1.32	2	28	0.018	1	U	L.ILNTA
2418	523.7787	1045.5429	1045.5444	-1.39	2	50	0.00017	1	U	L.LPQLG
2419	523.7788	1045.5431	1045.5444	-1.28	2	(34)	0.0073	1	U	L.LPQLG
2453	526.2744	1050.5341	1050.5345	-0.38	0	37	0.0042	1	U	Y.TQAQK
2454	526.2745	1050.5345	1050.5345	-0.02	0	(32)	0.012	1	U	Y.TQAQK
2455	526.2751	1050.5356	1050.5345	1.03	0	(30)	0.022	1	U	Y.TQAQK
2456	526.2751	1050.5356	1050.5345	1.03	0	(23)	0.1	1	U	Y.TQAQK
3133	559.3136	1116.6126	1116.6139	-1.10	0	(44)	0.00064	1	U	Y.KQAVV
3134	559.3149	1116.6153	1116.6139	1.30	0	56	3e-05	1	U	Y.KQAVV
3623	578.8198	1155.6251	1155.6247	0.30	0	58	2e-05	1	U	F.EKINE
3625	578.8212	1155.6279	1155.6247	2.74	0	(41)	0.00092	1	U	F.EKINE
3669	580.3372	1158.6599	1158.6609	-0.84	0	36	0.0024	1	U	Y.SVGTR
3670	580.3377	1158.6609	1158.6609	0.01	0	(33)	0.0039	1	U	Y.SVGTR
4221	605.8434	1209.6723	1209.6717	0.50	0	44	0.00025	1	U	F.KTDKP
4223	605.8442	1209.6739	1209.6717	1.82	0	(37)	0.0013	1	U	F.KTDKP
4240	606.3366	1210.6587	1210.6557	2.43	0	(22)	0.055	1	U	F.KTDKP
4970	639.2937	1276.5728	1276.5718	0.85	0	(47)	0.00031	1	U	Y.DDSNM
4971	639.2950	1276.5754	1276.5718	2.86	0	49	0.00022	1	U	Y.DDSNM
5023	642.3213	1282.6280	1282.6266	1.14	0	39	0.0024	1	U	Y.SGSKT
5036	642.8229	1283.6312	1283.6106	16.1	0	(23)	0.09	1	U	Y.SGSKT
5098	647.2905	1292.5664	1292.5667	-0.23	0	(37)	0.0021	1	U	Y.DDSNM
5100	647.2917	1292.5689	1292.5667	1.75	0	(26)	0.029	1	U	Y.DDSNM
5101	647.2922	1292.5698	1292.5667	2.42	0	(38)	0.0019	1	U	Y.DDSNM

5175	651.3223	1300.6301	1300.6299	0.16	1	(37)	0.0033	1	U	L.SYTQA
5176	651.3229	1300.6312	1300.6299	1.01	1	39	0.002	1	U	L.SYTQA
5417	661.8314	1321.6482	1321.6514	-2.43	0	(33)	0.012	1	U	L.QEKAA
5418	661.8323	1321.6501	1321.6514	-0.95	0	46	0.00058	1	U	L.QEKAA
5438	662.3868	1322.7590	1322.7558	2.44	1	47	7.1e-05	1	U	F.KTDKP
5439	662.3872	1322.7597	1322.7558	3.00	1	(44)	0.00013	1	U	F.KTDKP
5495	665.8049	1329.5953	1329.5936	1.27	1	47	0.00028	1	U	L.DLTAS
5496	665.8055	1329.5965	1329.5936	2.19	1	(35)	0.0042	1	U	L.DLTAS
5900	690.8414	1379.6683	1379.6681	0.18	0	79	2.7e-07	1	U	F.NNINA
5901	690.8426	1379.6706	1379.6681	1.86	0	(79)	3e-07	1	U	F.NNINA
5903	691.3302	1380.6458	1380.6521	-4.51	0	(29)	0.024	1	U	F.NNINA
5904	691.3349	1380.6552	1380.6521	2.30	0	(48)	0.00028	1	U	F.NNINA
6414	724.8774	1447.7403	1447.7419	-1.11	0	58	3.8e-05	1	U	L.VAITD
6416	724.8783	1447.7420	1447.7419	0.08	0	(52)	0.00015	1	U	L.VAITD
6424	725.3712	1448.7279	1448.7259	1.35	0	(41)	0.002	1	U	L.VAITD
6425	725.3716	1448.7287	1448.7259	1.93	0	(54)	9.9e-05	1	U	L.VAITD
6426	725.3723	1448.7301	1448.7259	2.85	0	(46)	0.00062	1	U	L.VAITD
6427	725.3724	1448.7302	1448.7259	2.95	0	(48)	0.00042	1	U	L.VAITD
6696	743.3483	1484.6821	1484.6817	0.28	2	(35)	0.0056	1	U	F.SLSQ
6697	743.3492	1484.6838	1484.6817	1.43	2	43	0.00096	1	U	F.SLSQ
6742	745.8644	1489.7142	1489.7121	1.44	0	(47)	0.00049	1	U	Y.RDANG
6743	745.8658	1489.7170	1489.7121	3.32	0	(62)	1.5e-05	1	U	Y.RDANG
6744	745.8658	1489.7171	1489.7121	3.40	0	81	1.6e-07	1	U	Y.RDANG
6748	746.3566	1490.6987	1490.6961	1.77	0	(72)	1.4e-06	1	U	Y.RDANG
6882	758.4037	1514.7928	1514.7940	-0.78	2	59	2.3e-05	1	U	L.NIKSA
6883	758.4072	1514.7999	1514.7940	3.90	2	(40)	0.0018	1	U	L.NIKSA
7057	768.8999	1535.7852	1535.7831	1.38	1	(59)	3e-05	1	U	L.TLQEK
7058	768.9002	1535.7857	1535.7831	1.71	1	65	6.6e-06	1	U	L.TLQEK
7059	768.9013	1535.7879	1535.7831	3.14	1	(39)	0.0029	1	U	L.TLQEK
7060	768.9017	1535.7889	1535.7831	3.76	1	(43)	0.00095	1	U	L.TLQEK
7064	769.3908	1536.7671	1536.7671	-0.04	1	(42)	0.0016	1	U	L.TLQEK
7065	769.3922	1536.7697	1536.7671	1.70	1	(51)	0.0002	1	U	L.TLQEK
7066	769.3946	1536.7746	1536.7671	4.88	1	(49)	0.00029	1	U	L.TLQEK
7067	769.3991	1536.7837	1536.7671	10.8	1	(48)	0.00031	1	U	L.TLQEK
7172	777.3734	1552.7323	1552.7304	1.21	0	(50)	0.00022	1	U	Y.QGMV
7173	777.3755	1552.7365	1552.7304	3.96	0	(52)	0.00014	1	U	Y.QGMV
7181	777.8662	1553.7179	1553.7144	2.23	0	(53)	0.00011	1	U	Y.QGMV
7182	777.8669	1553.7193	1553.7144	3.17	0	54	8.2e-05	1	U	Y.QGMV
7185	777.8727	1553.7309	1553.7144	10.6	0	(43)	0.0011	1	U	Y.QGMV
7511	804.9230	1607.8314	1607.8307	0.42	2	(38)	0.0027	1	U	L.RQITG
7512	804.9233	1607.8320	1607.8307	0.80	2	(39)	0.0025	1	U	L.RQITG
7513	804.9236	1607.8327	1607.8307	1.26	2	47	0.0004	1	U	L.RQITG
7518	805.4172	1608.8199	1608.8147	3.23	2	(26)	0.05	1	U	L.RQITG
7519	805.4183	1608.8220	1608.8147	4.51	2	(36)	0.0052	1	U	L.RQITG
8248	874.4428	1746.8711	1746.8649	3.55	1	26	0.059	1	U	L.SNPFL
8580	916.4871	1830.9572	1830.9588	-0.86	1	(44)	0.00079	1	U	F.NVGLV
8581	916.4871	1830.9597	1830.9588	0.48	1	103	9.2e-10	1	U	F.NVGLV
8582	916.4872	1830.9599	1830.9588	0.62	1	(92)	1.3e-08	1	U	F.NVGLV
8584	916.9792	1831.9438	1831.9428	0.56	1	(38)	0.0034	1	U	F.NVGLV
8657	927.9488	1853.8831	1853.8829	0.13	1	(75)	7.2e-07	1	U	Y.KQAVV
8658	927.9515	1853.8885	1853.8829	3.03	1	(77)	5.2e-07	1	U	Y.KQAVV
8714	935.9456	1869.8767	1869.8778	-0.61	1	81	1.8e-07	1	U	Y.KQAVV
8715	935.9495	1869.8844	1869.8778	3.50	1	(77)	4.5e-07	1	U	Y.KQAVV
8716	935.9668	1869.9190	1869.9180	0.54	1	(70)	2e-06	1	U	L.ANEVT
8717	935.9691	1869.9237	1869.9180	3.03	1	(65)	6.2e-06	1	U	L.ANEVT
8720	936.4600	1870.9054	1870.9020	1.78	1	(66)	4.5e-06	1	U	L.ANEVT
8721	936.4604	1870.9062	1870.9020	2.24	1	76	5e-07	1	U	L.ANEVT

8842	956.9357	1911.8569	1911.8558	0.57	1	71	1.4e-06	1	U	Y.SNGYR
8843	956.9387	1911.8629	1911.8558	3.70	1	(53)	0.00011	1	U	Y.SNGYR
8846	957.4304	1912.8463	1912.8398	3.38	1	(40)	0.0015	1	U	Y.SNGYR
8847	957.4342	1912.8538	1912.8398	7.33	1	(45)	0.00054	1	U	Y.SNGYR

2. [2::sp|POA9P0|DLDH_ECOLI](#) Mass: 50942 Score: 1436 Matches: 99(84) Sequences:
 Dihydrolipoyl dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=lpdA PE=1 S
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
543	416.1975	830.3805	830.3810	-0.67	0	24	0.025	1	U	Y.TEPEV
544	416.1979	830.3811	830.3810	0.15	0	(21)	0.045	1	U	Y.TEPEV
570	417.2127	832.4108	832.4113	-0.59	1	(27)	0.035	1	U	Y.NTLGG
571	417.2131	832.4116	832.4113	0.42	1	28	0.028	1	U	Y.NTLGG
737	426.2002	850.3858	850.3861	-0.42	0	34	0.0044	1	U	Y.ETATF
738	426.2002	850.3859	850.3861	-0.25	0	(31)	0.0088	1	U	Y.ETATF
838	435.7560	869.4975	869.4970	0.49	0	24	0.016	1	U	L.KEVPE
848	436.2719	870.5293	870.5287	0.67	0	27	0.0083	3	U	F.IRVDK
849	436.2719	870.5293	870.5287	0.74	0	(25)	0.013	3	U	F.IRVDK
1423	473.2760	944.5374	944.5365	0.94	1	20	0.11	1	U	L.LVMGG
1690	486.2978	970.5810	970.5811	-0.07	0	26	0.011	1	U	W.KEKVI
2533	529.7866	1057.5586	1057.5590	-0.41	0	31	0.012	1	U	L.NVGC
2534	529.7871	1057.5597	1057.5590	0.63	0	(27)	0.029	1	U	L.NVGC
3070	556.8192	1111.6239	1111.6237	0.16	1	23	0.036	1	U	L.ELKEV
3392	570.7664	1139.5183	1139.5169	1.23	0	(21)	0.11	1	U	L.GSQID
3393	570.7665	1139.5185	1139.5169	1.44	0	28	0.023	1	U	L.GSQID
3699	388.2045	1161.5918	1161.5931	-1.13	0	(26)	0.056	1	U	F.IPHED
3700	388.2047	1161.5921	1161.5931	-0.82	0	28	0.033	1	U	F.IPHED
3822	586.3285	1170.6424	1170.6431	-0.54	1	47	0.00027	1	U	L.NVGC
3823	586.3285	1170.6425	1170.6431	-0.44	1	(43)	0.00052	1	U	L.NVGC
3888	589.8247	1177.6347	1177.6343	0.40	1	(46)	0.00034	1	U	L.GLETV
3889	589.8259	1177.6372	1177.6343	2.47	1	53	6.7e-05	1	U	L.GLETV
4316	608.8607	1215.7068	1215.7075	-0.57	0	36	0.0015	1	U	M.STEIK
4317	608.8611	1215.7076	1215.7075	0.12	0	(34)	0.0024	1	U	M.STEIK
4561	619.3720	1236.7295	1236.7302	-0.62	0	55	5.9e-06	1	U	L.VAIGR
4564	619.3734	1236.7323	1236.7302	1.64	0	(41)	0.00015	1	U	L.VAIGR
4576	619.8646	1237.7146	1237.7142	0.26	0	(46)	8.1e-05	1	U	L.VAIGR
4577	413.5790	1237.7152	1237.7142	0.77	0	(22)	0.019	1	U	L.VAIGR
4578	619.8660	1237.7174	1237.7142	2.54	0	(52)	1.9e-05	1	U	L.VAIGR
4683	625.3459	1248.6772	1248.6754	1.45	1	38	0.0021	1	U	Y.FDPKV
4685	625.3466	1248.6786	1248.6754	2.53	1	(38)	0.0019	1	U	Y.FDPKV
5268	436.5938	1306.7597	1306.7608	-0.89	0	(21)	0.022	1	U	L.HVAKV
5269	436.5942	1306.7608	1306.7608	-0.04	0	(25)	0.0085	1	U	L.HVAKV
5270	436.5944	1306.7615	1306.7608	0.52	0	27	0.0062	1	U	L.HVAKV
5915	461.5770	1381.7093	1381.7089	0.29	0	(23)	0.082	1	U	L.TEKEA
5916	691.8632	1381.7119	1381.7089	2.19	0	24	0.057	1	U	L.TEKEA
6076	704.3112	1406.6079	1406.6057	1.52	0	(32)	0.0072	1	U	L.AIEMG
6077	704.3119	1406.6092	1406.6057	2.48	0	44	0.00051	1	U	L.AIEMG
6178	474.2881	1419.8424	1419.8449	-1.74	1	(30)	0.0017	1	U	L.LHVAK
6179	474.2888	1419.8446	1419.8449	-0.20	1	(42)	8.7e-05	1	U	L.LHVAK
6180	710.9313	1419.8481	1419.8449	2.27	1	(35)	0.0005	1	U	L.LHVAK
6181	710.9320	1419.8493	1419.8449	3.13	1	44	6.2e-05	1	U	L.LHVAK

6204	712.3099	1422.6053	1422.6007	3.28	0	(20)	0.1	1	U	L.AIEMG
6303	479.2316	1434.6729	1434.6739	-0.73	0	(34)	0.0082	1	U	L.DAGKA
6304	479.2321	1434.6746	1434.6739	0.48	0	(21)	0.18	1	U	L.DAGKA
6305	479.2323	1434.6752	1434.6739	0.86	0	(21)	0.18	1	U	L.DAGKA
6307	718.3457	1434.6768	1434.6739	2.03	0	59	2.6e-05	1	U	L.DAGKA
6308	718.3461	1434.6776	1434.6739	2.55	0	(55)	6.4e-05	1	U	L.DAGKA
6309	718.3466	1434.6786	1434.6739	3.23	0	(32)	0.014	1	U	L.DAGKA
6310	718.3562	1434.6978	1434.6991	-0.85	0	54	0.00011	1	U	L.EVEGE
6311	718.3586	1434.7027	1434.6991	2.55	0	(48)	0.00038	1	U	L.EVEGE
6312	718.8496	1435.6847	1435.6831	1.11	0	(50)	0.00023	1	U	L.EVEGE
6313	718.8498	1435.6850	1435.6831	1.36	0	(37)	0.0045	1	U	L.EVEGE
6384	723.3584	1444.7022	1444.7021	0.13	1	(24)	0.082	1	U	Y.HALGS
6385	723.3604	1444.7063	1444.7021	2.91	1	(20)	0.21	1	U	Y.HALGS
6524	731.3555	1460.6964	1460.6970	-0.40	1	70	2.2e-06	1	U	Y.HALGS
6525	731.3557	1460.6969	1460.6970	-0.07	1	(58)	3.7e-05	1	U	Y.HALGS
6526	731.3562	1460.6978	1460.6970	0.60	1	(21)	0.18	1	U	Y.HALGS
6527	731.3566	1460.6987	1460.6970	1.19	1	(22)	0.14	1	U	Y.HALGS
6528	731.3580	1460.7014	1460.6970	3.02	1	(21)	0.16	1	U	Y.HALGS
6856	504.6036	1510.7891	1510.7892	-0.09	1	39	0.002	1	U	L.TIHAH
6986	764.8750	1527.7354	1527.7313	2.70	1	(36)	0.005	1	U	L.VMGGG
6987	764.8756	1527.7367	1527.7313	3.50	1	36	0.0042	1	U	L.VMGGG
7203	779.9157	1557.8167	1557.8151	1.06	0	(50)	0.00018	1	U	F.GEPKT
7205	779.9171	1557.8197	1557.8151	2.94	0	70	1.6e-06	1	U	F.GEPKT
7665	821.4158	1640.8170	1640.8154	0.98	2	(46)	0.00052	1	U	L.LVMGG
7666	821.4177	1640.8208	1640.8154	3.28	2	58	3.7e-05	1	U	L.LVMGG
7735	551.3016	1650.8829	1650.8828	0.04	1	(28)	0.017	1	U	W.VGLTE
7736	551.3026	1650.8860	1650.8828	1.93	1	(22)	0.077	1	U	W.VGLTE
7737	826.4504	1650.8862	1650.8828	2.06	1	(40)	0.0011	1	U	W.VGLTE
7738	826.4504	1650.8863	1650.8828	2.13	1	48	0.00019	1	U	W.VGLTE
7785	829.4611	1656.9076	1656.9087	-0.67	0	(37)	0.0024	1	U	F.DQVIP
7786	829.4615	1656.9085	1656.9087	-0.08	0	(36)	0.003	1	U	F.DQVIP
7787	553.3107	1656.9104	1656.9087	1.02	0	(23)	0.06	1	U	F.DQVIP
7788	829.4625	1656.9105	1656.9087	1.09	0	62	8.5e-06	1	U	F.DQVIP
7791	553.3117	1656.9133	1656.9087	2.79	0	(28)	0.02	1	U	F.DQVIP
7792	553.3118	1656.9137	1656.9087	3.01	0	(32)	0.0069	1	U	F.DQVIP
7793	829.4642	1656.9138	1656.9087	3.09	0	(52)	7.9e-05	1	U	F.DQVIP
7931	841.9650	1681.9155	1681.9151	0.22	0	62	5.1e-06	1	U	F.DNAII
7932	841.9666	1681.9187	1681.9151	2.10	0	(59)	1.1e-05	1	U	F.DNAII
7934	841.9697	1681.9248	1681.9151	5.74	0	(30)	0.0075	1	U	F.DNAII
8039	568.9642	1703.8709	1703.8665	2.59	0	(44)	0.00079	1	U	Y.VTMEG
8105	574.2941	1719.8606	1719.8614	-0.47	0	(45)	0.0009	1	U	Y.VTMEG
8106	574.2941	1719.8606	1719.8614	-0.47	0	55	8.4e-05	1	U	Y.VTMEG
8107	860.9385	1719.8625	1719.8614	0.67	0	(40)	0.0027	1	U	Y.VTMEG
8110	860.9387	1719.8629	1719.8614	0.88	0	(35)	0.0089	1	U	Y.VTMEG
8444	598.6454	1792.9143	1792.9142	0.10	2	(32)	0.013	1	U	F.RCADL
8445	897.4649	1792.9152	1792.9142	0.61	2	(40)	0.0022	1	U	F.RCADL
8446	598.6469	1792.9189	1792.9142	2.65	2	(43)	0.001	1	U	F.RCADL
8448	897.4674	1792.9203	1792.9142	3.41	2	49	0.00024	1	U	F.RCADL
8802	632.9943	1895.9610	1895.9550	3.14	1	23	0.1	1	U	L.MLETK
9066	665.0004	1991.9795	1991.9800	-0.27	1	(38)	0.0043	1	U	F.TGANT
9067	665.0005	1991.9796	1991.9800	-0.18	1	(42)	0.0018	1	U	F.TGANT
9068	996.9978	1991.9810	1991.9800	0.53	1	(52)	0.00017	1	U	F.TGANT
9069	996.9979	1991.9813	1991.9800	0.65	1	(52)	0.00015	1	U	F.TGANT
9072	997.4899	1992.9653	1992.9640	0.65	1	(75)	7.8e-07	1	U	F.TGANT
9073	997.4926	1992.9705	1992.9640	3.28	1	76	6e-07	1	U	F.TGANT
9074	665.3321	1992.9744	1992.9640	5.24	1	(33)	0.014	1	U	F.TGANT
9345	714.0347	2139.0824	2139.0769	2.55	2	27	0.038	1	U	F.NLMLE

3. [2::sp|P0ABB4|ATPB_ECOLI](#) Mass: 50351 Score: 1301 Matches: 85(71) Sequences:
 ATP synthase subunit beta OS=Escherichia coli (strain K12) OX=83333 GN=atpD PE=1 SV=
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
126	387.7269	773.4392	773.4395	-0.36	0	29	0.012	1	U	L.SRQIA
127	387.7273	773.4401	773.4395	0.75	0	(29)	0.013	1	U	L.SRQIA
545	416.2031	830.3917	830.3923	-0.68	0	33	0.0039	1	U	L.VVGQE
546	416.2033	830.3921	830.3923	-0.25	0	(22)	0.051	1	U	L.VVGQE
901	438.7687	875.5229	875.5229	-0.02	1	29	0.005	1	U	F.AKGGK
1231	463.7182	925.4218	925.4215	0.32	0	21	0.11	1	U	F.KGIME
1319	469.2319	936.4493	936.4487	0.62	0	(24)	0.072	1	U	L.GRMPS
1492	477.2300	952.4455	952.4436	1.91	0	(24)	0.059	1	U	L.GRMPS
1493	477.2303	952.4460	952.4436	2.50	0	33	0.0077	1	U	L.GRMPS
1520	478.7272	955.4398	955.4399	-0.10	0	25	0.033	1	U	Y.DHLPE
1531	478.7743	955.5341	955.5338	0.26	1	39	0.00075	1	U	L.VLEVQ
1532	478.7748	955.5350	955.5338	1.22	1	(35)	0.002	1	U	L.VLEVQ
1558	480.2491	958.4836	958.4832	0.43	0	24	0.049	1	U	F.RDEGR
1869	494.2888	986.5630	986.5648	-1.86	0	(27)	0.024	1	U	L.ETGIK
1870	494.2896	986.5646	986.5648	-0.20	0	33	0.0059	1	U	L.ETGIK
2130	507.2523	1012.4901	1012.4899	0.16	1	42	0.0008	1	U	L.TGLTM
2131	507.2528	1012.4910	1012.4899	1.07	1	(40)	0.0012	1	U	L.TGLTM
2557	530.2939	1058.5733	1058.5720	1.25	0	23	0.071	1	U	Y.DTARG
2635	533.7714	1065.5283	1065.5277	0.54	1	(25)	0.058	1	U	L.LGRMP
2636	533.7717	1065.5289	1065.5277	1.12	1	35	0.0057	1	U	L.LGRMP
2673	537.8063	1073.5981	1073.5968	1.21	2	44	0.00051	1	U	Y.TLAGT
2943	550.8310	1099.6474	1099.6489	-1.31	1	58	1.2e-05	1	U	L.LETGI
2944	550.8320	1099.6495	1099.6489	0.58	1	(43)	0.00034	1	U	L.LETGI
3144	560.2595	1118.5045	1118.5033	1.09	1	(23)	0.058	1	U	Y.DHLPE
3145	560.2596	1118.5047	1118.5033	1.31	1	25	0.038	1	U	Y.DHLPE
3337	568.3264	1134.6383	1134.6397	-1.25	1	39	0.0012	1	U	Y.VSLKD
3338	568.3267	1134.6389	1134.6397	-0.72	1	(33)	0.0045	1	U	Y.VSLKD
3605	578.3532	1154.6919	1154.6910	0.72	1	(29)	0.0065	1	U	Y.QELKD
3606	578.3543	1154.6941	1154.6910	2.62	1	44	0.00018	1	U	Y.QELKD
3608	578.7861	1155.5577	1155.5560	1.44	1	(32)	0.0099	1	U	L.DPLVV
3609	578.7862	1155.5578	1155.5560	1.54	1	44	0.00062	1	U	L.DPLVV
4246	606.7935	1211.5724	1211.5717	0.56	0	(23)	0.079	1	U	Y.GQMNE
4247	606.7936	1211.5727	1211.5717	0.86	0	(25)	0.053	1	U	Y.GQMNE
4248	606.7939	1211.5733	1211.5717	1.37	0	(31)	0.012	1	U	Y.GQMNE
4249	606.7952	1211.5759	1211.5717	3.48	0	(21)	0.13	1	U	Y.GQMNE
4440	614.7906	1227.5666	1227.5666	0.02	0	37	0.0029	1	U	Y.GQMNE
4441	614.7913	1227.5680	1227.5666	1.11	0	(35)	0.0047	1	U	Y.GQMNE
4442	614.7927	1227.5709	1227.5666	3.49	0	(31)	0.012	1	U	Y.GQMNE
4820	633.2819	1264.5493	1264.5493	0.01	1	(59)	1.3e-05	1	U	L.GMDEL
4821	633.2823	1264.5500	1264.5493	0.60	1	(45)	0.00041	1	U	L.GMDEL
4913	424.8949	1271.6628	1271.6622	0.46	0	(30)	0.018	1	U	L.IRNIA
4914	636.8394	1271.6643	1271.6622	1.64	0	(36)	0.0039	1	U	L.IRNIA
4915	424.8954	1271.6645	1271.6622	1.83	0	(34)	0.0072	1	U	L.IRNIA
4916	636.8403	1271.6660	1271.6622	2.98	0	41	0.0015	1	U	L.IRNIA
5008	641.2796	1280.5446	1280.5442	0.36	1	(59)	1.1e-05	1	U	L.GMDEL
5009	641.2802	1280.5459	1280.5442	1.31	1	60	9.6e-06	1	U	L.GMDEL
5706	679.3391	1356.6637	1356.6633	0.25	1	(52)	0.0001	1	U	Y.DALEV
5707	679.3409	1356.6673	1356.6633	2.95	1	(51)	0.00012	1	U	Y.DALEV

5713	679.8301	1357.6457	1357.6473	-1.19	1	52	9.5e-05	1	U	Y.DALEV
5714	679.8308	1357.6471	1357.6473	-0.20	1	(39)	0.0022	1	U	Y.DALEV
5897	690.3364	1378.6582	1378.6585	-0.22	0	(43)	0.0013	1	U	F.GGAGV
5898	690.3381	1378.6616	1378.6585	2.26	0	(51)	0.00018	1	U	F.GGAGV
5992	698.3347	1394.6548	1394.6534	0.98	0	(56)	6e-05	1	U	F.GGAGV
5993	698.3362	1394.6578	1394.6534	3.16	0	58	3.6e-05	1	U	F.GGAGV
7069	769.8827	1537.7508	1537.7520	-0.79	1	(39)	0.0034	1	U	L.ETGIK
7070	769.8830	1537.7514	1537.7520	-0.39	1	39	0.0033	1	U	L.ETGIK
7135	773.8680	1545.7215	1545.7199	1.06	1	35	0.0054	1	U	Y.VPADD
7136	773.8696	1545.7247	1545.7199	3.11	1	(22)	0.12	1	U	Y.VPADD
7291	785.4145	1568.8144	1568.8158	-0.88	2	62	8.8e-06	1	U	Y.DALEV
7292	785.4167	1568.8189	1568.8158	2.00	2	(55)	5.1e-05	1	U	Y.DALEV
7300	785.9105	1569.8064	1569.7998	4.17	2	(52)	0.0001	1	U	Y.DALEV
7301	785.9106	1569.8066	1569.7998	4.32	2	(45)	0.00061	1	U	Y.DALEV
7382	529.9278	1586.7616	1586.7610	0.35	0	(27)	0.04	1	U	Y.HEMTD
7384	794.3892	1586.7638	1586.7610	1.73	0	(34)	0.0083	1	U	Y.HEMTD
7385	794.3898	1586.7651	1586.7610	2.58	0	(42)	0.0012	1	U	Y.HEMTD
7461	535.2600	1602.7580	1602.7559	1.30	0	(21)	0.16	1	U	Y.HEMTD
7462	802.3867	1602.7588	1602.7559	1.77	0	43	0.0011	1	U	Y.HEMTD
7463	802.3880	1602.7614	1602.7559	3.44	0	(42)	0.0013	1	U	Y.HEMTD
7626	408.7310	1630.8947	1630.8963	-0.99	0	(36)	0.003	1	U	Y.MVGS
7627	408.7311	1630.8955	1630.8963	-0.55	0	(34)	0.0045	1	U	Y.MVGS
7696	412.7301	1646.8914	1646.8913	0.09	0	(24)	0.064	1	U	Y.MVGS
7698	549.9719	1646.8938	1646.8913	1.51	0	(45)	0.0004	1	U	Y.MVGS
7699	824.4543	1646.8941	1646.8913	1.75	0	52	9.1e-05	1	U	Y.MVGS
8177	866.4518	1730.8891	1730.8839	3.01	1	(58)	3.6e-05	1	U	L.GIYPA
8178	866.4523	1730.8900	1730.8839	3.51	1	59	2.6e-05	1	U	L.GIYPA
8699	622.6372	1864.8896	1864.8877	1.04	1	(22)	0.15	1	U	Y.HEMTD
8700	933.4522	1864.8899	1864.8877	1.17	1	(25)	0.09	1	U	Y.HEMTD
8702	933.4543	1864.8941	1864.8877	3.47	1	34	0.011	1	U	Y.HEMTD
8973	654.0299	1959.0677	1959.0677	0.02	1	68	1.6e-06	1	U	L.DVKDL
8974	980.5413	1959.0680	1959.0677	0.14	1	(55)	3.8e-05	1	U	L.DVKDL
8975	654.0314	1959.0725	1959.0677	2.44	1	(58)	1.7e-05	1	U	L.DVKDL
8976	980.5457	1959.0769	1959.0677	4.70	1	(40)	0.001	1	U	L.DVKDL
9813	669.8239	2675.2665	2675.2683	-0.66	1	(21)	0.15	1	U	L.GRIMN
9814	892.7634	2675.2685	2675.2683	0.06	1	(45)	0.00065	1	U	L.GRIMN
9815	892.7645	2675.2718	2675.2683	1.29	1	46	0.00057	1	U	L.GRIMN

4. [2::sp|P0A850|TIG_ECOLI](#) Mass: 48163 Score: 1173 Matches: 67(58) Sequences: 2

Trigger factor OS=Escherichia coli (strain K12) OX=833333 GN=tig PE=1 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
1054	452.2505	902.4865	902.4861	0.38	1	21	0.13	2	U	L.ELPR
1395	472.7622	943.5098	943.5087	1.18	0	25	0.043	1	U	Y.GASV
1396	472.7624	943.5102	943.5087	1.62	0	(21)	0.11	1	U	Y.GASV
1574	481.2273	960.4400	960.4400	-0.05	0	(42)	0.0007	1	U	F.GVED
1575	481.2276	960.4406	960.4400	0.66	0	50	0.00013	1	U	F.GVED
1592	482.2112	962.4078	962.4127	-5.10	1	(22)	0.058	1	U	F.NELM
1593	482.2246	962.4345	962.4127	22.7	1	23	0.076	1	U	F.NELM
1698	486.7376	971.4606	971.4600	0.62	2	(42)	0.0007	1	U	Y.KLGE
1699	486.7376	971.4607	971.4600	0.74	2	42	0.00062	1	U	Y.KLGE
2990	553.2737	1104.5329	1104.5339	-0.87	0	38	0.0032	1	U	Y.EDPK
2991	553.2738	1104.5330	1104.5339	-0.76	0	(27)	0.037	1	U	Y.EDPK

<u>3457</u>	572.3214	1142.6283	1142.6295	-1.09	1	33	0.0068	1	U	L.LGEV
<u>3458</u>	572.3231	1142.6316	1142.6295	1.79	1	(28)	0.018	1	U	L.LGEV
<u>3475</u>	572.8198	1143.6251	1143.6248	0.29	0	34	0.0058	1	U	L.KADE
<u>3476</u>	572.8199	1143.6253	1143.6248	0.52	0	(33)	0.0064	1	U	L.KADE
<u>4016</u>	596.7980	1191.5815	1191.5806	0.80	0	(61)	1.7e-05	1	U	-.MQVS
<u>4017</u>	596.7992	1191.5838	1191.5806	2.75	0	62	1.5e-05	1	U	-.MQVS
<u>4208</u>	604.7947	1207.5749	1207.5755	-0.45	0	(33)	0.011	1	U	-.MQVS
<u>4209</u>	604.7949	1207.5752	1207.5755	-0.25	0	(26)	0.049	1	U	-.MQVS
<u>4257</u>	607.2847	1212.5548	1212.5550	-0.21	0	47	0.00027	1	U	F.TIDV
<u>4258</u>	607.2858	1212.5570	1212.5550	1.61	0	(39)	0.0017	1	U	F.TIDV
<u>4457</u>	615.3270	1228.6395	1228.6412	-1.36	1	(36)	0.0045	1	U	Y.GASV
<u>4460</u>	615.3292	1228.6439	1228.6412	2.21	1	44	0.00067	1	U	Y.GASV
<u>4741</u>	628.8638	1255.7131	1255.7136	-0.37	2	(58)	1.3e-05	1	U	L.LLGE
<u>4743</u>	628.8660	1255.7175	1255.7136	3.13	2	60	7.3e-06	1	U	L.LLGE
<u>4763</u>	629.3544	1256.6943	1256.6976	-2.61	2	(40)	0.00099	1	U	L.LLGE
<u>4764</u>	629.3545	1256.6944	1256.6976	-2.51	2	(48)	0.00018	1	U	L.LLGE
<u>4859</u>	634.8054	1267.5962	1267.5972	-0.83	1	43	0.00095	1	U	Y.EDPK
<u>4860</u>	634.8068	1267.5990	1267.5972	1.38	1	(42)	0.0011	1	U	Y.EDPK
<u>4952</u>	638.3265	1274.6385	1274.6394	-0.70	1	(52)	0.00014	1	U	F.EVYP
<u>4953</u>	638.3288	1274.6430	1274.6394	2.85	1	68	3.6e-06	1	U	F.EVYP
<u>5657</u>	451.5853	1351.7340	1351.7347	-0.54	0	(31)	0.0093	1	U	L.AKAK
<u>5658</u>	451.5854	1351.7344	1351.7347	-0.21	0	(20)	0.11	1	U	L.AKAK
<u>5659</u>	676.8748	1351.7351	1351.7347	0.28	0	53	6e-05	1	U	L.AKAK
<u>5660</u>	676.8763	1351.7381	1351.7347	2.53	0	(52)	6e-05	1	U	L.AKAK
<u>8175</u>	866.3717	1730.7288	1730.7272	0.98	1	76	2.4e-07	1	U	F.TGSV
<u>8176</u>	866.3743	1730.7341	1730.7272	4.02	1	(59)	1.3e-05	1	U	F.TGSV
<u>8508</u>	907.5069	1812.9992	1812.9985	0.41	0	(48)	0.00015	1	U	F.IDAI
<u>8511</u>	907.5087	1813.0029	1812.9985	2.43	0	66	2.5e-06	1	U	F.IDAI
<u>8529</u>	909.4856	1816.9566	1816.9570	-0.21	1	(39)	0.0025	1	U	L.KKVE
<u>8533</u>	909.4893	1816.9640	1816.9570	3.82	1	46	0.00042	1	U	L.KKVE
<u>8745</u>	627.6475	1879.9207	1879.9211	-0.17	2	(28)	0.039	1	U	Y.GASV
<u>8746</u>	627.6494	1879.9264	1879.9211	2.85	2	34	0.0096	1	U	Y.GASV
<u>8864</u>	641.3182	1920.9328	1920.9429	-5.26	0	(23)	0.13	1	U	W.KEKD
<u>8866</u>	641.3211	1920.9415	1920.9429	-0.71	0	(30)	0.028	1	U	W.KEKD
<u>8868</u>	641.3217	1920.9433	1920.9429	0.24	0	(22)	0.17	1	U	W.KEKD
<u>8869</u>	641.3218	1920.9435	1920.9429	0.33	0	(30)	0.028	1	U	W.KEKD
<u>8871</u>	641.3219	1920.9439	1920.9429	0.52	0	54	0.0001	1	U	W.KEKD
<u>8875</u>	961.4812	1920.9478	1920.9429	2.59	0	(51)	0.00022	1	U	W.KEKD
<u>8876</u>	641.3234	1920.9483	1920.9429	2.80	0	(23)	0.15	1	U	W.KEKD
<u>9209</u>	1028.0056	2053.9967	2053.9990	-1.11	1	(29)	0.027	1	U	L.KADE
<u>9213</u>	685.6753	2054.0042	2053.9990	2.56	1	(20)	0.23	1	U	L.KADE
<u>9214</u>	1028.0105	2054.0064	2053.9990	3.64	1	30	0.021	1	U	L.KADE
<u>9305</u>	1055.5659	2109.1173	2109.1205	-1.52	1	(27)	0.022	1	U	L.VKAN
<u>9306</u>	1055.5671	2109.1197	2109.1205	-0.37	1	47	0.00024	1	U	L.VKAN
<u>9556</u>	1180.1307	2358.2469	2358.2471	-0.06	1	(46)	0.00034	1	U	F.IDAI
<u>9557</u>	1180.1309	2358.2472	2358.2471	0.04	1	51	0.00011	1	U	F.IDAI
<u>9558</u>	787.0905	2358.2495	2358.2471	1.04	1	(38)	0.0022	1	U	F.IDAI
<u>9559</u>	787.0912	2358.2517	2358.2471	1.98	1	(40)	0.0014	1	U	F.IDAI
<u>9771</u>	873.0989	2616.2750	2616.2728	0.84	1	73	1.2e-06	1	U	L.EAIE
<u>9772</u>	873.0996	2616.2768	2616.2728	1.54	1	(63)	1.2e-05	1	U	L.EAIE
<u>9773</u>	1309.1461	2616.2777	2616.2728	1.87	1	(58)	3.3e-05	1	U	L.EAIE
<u>9774</u>	873.0998	2616.2777	2616.2728	1.88	1	(60)	2.1e-05	1	U	L.EAIE
<u>9775</u>	1309.1464	2616.2782	2616.2728	2.05	1	(61)	1.9e-05	1	U	L.EAIE
<u>9776</u>	1309.1494	2616.2843	2616.2728	4.38	1	(59)	3.1e-05	1	U	L.EAIE
<u>9777</u>	1309.1498	2616.2850	2616.2728	4.67	1	(70)	2e-06	1	U	L.EAIE
<u>9898</u>	948.4475	2842.3205	2842.3145	2.12	1	59	1.8e-05	1	U	W.KEKD

5. [2::sp|P02931|OMP_F_ECOLI](#) Mass: 39309 Score: 990 Matches: 60 (54) Sequences:
 Outer membrane protein F OS=Escherichia coli (strain K12) OX=83333 GN=ompF PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
172	394.1722	786.3299	786.3297	0.35	1	26	0.015	1		F.DYGR
431	409.2119	816.4091	816.4090	0.22	0	(29)	0.018	1	U	Y.GAAD
432	409.2122	816.4099	816.4090	1.20	0	35	0.0043	1	U	Y.GAAD
578	417.7212	833.4278	833.4283	-0.60	2	63	6.2e-06	1		F.GLVD
579	417.7212	833.4278	833.4283	-0.60	2	(46)	0.00034	1		F.GLVD
897	438.7505	875.4865	875.4865	0.08	1	(21)	0.077	1	U	F.GLRP
898	438.7506	875.4867	875.4865	0.21	1	24	0.04	1	U	F.GLRP
962	443.7188	885.4231	885.4232	-0.19	1	51	7.1e-05	1	U	L.KYAD
963	443.7193	885.4240	885.4232	0.85	1	(45)	0.00024	1	U	L.KYAD
1768	489.7719	977.5293	977.5294	-0.12	0	40	0.0013	1	U	F.VGRV
1769	489.7723	977.5300	977.5294	0.57	0	(39)	0.0014	1	U	F.VGRV
2005	500.7400	999.4655	999.4661	-0.64	1	21	0.091	1		L.KYDA
2032	501.2849	1000.5553	1000.5553	0.03	1	34	0.0048	2	U	F.ANKT
2033	501.2855	1000.5564	1000.5553	1.13	1	(32)	0.0084	1	U	F.ANKT
2048	502.7286	1003.4427	1003.4433	-0.57	1	(31)	0.0085	1		Y.FNKN
2049	502.7288	1003.4430	1003.4433	-0.27	1	31	0.0081	1		Y.FNKN
2719	540.2715	1078.5284	1078.5295	-0.98	0	(26)	0.06	1	U	L.VAGT
2720	540.2725	1078.5304	1078.5295	0.84	0	38	0.0032	1	U	L.VAGT
2957	551.7435	1101.4725	1101.4727	-0.16	1	(38)	0.0011	1	U	Y.FSKG
2958	551.7446	1101.4747	1101.4727	1.83	1	(38)	0.0012	1	U	Y.FSKG
2967	552.2357	1102.4569	1102.4567	0.17	1	(44)	0.00027	1	U	Y.FSKG
2968	552.2366	1102.4586	1102.4567	1.72	1	54	2.7e-05	1	U	Y.FSKG
2977	552.7795	1103.5445	1103.5459	-1.20	0	(43)	0.0008	1	U	F.KGET
2978	552.7801	1103.5456	1103.5459	-0.20	0	48	0.00027	1	U	F.KGET
2979	552.7802	1103.5459	1103.5459	0.01	0	(41)	0.0013	1	U	F.KGET
2980	552.7809	1103.5472	1103.5459	1.23	0	(37)	0.0037	1	U	F.KGET
3735	583.2958	1164.5770	1164.5775	-0.41	1	(34)	0.0072	1	U	Y.NKDG
3736	389.1999	1164.5779	1164.5775	0.38	1	(21)	0.16	1	U	Y.NKDG
3737	583.2974	1164.5803	1164.5775	2.41	1	39	0.0026	1	U	Y.NKDG
3928	592.2581	1182.5016	1182.5015	0.02	2	29	0.014	1		Y.YFNK
3929	592.2588	1182.5030	1182.5015	1.26	2	(25)	0.033	1		Y.YFNK
4917	636.8436	1271.6727	1271.6721	0.47	0	(71)	1.3e-06	1	U	Y.IINQ
4918	636.8438	1271.6731	1271.6721	0.76	0	72	9.3e-07	1	U	Y.IINQ
4934	637.3367	1272.6589	1272.6561	2.20	0	(47)	0.00043	1	U	Y.IINQ
6142	708.8035	1415.5924	1415.5915	0.62	1	(56)	2.1e-05	1	U	Y.TDML
6143	708.8048	1415.5951	1415.5915	2.52	1	66	2.1e-06	1	U	Y.TDML
6223	713.3462	1424.6778	1424.6783	-0.35	1	(45)	0.0006	1	U	F.KGET
6225	713.3464	1424.6783	1424.6783	-0.00	1	(46)	0.00048	1	U	F.KGET
6230	713.8400	1425.6655	1425.6623	2.22	1	(44)	0.0008	1	U	F.KGET
6231	713.8401	1425.6656	1425.6623	2.31	1	50	0.00022	1	U	F.KGET
6232	713.8403	1425.6660	1425.6623	2.56	1	(41)	0.0015	1	U	F.KGET
6233	713.8412	1425.6678	1425.6623	3.85	1	(36)	0.0055	1	U	F.KGET
6275	716.8000	1431.5854	1431.5864	-0.70	1	(61)	5.4e-06	1	U	Y.TDML
6276	716.8029	1431.5912	1431.5864	3.31	1	(58)	1.3e-05	1	U	Y.TDML
6685	742.3795	1482.7445	1482.7426	1.24	1	(26)	0.046	1	U	Y.GAAD
6686	742.3797	1482.7448	1482.7426	1.49	1	(27)	0.038	1	U	Y.GAAD
6687	742.3810	1482.7475	1482.7426	3.29	1	(22)	0.11	1	U	Y.GAAD
6688	742.3812	1482.7479	1482.7426	3.55	1	32	0.011	1	U	Y.GAAD
7611	815.3915	1628.7684	1628.7682	0.12	2	64	7.1e-06	1	U	L.GFKG

7612	815.3929	1628.7712	1628.7682	1.84	2	(64)	7.2e-06	1	U	L.GFKG
8683	620.9652	1859.8738	1859.8722	0.88	0	(42)	0.0014	1	U	F.QGNN
8684	620.9661	1859.8764	1859.8722	2.25	0	(34)	0.0092	1	U	F.QGNN
8685	930.9455	1859.8764	1859.8722	2.30	0	(40)	0.0022	1	U	F.QGNN
8686	930.9466	1859.8786	1859.8722	3.48	0	47	0.0004	1	U	F.QGNN
9319	708.0026	2120.9860	2120.9835	1.19	1	(37)	0.005	1	U	Y.NFQG
9320	708.0033	2120.9881	2120.9835	2.15	1	(48)	0.00039	1	U	Y.NFQG
9321	1061.5024	2120.9903	2120.9835	3.22	1	76	5.7e-07	1	U	Y.NFQG
9753	1303.1719	2604.3292	2604.3283	0.35	1	(32)	0.011	1	U	Y.IINQ
9754	869.1200	2604.3382	2604.3283	3.79	1	(24)	0.063	1	U	Y.IINQ
9755	1303.1776	2604.3407	2604.3283	4.75	1	52	9.5e-05	1	U	Y.IINQ

Proteins matching a subset of these peptides:

2::sp P21420 NMPC_ECOLI	Mass: 40277	Score: 84	Matches: 3(2)	Sequences: 2
Putative outer membrane porin protein NmpC OS=Escherichia coli (strain K12) OX=833333 GN=nmnC PE=1 SV=1				
2::sp P76335 YEDS_ECOLI	Mass: 17285	Score: 26	Matches: 1(1)	Sequences: 1
Putative outer membrane protein YedS OS=Escherichia coli (strain K12) OX=833333 GN=yedS PE=1 SV=1				
2::sp P02932 PHOE_ECOLI	Mass: 38898	Score: 21	Matches: 1(0)	Sequences: 1
Outer membrane pore protein E OS=Escherichia coli (strain K12) OX=833333 GN=phoE PE=1 SV=1				

6. [2::sp|P0CE47|EFTU1_ECOLI](#) Mass: 43427 Score: 965 Matches: 59(58) Sequences: 59
Elongation factor Tu 1 OS=Escherichia coli (strain K12) OX=833333 GN=tufA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
197	395.2393	788.4640	788.4644	-0.51	0	22	0.053	1	U	L.TAAI
1420	473.2684	944.5223	944.5219	0.45	1	38	0.0022	1	U	F.LLPI
1421	473.2684	944.5223	944.5219	0.45	1	(36)	0.0033	1	U	F.LLPI
2189	509.7455	1017.4764	1017.4767	-0.29	1	35	0.0047	1	U	L.KALE
2740	541.2718	1080.5291	1080.5274	1.64	0	61	1.3e-05	1	U	L.IHPI
2741	541.2719	1080.5293	1080.5274	1.75	0	(52)	0.00012	1	U	L.IHPI
2912	549.2691	1096.5236	1096.5223	1.24	0	(44)	0.00055	1	U	L.IHPI
2913	549.2698	1096.5250	1096.5223	2.48	0	(39)	0.0019	1	U	L.IHPI
4289	608.3022	1214.5898	1214.5891	0.58	0	48	0.00024	1	U	L.DEGR
4290	608.3036	1214.5927	1214.5891	2.98	0	(42)	0.001	1	U	L.DEGR
4591	414.5047	1240.4924	1240.4931	-0.62	0	(24)	0.021	1	U	Y.AHVD
4593	621.2537	1240.4929	1240.4931	-0.20	0	35	0.0015	1	U	Y.AHVD
4594	621.2546	1240.4946	1240.4931	1.19	0	(27)	0.0098	1	U	Y.AHVD
4651	623.8206	1245.6267	1245.6275	-0.62	1	(56)	5.7e-05	1	U	L.ELVE
4652	623.8226	1245.6306	1245.6275	2.51	1	58	3.1e-05	1	U	L.ELVE
4802	631.8192	1261.6239	1261.6224	1.18	1	(36)	0.0058	1	U	L.ELVE
4803	631.8201	1261.6257	1261.6224	2.64	1	(53)	0.00012	1	U	L.ELVE
5484	664.8436	1327.6727	1327.6732	-0.36	1	35	0.0046	1	U	L.DEGR
5485	664.8437	1327.6728	1327.6732	-0.27	1	58	2.2e-05	1	U	L.LDEG
5486	664.8450	1327.6754	1327.6732	1.66	1	(45)	0.00042	1	U	L.LDEG
5487	664.8453	1327.6761	1327.6732	2.22	1	(34)	0.0063	1	U	L.DEGR
5863	688.3606	1374.7066	1374.7064	0.15	2	(42)	0.0013	1	U	L.ELVE
5864	688.3609	1374.7072	1374.7064	0.59	2	45	0.0006	2	U	L.ELVE
5919	462.2396	1383.6969	1383.6969	-0.03	1	(38)	0.0028	1	U	L.IHPI
5920	462.2398	1383.6974	1383.6969	0.38	1	(38)	0.0025	1	U	L.IHPI
6039	700.8525	1399.6904	1399.6918	-1.01	1	(33)	0.01	1	U	L.IHPI
6040	467.5716	1399.6930	1399.6918	0.87	1	49	0.00021	1	U	L.IHPI
6041	467.5718	1399.6936	1399.6918	1.27	1	(45)	0.00052	1	U	L.IHPI

6042	700.8552	1399.6958	1399.6918	2.82	1	(45)	0.00064	1	U	L.IHPI
6107	706.3852	1410.7558	1410.7507	3.64	0	34	0.0048	1	U	Y.IPEP
6108	706.3862	1410.7579	1410.7507	5.12	0	(30)	0.012	1	U	Y.IPEP
6350	721.3859	1440.7573	1440.7572	0.04	2	44	0.00058	1	U	L.LDEG
6351	721.3868	1440.7591	1440.7572	1.30	2	(40)	0.0016	1	U	L.LDEG
6489	728.8824	1455.7503	1455.7470	2.28	1	(35)	0.0058	1	U	Y.ILSK
6490	728.8827	1455.7508	1455.7470	2.61	1	50	0.00017	1	U	Y.ILSK
6667	740.8177	1479.6208	1479.6221	-0.88	1	32	0.0051	1	U	L.NKCD
6668	740.8190	1479.6235	1479.6221	0.93	1	(31)	0.0066	1	U	L.NKCD
7206	780.3892	1558.7638	1558.7628	0.65	0	(49)	0.00029	1	U	Y.DFPG
7207	780.3892	1558.7639	1558.7628	0.73	0	(63)	9.8e-06	1	U	Y.DFPG
7208	780.3893	1558.7640	1558.7628	0.80	0	(60)	2.3e-05	1	U	Y.DFPG
7209	780.3895	1558.7645	1558.7628	1.12	0	63	9.5e-06	1	U	Y.DFPG
7414	797.3611	1592.7076	1592.7062	0.89	2	61	1.2e-05	1	U	F.LNKC
7415	797.3613	1592.7081	1592.7062	1.20	2	(55)	4.7e-05	1	U	F.LNKC
7515	805.3583	1608.7021	1608.7011	0.63	2	(48)	0.0002	1	U	F.LNKC
7516	805.3602	1608.7058	1608.7011	2.91	2	(51)	0.00011	1	U	F.LNKC
7706	824.9243	1647.8341	1647.8324	1.03	0	(37)	0.0048	1	U	Y.VKNM
7707	824.9258	1647.8370	1647.8324	2.80	0	46	0.00068	1	U	Y.VKNM
7843	832.9213	1663.8281	1663.8273	0.48	0	(37)	0.0049	1	U	Y.VKNM
7844	832.9217	1663.8288	1663.8273	0.91	0	(34)	0.009	1	U	Y.VKNM
8137	575.9920	1724.9542	1724.9533	0.50	2	(32)	0.006	1	U	F.RKLL
8139	863.4848	1724.9550	1724.9533	1.01	2	(34)	0.004	1	U	F.RKLL
8140	863.4854	1724.9561	1724.9533	1.65	2	38	0.0014	1	U	F.RKLL
8381	888.9462	1775.8778	1775.8730	2.70	1	30	0.026	1	U	L.DSYI
8782	630.6593	1888.9561	1888.9570	-0.52	2	(27)	0.042	1	U	F.LDSY
8783	945.4863	1888.9581	1888.9570	0.56	2	29	0.029	1	U	F.LDSY
8784	630.6611	1888.9616	1888.9570	2.39	2	(23)	0.12	1	U	F.LDSY
8785	945.4890	1888.9633	1888.9570	3.34	2	(29)	0.031	1	U	F.LDSY
9971	1098.5492	3292.6257	3292.6241	0.50	0	(37)	0.0032	1	U	F.RTTD
9972	1098.5527	3292.6364	3292.6241	3.72	0	64	5.9e-06	1	U	F.RTTD

Proteins matching the same set of peptides:

[2::sp|P0CE48|EFTU2_ECOLI](#) Mass: 43457 Score: 965 Matches: 59(58) Sequences:
Elongation factor Tu 2 OS=Escherichia coli (strain K12) OX=83333 GN=tufB PE=1 SV=1

7. [2::sp|P0AE06|ACRA_ECOLI](#) Mass: 42228 Score: 932 Matches: 56(49) Sequences:
Multidrug efflux pump subunit AcrA OS=Escherichia coli (strain K12) OX=83333 GN=acrA
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
67	384.1996	766.3847	766.3861	-1.83	0	(23)	0.048	1	U	Y.ISKQ
68	384.2007	766.3869	766.3861	1.09	0	35	0.0032	1	U	Y.ISKQ
167	393.7451	785.4756	785.4759	-0.43	1	20	0.063	1	U	L.RLKQ
342	404.1979	806.3813	806.3810	0.30	0	21	0.11	1		Y.QIDP
1014	450.2871	898.5595	898.5600	-0.47	2	24	0.015	1	U	F.LRLK
1032	451.2404	900.4662	900.4665	-0.29	0	(23)	0.055	1	U	L.VQNG
1033	451.2407	900.4668	900.4665	0.31	0	28	0.015	1	U	L.VQNG
1458	475.7691	949.5236	949.5233	0.40	2	28	0.014	1	U	Y.QKLL
1707	487.2697	972.5247	972.5240	0.78	1	(54)	6.9e-05	1	U	L.KQEL
1708	487.2697	972.5248	972.5240	0.84	1	58	2.3e-05	1	U	L.KQEL
1715	487.7611	973.5076	973.5080	-0.40	1	(27)	0.037	1	U	L.KQEL
1716	487.7617	973.5088	973.5080	0.79	1	(36)	0.0049	1	U	L.KQEL
1717	487.7618	973.5090	973.5080	1.04	1	(30)	0.019	1	U	L.KQEL

<u>1718</u>	487.7627	973.5108	973.5080	2.85	1	(34)	0.0081	1	U	L.KQEL
<u>3102</u>	557.8334	1113.6523	1113.6506	1.55	0	38	0.0014	1	U	L.KAGD
<u>4047</u>	597.8055	1193.5964	1193.5928	3.03	1	33	0.0092	1	U	Y.ISKQ
<u>4048</u>	597.8058	1193.5970	1193.5928	3.55	1	(32)	0.012	1	U	Y.ISKQ
<u>4144</u>	601.8399	1201.6652	1201.6666	-1.13	0	29	0.014	1	U	L.KQEN
<u>4146</u>	601.8412	1201.6678	1201.6666	1.01	0	(26)	0.023	1	U	L.KQEN
<u>4161</u>	602.8067	1203.5988	1203.5983	0.47	0	26	0.051	2	U	F.KEGS
<u>4162</u>	602.8076	1203.6007	1203.5983	2.00	0	(25)	0.062	1	U	F.KEGS
<u>4603</u>	621.8620	1241.7094	1241.7092	0.24	2	32	0.0056	1	U	L.RLKQ
<u>4604</u>	621.8620	1241.7094	1241.7092	0.24	2	(28)	0.013	1	U	L.RLKQ
<u>4621</u>	622.3556	1242.6967	1242.6932	2.89	2	(26)	0.027	1	U	L.RLKQ
<u>5787</u>	684.3378	1366.6610	1366.6616	-0.45	1	52	0.00012	1	U	F.KEGS
<u>5789</u>	684.3397	1366.6649	1366.6616	2.40	1	(43)	0.001	1	U	F.KEGS
<u>5790</u>	684.3398	1366.6650	1366.6616	2.49	1	(26)	0.052	1	U	F.KEGS
<u>5791</u>	684.3398	1366.6651	1366.6616	2.58	1	(39)	0.0029	1	U	F.KEGS
<u>5792</u>	684.3402	1366.6659	1366.6616	3.12	1	(23)	0.11	1	U	F.KEGS
<u>6315</u>	718.8732	1435.7319	1435.7307	0.84	0	45	0.00068	1	U	L.QITT
<u>6316</u>	718.8748	1435.7350	1435.7307	2.97	0	(25)	0.058	1	U	L.QITT
<u>6749</u>	746.3887	1490.7628	1490.7617	0.74	0	(49)	0.00031	1	U	L.ITSD
<u>6750</u>	746.3906	1490.7667	1490.7617	3.37	0	(41)	0.0018	1	U	L.ITSD
<u>6751</u>	746.3907	1490.7668	1490.7617	3.45	0	64	8.6e-06	1	U	L.ITSD
<u>6752</u>	746.3911	1490.7677	1490.7617	4.01	0	(60)	2.2e-05	1	U	L.ITSD
<u>7158</u>	775.9729	1549.9312	1549.9304	0.55	0	30	0.0012	1	U	Y.RIAE
<u>7161</u>	775.9737	1549.9329	1549.9304	1.65	0	(22)	0.0067	1	U	Y.RIAE
<u>8336</u>	884.4429	1766.8712	1766.8727	-0.85	1	(53)	0.0001	1	U	L.ITSD
<u>8337</u>	884.4436	1766.8726	1766.8727	-0.03	1	62	1.3e-05	1	U	L.ITSD
<u>8613</u>	614.6500	1840.9281	1840.9294	-0.75	1	(26)	0.051	1	U	L.RAIF
<u>8615</u>	921.4727	1840.9309	1840.9294	0.79	1	44	0.00068	1	U	L.RAIF
<u>8616</u>	921.4755	1840.9364	1840.9294	3.77	1	(41)	0.0015	1	U	L.RAIF
<u>8671</u>	928.4979	1854.9812	1854.9799	0.69	1	62	8.1e-06	1	U	Y.DSAK
<u>8673</u>	928.5005	1854.9864	1854.9799	3.53	1	(60)	1.5e-05	1	U	Y.DSAK
<u>9475</u>	1120.5386	2239.0626	2239.0645	-0.85	2	(56)	5.3e-05	1		L.ATVQ
<u>9476</u>	1120.5430	2239.0714	2239.0645	3.08	2	92	1.5e-08	1		L.ATVQ
<u>9667</u>	818.7718	2453.2935	2453.2914	0.86	0	(44)	0.00047	1	U	L.VVGA
<u>9668</u>	818.7720	2453.2943	2453.2914	1.15	0	(44)	0.00057	1	U	L.VVGA
<u>9669</u>	1227.6545	2453.2945	2453.2914	1.26	0	53	6.7e-05	1	U	L.VVGA
<u>9670</u>	1227.6567	2453.2989	2453.2914	3.05	0	(37)	0.0025	1	U	L.VVGA
<u>9671</u>	614.5783	2454.2841	2454.2755	3.54	0	(21)	0.11	1	U	L.VVGA
<u>9672</u>	614.5784	2454.2844	2454.2755	3.64	0	(22)	0.088	1	U	L.VVGA
<u>9673</u>	819.1021	2454.2845	2454.2755	3.69	0	(40)	0.0014	1	U	L.VVGA
<u>9674</u>	819.1028	2454.2865	2454.2755	4.51	0	(45)	0.00044	1	U	L.VVGA
<u>9965</u>	1048.1896	3141.5469	3141.5435	1.09	1	60	1.9e-05	1	U	L.ALTG
<u>9966</u>	1048.1926	3141.5561	3141.5435	4.00	1	(44)	0.00075	1	U	L.ALTG

8. [1::sp|cRAP022|P00766|CTRA_BOVIN](#) Mass: 26220 Score: 932 Matches: 70 (60) Seq

Chymotrypsinogen A OS=Bos taurus PE=1 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
<u>472</u>	412.7284	823.4422	823.4440	-2.10	1	(22)	0.044	1	U	L.KLST
<u>474</u>	412.7293	823.4440	823.4440	0.07	1	55	2e-05	1	U	L.KLST
<u>475</u>	412.7293	823.4441	823.4440	0.14	1	(48)	9.9e-05	1	U	L.KLST
<u>476</u>	412.7300	823.4454	823.4440	1.77	1	(28)	0.011	1	U	L.KLST
<u>882</u>	437.7552	873.4958	873.4960	-0.22	1	47	0.0003	1	U	W.TLVG

883	437.7552	873.4959	873.4960	-0.08	1	(33)	0.0066	1	U	W.TLVG
1583	481.7476	961.4807	961.4804	0.34	0	(24)	0.076	1	U	L.VCKK
1584	481.7478	961.4810	961.4804	0.71	0	(20)	0.16	1	U	L.VCKK
1594	482.2392	962.4638	962.4644	-0.61	0	29	0.019	1	U	L.VCKK
1595	482.2394	962.4641	962.4644	-0.23	0	(28)	0.022	1	U	L.VCKK
1876	494.7587	987.5028	987.5025	0.24	1	34	0.0055	1	U	L.VNWW
1877	494.7591	987.5036	987.5025	1.03	1	(24)	0.065	1	U	L.VNWW
2026	501.2546	1000.4946	1000.4938	0.85	0	(27)	0.027	1	U	Y.TNAN
2027	501.2548	1000.4950	1000.4938	1.21	0	(30)	0.013	1	U	Y.TNAN
2037	501.7452	1001.4758	1001.4778	-1.96	0	(29)	0.015	1	U	Y.TNAN
2038	501.7454	1001.4763	1001.4778	-1.48	0	37	0.0023	1	U	Y.TNAN
2172	508.7848	1015.5551	1015.5550	0.12	1	(47)	0.00032	1	U	L.TINN
2173	508.7851	1015.5556	1015.5550	0.60	1	53	6.7e-05	1	U	L.TINN
2174	508.7851	1015.5556	1015.5550	0.68	1	(35)	0.0042	1	U	L.TINN
2175	508.7852	1015.5558	1015.5550	0.85	1	(26)	0.032	1	U	L.TINN
2176	508.7852	1015.5559	1015.5550	0.91	1	(27)	0.03	1	U	L.TINN
2177	508.7854	1015.5562	1015.5550	1.21	1	(41)	0.001	1	U	L.TINN
2178	508.7854	1015.5563	1015.5550	1.33	1	(32)	0.0079	1	U	L.TINN
2318	515.2953	1028.5760	1028.5767	-0.66	1	31	0.0085	1	U	Y.ARVTF
2319	515.2953	1028.5760	1028.5767	-0.66	1	(22)	0.062	1	U	Y.ARVTF
3174	561.7931	1121.5716	1121.5717	-0.07	1	(44)	0.00079	1	U	W.QVSL
3175	561.7931	1121.5717	1121.5717	0.04	1	67	4.1e-06	1	U	W.QVSL
3177	561.7935	1121.5724	1121.5717	0.59	1	(36)	0.0047	1	U	W.QVSL
3179	561.7936	1121.5727	1121.5717	0.92	1	(38)	0.0032	1	U	W.QVSL
3183	561.7940	1121.5735	1121.5717	1.58	1	(33)	0.0097	1	U	W.QVSL
3184	561.7942	1121.5738	1121.5717	1.90	1	(48)	0.0003	1	U	W.QVSL
3187	561.7944	1121.5742	1121.5717	2.22	1	(49)	0.00026	1	U	W.QVSL
3188	561.7944	1121.5743	1121.5717	2.32	1	(64)	7.2e-06	1	U	W.QVSL
3189	561.7944	1121.5743	1121.5717	2.32	1	(42)	0.0012	1	U	W.QVSL
3252	564.2779	1126.5412	1126.5441	-2.52	1	23	0.084	1	U	L.LSNT
3522	575.2533	1148.4920	1148.4921	-0.00	1	39	0.0011	1	U	F.CGGS
3523	575.2536	1148.4926	1148.4921	0.52	1	(37)	0.0017	1	U	F.CGGS
4105	600.7768	1199.5390	1199.5393	-0.25	1	22	0.081	1	U	L.SNTN
5209	652.2776	1302.5407	1302.5398	0.71	0	27	0.012	1	U	W.GSST
5210	652.2790	1302.5435	1302.5398	2.86	0	(23)	0.032	1	U	W.GSST
5302	655.8601	1309.7057	1309.7064	-0.57	1	(20)	0.1	1	U	-.CGVP
5303	655.8626	1309.7107	1309.7064	3.24	1	33	0.005	1	U	-.CGVP
5383	660.3434	1318.6723	1318.6728	-0.39	0	(53)	0.00011	1	U	F.DQGS
5388	440.5653	1318.6742	1318.6728	1.03	0	(26)	0.054	1	U	F.DQGS
5389	660.3448	1318.6750	1318.6728	1.66	0	(52)	0.00012	1	U	F.DQGS
5391	660.3458	1318.6770	1318.6728	3.13	0	58	3.3e-05	1	U	F.DQGS
5392	660.3459	1318.6772	1318.6728	3.33	0	(47)	0.0004	1	U	F.DQGS
5393	660.3461	1318.6777	1318.6728	3.69	0	(37)	0.0041	1	U	F.DQGS
5405	440.8912	1319.6519	1319.6568	-3.75	0	(28)	0.038	1	U	F.DQGS
5406	440.8925	1319.6556	1319.6568	-0.91	0	(22)	0.14	1	U	F.DQGS
5407	660.8357	1319.6568	1319.6568	-0.01	0	(38)	0.0037	1	U	F.DQGS
5408	660.8357	1319.6569	1319.6568	0.08	0	(42)	0.0012	1	U	F.DQGS
5501	665.8642	1329.7138	1329.7140	-0.09	2	(57)	3.2e-05	1	U	Y.NSLT
5503	665.8657	1329.7168	1329.7140	2.10	2	79	1.7e-07	1	U	Y.NSLT
6283	717.3172	1432.6198	1432.6194	0.32	2	49	0.00013	1	U	F.HFCG
6285	717.3187	1432.6229	1432.6194	2.46	2	(38)	0.0019	1	U	F.HFCG
7947	842.3804	1682.7463	1682.7458	0.31	0	62	9.4e-06	1	U	F.SQTV
7949	842.3821	1682.7496	1682.7458	2.27	0	(52)	0.00011	1	U	F.SQTV
8194	869.9560	1737.8974	1737.9009	-2.02	1	(29)	0.021	1	U	Y.TNAN
8196	869.9578	1737.9011	1737.9009	0.09	1	(44)	0.00062	1	U	Y.TNAN
8198	869.9582	1737.9018	1737.9009	0.51	1	(22)	0.1	1	U	Y.TNAN
8200	869.9601	1737.9056	1737.9009	2.69	1	50	0.00015	1	U	Y.TNAN

8205	870.4543	1738.8940	1738.8849	5.21	1	(35)	0.0053	1	U	Y.TNAN
8206	870.4568	1738.8990	1738.8849	8.10	1	(33)	0.0076	1	U	Y.TNAN
8403	892.4426	1782.8707	1782.8689	1.00	0	(37)	0.0046	1	U	L.SRIV
8404	892.4450	1782.8755	1782.8689	3.67	0	50	0.00023	1	U	L.SRIV
8645	926.5021	1850.9896	1850.9850	2.49	2	42	0.0007	1	U	Y.TNAN
8647	926.5037	1850.9928	1850.9850	4.20	2	(32)	0.0065	1	U	Y.TNAN
9135	1009.9976	2017.9806	2017.9780	1.30	0	(41)	0.0017	1	U	W.VVTA
9136	1009.9980	2017.9814	2017.9780	1.72	0	46	0.00051	1	U	W.VVTA

Proteins matching a subset of these peptides:

[1::sp|cRAP023|P00767|CTRB_BOVIN](#) Mass: 26309 Score: 79 Matches: 4(3) Sequences:
 Chymotrypsinogen B OS=Bos taurus PE=1 SV=1

9. [2::sp|P0A6F3|GLPK_ECOLI](#) Mass: 56480 Score: 750 Matches: 44(38) Sequences:
 Glycerol kinase OS=Escherichia coli (strain K12) OX=833333 GN=glpK PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
19	380.7189	759.4232	759.4239	-0.84	0	42	0.00074	1	U	Y.IRSNT
22	380.7195	759.4245	759.4239	0.84	0	(38)	0.0021	1	U	Y.IRSNT
312	402.2369	802.4593	802.4589	0.45	1	24	0.043	1	U	Y.VVPAF
313	402.2370	802.4594	802.4589	0.60	1	(21)	0.085	1	U	Y.VVPAF
778	432.2076	862.4007	862.4007	-0.05	0	35	0.0052	1	U	F.MAGAS
779	432.2076	862.4007	862.4007	-0.05	0	(24)	0.066	1	U	F.MAGAS
1485	476.7661	951.5176	951.5178	-0.21	1	44	0.00028	1	U	Y.FSGTK
1486	476.7669	951.5193	951.5178	1.60	1	(43)	0.00038	1	U	Y.FSGTK
1962	498.2447	994.4749	994.4720	2.95	1	(28)	0.031	1	U	L.KRDGL
1963	498.2448	994.4751	994.4720	3.13	1	29	0.021	1	U	L.KRDGL
2507	528.7709	1055.5273	1055.5070	19.3	1	21	0.089	1	U	Y.TNASR
2618	532.7839	1063.5532	1063.5549	-1.65	0	(21)	0.15	1	U	W.EKETG
2619	532.7839	1063.5533	1063.5549	-1.52	0	27	0.036	1	U	W.EKETG
3148	560.2816	1118.5486	1118.5469	1.51	0	(29)	0.024	1	U	L.RVDGG
3149	560.2825	1118.5505	1118.5469	3.25	0	40	0.0018	1	U	L.RVDGG
3996	595.7955	1189.5764	1189.5761	0.25	0	46	0.00058	1	U	L.EAMQA
3997	595.7955	1189.5765	1189.5761	0.35	0	(37)	0.0045	1	U	L.EAMQA
4051	597.8093	1193.6041	1193.6040	0.05	0	43	0.0011	1	U	F.ATKVQ
4052	597.8095	1193.6045	1193.6040	0.35	0	(38)	0.0032	1	U	F.ATKVQ
4187	603.7930	1205.5714	1205.5710	0.31	0	(44)	0.00078	1	U	L.EAMQA
4188	603.7938	1205.5731	1205.5710	1.72	0	(41)	0.0018	1	U	L.EAMQA
4991	640.2970	1278.5794	1278.5802	-0.59	2	32	0.012	1	U	L.DWDDK
4992	640.2993	1278.5841	1278.5802	3.04	2	(25)	0.054	1	U	L.DWDDK
5350	658.8043	1315.5941	1315.5900	3.08	0	24	0.055	1	U	L.CVKEG
5540	445.8933	1334.6580	1334.6579	0.12	0	(34)	0.0094	1	U	F.RPGIE
5541	445.8935	1334.6586	1334.6579	0.59	0	35	0.0075	1	U	F.RPGIE
5542	668.3374	1334.6602	1334.6579	1.80	0	(28)	0.04	1	U	F.RPGIE
5544	668.3384	1334.6622	1334.6579	3.26	0	(34)	0.0096	1	U	F.RPGIE
5573	671.3434	1340.6723	1340.6725	-0.11	1	(40)	0.0015	1	U	Y.FATKV
5574	671.3442	1340.6738	1340.6725	1.00	1	(24)	0.059	1	U	Y.FATKV
5576	671.8357	1341.6569	1341.6565	0.35	1	49	0.00026	1	U	Y.FATKV
5577	671.8386	1341.6626	1341.6565	4.54	1	(33)	0.0086	1	U	Y.FATKV
5612	674.3687	1346.7229	1346.7194	2.57	1	26	0.043	1	U	Y.IRSNT
5613	674.3687	1346.7229	1346.7194	2.57	1	(25)	0.049	1	U	Y.IRSNT
5910	691.8171	1381.6197	1381.6184	0.97	0	(57)	2.9e-05	1	U	L.TTIAC
5911	691.8184	1381.6222	1381.6184	2.73	0	58	2.9e-05	1	U	L.TTIAC

6777	748.8760	1495.7374	1495.7340	2.25	2	24	0.091	1	U	W.LRDEM
7496	803.9115	1605.8084	1605.8032	3.27	1	(35)	0.0085	1	U	L.MNTGE
7498	803.9117	1605.8088	1605.8032	3.50	1	36	0.0066	1	U	L.MNTGE
8977	981.0034	1959.9922	1959.9901	1.04	2	76	6.7e-07	1	U	W.QNLDE
8978	654.3390	1959.9951	1959.9901	2.56	2	(38)	0.0038	1	U	W.QNLDE
8979	654.3391	1959.9953	1959.9901	2.65	2	(49)	0.00033	1	U	W.QNLDE
8980	981.0070	1959.9995	1959.9901	4.78	2	(46)	0.00067	1	U	W.QNLDE
9706	827.4485	2479.3236	2479.3143	3.77	0	50	8.4e-05	1	U	Y.GQTNI

10. [2::sp|P0ABBO|ATPA_ECOLI](#) Mass: 55416 Score: 732 Matches: 38(33) Sequences:
 ATP synthase subunit alpha OS=Escherichia coli (strain K12) OX=83333 GN=atpA PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
139	390.2181	778.4215	778.4225	-1.22	1	35	0.0031	1	U	L.KGIL
140	390.2181	778.4217	778.4225	-1.07	1	(33)	0.0044	1	U	L.KGIL
1176	459.2322	916.4499	916.4502	-0.31	0	34	0.0061	1	U	Y.NDEI
1177	459.2324	916.4502	916.4502	0.02	0	(27)	0.028	1	U	Y.NDEI
2272	513.7640	1025.5135	1025.5142	-0.63	0	23	0.06	1	U	L.DHGQ
3377	570.3077	1138.6009	1138.5982	2.36	1	(25)	0.031	1	U	L.DHGQ
3378	570.3082	1138.6019	1138.5982	3.23	1	27	0.019	1	U	L.DHGQ
3615	578.7904	1155.5663	1155.5673	-0.86	1	28	0.023	1	U	L.AYVD
3616	578.7910	1155.5675	1155.5673	0.20	1	(22)	0.097	1	U	L.AYVD
4172	602.8483	1203.6820	1203.6823	-0.26	0	(37)	0.0018	1	U	F.TKGE
4174	602.8497	1203.6848	1203.6823	2.07	0	49	0.00011	1	U	F.TKGE
4921	636.8682	1271.7219	1271.7197	1.70	0	38	0.0014	1	U	L.IIGD
4923	636.8691	1271.7236	1271.7197	3.04	0	(33)	0.0042	1	U	L.IIGD
4984	639.8507	1277.6869	1277.6867	0.13	2	(62)	7.6e-06	1	U	Y.LADV
4985	639.8511	1277.6876	1277.6867	0.69	2	68	2e-06	1	U	Y.LADV
5514	666.8415	1331.6685	1331.6681	0.34	1	61	1.6e-05	1	U	F.ASDL
5517	666.8436	1331.6726	1331.6681	3.38	1	(53)	0.0001	1	U	F.ASDL
6766	748.3628	1494.7111	1494.7103	0.55	1	(52)	0.00016	1	U	L.GAPI
6768	748.3633	1494.7121	1494.7103	1.20	1	56	5.5e-05	1	U	L.GAPI
6795	749.8929	1497.7713	1497.7715	-0.10	2	(32)	0.0094	1	U	L.IIYD
6796	749.8957	1497.7768	1497.7715	3.57	2	37	0.0031	1	U	L.IIYD
6829	752.4066	1502.7987	1502.7981	0.40	0	(20)	0.15	1	U	F.VPTN
6830	752.4080	1502.8015	1502.7981	2.27	0	24	0.066	1	U	F.VPTN
7493	803.8981	1605.7816	1605.7821	-0.31	1	(59)	3.3e-05	1	U	L.NLER
7494	803.9004	1605.7863	1605.7821	2.65	1	63	1.3e-05	1	U	L.NLER
7577	811.8957	1621.7768	1621.7770	-0.11	1	(47)	0.00055	1	U	L.NLER
7578	811.8981	1621.7817	1621.7770	2.90	1	(47)	0.00048	1	U	L.NLER
7836	555.2811	1662.8214	1662.8213	0.06	2	(27)	0.048	1	U	F.RDRG
7837	832.4196	1662.8246	1662.8213	1.97	2	(24)	0.097	1	U	F.RDRG
7838	555.2825	1662.8256	1662.8213	2.58	2	29	0.029	1	U	F.RDRG
8007	847.9195	1693.8244	1693.8271	-1.59	2	26	0.06	1	U	F.SQFA
9168	1019.9731	2037.9317	2037.9313	0.21	1	99	2.8e-09	1	U	L.MQEI
9169	1019.9749	2037.9353	2037.9313	1.94	1	(77)	3.9e-07	1	U	L.MQEI
9207	1027.9700	2053.9254	2053.9262	-0.41	1	(85)	5e-08	1	U	L.MQEI
9208	1027.9705	2053.9264	2053.9262	0.07	1	(76)	4.7e-07	1	U	L.MQEI
9715	1257.6453	2513.2760	2513.2762	-0.09	0	(34)	0.0062	1	U	F.SAVE
9716	838.7667	2513.2782	2513.2762	0.78	0	(34)	0.0062	1	U	F.SAVE
9717	838.7672	2513.2798	2513.2762	1.44	0	38	0.0026	1	U	F.SAVE

11. [2::sp|P0A6P9|ENO_ECOLI](#) Mass: 45683 Score: 723 Matches: 34(31) Sequences: 1

Enolase OS=Escherichia coli (strain K12) OX=83333 GN=eno PE=1 SV=2

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
968	444.7556	887.4965	887.4964	0.18	1	40	0.0013	1	U	Y.ELGK
969	444.7557	887.4968	887.4964	0.48	1	(38)	0.0021	1	U	Y.ELGK
2059	503.2715	1004.5284	1004.5291	-0.67	1	51	0.00014	1	U	Y.VLAG
2060	503.2724	1004.5302	1004.5291	1.10	1	(43)	0.00085	1	U	Y.VLAG
2676	538.2858	1074.5570	1074.5557	1.20	1	(49)	0.00023	1	U	F.NQIG
2677	538.2859	1074.5573	1074.5557	1.54	1	61	1.5e-05	1	U	F.NQIG
2939	550.8130	1099.6115	1099.6098	1.62	0	37	0.0026	1	U	Y.NGRK
2940	550.8132	1099.6118	1099.6098	1.83	0	(35)	0.0042	1	U	Y.NGRK
2955	551.3027	1100.5908	1100.5938	-2.72	0	(23)	0.064	1	U	Y.NGRK
2956	551.3033	1100.5921	1100.5938	-1.50	0	(29)	0.019	1	U	Y.NGRK
3588	385.5340	1153.5803	1153.5801	0.13	0	(22)	0.093	1	U	L.AAIK
3589	385.5344	1153.5815	1153.5801	1.22	0	24	0.061	1	U	L.AAIK
3703	581.8278	1161.6410	1161.6393	1.40	0	(84)	4.4e-08	1	U	L.AVIA
3704	581.8281	1161.6416	1161.6393	1.92	0	86	2.9e-08	1	U	L.AVIA
5390	660.3458	1318.6770	1318.6769	0.06	2	(39)	0.0024	1	U	L.GDKI
5394	660.3473	1318.6800	1318.6769	2.38	2	40	0.002	1	U	L.GDKI
6248	715.3563	1428.6980	1428.6885	6.64	1	31	0.014	1	U	Y.EHIA
6721	744.9073	1487.8001	1487.7983	1.22	1	(37)	0.0041	1	U	L.IRIE
6722	744.9081	1487.8016	1487.7983	2.20	1	45	0.00057	1	U	L.IRIE
6723	496.9412	1487.8017	1487.7983	2.23	1	(37)	0.0036	1	U	L.IRIE
6724	496.9412	1487.8017	1487.7983	2.23	1	(27)	0.035	1	U	L.IRIE
6866	505.2365	1512.6878	1512.6879	-0.04	0	(38)	0.003	1	U	L.KAKG
6867	757.3517	1512.6888	1512.6879	0.63	0	(63)	9.5e-06	1	U	L.KAKG
6868	505.2372	1512.6897	1512.6879	1.23	0	(42)	0.0012	1	U	L.KAKG
6869	757.3533	1512.6921	1512.6879	2.81	0	70	1.8e-06	1	U	L.KAKG
7704	824.9021	1647.7896	1647.7886	0.62	0	(35)	0.0078	1	U	F.VGMA
7705	824.9044	1647.7943	1647.7886	3.44	0	54	8.6e-05	1	U	F.VGMA
8617	615.3346	1842.9819	1842.9839	-1.06	2	69	2.1e-06	1	U	Y.NQLI
8618	922.4988	1842.9831	1842.9839	-0.42	2	(46)	0.00038	1	U	Y.NQLI
8619	922.4992	1842.9839	1842.9839	-0.02	2	(54)	5.7e-05	1	U	Y.NQLI
8620	615.3364	1842.9875	1842.9839	1.93	2	(50)	0.00014	1	U	Y.NQLI
8769	943.9299	1885.8452	1885.8438	0.76	2	51	0.00015	1	U	Y.ELGK
8770	943.9301	1885.8455	1885.8438	0.95	2	(42)	0.0011	1	U	Y.ELGK
9274	1048.0018	2093.9891	2093.9793	4.67	1	65	7.8e-06	1	U	L.TKQY

12. [2::sp|P00350|6PGD_ECOLI](#) Mass: 51563 Score: 705 Matches: 32(30) Sequences: 1

6-phosphogluconate dehydrogenase, decarboxylating OS=Escherichia coli (strain K12) OX=83333 GN=6pgd PE=1 SV=2

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
159	393.7048	785.3950	785.3959	-1.15	1	(23)	0.033	1	U	Y.YTVKE
160	393.7051	785.3955	785.3959	-0.51	1	24	0.029	1	U	Y.YTVKE
983	448.2422	894.4699	894.4698	0.04	1	(27)	0.024	1	U	L.SLITE
984	448.2423	894.4699	894.4698	0.11	1	27	0.022	1	U	L.SLITE
1225	462.7848	923.5551	923.5552	-0.15	0	30	0.0021	1	U	Y.RAAVL
1472	476.2614	950.5082	950.5073	0.98	1	27	0.019	1	U	F.LQKIT
1473	476.2615	950.5084	950.5073	1.17	1	(25)	0.026	1	U	F.LQKIT
1992	500.2423	998.4701	998.4709	-0.83	1	(47)	0.00021	1	U	Y.FKQIA
1993	500.2430	998.4715	998.4709	0.57	1	49	0.00012	1	U	Y.FKQIA

2230	511.7668	1021.5189	1021.5192	-0.27	1	39	0.003	1	U	L.ALNIE
2232	511.7672	1021.5199	1021.5192	0.69	1	(34)	0.0077	1	U	L.ALNIE
2377	520.7615	1039.5084	1039.5087	-0.28	1	41	0.001	1	U	L.IQAQR
2378	520.7617	1039.5089	1039.5087	0.20	1	(38)	0.0023	1	U	L.IQAQR
2700	539.3128	1076.6111	1076.6118	-0.64	1	45	0.0003	1	U	Y.LIDIT
2701	539.3143	1076.6140	1076.6118	2.07	1	(38)	0.0011	1	U	Y.LIDIT
2750	541.7963	1081.5780	1081.5767	1.14	1	36	0.0021	1	U	Y.AENPO
5025	642.3237	1282.6328	1282.6445	-9.12	2	20	0.16	1	U	W.DLNYG
5092	646.8289	1291.6432	1291.6408	1.83	1	(29)	0.027	1	U	F.KQIAD
5093	646.8296	1291.6446	1291.6408	2.96	1	45	0.00063	1	U	F.KQIAD
6080	704.3401	1406.6657	1406.6678	-1.45	1	43	0.0012	1	U	F.NFIGT
6652	739.3791	1476.7437	1476.7460	-1.55	1	74	9.5e-07	1	U	Y.LDKGD
6653	739.3805	1476.7464	1476.7460	0.27	1	(66)	5.8e-06	1	U	Y.LDKGD
6658	493.5818	1477.7235	1477.7235	-0.03	0	(33)	0.013	1	U	L.KGPSI
6659	493.5822	1477.7247	1477.7235	0.82	0	34	0.01	1	U	L.KGPSI
6660	739.8697	1477.7248	1477.7235	0.90	0	(24)	0.11	1	U	L.KGPSI
8566	610.3307	1827.9702	1827.9731	-1.54	2	(29)	0.018	1	U	Y.LVDVI
8567	914.9937	1827.9729	1827.9731	-0.10	2	69	2.1e-06	1	U	Y.LVDVI
8568	914.9945	1827.9743	1827.9731	0.71	2	(58)	2.2e-05	1	U	Y.LVDVI
8569	610.3333	1827.9781	1827.9731	2.76	2	(44)	0.00054	1	U	Y.LVDVI
9904	951.1363	2850.3870	2850.3858	0.43	2	(45)	0.00072	1	U	F.NFIGT
9909	956.4706	2866.3899	2866.3807	3.21	2	(61)	1.6e-05	1	U	F.NFIGT
9910	956.4711	2866.3914	2866.3807	3.72	2	108	2.8e-10	1	U	F.NFIGT

13. [2::sp|P0A6H5|HSLU_ECOLI](#) Mass: 49677 Score: 701 Matches: 35(30) Sequences:
 ATP-dependent protease ATPase subunit HslU OS=Escherichia coli (strain K12) OX=83333
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
553	416.2398	830.4650	830.4650	-0.00	1	52	8e-05	1	U	L.AKLAN
554	416.2400	830.4654	830.4650	0.50	1	(48)	0.0002	1	U	L.AKLAN
1046	451.7449	901.4752	901.4756	-0.47	0	32	0.011	1	U	L.IEEEE
1047	451.7449	901.4753	901.4756	-0.34	0	(25)	0.051	1	U	L.IEEEE
1309	468.2812	934.5479	934.5488	-0.86	0	(36)	0.0007	1	U	F.IKVEA
1310	468.2816	934.5486	934.5488	-0.20	0	41	0.00025	1	U	F.IKVEA
1588	481.7887	961.5628	961.5630	-0.22	0	25	0.017	1	U	L.KIKDA
1589	481.7894	961.5642	961.5630	1.23	0	(23)	0.029	1	U	L.KIKDA
2166	508.2878	1014.5611	1014.5597	1.37	1	64	5.4e-06	1	U	L.LIEEE
2167	508.2879	1014.5612	1014.5597	1.49	1	(47)	0.00026	1	U	L.LIEEE
2742	541.2800	1080.5455	1080.5451	0.35	1	(21)	0.13	1	U	L.TTSDF
2744	541.2814	1080.5482	1080.5451	2.83	1	25	0.051	1	U	L.TTSDF
3041	555.7605	1109.5064	1109.5063	0.13	0	(29)	0.021	1	U	L.MATEG
3043	555.7611	1109.5077	1109.5063	1.23	0	(22)	0.095	1	U	L.MATEG
3228	563.7577	1125.5008	1125.5012	-0.35	0	32	0.0077	1	U	L.MATEG
3229	563.7592	1125.5038	1125.5012	2.26	0	(25)	0.04	1	U	L.MATEG
3771	585.2801	1168.5456	1168.5434	1.92	1	(27)	0.031	1	U	L.ERLME
3772	585.2802	1168.5459	1168.5434	2.13	1	36	0.004	1	U	L.ERLME
3941	593.2786	1184.5427	1184.5383	3.72	1	(22)	0.09	1	U	L.ERLME
4067	598.7768	1195.5390	1195.5357	2.79	0	20	0.15	1	U	L.SQONI
4365	611.8025	1221.5904	1221.5877	2.21	0	25	0.067	1	U	L.TEPNA
5488	664.8622	1327.7099	1327.7095	0.31	1	40	0.0013	1	U	Y.RAEEL
5489	664.8641	1327.7136	1327.7095	3.07	1	(39)	0.0019	1	U	Y.RAEEL
5589	448.5895	1342.7467	1342.7456	0.81	0	28	0.02	1	U	Y.VGKEV
5632	675.8319	1349.6491	1349.6463	2.11	2	50	0.00022	1	U	L.DALVA

5633	675.8319	1349.6493	1349.6463	2.20	2	(36)	0.0057	1	U	L.DALVA
6070	703.8438	1405.6731	1405.6759	-2.00	0	47	0.00053	1	U	M.SEMTP
6071	703.8468	1405.6790	1405.6759	2.26	0	(41)	0.002	1	U	M.SEMTP
7867	835.4314	1668.8482	1668.8471	0.67	0	59	2.4e-05	1	U	L.KQDAI
7868	835.4315	1668.8484	1668.8471	0.74	0	(53)	0.0001	1	U	L.KQDAI
7888	836.9269	1671.8392	1671.8315	4.60	1	48	0.00033	1	U	L.REGQL
8021	849.3768	1696.7391	1696.7428	-2.17	1	47	0.00023	1	U	Y.DASDL
8022	849.3792	1696.7439	1696.7428	0.64	1	(31)	0.0096	1	U	Y.DASDL
8181	867.4584	1732.9023	1732.8995	1.61	1	(27)	0.037	1	U	F.ERILT
8182	867.4592	1732.9039	1732.8995	2.52	1	31	0.016	1	U	F.ERILT

14. [2::sp|P0A8M0|SYN_ECOLI](#) Mass: 52766 Score: 624 Matches: 31(29) Sequences: 1
 Asparagine--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=asnS PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
204	396.2240	790.4335	790.4337	-0.28	2	(25)	0.034	1	U	F.GLGFE
205	396.2240	790.4335	790.4337	-0.28	2	27	0.024	1	U	F.GLGFE
1003	449.7657	897.5168	897.5172	-0.43	0	43	0.00023	1	U	M.SVVPV
1004	449.7657	897.5169	897.5172	-0.29	0	(32)	0.0029	1	U	M.SVVPV
1301	468.2310	934.4474	934.4470	0.40	1	(33)	0.0089	1	U	W.MLEPE
1302	468.2310	934.4475	934.4470	0.53	1	(30)	0.017	1	U	W.MLEPE
1465	476.2276	950.4406	950.4419	-1.33	1	37	0.0028	1	U	W.MLEPE
1466	476.2284	950.4422	950.4419	0.27	1	(32)	0.0088	1	U	W.MLEPE
2270	513.7475	1025.4804	1025.4818	-1.31	1	29	0.02	1	U	L.ERFIE
2271	513.7483	1025.4821	1025.4818	0.34	1	(29)	0.02	1	U	L.ERFIE
3759	584.7787	1167.5428	1167.5408	1.75	1	(30)	0.016	1	U	L.TVSGQ
3760	584.7794	1167.5443	1167.5408	3.00	1	49	0.00022	1	U	L.TVSGQ
3783	585.7692	1169.5239	1169.5241	-0.13	1	33	0.007	1	U	F.IEADF
3784	585.7703	1169.5260	1169.5241	1.63	1	(27)	0.029	1	U	F.IEADF
5077	646.2999	1290.5853	1290.5840	0.99	1	66	4.3e-06	1	U	W.GVDLS
5078	646.3013	1290.5881	1290.5840	3.16	1	(55)	5.6e-05	1	U	W.GVDLS
5273	654.8381	1307.6617	1307.6609	0.61	1	27	0.042	1	U	F.AQVDY
5357	658.8455	1315.6765	1315.6772	-0.54	0	(68)	3.8e-06	1	U	F.EIQAS
5358	658.8480	1315.6814	1315.6772	3.17	0	69	2.6e-06	1	U	F.EIQAS
5479	664.7871	1327.5595	1327.5602	-0.49	0	(38)	0.0012	1	U	L.ITASD
5592	672.7847	1343.5549	1343.5551	-0.15	0	(42)	0.00037	1	U	L.ITASD
5593	672.7851	1343.5556	1343.5551	0.40	0	43	0.00031	1	U	L.ITASD
5723	679.8724	1357.7303	1357.7314	-0.76	0	38	0.0026	1	U	F.AERVD
5725	679.8731	1357.7317	1357.7314	0.23	0	(28)	0.022	1	U	F.AERVD
6138	708.3632	1414.7119	1414.7126	-0.48	2	32	0.011	1	U	F.ANLND
6139	708.3650	1414.7154	1414.7126	2.02	2	(32)	0.013	1	U	F.ANLND
7250	784.3953	1566.7761	1566.7712	3.14	1	(48)	0.00034	1	U	F.KAVLE
7251	784.3966	1566.7785	1566.7712	4.71	1	65	6.4e-06	1	U	F.KAVLE
8079	572.2873	1713.8402	1713.8396	0.37	2	(23)	0.12	1	U	F.KAVLE
8080	857.9311	1713.8476	1713.8396	4.69	2	44	0.00082	1	U	F.KAVLE
8299	880.4371	1758.8596	1758.8537	3.37	1	25	0.071	1	U	L.DLENL

15. [2::sp|P0AFG6|ODO2_ECOLI](#) Mass: 43984 Score: 512 Matches: 30(28) Sequences: 1
 Dihydropolyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
418	408.2653	814.5160	814.5164	-0.44	1	34	0.0012	1	U	F.LVTIK
419	408.2654	814.5162	814.5164	-0.22	1	(31)	0.0028	1	U	F.LVTIK
528	414.7629	827.5111	827.5116	-0.60	0	(46)	0.00015	1	U	Y.VKAVV
529	414.7631	827.5116	827.5116	-0.09	0	52	3.1e-05	1	U	Y.VKAVV
649	422.2326	842.4507	842.4498	1.14	1	(27)	0.019	1	U	L.LEDPT
650	422.2328	842.4510	842.4498	1.42	1	27	0.019	1	U	L.LEDPT
1777	490.7395	979.4645	979.4644	0.09	0	23	0.094	1	U	L.EAKNS
1920	496.2939	990.5733	990.5750	-1.71	1	33	0.004	1	U	F.YVKAV
1921	496.2948	990.5750	990.5750	0.08	1	(31)	0.0041	1	U	F.YVKAV
2461	526.7484	1051.4823	1051.4822	0.04	1	58	2.5e-05	1	U	L.TVEDL
2462	526.7488	1051.4831	1051.4822	0.86	1	(48)	0.00025	1	U	L.TVEDL
2874	547.2815	1092.5484	1092.5485	-0.04	1	34	0.0075	1	U	L.LEAKN
2875	547.2819	1092.5493	1092.5485	0.74	1	(32)	0.012	1	U	L.LEAKN
4433	614.3508	1226.6871	1226.6871	0.03	1	(31)	0.007	1	U	L.VTPVL
4434	614.3525	1226.6904	1226.6871	2.72	1	43	0.00053	1	U	L.VTPVL
5179	434.5772	1300.7098	1300.7099	-0.09	0	(29)	0.02	1	U	L.DASAI
5180	434.5774	1300.7103	1300.7099	0.33	0	(27)	0.03	1	U	L.DASAI
5182	651.3640	1300.7133	1300.7099	2.64	0	(52)	0.0001	1	U	L.DASAI
5184	651.3646	1300.7147	1300.7099	3.67	0	56	3.5e-05	1	U	L.DASAI
5212	652.3225	1302.6303	1302.6312	-0.63	0	66	5.4e-06	1	U	F.NEVNM
5213	652.3247	1302.6347	1302.6312	2.75	0	(65)	6.5e-06	1	U	F.NEVNM
5380	660.3188	1318.6230	1318.6261	-2.32	0	(53)	0.00011	1	U	F.NEVNM
5381	660.3200	1318.6255	1318.6261	-0.47	0	(52)	0.00012	1	U	F.NEVNM
5534	668.3185	1334.6224	1334.6210	1.05	0	(40)	0.0018	1	U	F.NEVNM
5535	668.3202	1334.6258	1334.6210	3.62	0	(47)	0.00042	1	U	F.NEVNM
6789	749.4031	1496.7916	1496.7908	0.51	0	26	0.035	1	U	L.MSTPI
8268	877.9721	1753.9297	1753.9284	0.72	1	(24)	0.055	1	U	F.GSLMS
8269	877.9746	1753.9345	1753.9284	3.50	1	30	0.013	1	U	F.GSLMS
8931	970.4768	1938.9389	1938.9323	3.42	0	39	0.0031	1	U	L.KRYPE
8932	970.4780	1938.9414	1938.9323	4.68	0	(25)	0.075	1	U	L.KRYPE

16. [2::sp|P0A7D4|PURA_ECOLI](#) Mass: 47543 Score: 459 Matches: 27(21) Sequences:
 Adenylosuccinate synthetase OS=Escherichia coli (strain K12) OX=83333 GN=purA PE=1 S
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
1040	451.2712	900.5279	900.5280	-0.10	1	23	0.039	2	U	L.DGLK
1041	451.2714	900.5282	900.5280	0.17	1	(23)	0.044	1	U	L.DGLK
1702	486.7900	971.5654	971.5651	0.28	0	(21)	0.073	1	U	L.VING
1703	486.7902	971.5658	971.5651	0.71	0	32	0.0052	1	U	L.VING
1961	498.2338	994.4530	994.4542	-1.17	1	27	0.03	1	U	F.LCKQ
4449	614.8596	1227.7046	1227.7074	-2.34	2	41	0.00061	1	U	L.DVLD
4452	614.8611	1227.7077	1227.7074	0.25	2	(25)	0.025	1	U	L.DVLD
4582	620.3201	1238.6256	1238.6216	3.20	1	(23)	0.091	1	U	F.AEKL
4583	620.3202	1238.6259	1238.6216	3.49	1	(29)	0.021	1	U	F.AEKL
4613	622.3472	1242.6799	1242.6820	-1.65	1	23	0.063	1	U	W.GDEG
4728	628.3152	1254.6159	1254.6165	-0.48	1	31	0.015	1	U	F.AEKL
5457	442.8944	1325.6614	1325.6616	-0.13	2	25	0.061	1	U	L.RVGD
5458	442.8945	1325.6618	1325.6616	0.14	2	(21)	0.13	1	U	L.RVGD
6596	735.9177	1469.8208	1469.8202	0.39	0	(47)	0.00021	1	U	L.RENV
6597	735.9194	1469.8242	1469.8202	2.72	0	(51)	7.5e-05	1	U	L.RENV
6601	736.4089	1470.8033	1470.8042	-0.59	0	(53)	6.3e-05	1	U	L.RENV
6603	736.4116	1470.8086	1470.8042	2.97	0	58	1.8e-05	1	U	L.RENV

6665	740.3667	1478.7188	1478.7213	-1.66	0	56	7e-05	1	U	Y.VTSS
6666	740.3677	1478.7209	1478.7213	-0.25	0	(43)	0.0012	1	U	Y.VTSS
6839	753.8718	1505.7291	1505.7224	4.43	1	(21)	0.19	1	U	W.KGVE
6919	761.8657	1521.7168	1521.7174	-0.39	1	(37)	0.0049	1	U	W.KGVE
6920	761.8661	1521.7177	1521.7174	0.25	1	38	0.0033	1	U	W.KGVE
7021	766.4058	1530.7971	1530.7963	0.49	1	(33)	0.011	2	U	Y.QKVL
7149	774.4028	1546.7910	1546.7913	-0.18	1	56	6.5e-05	1	U	Y.QKVL
7150	774.4034	1546.7922	1546.7913	0.61	1	(33)	0.011	1	U	Y.QKVL
9244	1037.4797	2072.9449	2072.9401	2.32	2	(47)	0.00033	1	U	W.KGVE
9245	1037.4808	2072.9471	2072.9401	3.38	2	51	0.00012	1	U	W.KGVE

17. [2::sp|P0A6P1|EFTS_ECOLI](#) Mass: 30518 Score: 437 Matches: 20(20) Sequences:
Elongation factor Ts OS=Escherichia coli (strain K12) OX=83333 GN=tsf PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3333	568.2858	1134.5570	1134.5557	1.11	1	45	0.00062	1	U	F.TGEVS
3334	568.2862	1134.5578	1134.5557	1.85	1	(43)	0.0011	1	U	F.TGEVS
4166	602.8166	1203.6186	1203.6169	1.41	0	(27)	0.039	1	U	F.VMEPS
4167	602.8176	1203.6206	1203.6169	3.04	0	32	0.013	1	U	F.VMEPS
5181	651.3627	1300.7108	1300.7061	3.63	1	36	0.0034	1	U	F.VMEPS
5183	651.3642	1300.7138	1300.7061	5.98	1	(30)	0.014	1	U	F.VMEPS
5395	660.3516	1318.6887	1318.6881	0.46	1	48	0.0003	1	U	L.KAQFE
5396	440.5702	1318.6888	1318.6881	0.57	1	(45)	0.00059	1	U	L.KAQFE
5397	440.5703	1318.6891	1318.6881	0.78	1	(30)	0.019	1	U	L.KAQFE
5398	660.3536	1318.6926	1318.6881	3.43	1	(45)	0.00057	1	U	L.KAQFE
6043	700.8842	1399.7539	1399.7559	-1.41	0	(53)	6.2e-05	1	U	L.DAAVA
6044	700.8872	1399.7599	1399.7559	2.86	0	60	1.3e-05	1	U	L.DAAVA
6434	726.3483	1450.6821	1450.6828	-0.45	0	(56)	7e-05	1	U	F.EVGEG
6435	726.3484	1450.6822	1450.6828	-0.36	0	60	2.5e-05	1	U	F.EVGEG
8710	623.3196	1866.9369	1866.9363	0.31	1	(49)	0.00031	1	U	F.IRFEV
8711	623.3210	1866.9411	1866.9363	2.56	1	54	8.6e-05	1	U	F.IRFEV
8893	643.0290	1926.0653	1926.0674	-1.05	1	(39)	0.001	1	U	F.ADKVL
8894	643.0295	1926.0668	1926.0674	-0.29	1	(33)	0.0035	1	U	F.ADKVL
8895	964.0413	1926.0681	1926.0674	0.38	1	102	5.2e-10	1	U	F.ADKVL
8896	964.0415	1926.0684	1926.0674	0.57	1	(64)	2.8e-06	1	U	F.ADKVL

18. [2::sp|P0A836|SUCC_ECOLI](#) Mass: 41652 Score: 432 Matches: 22(18) Sequences:
Succinate--CoA ligase [ADP-forming] subunit beta OS=Escherichia coli (strain K12) OX=83333 GN=tsf PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3140	559.8135	1117.6125	1117.6132	-0.56	2	40	0.0015	1	U	L.GLEGK
3141	559.8151	1117.6157	1117.6132	2.26	2	(40)	0.0015	1	U	L.GLEGK
3659	580.3135	1158.6125	1158.6132	-0.57	0	56	4.8e-05	1	U	L.VEAAT
3663	580.3158	1158.6170	1158.6132	3.33	0	(46)	0.00045	1	U	L.VEAAT
3867	589.2963	1176.5781	1176.5775	0.52	2	(38)	0.0033	1	U	L.DGKLG
3869	589.2973	1176.5800	1176.5775	2.17	2	(22)	0.12	1	U	L.DGKLG
3871	589.2976	1176.5807	1176.5775	2.69	2	44	0.00095	1	U	L.DGKLG
4780	630.3549	1258.6953	1258.6955	-0.18	1	28	0.019	1	U	L.VITKQ
4781	630.3565	1258.6985	1258.6955	2.35	1	(25)	0.042	1	U	L.VITKQ
4971	639.2950	1276.5754	1276.5540	16.8	0	(22)	0.088	3	U	L.DGNIG

5098	647.2905	1292.5664	1292.5489	13.5	0	(20)	0.1	2	U	L.DGNIG
5101	647.2922	1292.5698	1292.5489	16.1	0	23	0.064	2	U	L.DGNIG
5423	661.8464	1321.6783	1321.6765	1.37	1	40	0.0018	1	U	L.VEAAT
5936	693.8651	1385.7157	1385.7151	0.44	0	99	2.5e-09	1	U	L.TDAAQ
5947	694.3651	1386.7157	1386.6991	12.0	0	(42)	0.0013	1	U	L.TDAAQ
6032	467.2323	1398.6751	1398.6627	8.86	0	26	0.046	1	U	Y.QTDAN
7055	768.8876	1535.7607	1535.7580	1.77	0	(40)	0.0028	1	U	L.DVGGG
7056	768.8879	1535.7613	1535.7580	2.17	0	42	0.0015	1	U	L.DVGGG
7714	550.6220	1648.8442	1648.8421	1.30	1	(28)	0.04	1	U	F.LDVGG
7715	550.6222	1648.8447	1648.8421	1.63	1	39	0.0031	1	U	F.LDVGG
7716	825.4305	1648.8465	1648.8421	2.71	1	(30)	0.023	1	U	F.LDVGG
7717	825.4305	1648.8465	1648.8421	2.71	1	(34)	0.01	1	U	F.LDVGG

19. [2::sp|P0A9B2|G3P1_ECOLI](#) Mass: 35681 Score: 419 Matches: 23(23) Sequences:
 Glyceraldehyde-3-phosphate dehydrogenase A OS=Escherichia coli (strain K12) OX=83333
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
188	394.7292	787.4439	787.4440	-0.01	1	26	0.032	1	U	Y.SNKVL
976	447.7574	893.5003	893.5011	-0.89	2	(27)	0.013	1	U	F.VKLVS
977	447.7576	893.5006	893.5011	-0.49	2	35	0.0021	1	U	F.VKLVS
994	448.7636	895.5125	895.5127	-0.16	1	25	0.0073	1	U	L.DLIAH
995	448.7636	895.5126	895.5127	-0.10	1	(23)	0.013	1	U	L.DLIAH
1201	460.7457	919.4768	919.4763	0.51	0	(50)	0.00018	1	U	L.AKVIN
1202	460.7459	919.4772	919.4763	0.97	0	53	8.7e-05	1	U	L.AKVIN
1442	474.7793	947.5440	947.5440	0.03	0	(36)	0.0015	1	U	M.TIKVG
1443	474.7797	947.5448	947.5440	0.85	0	40	0.00056	1	U	M.TIKVG
1452	475.2710	948.5274	948.5280	-0.61	0	(40)	0.00093	1	U	M.TIKVG
1453	475.2711	948.5276	948.5280	-0.49	0	(38)	0.0015	1	U	M.TIKVG
1454	475.2711	948.5276	948.5280	-0.42	0	(30)	0.0094	1	U	M.TIKVG
1455	475.2712	948.5278	948.5280	-0.23	0	(31)	0.0068	1	U	M.TIKVG
3561	576.3246	1150.6346	1150.6346	0.01	1	40	0.00069	1	U	L.TVRLE
3563	576.3251	1150.6357	1150.6346	0.96	1	(35)	0.0025	1	U	L.TVRLE
4512	617.2577	1232.5009	1232.4986	1.92	2	26	0.0081	1	U	L.VSWYD
4665	624.8157	1247.6168	1247.6146	1.76	1	55	8.4e-05	1	U	F.DAKAG
4666	624.8159	1247.6173	1247.6146	2.16	1	(50)	0.00027	1	U	F.DAKAG
5126	648.3682	1294.7219	1294.7245	-2.02	0	47	0.00015	1	U	F.RVPTP
5127	648.3693	1294.7241	1294.7245	-0.33	0	(43)	0.00033	1	U	F.RVPTP
5608	674.2839	1346.5532	1346.5514	1.30	1	34	0.0029	1	U	L.GYTED
8971	653.6923	1958.0550	1958.0506	2.22	0	(36)	0.0032	1	U	Y.EQIKA
8972	653.6925	1958.0557	1958.0506	2.58	0	38	0.0021	1	U	Y.EQIKA

20. [2::sp|P21165|PEPQ_ECOLI](#) Mass: 50315 Score: 409 Matches: 19(19) Sequences:
 Xaa-Pro dipeptidase OS=Escherichia coli (strain K12) OX=83333 GN=pepQ PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
255	398.7379	795.4613	795.4603	1.28	0	31	0.0014	1	U	Y.KNHIA
256	398.7382	795.4618	795.4603	1.89	0	(31)	0.0015	1	U	Y.KNHIA
1286	467.2431	932.4716	932.4716	0.08	1	(40)	0.0015	1	U	Y.AADLT
1287	467.2434	932.4722	932.4716	0.68	1	47	0.00029	1	U	Y.AADLT
1476	476.2848	950.5551	950.5549	0.20	0	(21)	0.018	1	U	Y.IGPVP

1477	476.2850	950.5554	950.5549	0.58	0	28	0.0044	1	U	Y.IGPVP
2043	502.2294	1002.4443	1002.4447	-0.39	1	24	0.033	1	U	F.LDDHP
2044	502.2301	1002.4456	1002.4447	0.94	1	(23)	0.041	1	U	F.LDDHP
2548	530.2700	1058.5255	1058.5244	1.03	0	41	0.0012	1	U	L.VKDVN
2549	530.2700	1058.5255	1058.5244	1.03	0	(40)	0.0017	1	U	L.VKDVN
2665	537.3208	1072.6270	1072.6281	-0.94	1	24	0.025	1	U	W.QKIEA
4608	622.3300	1242.6454	1242.6456	-0.16	1	65	5e-06	1	U	L.VKDVN
4609	622.3303	1242.6461	1242.6456	0.42	1	(52)	0.00011	1	U	L.VKDVN
5639	675.8723	1349.7299	1349.7303	-0.25	1	(32)	0.0059	1	U	Y.SNIVA
5640	675.8740	1349.7334	1349.7303	2.28	1	34	0.0043	1	U	Y.SNIVA
5761	682.3192	1362.6237	1362.6245	-0.53	2	(33)	0.0097	1	U	F.NVFLD
5762	682.3212	1362.6278	1362.6245	2.44	2	35	0.0068	1	U	F.NVFLD
7392	795.4121	1588.8095	1588.8097	-0.07	0	34	0.01	1	U	L.GIEAS
8577	915.9844	1829.9543	1829.9523	1.11	1	52	0.00014	1	U	L.QLGIE

21. [2::sp|P04805|SYE_ECOLI](#) Mass: 54181 Score: 406 Matches: 27(22) Sequences: 1
 Glutamate--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=gltX PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
764	429.7563	857.4980	857.4971	1.06	0	(25)	0.028	1	U	L.EVVR
765	429.7565	857.4985	857.4971	1.69	0	28	0.016	1	U	L.EVVR
2890	548.2351	1094.4555	1094.4556	-0.09	2	44	0.00028	1	U	L.SLEW
2891	548.2352	1094.4558	1094.4556	0.13	2	(42)	0.00048	1	U	L.SLEW
4057	598.3198	1194.6250	1194.6244	0.45	1	(51)	0.0001	1	U	F.TLNA
4058	598.3207	1194.6268	1194.6244	1.99	1	56	3.3e-05	1	U	F.TLNA
4059	598.3212	1194.6278	1194.6244	2.81	1	(43)	0.00059	1	U	F.TLNA
4304	406.2054	1215.5943	1215.5958	-1.19	1	(22)	0.12	1	U	F.TREE
4305	406.2056	1215.5950	1215.5958	-0.65	1	(24)	0.072	1	U	F.TREE
4499	411.5373	1231.5901	1231.5907	-0.45	1	(25)	0.053	1	U	F.TREE
4500	411.5374	1231.5905	1231.5907	-0.13	1	26	0.049	1	U	F.TREE
4671	625.2957	1248.5769	1248.5735	2.75	1	(37)	0.0043	1	U	L.DFIA
4672	625.2960	1248.5774	1248.5735	3.13	1	45	0.00064	1	U	L.DFIA
4792	631.3257	1260.6369	1260.6350	1.53	2	21	0.16	1	U	Y.RDDG
4793	631.3278	1260.6411	1260.6350	4.83	2	(20)	0.2	1	U	Y.RDDG
6324	719.3904	1436.7662	1436.7663	-0.09	1	31	0.0097	1	U	Y.INAL
6325	719.3924	1436.7702	1436.7663	2.72	1	(24)	0.044	1	U	Y.INAL
6804	500.9199	1499.7378	1499.7402	-1.58	0	(26)	0.05	1	U	Y.AHVS
6805	750.8765	1499.7384	1499.7402	-1.23	0	(44)	0.00078	1	U	Y.AHVS
6806	750.8771	1499.7397	1499.7402	-0.33	0	51	0.00014	1	U	Y.AHVS
6807	500.9214	1499.7423	1499.7402	1.42	0	(21)	0.15	1	U	Y.AHVS
7169	777.3511	1552.6876	1552.7079	-13.04	1	(41)	0.0014	1	U	Y.NAVI
7170	777.3619	1552.7092	1552.7079	0.84	1	58	3.1e-05	1	U	Y.NAVI
7171	777.3621	1552.7096	1552.7079	1.07	1	(45)	0.00071	1	U	Y.NAVI
7279	785.3587	1568.7028	1568.7028	0.02	1	(46)	0.00041	1	U	Y.NAVI
7280	785.3588	1568.7030	1568.7028	0.09	1	(46)	0.00049	1	U	Y.NAVI
9889	942.1018	2823.2834	2823.2691	5.08	1	49	0.0002	1	U	L.RIED

22. [2::sp|P08200|IDH_ECOLI](#) Mass: 46070 Score: 402 Matches: 20(17) Sequences: 1
 Isocitrate dehydrogenase [NADP] OS=Escherichia coli (strain K12) OX=83333 GN=icd PE=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
751	427.2853	852.5561	852.5545	1.83	0	20	0.012	1	U	Y.RVAIK
1487	477.2219	952.4292	952.4290	0.19	1	32	0.0085	1	U	F.TEGAF
1488	477.2219	952.4293	952.4290	0.25	1	(26)	0.037	1	U	F.TEGAF
2119	506.7514	1011.4882	1011.4873	0.95	0	25	0.048	1	U	Y.TGEKS
2120	506.7515	1011.4884	1011.4873	1.07	0	(24)	0.056	1	U	Y.TGEKS
3600	578.3051	1154.5955	1154.5972	-1.39	0	(20)	0.12	1	U	L.NVPEN
3601	578.3068	1154.5991	1154.5972	1.68	0	25	0.036	1	U	L.NVPEN
3845	587.8079	1173.6012	1173.5990	1.89	0	(28)	0.029	1	U	Y.AIAND
3846	587.8080	1173.6015	1173.5990	2.19	0	30	0.021	1	U	Y.AIAND
4026	398.2236	1191.6491	1191.6499	-0.72	0	(20)	0.12	1	U	L.KVVDA
4027	596.8328	1191.6510	1191.6499	0.88	0	60	1.2e-05	1	U	L.KVVDA
4028	596.8329	1191.6512	1191.6499	1.10	0	(55)	4e-05	1	U	L.KVVDA
4029	398.2245	1191.6517	1191.6499	1.52	0	(23)	0.066	1	U	L.KVVDA
5315	656.3673	1310.7201	1310.7194	0.51	0	(44)	0.00032	1	U	Y.AGQDK
5316	656.3683	1310.7220	1310.7194	2.00	0	64	3.2e-06	1	U	Y.AGQDK
6191	711.3862	1420.7579	1420.7562	1.23	0	(43)	0.00071	1	U	W.KADSA
6192	711.3874	1420.7602	1420.7562	2.86	0	46	0.00037	1	U	W.KADSA
6821	751.8765	1501.7385	1501.7334	3.38	0	53	0.0001	1	U	Y.IEGDG
6822	751.8768	1501.7390	1501.7334	3.70	0	(44)	0.00079	1	U	Y.IEGDG
7630	816.8868	1631.7591	1631.7580	0.70	2	47	0.00043	1	U	L.AREEF

23. [2::sp|P0A910|OMPA_ECOLI](#) Mass: 37292 Score: 398 Matches: 19(16) Sequences:
 Outer membrane protein A OS=Escherichia coli (strain K12) OX=83333 GN=ompA PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1211	461.7659	921.5172	921.5171	0.12	2	23	0.041	1	U	F.TLKSD
1303	468.2420	934.4694	934.4695	-0.10	1	21	0.14	1	U	Y.TRLGG
1497	477.7022	953.3899	953.3879	2.04	1	23	0.035	1	U	W.SQYHD
2471	527.2443	1052.4741	1052.4749	-0.81	2	23	0.085	1	U	Y.DWLGR
2761	542.8215	1083.6285	1083.6288	-0.25	0	39	0.00081	1	U	Y.AITPE
2762	542.8217	1083.6288	1083.6288	-0.01	0	(36)	0.0018	1	U	Y.AITPE
4318	609.2766	1216.5387	1216.5360	2.17	1	(40)	0.0012	1	U	L.GYTDR
4319	609.2769	1216.5392	1216.5360	2.58	1	53	5.6e-05	1	U	L.GYTDR
4757	629.3157	1256.6168	1256.6150	1.44	0	31	0.011	1	U	Y.GKNHD
4758	629.3160	1256.6175	1256.6150	2.03	0	(28)	0.022	1	U	Y.GKNHD
5033	642.8029	1283.5912	1283.5921	-0.76	1	23	0.081	1	U	L.GYPIT
5515	666.8426	1331.6706	1331.6721	-1.11	2	(27)	0.04	1	U	L.KPEGQ
5516	666.8431	1331.6717	1331.6721	-0.28	2	33	0.011	1	U	L.KPEGQ
5569	670.8813	1339.7480	1339.7459	1.57	1	30	0.0063	1	U	F.NKATL
7878	835.9525	1669.8905	1669.8887	1.08	2	55	4e-05	1	U	Y.SQLSN
7879	835.9536	1669.8927	1669.8887	2.39	2	(42)	0.00076	1	U	Y.SQLSN
8260	877.4172	1752.8199	1752.8179	1.13	1	48	0.00041	1	U	F.INNNG
8261	877.4175	1752.8205	1752.8179	1.47	1	(44)	0.00094	1	U	F.INNNG
8265	877.9094	1753.8043	1753.8020	1.33	1	(39)	0.0024	1	U	F.INNNG

24. [2::sp|P0C8J8|GATZ_ECOLI](#) Mass: 47535 Score: 381 Matches: 16(15) Sequences:
 D-tagatose-1,6-bisphosphate aldolase subunit GatZ OS=Escherichia coli (strain K12) OX=83333 GN=gatz PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
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265	399.7070	797.3995	797.3993	0.25	0	25	0.032	1	U	L.IMDKI
566	416.7498	831.4851	831.4854	-0.35	1	(29)	0.0071	1	U	L.KVGPA
567	416.7499	831.4852	831.4854	-0.28	1	32	0.0035	1	U	L.KVGPA
1152	458.2375	914.4605	914.4610	-0.58	1	29	0.015	1	U	W.ELVRD
1153	458.2379	914.4612	914.4610	0.21	1	(27)	0.022	1	U	W.ELVRD
1276	466.2459	930.4773	930.4770	0.25	0	(25)	0.048	1	U	F.ERIQS
1277	466.2462	930.4777	930.4770	0.77	0	26	0.038	1	U	F.ERIQS
2145	507.7768	1013.5391	1013.5393	-0.20	1	(44)	0.00038	1	U	F.ALAQI
2146	507.7778	1013.5411	1013.5393	1.79	1	47	0.00023	1	U	F.ALAQI
4409	613.8403	1225.6660	1225.6666	-0.52	0	54	3.9e-05	1	U	L.APETV
4410	613.8405	1225.6663	1225.6666	-0.23	0	(50)	8.7e-05	1	U	L.APETV
4686	625.8054	1249.5963	1249.5939	1.93	0	49	0.00023	1	U	L.IEATS
7340	789.3669	1576.7192	1576.7151	2.59	0	62	1.2e-05	1	U	F.AAESV
7341	789.3676	1576.7205	1576.7151	3.44	0	(51)	0.00016	1	U	F.AAESV
7913	839.8851	1677.7556	1677.7515	2.41	0	58	3.3e-05	1	U	W.QQENA
7914	839.8857	1677.7569	1677.7515	3.21	0	(24)	0.07	1	U	W.QQENA

Proteins matching a subset of these peptides:

[2::sp|P0C8K0|KBAZ_ECOLI](#) Mass: 47562 Score: 32 Matches: 2(2) Sequences: 1
D-tagatose-1,6-bisphosphate aldolase subunit KbaZ OS=Escherichia coli (strain K12) C

25. [2::sp|P0A6E4|ASSY_ECOLI](#) Mass: 50038 Score: 375 Matches: 17(15) Sequences: 1
Argininosuccinate synthase OS=Escherichia coli (strain K12) OX=83333 GN=argG PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1766	489.7533	977.4921	977.4930	-0.94	0	40	0.0016	1	U	Y.KGNDI
1767	489.7540	977.4934	977.4930	0.43	0	(40)	0.0018	1	U	Y.KGNDI
2011	500.7566	999.4987	999.4985	0.17	0	35	0.0038	1	U	F.SPDDR
2012	500.7571	999.4997	999.4985	1.15	0	(28)	0.017	1	U	F.SPDDR
3131	559.3087	1116.6029	1116.6027	0.20	0	(24)	0.059	1	U	W.VASQI
3132	559.3088	1116.6031	1116.6027	0.42	0	29	0.019	1	U	W.VASQI
3419	571.2867	1140.5588	1140.5564	2.15	1	37	0.0031	1	U	Y.KGNDI
3420	571.2872	1140.5599	1140.5564	3.12	1	(32)	0.0085	1	U	Y.KGNDI
4559	619.3248	1236.6351	1236.6350	0.08	1	29	0.027	1	U	L.DITDT
4560	619.3259	1236.6372	1236.6350	1.76	1	(21)	0.15	1	U	L.DITDT
6164	710.3243	1418.6340	1418.6314	1.85	0	40	0.0012	1	U	L.TGIHN
6165	710.3246	1418.6346	1418.6314	2.28	0	(24)	0.049	1	U	L.TGIHN
8101	573.6372	1717.8898	1717.8887	0.67	0	36	0.0051	1	U	W.DESVK
8819	951.4644	1900.9142	1900.9126	0.81	1	75	6.3e-07	1	U	L.SSSAA
8820	951.4649	1900.9152	1900.9126	1.38	1	(64)	7.7e-06	1	U	L.SSSAA
8828	635.6633	1903.9680	1903.9680	0.01	1	(49)	0.00028	1	U	F.WDES
8829	635.6650	1903.9733	1903.9680	2.79	1	55	8e-05	1	U	F.WDES

26. [2::sp|P0AEX9|MALE_ECOLI](#) Mass: 43360 Score: 367 Matches: 17(14) Sequences: 1
Maltose-binding periplasmic protein OS=Escherichia coli (strain K12) OX=83333 GN=malM PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1913	496.2582	990.5019	990.5022	-0.33	0	(21)	0.13	1	U	L.AEITP
1914	496.2585	990.5025	990.5022	0.27	0	22	0.1	1	U	L.AEITP
2584	531.8005	1061.5865	1061.5869	-0.38	1	33	0.0055	1	U	Y.NGLAE

3395	570.7800	1139.5454	1139.5459	-0.41	0	(37)	0.003	1	U	W.SNIDT
3396	570.7803	1139.5460	1139.5459	0.12	0	54	6.2e-05	1	U	W.SNIDT
4899	636.3332	1270.6518	1270.6517	0.11	0	47	0.00028	1	U	L.SAGIN
4901	636.3341	1270.6535	1270.6517	1.46	0	(45)	0.0005	1	U	L.SAGIN
6292	717.8375	1433.6604	1433.6609	-0.37	0	64	7.1e-06	1	U	F.NKGET
6293	717.8395	1433.6645	1433.6609	2.53	0	(57)	4.5e-05	1	U	F.NKGET
7107	514.9422	1541.8048	1541.8049	-0.10	0	(32)	0.0096	1	U	Y.DIKDV
7108	514.9426	1541.8061	1541.8049	0.73	0	(30)	0.016	1	U	Y.DIKDV
7109	771.9114	1541.8083	1541.8049	2.20	0	63	7.6e-06	1	U	Y.DIKDV
7110	771.9121	1541.8095	1541.8049	2.99	0	(60)	1.7e-05	1	U	Y.DIKDV
7212	780.9164	1559.8183	1559.8195	-0.75	2	(50)	0.00019	1	U	Y.AQSGL
7213	780.9171	1559.8195	1559.8195	0.03	2	50	0.00018	1	U	Y.AQSGL
8432	597.6477	1789.9213	1789.9210	0.15	1	(24)	0.098	1	U	Y.DIKDV
8433	895.9680	1789.9215	1789.9210	0.25	1	37	0.004	1	U	Y.DIKDV

27. [2::sp|P0A799|PGK_ECOLI](#) Mass: 41264 Score: 347 Matches: 17(15) Sequences: 9
 Phosphoglycerate kinase OS=Escherichia coli (strain K12) OX=83333 GN=pgk PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
801	433.7343	865.4541	865.4545	-0.52	0	(22)	0.071	1	U	F.GIADK
802	433.7346	865.4546	865.4545	0.06	0	22	0.06	1	U	F.GIADK
1068	452.7604	903.5063	903.5066	-0.26	1	37	0.0029	1	U	F.SLLPV
1069	452.7605	903.5064	903.5066	-0.13	1	(36)	0.0033	1	U	F.SLLPV
1077	453.2641	904.5136	904.5130	0.60	1	26	0.018	1	U	L.DLAGK
1078	453.2641	904.5136	904.5130	0.60	1	(24)	0.03	1	U	L.DLAGK
5019	428.2667	1281.7782	1281.7768	1.09	2	20	0.023	1	U	Y.LKDKL
5719	679.8576	1357.7006	1357.6990	1.21	1	(44)	0.00065	1	U	F.IAAQG
5720	679.8584	1357.7022	1357.6990	2.39	1	47	0.00034	1	U	F.IAAQG
5820	686.3769	1370.7393	1370.7405	-0.85	2	(48)	0.00023	1	U	Y.EADLV
5821	457.9209	1370.7408	1370.7405	0.20	2	(25)	0.047	1	U	Y.EADLV
5824	686.3798	1370.7450	1370.7405	3.25	2	61	1.3e-05	1	U	Y.EADLV
6234	714.3063	1426.5981	1426.6001	-1.36	1	28	0.014	1	U	L.GRPTE
6508	729.8939	1457.7733	1457.7726	0.50	0	46	0.00043	1	U	L.KSVND
6509	729.8945	1457.7744	1457.7726	1.26	0	(37)	0.0033	1	U	L.KSVND
9676	820.0811	2457.2215	2457.2234	-0.78	1	65	7.6e-06	1	U	L.KSVND
9677	820.0813	2457.2221	2457.2234	-0.56	1	(52)	0.00014	1	U	L.KSVND

28. [2::sp|P0C0V0|DEGP_ECOLI](#) Mass: 49438 Score: 346 Matches: 17(13) Sequences: 9
 Periplasmic serine endoprotease DegP OS=Escherichia coli (strain K12) OX=83333 GN=de
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
714	425.2267	848.4389	848.4392	-0.38	0	31	0.012	1	U	L.NGKPI
715	425.2270	848.4395	848.4392	0.33	0	(23)	0.062	1	U	L.NGKPI
3332	568.2853	1134.5560	1134.5591	-2.68	0	(20)	0.18	1	U	L.TAIKM
3554	576.2853	1150.5560	1150.5540	1.77	0	31	0.014	1	U	L.TAIKM
3555	576.2938	1150.5730	1150.5540	16.6	0	(23)	0.093	1	U	L.TAIKM
3954	594.2540	1186.4934	1186.4931	0.21	2	41	0.00057	1	U	F.QQFFG
3955	594.2547	1186.4948	1186.4931	1.44	2	(29)	0.0082	1	U	F.QQFFG
4735	628.3611	1254.7076	1254.7044	2.54	1	39	0.00094	1	U	L.LRDGK
5634	675.8541	1349.6937	1349.6939	-0.15	1	35	0.0056	1	U	L.ALNIQ

5635	675.8560	1349.6975	1349.6939	2.65	1	(28)	0.028	1	U	L.ALNIQ
5737	680.3753	1358.7361	1358.7340	1.50	0	(22)	0.092	1	U	L.RAQVG
5738	680.3762	1358.7378	1358.7340	2.76	0	35	0.0058	1	U	L.RAQVG
6848	755.3844	1508.7542	1508.7545	-0.15	1	(87)	4.8e-08	1	U	F.MALGS
6849	755.3868	1508.7591	1508.7545	3.09	1	93	1e-08	1	U	F.MALGS
6956	763.3824	1524.7502	1524.7494	0.55	1	(81)	1.7e-07	1	U	F.MALGS
6957	763.3839	1524.7531	1524.7494	2.46	1	(87)	3.6e-08	1	U	F.MALGS
8454	898.9227	1795.8308	1795.8224	4.65	1	41	0.0018	1	U	L.ELQQS

29. [2::sp|P0ABH7|CISY_ECOLI](#) Mass: 48383 Score: 333 Matches: 18(17) Sequences:
Citrate synthase OS=Escherichia coli (strain K12) OX=83333 GN=glcA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2350	516.7641	1031.5136	1031.5135	0.14	1	27	0.033	1	U	L.TLNGD
2610	532.7594	1063.5042	1063.5047	-0.38	0	20	0.2	1	U	W.GPAHG
2748	541.7905	1081.5664	1081.5669	-0.45	0	34	0.005	1	U	L.HRGFP
2749	541.7914	1081.5682	1081.5669	1.23	0	(23)	0.055	1	U	L.HRGFP
3232	563.7802	1125.5457	1125.5455	0.26	1	29	0.02	1	U	F.VYPRN
3233	563.7803	1125.5461	1125.5455	0.58	1	(25)	0.05	1	U	F.VYPRN
4034	597.2760	1192.5374	1192.5360	1.20	0	(24)	0.057	1	U	L.NGEKP
4035	597.2760	1192.5374	1192.5360	1.20	0	33	0.0079	1	U	L.NGEKP
6420	725.3592	1448.7038	1448.7068	-2.08	2	(40)	0.0029	1	U	L.GTKDD
6421	725.3606	1448.7066	1448.7068	-0.14	2	44	0.0011	1	U	L.GTKDD
6997	510.2928	1527.8565	1527.8621	-3.67	1	(27)	0.02	1	U	L.KGTLG
6998	510.2938	1527.8596	1527.8621	-1.59	1	30	0.01	1	U	L.KGTLG
7035	767.3932	1532.7719	1532.7722	-0.17	2	42	0.0014	1	U	Y.ILLNG
7036	767.3951	1532.7757	1532.7722	2.30	2	(37)	0.0042	1	U	Y.ILLNG
7373	792.8444	1583.6743	1583.6740	0.20	1	41	0.00088	1	U	L.NGEKP
7374	792.8447	1583.6748	1583.6740	0.52	1	(37)	0.0022	1	U	L.NGEKP
7953	562.3072	1683.8997	1683.8978	1.18	1	(27)	0.027	1	U	Y.EVNPI
7954	562.3075	1683.9007	1683.8978	1.73	1	32	0.0086	1	U	Y.EVNPI

30. [2::sp|P0A825|GLYA_ECOLI](#) Mass: 45459 Score: 319 Matches: 13(13) Sequences:
Serine hydroxymethyltransferase OS=Escherichia coli (strain K12) OX=83333 GN=glyA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
410	408.2290	814.4435	814.4436	-0.15	0	42	0.00075	1	U	Y.VDIVE
411	408.2290	814.4435	814.4436	-0.15	0	(38)	0.0023	1	U	Y.VDIVE
888	438.2265	874.4385	874.4396	-1.24	0	28	0.032	1	U	L.TGKEA
2301	514.8029	1027.5913	1027.5914	-0.06	2	(31)	0.0073	1	U	F.LVDLV
2302	514.8031	1027.5916	1027.5914	0.29	2	37	0.0018	1	U	F.LVDLV
2572	531.2487	1060.4829	1060.4825	0.32	0	(47)	0.00024	1	U	Y.GIDAT
2573	531.2494	1060.4842	1060.4825	1.59	0	52	7e-05	1	U	Y.GIDAT
2585	531.8008	1061.5871	1061.5869	0.20	1	25	0.038	1	U	L.AIDRA
3265	564.8108	1127.6071	1127.6074	-0.23	2	(32)	0.0076	1	U	Y.TALLE
3266	564.8123	1127.6100	1127.6074	2.27	2	51	9.7e-05	1	U	Y.TALLE
3894	590.3157	1178.6168	1178.6183	-1.26	2	35	0.0051	1	U	L.ILAKG
4925	637.3311	1272.6477	1272.6463	1.11	1	49	0.00028	1	U	Y.KVVSQ
4928	637.3325	1272.6505	1272.6463	3.31	1	(41)	0.0017	1	U	Y.KVVSQ

31. [2::sp|P0AG30|RHO](#) [ECOLI](#) **Mass:** 47032 **Score:** 313 **Matches:** 18(17) **Sequences:** 9
 Transcription termination factor Rho OS=Escherichia coli (strain K12) OX=83333 GN=rh
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1000	449.7166	897.4187	897.4192	-0.51	1	29	0.012	1	U	F.LRSAD
1001	449.7168	897.4190	897.4192	-0.22	1	(26)	0.027	1	U	F.LRSAD
2365	518.7872	1035.5599	1035.5601	-0.16	0	(38)	0.002	1	U	L.VKGEV
2366	518.7875	1035.5604	1035.5601	0.32	0	48	0.00018	1	U	L.VKGEV
2763	542.8221	1083.6296	1083.6288	0.73	0	(42)	0.00046	1	U	Y.NTVVP
2764	542.8221	1083.6296	1083.6288	0.73	0	44	0.00029	1	U	Y.NTVVP
4175	603.2622	1204.5099	1204.5070	2.34	1	(23)	0.039	1	U	L.AMTKT
4176	603.2624	1204.5103	1204.5070	2.74	1	29	0.011	1	U	L.AMTKT
4282	607.8543	1213.6941	1213.6918	1.88	1	26	0.027	1	U	L.KNTPV
5218	652.3334	1302.6522	1302.6489	2.50	2	36	0.0047	1	U	L.ITLGE
5219	652.3336	1302.6526	1302.6489	2.80	2	(30)	0.02	1	U	L.ITLGE
5281	655.3085	1308.6024	1308.6020	0.30	1	38	0.0033	1	U	L.TTQEE
5282	655.3115	1308.6084	1308.6020	4.87	1	(30)	0.019	1	U	L.TTQEE
8367	888.4067	1774.7989	1774.7971	1.02	1	(37)	0.0031	1	U	L.IDTGS
8368	888.4083	1774.8021	1774.7971	2.81	1	(34)	0.0068	1	U	L.IDTGS
8436	896.4031	1790.7916	1790.7920	-0.24	1	(45)	0.00043	1	U	L.IDTGS
8437	896.4055	1790.7965	1790.7920	2.48	1	46	0.00036	1	U	L.IDTGS
8870	481.2432	1920.9435	1920.9060	19.5	2	24	0.11	1	U	L.KNTPV

32. [2::sp|P21599|KPYK2](#) [ECOLI](#) **Mass:** 51553 **Score:** 308 **Matches:** 17(13) **Sequences:** 17
 Pyruvate kinase II OS=Escherichia coli (strain K12) OX=83333 GN=pykA PE=1 SV=3
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
333	403.7240	805.4334	805.4334	0.07	1	35	0.0032	1	U	F.LNIGD
335	403.7243	805.4340	805.4334	0.74	1	(20)	0.094	1	U	F.LNIGD
854	436.7397	871.4649	871.4651	-0.26	0	29	0.012	1	U	F.TEVTV
855	436.7399	871.4652	871.4651	0.15	0	(25)	0.035	1	U	F.TEVTV
1864	494.2817	986.5489	986.5509	-1.96	0	26	0.038	1	U	L.SNNKG
1866	494.2826	986.5507	986.5509	-0.11	0	(22)	0.076	1	U	L.SNNKG
2294	514.7904	1027.5663	1027.5662	0.06	2	33	0.005	1	U	L.LLDDG
2296	514.7911	1027.5677	1027.5662	1.48	2	(26)	0.023	1	U	L.LLDDG
5107	647.3745	1292.7343	1292.7340	0.26	0	(25)	0.016	1	U	Y.KGLPA
5108	647.3757	1292.7368	1292.7340	2.15	0	36	0.0011	1	U	Y.KGLPA
5733	680.3572	1358.6998	1358.6976	1.61	1	22	0.14	1	U	L.SNNKG
6055	702.3936	1402.7727	1402.7667	4.25	0	59	1.6e-05	1	U	L.TEKDK
6056	702.3945	1402.7745	1402.7667	5.55	0	(44)	0.00047	1	U	L.TEKDK
6823	752.3503	1502.6860	1502.6849	0.76	0	40	0.0015	1	U	F.DSAND
6824	752.3516	1502.6886	1502.6849	2.47	0	(36)	0.0046	1	U	F.DSAND
7660	820.8896	1639.7647	1639.7664	-1.03	2	(23)	0.13	1	U	Y.LAVSF
7661	820.8922	1639.7697	1639.7664	2.02	2	32	0.015	1	U	Y.LAVSF

33. [2::sp|P0AC38|ASPA](#) [ECOLI](#) **Mass:** 52950 **Score:** 308 **Matches:** 13(13) **Sequences:** 13
 Aspartate ammonia-lyase OS=Escherichia coli (strain K12) OX=83333 GN=aspA PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3242	563.8456	1125.6767	1125.6757	0.88	1	56	1.1e-05	1	U	L.IKLVD
4196	604.2748	1206.5351	1206.5339	1.01	1	41	0.0011	1	U	L.ELMGH
4197	604.2756	1206.5366	1206.5339	2.22	1	(37)	0.003	1	U	L.ELMGH
4597	621.2947	1240.5748	1240.5724	1.94	1	27	0.03	1	U	L.GTREV
5334	658.3464	1314.6782	1314.6779	0.22	1	52	0.00012	1	U	M.SNNIR
5335	658.3475	1314.6804	1314.6779	1.89	1	(39)	0.0022	1	U	M.SNNIR
5875	688.8585	1375.7025	1375.6983	3.03	0	41	0.0017	1	U	Y.ISNNK
5876	688.8598	1375.7050	1375.6983	4.89	0	(28)	0.032	1	U	Y.ISNNK
7501	804.3703	1606.7260	1606.7257	0.21	0	26	0.042	1	U	Y.QGGAG
7506	804.8904	1607.7663	1607.7688	-1.51	1	43	0.0013	1	U	L.QLNVM
7507	804.8926	1607.7707	1607.7688	1.23	1	(28)	0.039	1	U	L.QLNVM
8030	851.8641	1701.7137	1701.7127	0.60	0	24	0.03	1	U	L.NNGKC
8031	851.8662	1701.7179	1701.7127	3.03	0	(23)	0.046	1	U	L.NNGKC

34. [2::sp|P0A8L1|SYS_ECOLI](#) Mass: 48669 Score: 297 Matches: 15(13) Sequences: 8
 Serine--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=serS PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
541	415.7515	829.4884	829.4909	-3.06	1	(23)	0.057	1	U	F.KLDVD
542	415.7517	829.4888	829.4909	-2.53	1	28	0.015	1	U	F.KLDVD
584	417.7395	833.4644	833.4647	-0.36	1	(39)	0.001	1	U	L.DFAAA
585	417.7396	833.4646	833.4647	-0.15	1	43	0.00046	1	U	L.DFAAA
2244	512.3075	1022.6004	1022.6012	-0.72	1	45	9.6e-05	1	U	Y.ALIPT
2245	512.3083	1022.6020	1022.6012	0.83	1	(31)	0.0021	1	U	Y.ALIPT
4472	615.8096	1229.6046	1229.6041	0.43	1	29	0.02	1	U	F.DFEVR
4474	615.8108	1229.6070	1229.6041	2.41	1	(27)	0.033	1	U	F.DFEVR
4598	621.3272	1240.6399	1240.6411	-1.02	0	(27)	0.023	1	U	L.RNEPD
4599	621.3286	1240.6427	1240.6411	1.24	0	32	0.0075	1	U	L.RNEPD
5636	675.8580	1349.7014	1349.6980	2.53	2	33	0.0077	1	U	Y.GTGQL
6453	727.3848	1452.7551	1452.7572	-1.47	0	(23)	0.081	1	U	Y.QQADG
6454	727.3878	1452.7610	1452.7572	2.56	0	32	0.0098	1	U	Y.QQADG
7815	831.3708	1660.7270	1660.7329	-3.51	1	53	5.3e-05	1	U	F.HTRPL
7816	831.3727	1660.7308	1660.7329	-1.24	1	(50)	0.00013	1	U	F.HTRPL

35. [2::sp|P02925|RBSB_ECOLI](#) Mass: 30931 Score: 295 Matches: 13(9) Sequences: 9
 Ribose import binding protein RbsB OS=Escherichia coli (strain K12) OX=83333 GN=rbsB
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
143	390.6976	779.3806	779.3814	-0.92	0	47	0.00032	1	U	L.GGKIA
144	390.6977	779.3809	779.3814	-0.61	0	(39)	0.0024	1	U	L.GGKIA
2757	542.7753	1083.5360	1083.5349	0.98	0	23	0.061	2	U	L.TAHPD
3106	558.2701	1114.5256	1114.5254	0.15	0	24	0.055	2	U	L.DSQNN
5670	677.8375	1353.6605	1353.6599	0.45	0	22	0.13	1	U	L.QTAGK
6196	474.9136	1421.7190	1421.7150	2.77	1	25	0.066	1	U	L.KDGAQ
6876	757.9255	1513.8364	1513.8286	5.15	2	(23)	0.062	1	U	F.DRIKG
6877	757.9278	1513.8410	1513.8286	8.21	2	24	0.054	1	U	F.DRIKG
6878	758.3687	1514.7227	1514.7213	0.98	0	39	0.0025	1	U	F.DGTPD
6879	758.3690	1514.7234	1514.7213	1.39	0	(32)	0.013	1	U	F.DGTPD

7754	827.4441	1652.8736	1652.8733	0.19	2	70	1.5e-06	1	U	Y.NLVVL
7755	827.4460	1652.8774	1652.8733	2.47	2	(67)	2.4e-06	1	U	Y.NLVVL
9536	770.4290	2308.2652	2308.2638	0.62	0	27	0.013	1	U	L.AATIA

36. [2::sp|P27306|STHA_ECOLI](#) Mass: 51984 Score: 282 Matches: 12(11) Sequences: 7
Soluble pyridine nucleotide transhydrogenase OS=Escherichia coli (strain K12) OX=833333 GN=rpsA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
486	413.2124	824.4102	824.4102	0.04	0	35	0.0041	1	U	L.TAMKV
487	413.2124	824.4103	824.4102	0.11	0	(33)	0.0055	1	U	L.TAMKV
2988	553.2654	1104.5162	1104.5160	0.22	0	37	0.0028	1	U	Y.ANGRT
2989	553.2657	1104.5168	1104.5160	0.78	0	(32)	0.011	1	U	Y.ANGRT
4888	636.2788	1270.5431	1270.5387	3.42	2	(46)	0.0003	1	U	L.AFLDQ
4889	636.2790	1270.5435	1270.5387	3.79	2	62	7.9e-06	1	U	L.AFLDQ
7176	777.3961	1552.7776	1552.7773	0.16	1	29	0.029	1	U	Y.AVGDV
7177	777.3976	1552.7807	1552.7773	2.20	1	(23)	0.11	1	U	Y.AVGDV
7532	807.9269	1613.8392	1613.8373	1.19	2	(63)	1e-05	1	U	L.ALQNI
7533	807.9281	1613.8416	1613.8373	2.71	2	70	1.8e-06	1	U	L.ALQNI
7613	815.4407	1628.8668	1628.8621	2.87	0	49	0.00019	1	U	Y.TIPEI
7614	815.4407	1628.8668	1628.8621	2.87	0	(47)	0.00032	1	U	Y.TIPEI

37. [2::sp|P0AB71|ALF_ECOLI](#) Mass: 39351 Score: 258 Matches: 18(17) Sequences: 7
Fructose-bisphosphate aldolase class 2 OS=Escherichia coli (strain K12) OX=833333 GN=rpsA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5328	438.8946	1313.6619	1313.6616	0.29	2	30	0.015	1	U	W.IDGL
5329	438.8948	1313.6626	1313.6616	0.79	2	(27)	0.03	1	U	W.IDGL
6629	492.2476	1473.7210	1473.7212	-0.10	0	26	0.06	1	U	L.GNPK
6918	761.8649	1521.7152	1521.7134	1.20	0	37	0.0046	1	U	Y.GVVK
6921	761.8663	1521.7181	1521.7134	3.12	0	(31)	0.019	1	U	Y.GVVK
7584	541.9868	1622.9386	1622.9355	1.90	0	(29)	0.0046	1	U	F.IAGK
7585	812.4773	1622.9400	1622.9355	2.76	0	(25)	0.0099	1	U	F.IAGK
7586	812.4779	1622.9413	1622.9355	3.53	0	35	0.0011	1	U	F.IAGK
8117	574.9363	1721.7872	1721.7857	0.89	0	(22)	0.13	1	U	F.HGGS
8118	861.9023	1721.7900	1721.7857	2.53	0	(37)	0.0038	1	U	F.HGGS
8119	574.9376	1721.7909	1721.7857	3.02	0	(32)	0.013	1	U	F.HGGS
8120	861.9027	1721.7909	1721.7857	3.02	0	51	0.00017	1	U	F.HGGS
8695	932.4958	1862.9770	1862.9779	-0.45	1	40	0.0015	1	U	F.DFVK
8696	621.9999	1862.9778	1862.9779	-0.03	1	(30)	0.017	1	U	F.DFVK
8698	932.4989	1862.9832	1862.9779	2.89	1	(36)	0.0036	1	U	F.DFVK
9122	1007.5216	2013.0285	2013.0279	0.31	2	39	0.0024	1	U	Y.LQQQ
9123	672.0169	2013.0289	2013.0279	0.49	2	(28)	0.028	1	U	Y.LQQQ
9124	672.0178	2013.0315	2013.0279	1.75	2	(34)	0.0065	1	U	Y.LQQQ

38. [2::sp|P0AG67|RS1_ECOLI](#) Mass: 61235 Score: 252 Matches: 10(10) Sequences: 7
30S ribosomal protein S1 OS=Escherichia coli (strain K12) OX=833333 GN=rpsA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
490	413.2265	824.4384	824.4392	-0.98	1	24	0.031	1	U	L.HLEGGK
3441	571.7967	1141.5789	1141.5768	1.91	2	(32)	0.008	1	U	L.GLKQL
3442	571.7968	1141.5791	1141.5768	2.02	2	52	6.8e-05	1	U	L.GLKQL
3449	381.5643	1141.6710	1141.6707	0.29	0	22	0.031	1	U	Y.KKGDE
4189	603.8052	1205.5959	1205.5928	2.60	0	27	0.047	1	U	L.KSESA
4542	618.7963	1235.5780	1235.5782	-0.19	0	(38)	0.0032	1	U	W.NVAGE
4543	618.7978	1235.5810	1235.5782	2.29	0	40	0.002	1	U	W.NVAGE
5094	646.8399	1291.6652	1291.6660	-0.57	1	60	1.7e-05	1	U	L.VLSVG
5097	646.8422	1291.6698	1291.6660	2.93	1	(58)	3.3e-05	1	U	L.VLSVG
7650	546.3186	1635.9340	1635.9308	1.93	1	26	0.01	1	U	F.LPGSL

39. [2::sp|P21888|SYC_ECOLI](#) Mass: 52454 Score: 246 Matches: 10(9) Sequences: 6
 Cysteine--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=cysS PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2006	500.7402	999.4658	999.4662	-0.37	1	35	0.0034	1	U	Y.DAETV
2009	500.7406	999.4666	999.4662	0.49	1	(33)	0.0057	1	U	Y.DAETV
2168	508.7374	1015.4602	1015.4611	-0.80	1	(28)	0.017	1	U	Y.YDAET
2169	508.7381	1015.4617	1015.4611	0.64	1	29	0.016	1	U	Y.YDAET
3305	566.7796	1131.5446	1131.5448	-0.12	2	45	0.00058	1	U	L.GLLEQ
3307	566.7805	1131.5464	1131.5448	1.40	2	(29)	0.022	1	U	L.GLLEQ
6643	738.8767	1475.7387	1475.7369	1.28	0	(49)	0.00026	1	U	L.RGTDK
6644	738.8784	1475.7422	1475.7369	3.60	0	70	2.3e-06	1	U	L.RGTDK
8623	923.4387	1844.8628	1844.8639	-0.63	1	49	0.00027	1	U	F.LQSGA
9191	683.6661	2047.9764	2047.9745	0.91	0	21	0.19	1	U	L.QAGAR

40. [2::sp|P06715|GSHR_ECOLI](#) Mass: 49084 Score: 246 Matches: 10(6) Sequences: 7
 Glutathione reductase OS=Escherichia coli (strain K12) OX=83333 GN=gor PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4839	633.8215	1265.6284	1265.6252	2.56	0	26	0.043	1	U	L.EAAGV
5310	656.3172	1310.6198	1310.6176	1.68	1	20	0.2	1	U	L.RSFDP
5999	698.8626	1395.7105	1395.7106	-0.04	0	(23)	0.081	1	U	W.AIGRE
6000	698.8633	1395.7121	1395.7106	1.09	0	25	0.055	1	U	W.AIGRE
6104	706.3566	1410.6987	1410.6991	-0.25	0	53	9.3e-05	1	U	L.EVNGE
6916	761.8388	1521.6631	1521.6617	0.90	1	(34)	0.0055	1	U	L.ELEDG
6917	761.8390	1521.6634	1521.6617	1.14	1	39	0.0016	1	U	L.ELEDG
7358	791.9514	1581.8881	1581.8879	0.18	0	(43)	0.0004	1	U	F.ALPAL
7359	791.9517	1581.8888	1581.8879	0.57	0	57	1.6e-05	1	U	F.ALPAL
8328	883.4534	1764.8922	1764.8795	7.19	0	26	0.061	1	U	L.IATGG

41. [2::sp|P0A7Z4|RPOA_ECOLI](#) Mass: 36717 Score: 242 Matches: 12(8) Sequences: 7
 DNA-directed RNA polymerase subunit alpha OS=Escherichia coli (strain K12) OX=83333
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
437	409.2365	816.4585	816.4593	-0.91	0	(24)	0.061	2	U	L.TEIKD

438	409.2375	816.4604	816.4593	1.34	0	24	0.056	2	U	L.TEIKD
547	416.2216	830.4286	830.4286	-0.06	0	24	0.063	1	U	L.KAEAI
1295	467.7532	933.4918	933.4920	-0.18	0	44	0.00063	1	U	Y.SPVER
1296	467.7536	933.4927	933.4920	0.80	0	(43)	0.00071	1	U	Y.SPVER
4457	615.3270	1228.6395	1228.6452	-4.60	1	26	0.04	2	U	L.KAEAI
4460	615.3292	1228.6439	1228.6452	-1.03	1	(26)	0.038	2	U	L.KAEAI
5467	663.8917	1325.7689	1325.7667	1.66	0	48	7.7e-05	1	U	L.AVRVQ
5468	663.8924	1325.7702	1325.7667	2.68	0	(29)	0.0058	1	U	L.AVRVQ
6694	742.9199	1483.8253	1483.8246	0.46	2	55	3.1e-05	1	U	Y.IGDLV
6695	742.9216	1483.8286	1483.8246	2.69	2	(47)	0.00018	1	U	Y.IGDLV
8679	619.6669	1855.9790	1855.9752	2.05	1	21	0.11	1	U	Y.NVEAA

42. [2::sp|P0AAI5|FABF_ECOLI](#) Mass: 43247 Score: 234 Matches: 9(6) Sequences: 5
 3-oxoacyl-[acyl-carrier-protein] synthase 2 OS=Escherichia coli (strain K12) OX=83333
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3062	556.7834	1111.5522	1111.5509	1.16	1	21	0.1	1	U	L.GLIEE
4626	622.8165	1243.6185	1243.6197	-0.96	1	51	0.00012	1	U	L.AGQSG
4627	622.8170	1243.6195	1243.6197	-0.17	1	(36)	0.0044	1	U	L.AGQSG
5709	679.3586	1356.7026	1356.7038	-0.85	2	80	1.6e-07	1	U	L.LAGQS
5710	679.3592	1356.7039	1356.7038	0.13	2	(76)	4.2e-07	1	U	L.LAGQS
5801	684.8107	1367.6068	1367.6140	-5.24	0	(23)	0.095	1	U	Y.HMTSP
5803	684.8182	1367.6218	1367.6140	5.74	0	51	0.00017	1	U	Y.HMTSP
7448	533.9253	1598.7542	1598.7549	-0.45	0	(24)	0.076	1	U	L.STRND
7449	533.9257	1598.7553	1598.7549	0.24	0	34	0.0072	1	U	L.STRND

43. [2::sp|P68767|AMPA_ECOLI](#) Mass: 55358 Score: 232 Matches: 7(7) Sequences: 4
 Cytosol aminopeptidase OS=Escherichia coli (strain K12) OX=83333 GN=pepA PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5067	645.8075	1289.6004	1289.6000	0.34	0	(41)	0.0014	1	U	L.IAASE
5068	645.8085	1289.6025	1289.6000	1.94	0	64	7.8e-06	1	U	L.IAASE
5812	685.3755	1368.7365	1368.7361	0.33	0	54	4.8e-05	1	U	Y.KGNAS
5813	685.3760	1368.7374	1368.7361	0.96	0	(37)	0.0024	1	U	Y.KGNAS
6518	730.8723	1459.7301	1459.7307	-0.42	2	31	0.017	1	U	W.RLPLG
7047	768.3832	1534.7519	1534.7515	0.29	1	(78)	3.8e-07	1	U	L.SPIAE
7048	768.3841	1534.7536	1534.7515	1.40	1	84	1.1e-07	1	U	L.SPIAE

44. [2::sp|P06996|OMPC_ECOLI](#) Mass: 40343 Score: 222 Matches: 11(9) Sequences: 7
 Outer membrane protein C OS=Escherichia coli (strain K12) OX=83333 GN=ompC PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
172	394.1722	786.3299	786.3297	0.35	1	26	0.015	1		F.DYGRN
578	417.7212	833.4278	833.4283	-0.60	2	63	6.2e-06	1		F.GLV DG
579	417.7212	833.4278	833.4283	-0.60	2	(46)	0.00034	1		F.GLV DG
897	438.7505	875.4865	875.4865	0.08	2	(21)	0.077	1	U	F.GLRPS

898	438.7506	875.4867	875.4865	0.21	2	24	0.04	1	U	F.GLRPS
2005	500.7400	999.4655	999.4661	-0.64	1	21	0.091	1		L.KYDAN
2048	502.7286	1003.4427	1003.4433	-0.57	1	(31)	0.0085	1		Y.FNKNM
2049	502.7288	1003.4430	1003.4433	-0.27	1	31	0.0081	1		Y.FNKNM
3928	592.2581	1182.5016	1182.5015	0.02	2	29	0.014	1		Y.YFNKN
3929	592.2588	1182.5030	1182.5015	1.26	2	(25)	0.033	1		Y.YFNKN
6618	736.9030	1471.7915	1471.7631	19.3	0	28	0.022	1	U	F.TRDAG

45. [2::sp|P31224|ACRB_ECOLI](#) Mass: 113615 Score: 222 Matches: 7(4) Sequences: 6
 Multidrug efflux pump subunit AcrB OS=Escherichia coli (strain K12) OX=83333 GN=acrB
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2324	515.7801	1029.5456	1029.5454	0.18	0	46	0.00039	1	U	L.DTAA
3005	553.7686	1105.5225	1105.5226	-0.05	1	23	0.087	1	U	W.MNPN
3006	553.7695	1105.5245	1105.5226	1.73	1	(21)	0.12	1	U	W.MNPN
3501	573.8035	1145.5924	1145.5928	-0.38	0	24	0.091	1	U	L.GVSI
7337	526.2822	1575.8247	1575.8256	-0.61	2	27	0.039	1	U	L.LRDV
7604	814.9341	1627.8537	1627.8529	0.51	1	56	3.7e-05	1	U	L.ATGA
9226	1032.5210	2063.0274	2063.0171	5.01	0	48	0.00044	1	U	L.LPQE

46. [2::sp|P0A870|TALB_ECOLI](#) Mass: 35368 Score: 220 Matches: 11(10) Sequences: 1
 Transaldolase B OS=Escherichia coli (strain K12) OX=83333 GN=talB PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
443	409.7420	817.4694	817.4698	-0.47	1	(39)	0.001	1	U	L.IKLAS
444	409.7421	817.4696	817.4698	-0.23	1	42	0.00045	1	U	L.IKLAS
2518	528.8055	1055.5965	1055.5975	-0.90	1	(31)	0.0071	1	U	F.RNIGE
2520	528.8066	1055.5987	1055.5975	1.19	1	32	0.0064	1	U	F.RNIGE
3960	594.3048	1186.5949	1186.5942	0.64	0	41	0.0011	1	U	Y.NDAGI
3961	594.3051	1186.5957	1186.5942	1.24	0	(34)	0.0063	1	U	Y.NDAGI
6032	467.2323	1398.6751	1398.6878	-9.11	1	23	0.088	3	U	Y.QPQDA
7030	766.8776	1531.7406	1531.7406	-0.02	0	(36)	0.0054	1	U	Y.APAED
7031	766.8780	1531.7414	1531.7406	0.54	0	40	0.0024	1	U	Y.APAED
7312	524.9580	1571.8522	1571.8518	0.24	1	42	0.001	1	U	L.KELAE
7313	524.9583	1571.8529	1571.8518	0.70	1	(35)	0.0047	1	U	L.KELAE

Proteins matching a subset of these peptides:

[2::sp|P0A867|TALA_ECOLI](#) Mass: 35865 Score: 42 Matches: 2(2) Sequences: 1
 Transaldolase A OS=Escherichia coli (strain K12) OX=83333 GN=talA PE=3 SV=1

47. [2::sp|P0A6F5|CH60_ECOLI](#) Mass: 57464 Score: 215 Matches: 10(10) Sequences: 1
 60 kDa chaperonin OS=Escherichia coli (strain K12) OX=83333 GN=groL PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5368	659.3562	1316.6978	1316.6976	0.19	1	(39)	0.0018	1	U	Y.FINKP

5369	659.3562	1316.6978	1316.6976	0.19	1	40	0.0014	1	U	Y.FINKP
6436	726.3496	1450.6845	1450.6861	-1.09	0	(27)	0.049	1	U	L.TGGTV
6437	726.3517	1450.6888	1450.6861	1.85	0	29	0.033	1	U	L.TGGTV
7623	815.9200	1629.8254	1629.8250	0.26	1	43	0.0011	1	U	F.INKPE
7625	816.4211	1630.8277	1630.8090	11.5	1	(26)	0.055	1	U	F.INKPE
8382	889.4544	1776.8943	1776.8934	0.49	2	(48)	0.00039	1	U	Y.FINKP
8383	889.4573	1776.9001	1776.8934	3.79	2	54	0.00011	1	U	Y.FINKP
8933	647.3457	1939.0153	1939.0123	1.54	1	(36)	0.0041	1	U	L.ADLRG
8934	647.3469	1939.0188	1939.0123	3.34	1	49	0.00019	1	U	L.ADLRG

48. [2::sp|P76658|HLDE_ECOLI](#) Mass: 51247 Score: 214 Matches: 8(8) Sequences: 5
 Bifunctional protein HldE OS=Escherichia coli (strain K12) OX=83333 GN=hldE PE=1 SV=
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2751	541.8010	1081.5874	1081.5880	-0.58	0	23	0.033	1	U	L.KGDSR
4310	608.8252	1215.6358	1215.6347	0.93	0	(43)	0.00087	1	U	Y.DVTGA
4311	608.8253	1215.6360	1215.6347	1.03	0	55	5.5e-05	1	U	Y.DVTGA
4550	618.8166	1235.6187	1235.6180	0.62	1	(42)	0.0013	1	U	L.LVTRS
4551	618.8174	1235.6202	1235.6180	1.80	1	46	0.00059	1	U	L.LVTRS
6169	710.3587	1418.7028	1418.7042	-0.93	1	(56)	6e-05	1	U	W.VVSFE
6170	710.3610	1418.7075	1418.7042	2.34	1	57	5.2e-05	1	U	W.VVSFE
7348	789.8497	1577.6848	1577.6886	-2.41	2	35	0.0034	1	U	L.DFEEG

49. [2::sp|P0AGG8|TLDD_ECOLI](#) Mass: 51446 Score: 211 Matches: 7(6) Sequences: 4
 Metalloprotease TldD OS=Escherichia coli (strain K12) OX=83333 GN=tldD PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1830	492.7902	983.5659	983.5651	0.78	1	42	0.00036	1	U	Y.NVLIE
1946	497.2654	992.5161	992.5178	-1.70	2	(42)	0.0012	1	U	F.AYADQ
1947	497.2659	992.5173	992.5178	-0.53	2	50	0.00019	1	U	F.AYADQ
7424	797.8970	1593.7795	1593.7787	0.48	1	96	7.4e-09	1	U	Y.APNFG
7426	797.8982	1593.7819	1593.7787	2.01	1	(71)	1.9e-06	1	U	Y.APNFG
8921	968.9841	1935.9536	1935.9499	1.89	0	(25)	0.071	1	U	Y.MLP GK
8922	968.9855	1935.9565	1935.9499	3.40	0	27	0.05	1	U	Y.MLP GK

50. [2::sp|P24182|ACCC_ECOLI](#) Mass: 49745 Score: 198 Matches: 9(8) Sequences: 5
 Biotin carboxylase OS=Escherichia coli (strain K12) OX=83333 GN=accC PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1981	499.7324	997.4502	997.4505	-0.33	2	44	0.0005	1	U	Y.GFLSE
2222	511.7490	1021.4834	1021.4829	0.49	0	55	7.1e-05	1	U	F.AEQVE
2223	511.7492	1021.4838	1021.4829	0.92	0	(54)	9.1e-05	1	U	F.AEQVE
2226	511.7590	1021.5035	1021.4829	20.2	0	(20)	0.21	1	U	F.AEQVE
2227	511.7606	1021.5066	1021.4829	23.3	0	(30)	0.019	1	U	F.AEQVE
2919	549.3378	1096.6611	1096.6604	0.63	0	40	0.00026	1	U	F.IGPKA
2920	549.3387	1096.6628	1096.6604	2.18	0	(26)	0.0056	1	U	F.IGPKA
4127	600.8452	1199.6759	1199.6761	-0.23	0	29	0.014	1	U	L.IIDGI

[6400](#) 723.9091 1445.8036 1445.7990 3.13 1 32 0.0063 1 U Y.LENPR

51. [2::sp|P0A6H1|CLPX_ECOLI](#) Mass: 46726 Score: 197 Matches: 11(8) Sequences: 6
ATP-dependent Clp protease ATP-binding subunit ClpX OS=Escherichia coli (strain K12)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1264	465.7739	929.5332	929.5334	-0.30	2	(21)	0.089	1	U	L.ARLLD
1265	465.7743	929.5340	929.5334	0.56	2	23	0.055	1	U	L.ARLLD
1691	486.2980	970.5814	970.5811	0.30	1	(26)	0.011	1	U	L.RSIVE
1693	486.2980	970.5815	970.5811	0.42	1	28	0.0076	1	U	L.RSIVE
2173	508.7851	1015.5556	1015.5437	11.7	1	20	0.13	7	U	L.SEEAL
2404	522.3077	1042.6009	1042.6023	-1.28	1	42	0.00056	1	U	L.LIGPT
2405	522.3088	1042.6031	1042.6023	0.83	1	(33)	0.0047	1	U	L.LIGPT
3718	582.3373	1162.6600	1162.6598	0.20	2	(30)	0.0066	1	U	F.LQVDT
3719	582.3388	1162.6629	1162.6598	2.73	2	38	0.0011	1	U	F.LQVDT
5056	644.8442	1287.6739	1287.6711	2.23	1	(44)	0.00091	1	U	L.AQVEP
5057	644.8445	1287.6745	1287.6711	2.70	1	51	0.00015	1	U	L.AQVEP

52. [2::sp|P0A6A3|ACKA_ECOLI](#) Mass: 43605 Score: 196 Matches: 11(11) Sequences: 6
Acetate kinase OS=Escherichia coli (strain K12) OX=83333 GN=ackA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
942	442.2171	882.4197	882.4195	0.21	0	(28)	0.023	1	U	L.GAGAA
943	442.2174	882.4202	882.4195	0.77	0	30	0.013	1	U	L.GAGAA
2068	503.7662	1005.5178	1005.5165	1.32	0	31	0.014	1	U	Y.VTQEA
2069	503.7671	1005.5196	1005.5165	3.09	0	(30)	0.019	1	U	Y.VTQEA
2759	542.8041	1083.5936	1083.5924	1.12	1	34	0.0033	1	U	L.AQKPE
2760	542.8045	1083.5944	1083.5924	1.90	1	(34)	0.0035	1	U	L.AQKPE
3344	569.2304	1136.4461	1136.4444	1.51	0	24	0.016	1	U	F.HQTMP
5159	650.7958	1299.5771	1299.5765	0.47	1	(46)	0.00033	1	U	L.GLTEV
5160	650.7977	1299.5809	1299.5765	3.37	1	49	0.00017	1	U	L.GLTEV
9033	990.5417	1979.0688	1979.0687	0.05	0	(26)	0.029	1	U	F.INKEG
9034	990.5433	1979.0720	1979.0687	1.65	0	31	0.0081	1	U	F.INKEG

53. [2::sp|P0A817|METK_ECOLI](#) Mass: 42153 Score: 195 Matches: 11(7) Sequences: 6
S-adenosylmethionine synthase OS=Escherichia coli (strain K12) OX=83333 GN=metK PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
652	422.2555	842.4964	842.4974	-1.20	2	(21)	0.058	1	U	L.LRDAA
653	422.2559	842.4973	842.4974	-0.10	2	28	0.012	1	U	L.LRDAA
1517	478.2998	954.5851	954.5862	-1.12	0	35	0.00087	1	U	Y.VAKNI
2805	544.2843	1086.5540	1086.5557	-1.52	0	(24)	0.063	1	U	F.GTEKV
2807	544.2857	1086.5569	1086.5557	1.08	0	25	0.052	1	U	F.GTEKV
4586	620.7862	1239.5579	1239.5554	2.08	0	(22)	0.097	1	U	L.ADRCE
4587	620.7862	1239.5579	1239.5554	2.08	0	25	0.059	1	U	L.ADRCE
4798	631.3503	1260.6861	1260.6826	2.77	1	(21)	0.12	1	U	W.LRPDA
4799	631.3506	1260.6866	1260.6826	3.17	1	24	0.054	1	U	W.LRPDA

7473	802.9313	1603.8480	1603.8457	1.40	1	(52)	0.00013	1	U	F.QYDDG
7475	802.9331	1603.8517	1603.8457	3.69	1	58	2.6e-05	1	U	F.QYDDG

54. [2::sp|P25553|ALDA_ECOLI](#) Mass: 52411 Score: 193 Matches: 9(9) Sequences: 5
 Lactaldehyde dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=aldA PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1616	483.2566	964.4987	964.4978	1.00	0	41	0.0013	1	U	F.GGKAV
1617	483.2570	964.4994	964.4978	1.64	0	(35)	0.0056	1	U	F.GGKAV
4761	629.3431	1256.6717	1256.6725	-0.59	1	30	0.013	1	U	L.VLGRG
4762	629.3455	1256.6765	1256.6725	3.20	1	(25)	0.038	1	U	L.VLGRG
5239	653.3583	1304.7021	1304.6976	3.46	0	40	0.0017	1	U	L.TGNTI
6582	735.8544	1469.6943	1469.6933	0.72	0	(33)	0.011	1	U	F.GNPAE
6583	735.8544	1469.6943	1469.6933	0.72	0	36	0.0048	1	U	F.GNPAE
7864	835.4251	1668.8357	1668.8318	2.29	0	51	0.00015	1	U	Y.EGEII
7865	835.4261	1668.8376	1668.8318	3.46	0	(37)	0.004	1	U	Y.EGEII

55. [2::sp|P0AGD7|SRP54_ECOLI](#) Mass: 49812 Score: 181 Matches: 9(6) Sequences: 5
 Signal recognition particle protein OS=Escherichia coli (strain K12) OX=83333 GN=ffh
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2868	546.8244	1091.6342	1091.6339	0.34	1	(20)	0.039	1	U	L.NLAAQ
2869	546.8249	1091.6352	1091.6339	1.23	1	31	0.0034	1	U	L.NLAAQ
4475	615.8253	1229.6360	1229.6364	-0.36	0	25	0.057	1	U	L.TKVDG
4476	615.8268	1229.6391	1229.6364	2.21	0	(23)	0.082	1	U	L.TKVDG
5596	672.8618	1343.7090	1343.7085	0.34	0	(49)	0.00027	1	U	L.EADVA
5597	672.8634	1343.7122	1343.7085	2.78	0	52	0.00013	1	U	L.EADVA
5958	695.3664	1388.7182	1388.7187	-0.37	2	29	0.024	1	U	F.LGVGE
9177	682.0358	2043.0857	2043.0847	0.45	1	46	0.00035	1	U	L.SLIED
9180	682.0373	2043.0902	2043.0847	2.68	1	(21)	0.1	1	U	L.SLIED

56. [2::sp|P0A6M8|EFG_ECOLI](#) Mass: 77704 Score: 177 Matches: 5(4) Sequences: 4(3)
 Elongation factor G OS=Escherichia coli (strain K12) OX=83333 GN=fusA PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3096	557.7802	1113.5457	1113.5455	0.26	1	40	0.0013	1	U	L.QLAIG
5255	653.8447	1305.6749	1305.6751	-0.15	0	22	0.15	1	U	L.AGYPV
7005	765.4069	1528.7993	1528.7984	0.57	2	(52)	0.00012	1	U	Y.LGGEE
7008	765.4093	1528.8040	1528.7984	3.68	2	73	8.1e-07	1	U	Y.LGGEE
8945	972.4865	1942.9585	1942.9558	1.38	1	42	0.0013	1	U	L.KDVTT

57. [2::sp|P21507|SRMB_ECOLI](#) Mass: 49998 Score: 174 Matches: 6(6) Sequences: 4
 ATP-dependent RNA helicase SrmB OS=Escherichia coli (strain K12) OX=83333 GN=srmB PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1090	454.2294	906.4443	906.4447	-0.42	1	(37)	0.0037	1	U	L.EALQD
1091	454.2299	906.4452	906.4447	0.53	1	46	0.00045	1	U	L.EALQD
3910	591.2939	1180.5732	1180.5724	0.67	0	46	0.00046	1	U	L.GSAPT
3911	591.2944	1180.5742	1180.5724	1.50	0	(43)	0.0009	1	U	L.GSAPT
5373	659.7744	1317.5343	1317.5296	3.56	1	34	0.0024	1	U	F.NFDMP
6955	763.3737	1524.7328	1524.7321	0.45	0	50	0.0002	1	U	F.AQDIE

58. [2::sp|P02943|LAMB_ECOLI](#) Mass: 49995 Score: 164 Matches: 7(6) Sequences: 4
Maltoporin OS=Escherichia coli (strain K12) OX=83333 GN=lamB PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
318	402.7162	803.4178	803.4178	0.09	0	(21)	0.11	1	U	F.GKAVP
319	402.7163	803.4181	803.4178	0.39	0	25	0.042	1	U	F.GKAVP
4155	602.3106	1202.6067	1202.6044	1.90	1	(32)	0.014	1	U	Y.RLV DG
4156	602.3109	1202.6073	1202.6044	2.40	1	41	0.0016	1	U	Y.RLV DG
4232	606.2828	1210.5510	1210.5500	0.85	0	60	1.6e-05	1	U	Y.ATDSM
4233	606.2835	1210.5523	1210.5500	1.96	0	(54)	6.4e-05	1	U	Y.ATDSM
8335	884.4007	1766.7868	1766.7820	2.77	0	38	0.0029	1	U	Y.DNVES

59. [2::sp|P0AE08|AHPC_ECOLI](#) Mass: 20862 Score: 151 Matches: 9(8) Sequences: 4
Alkyl hydroperoxide reductase C OS=Escherichia coli (strain K12) OX=83333 GN=ahpC PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2123	506.8062	1011.5977	1011.5964	1.30	2	47	8.6e-05	1	U	L.APSLD
2124	506.8065	1011.5985	1011.5964	2.03	2	(39)	0.00056	1	U	L.APSLD
8273	585.9254	1754.7544	1754.7530	0.84	1	(32)	0.008	1	U	F.DNMRE
8274	585.9260	1754.7563	1754.7530	1.88	1	(25)	0.038	1	U	F.DNMRE
8275	878.3855	1754.7564	1754.7530	1.99	1	(20)	0.12	1	U	F.DNMRE
8276	878.3856	1754.7567	1754.7530	2.12	1	33	0.0063	1	U	F.DNMRE
8629	923.9118	1845.8090	1845.8091	-0.03	2	35	0.0038	1	U	F.VCPTPE
9201	684.6723	2050.9951	2050.9960	-0.43	1	(35)	0.0088	1	U	F.KNGEF
9202	684.6741	2051.0004	2050.9960	2.16	1	35	0.008	1	U	F.KNGEF

60. [2::sp|P0A953|FABB_ECOLI](#) Mass: 42928 Score: 150 Matches: 7(6) Sequences: 4
3-oxoacyl-[acyl-carrier-protein] synthase 1 OS=Escherichia coli (strain K12) OX=83333 GN=fabB PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
323	403.2319	804.4492	804.4494	-0.23	0	(39)	0.0012	1	U	L.AAIRE
325	403.2320	804.4494	804.4494	-0.00	0	46	0.00023	1	U	L.AAIRE
5073	645.8341	1289.6537	1289.6463	5.71	0	(34)	0.011	1	U	L.NIVTE
5074	645.8342	1289.6539	1289.6463	5.90	0	38	0.004	1	U	L.NIVTE
6500	729.3853	1456.7561	1456.7522	2.68	0	46	0.00053	1	U	L.GIVSS
6501	729.3858	1456.7570	1456.7522	3.35	0	(44)	0.00084	1	U	L.GIVSS
7753	551.9536	1652.8390	1652.8370	1.23	1	21	0.16	1	U	Y.LNSHG

61. [2::sp|P0AGE9|SUCD_ECOLI](#) Mass: 30044 Score: 149 Matches: 5(5) Sequences: 3(3)
 Succinate--CoA ligase [ADP-forming] subunit alpha OS=Escherichia coli (strain K12) OX=83333 GN=sucC PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1254	465.2689	928.5232	928.5229	0.27	0	45	0.00035	1	U	L.EAIDA
1255	465.2690	928.5234	928.5229	0.53	0	(34)	0.0049	1	U	L.EAIDA
2487	527.7559	1053.4973	1053.4978	-0.53	0	46	0.00037	1	U	Y.EAVKQ
2488	527.7571	1053.4996	1053.4978	1.67	0	(46)	0.00043	1	U	Y.EAVKQ
8449	897.4768	1792.9389	1792.9319	3.92	0	58	2.8e-05	1	U	F.NTVRE

62. [2::sp|P31979|NUOF_ECOLI](#) Mass: 49774 Score: 148 Matches: 5(5) Sequences: 4(4)
 NADH-quinone oxidoreductase subunit F OS=Escherichia coli (strain K12) OX=83333 GN=nuoF PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2478	527.2727	1052.5309	1052.5291	1.70	2	27	0.035	1	U	L.VRNLE
2479	527.2728	1052.5310	1052.5291	1.81	2	(26)	0.042	1	U	L.VRNLE
5509	666.3345	1330.6545	1330.6551	-0.45	0	34	0.0079	1	U	W.GKPTC
7435	533.2723	1596.7950	1596.7936	0.87	2	32	0.012	1	U	Y.FREEF
8348	885.9316	1769.8486	1769.8432	3.08	1	60	2.1e-05	1	U	L.EREGE

63. [2::sp|P37095|PEPB_ECOLI](#) Mass: 46436 Score: 146 Matches: 7(6) Sequences: 4(4)
 Peptidase B OS=Escherichia coli (strain K12) OX=83333 GN=pepB PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
672	423.2476	844.4806	844.4807	-0.05	1	21	0.075	1	U	W.RLPLA
7238	522.2760	1563.8062	1563.8005	3.63	1	32	0.013	1	U	Y.RITKG
7239	522.2772	1563.8097	1563.8005	5.86	1	(28)	0.033	1	U	Y.RITKG
7739	826.8939	1651.7732	1651.7729	0.13	2	47	0.00047	1	U	L.ALDYN
7740	826.8955	1651.7765	1651.7729	2.13	2	(36)	0.0052	1	U	L.ALDYN
8489	905.4720	1808.9294	1808.9268	1.43	1	(42)	0.0014	1	U	W.VRDTI
8490	905.4738	1808.9331	1808.9268	3.47	1	52	0.00014	1	U	W.VRDTI

64. [2::sp|P60906|SYH_ECOLI](#) Mass: 47285 Score: 135 Matches: 6(4) Sequences: 4(3)
 Histidine--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=hisS PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1706	487.2467	972.4788	972.4777	1.11	1	23	0.058	1	U	Y.NQEQ
4263	607.3264	1212.6381	1212.6350	2.60	1	(22)	0.071	1	U	L.DSKN
4264	607.3265	1212.6385	1212.6350	2.91	1	23	0.057	1	U	L.DSKN
6763	747.9299	1493.8453	1493.8453	-0.01	0	51	4.7e-05	1	U	Y.SEIR
6764	747.9301	1493.8455	1493.8453	0.15	0	(29)	0.0063	1	U	Y.SEIR
9125	1009.0399	2016.0653	2016.0568	4.21	2	40	0.0016	1	U	L.LVQA

65. [2::sp|P61889|MDH_ECOLI](#) Mass: 32488 Score: 135 Matches: 5(4) Sequences: 4(3)

Malate dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=mdh PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1613	483.2561	964.4977	964.4978	-0.08	0	23	0.081	1	U	L.DIIRS
2556	530.2879	1058.5612	1058.5608	0.45	0	42	0.00099	1	U	L.KTQLP
3829	586.8300	1171.6454	1171.6448	0.45	1	44	0.00041	1	U	L.LKTQL
3830	586.8300	1171.6455	1171.6448	0.56	1	(40)	0.0011	1	U	L.LKTQL
7112	772.3799	1542.7452	1542.7413	2.51	1	28	0.029	1	U	F.SGEDA

66. [2::sp|P0A855|TOLB_ECOLI](#) Mass: 45927 Score: 130 Matches: 4(3) Sequences: 3(3)
 Tol-Pal system protein TolB OS=Escherichia coli (strain K12) OX=83333 GN=tolB PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4360	611.2977	1220.5808	1220.5786	1.82	0	28	0.03	1	U	F.TSDQ
7945	842.3580	1682.7015	1682.7020	-0.29	0	76	2.3e-07	1	U	W.EGSQ
7946	842.3596	1682.7047	1682.7020	1.60	0	(58)	1.4e-05	1	U	W.EGSQ
9221	1030.0201	2058.0257	2058.0270	-0.61	1	26	0.062	1	U	W.SALG

67. [2::sp|P11447|ARLY_ECOLI](#) Mass: 50686 Score: 130 Matches: 5(4) Sequences: 3(3)
 Argininosuccinate lyase OS=Escherichia coli (strain K12) OX=83333 GN=argH PE=1 SV=3
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1311	468.7306	935.4467	935.4461	0.64	0	35	0.0063	1	U	F.TQAAD
1312	468.7308	935.4471	935.4461	1.09	0	(24)	0.065	1	U	F.TQAAD
1858	493.8167	985.6189	985.6172	1.71	1	42	0.00016	1	U	W.SKALV
6367	722.3834	1442.7522	1442.7518	0.28	1	(42)	0.0011	1	U	Y.RLAEQ
6368	722.3850	1442.7553	1442.7518	2.48	1	55	5.2e-05	1	U	Y.RLAEQ

68. [2::sp|P30845|EPTA_ECOLI](#) Mass: 62369 Score: 129 Matches: 6(4) Sequences: 4(4)
 Phosphoethanolamine transferase EptA OS=Escherichia coli (strain K12) OX=83333 GN=epa
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2407	522.7782	1043.5418	1043.5400	1.79	1	21	0.1	1	U	L.LKEHQ
4366	611.8071	1221.5996	1221.5990	0.52	0	43	0.0012	1	U	L.IVGET
4367	611.8076	1221.6007	1221.5990	1.42	0	(34)	0.0087	1	U	L.IVGET
4498	616.7891	1231.5637	1231.5622	1.21	1	24	0.058	1	U	L.HTIGS
4719	627.8562	1253.6978	1253.6980	-0.08	1	(36)	0.0021	1	U	Y.INNLQ
4721	627.8578	1253.7010	1253.6980	2.45	1	44	0.00027	1	U	Y.INNLQ

69. [2::sp|P00509|AAT_ECOLI](#) Mass: 43831 Score: 129 Matches: 4(4) Sequences: 3(3)
 Aspartate aminotransferase OS=Escherichia coli (strain K12) OX=83333 GN=aspC PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3346	569.2812	1136.5478	1136.5462	1.46	1	28	0.037	1	U	F.NSAGL
4387	612.8101	1223.6056	1223.6033	1.81	2	42	0.0012	1	U	Y.LLENE
4388	612.8120	1223.6095	1223.6033	5.00	2	(33)	0.0098	1	U	Y.LLENE
5003	640.8120	1279.6093	1279.6044	3.83	0	62	1.5e-05	1	U	L.VAADS

70. [2::sp|P60438|RL3_ECOLI](#) Mass: 22230 Score: 128 Matches: 5(4) Sequences: 4(3)
 50S ribosomal protein L3 OS=Escherichia coli (strain K12) OX=83333 GN=rplC PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
498	413.2809	824.5472	824.5484	-1.39	0	24	0.0037	1	U	L.IVKPA
4101	600.2926	1198.5706	1198.5691	1.32	0	40	0.0013	1	U	F.RTQDA
4274	405.5599	1213.6578	1213.6567	0.88	1	20	0.14	1	U	F.AKAGV
5037	642.8627	1283.7109	1283.7085	1.85	1	(26)	0.025	1	U	L.LVKGA
5039	642.8641	1283.7136	1283.7085	3.94	1	43	0.00051	1	U	L.LVKGA

71. [2::sp|P0AEI4|RIMO_ECOLI](#) Mass: 50064 Score: 125 Matches: 5(4) Sequences: 3(3)
 Ribosomal protein S12 methylthiotransferase RimO OS=Escherichia coli (strain K12) OX=83333 GN=rpsL2 PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3925	591.8584	1181.7022	1181.7020	0.24	2	(30)	0.0028	1	U	F.LSLVP
3926	591.8593	1181.7041	1181.7020	1.78	2	38	0.00045	1	U	F.LSLVP
9811	889.0967	2664.2682	2664.2667	0.56	0	65	6.3e-06	1	U	Y.SPVEG
9812	889.0974	2664.2704	2664.2667	1.39	0	(58)	3.3e-05	1	U	Y.SPVEG
9900	950.7863	2849.3371	2849.3277	3.32	0	22	0.12	1	U	L.VIIDE

72. [2::sp|P37349|DHAM_ECOLI](#) Mass: 51872 Score: 124 Matches: 5(5) Sequences: 3(3)
 Protein-lysine deacetylase OS=Escherichia coli (strain K12) OX=83333 GN=dhaM PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3257	564.3015	1126.5885	1126.5870	1.34	0	(44)	0.00035	1	U	L.IAKGP
3258	564.3032	1126.5919	1126.5870	4.37	0	46	0.00023	1	U	L.IAKGP
6510	729.8953	1457.7761	1457.7766	-0.32	1	(31)	0.013	1	U	L.IAKGP
6511	729.8962	1457.7779	1457.7766	0.95	1	44	0.00067	1	U	L.IAKGP
8624	923.4861	1844.9576	1844.9520	3.05	1	35	0.0058	1	U	L.TQTKE

73. [2::sp|P60422|RL2_ECOLI](#) Mass: 29956 Score: 123 Matches: 5(3) Sequences: 3(2)
 50S ribosomal protein L2 OS=Escherichia coli (strain K12) OX=83333 GN=rplB PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1205	461.2498	920.4850	920.4868	-1.98	0	22	0.078	1	U	F.GKHPV
2847	546.2962	1090.5778	1090.5771	0.68	0	62	1.1e-05	1	U	Y.VQIVA
2848	546.2971	1090.5796	1090.5771	2.26	0	(51)	0.00012	1	U	Y.VQIVA
5754	681.8377	1361.6607	1361.6575	2.38	1	39	0.0029	1	U	L.EYDPN

[5755](#) 681.8380 1361.6615 1361.6575 2.91 1 (23) 0.13 1 U L.EYDPN

74. [2::sp|P76403|YEQQ_ECOLI](#) Mass: 51446 Score: 117 Matches: 8(7) Sequences: 3
Uncharacterized protease YegQ OS=Escherichia coli (strain K12) OX=83333 GN=yegQ PE=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1629	483.7362	965.4577	965.4567	1.12	0	26	0.046	1	U	Y.SVSDR
1630	483.7363	965.4580	965.4567	1.37	0	(22)	0.12	1	U	Y.SVSDR
5415	661.8090	1321.6034	1321.5972	4.66	0	(34)	0.0078	1	U	F.MIEEA
5554	669.8035	1337.5925	1337.5921	0.28	0	(44)	0.00069	1	U	F.MIEEA
5555	669.8055	1337.5965	1337.5921	3.29	0	47	0.00038	1	U	F.MIEEA
5734	453.9174	1358.7304	1358.7306	-0.14	0	(38)	0.0026	1	U	Y.RKAID
5735	453.9175	1358.7307	1358.7306	0.06	0	(34)	0.0077	1	U	Y.RKAID
5736	680.3732	1358.7318	1358.7306	0.86	0	44	0.00066	1	U	Y.RKAID

75. [2::sp|P0A7V8|RS4_ECOLI](#) Mass: 23512 Score: 116 Matches: 7(4) Sequences: 4(2)
30S ribosomal protein S4 OS=Escherichia coli (strain K12) OX=83333 GN=rpsD PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
709	424.7347	847.4549	847.4552	-0.39	1	28	0.015	1	U	Y.GVLER
711	424.7353	847.4561	847.4552	1.12	1	(26)	0.025	1	U	Y.GVLER
1413	473.2486	944.4826	944.4927	-10.63	1	25	0.052	5	U	L.KGNTG
1414	473.2530	944.4915	944.4927	-1.21	1	(22)	0.1	1	U	L.KGNTG
2734	540.7750	1079.5354	1079.5360	-0.55	1	21	0.13	1	U	L.SRREG
6880	758.3852	1514.7558	1514.7616	-3.84	2	41	0.0014	1	U	L.SADIN
6881	758.3882	1514.7619	1514.7616	0.19	2	(34)	0.0076	1	U	L.SADIN

76. [2::sp|P05793|ILVC_ECOLI](#) Mass: 54376 Score: 106 Matches: 4(3) Sequences: 3(1)
Ketol-acid reductoisomerase (NADP(+)) OS=Escherichia coli (strain K12) OX=83333 GN=i
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
7708	824.9269	1647.8393	1647.8389	0.24	1	53	0.00012	1	U	F.VAEVK
7709	824.9285	1647.8424	1647.8389	2.10	1	(49)	0.00033	1	U	F.VAEVK
8209	871.4013	1740.7881	1740.7842	2.21	1	35	0.0053	1	U	F.ETAPQ
8776	944.9357	1887.8569	1887.8526	2.26	2	23	0.086	1	U	F.ETAPQ

77. [2::sp|P0A7V3|RS3_ECOLI](#) Mass: 25967 Score: 103 Matches: 3(3) Sequences: 2(2)
30S ribosomal protein S3 OS=Escherichia coli (strain K12) OX=83333 GN=rpsC PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1288	467.2482	932.4818	932.4815	0.33	0	(39)	0.002	1	U	L.VADSI
1289	467.2486	932.4826	932.4815	1.19	0	46	0.00042	1	U	L.VADSI
7377	793.8485	1585.6825	1585.6896	-4.51	2	57	2.4e-05	1	U	F.ANTKE

78. [2::sp|P22188|MURE_ECOLI](#) **Mass:** 53766 **Score:** 102 **Matches:** 4(3) **Sequences:** 3
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase OS=Escherichia coli
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1732	488.2303	974.4461	974.4458	0.34	0	31	0.0074	1	U	L.VAGKG
1733	488.2305	974.4465	974.4458	0.77	0	(27)	0.022	1	U	L.VAGKG
4654	623.8389	1245.6632	1245.6605	2.14	0	22	0.1	1	U	F.TAPGK
9275	699.0284	2094.0633	2094.0593	1.90	0	48	0.00029	1	U	L.GKVIP

79. [2::sp|P0A9K3|PHOL_ECOLI](#) **Mass:** 39129 **Score:** 97 **Matches:** 4(4) **Sequences:** 3
PhoH-like protein OS=Escherichia coli (strain K12) OX=83333 GN=ybeZ PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
694	424.2025	846.3905	846.3970	-7.78	0	24	0.044	1	U	F.DDNIK
3800	585.8268	1169.6390	1169.6404	-1.20	0	24	0.042	1	U	L.TRPAV
4703	626.8683	1251.7220	1251.7187	2.69	0	(22)	0.026	1	U	L.IERNV
4704	626.8691	1251.7236	1251.7187	3.95	0	49	4.8e-05	1	U	L.IERNV

80. [2::sp|P0A858|TPIS_ECOLI](#) **Mass:** 27126 **Score:** 94 **Matches:** 4(3) **Sequences:** 2
Triosephosphate isomerase OS=Escherichia coli (strain K12) OX=83333 GN=tpiA PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
216	397.2132	792.4119	792.4130	-1.37	0	24	0.054	1	U	L.KTQGA
217	397.2134	792.4123	792.4130	-0.92	0	(23)	0.064	1	U	L.KTQGA
4881	635.3807	1268.7469	1268.7452	1.37	0	70	4.6e-07	1	U	F.AVIVK
4882	635.3818	1268.7491	1268.7452	3.10	0	(58)	5.9e-06	1	U	F.AVIVK

81. [2::sp|P0AEK4|FABI_ECOLI](#) **Mass:** 28074 **Score:** 93 **Matches:** 1(1) **Sequences:** 1
Enoyl-[acyl-carrier-protein] reductase [NADH] FabI OS=Escherichia coli (strain K12)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
9139	1012.4739	2022.9333	2022.9283	2.48	2	95	6.8e-09	1	U	F.APGD

82. [2::sp|P00448|SODM_ECOLI](#) **Mass:** 23083 **Score:** 93 **Matches:** 4(3) **Sequences:** 2
Superoxide dismutase [Mn] OS=Escherichia coli (strain K12) OX=83333 GN=sodA PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5756	454.9052	1361.6938	1361.6939	-0.08	1	(20)	0.22	1	U	L.QGDLK
5757	454.9055	1361.6947	1361.6939	0.60	1	34	0.0092	1	U	L.QGDLK
5970	696.3389	1390.6632	1390.6629	0.17	1	59	3.1e-05	1	U	W.NVVNW

[5971](#) 696.3407 1390.6668 1390.6629 2.80 1 (41) 0.0019 1 U W.NVVNW

83. [2::sp|P15034|AMPP_ECOLI](#) Mass: 50012 Score: 84 Matches: 5(2) Sequences: 3
Xaa-Pro aminopeptidase OS=Escherichia coli (strain K12) OX=83333 GN=pepP PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1413	473.2486	944.4826	944.5039	-22.52	0	22	0.096	7	U	Y.GQDRS
2086	504.7582	1007.5019	1007.5036	-1.65	0	28	0.03	1	U	F.TQAQR
2087	504.7584	1007.5023	1007.5036	-1.29	0	(21)	0.14	1	U	F.TQAQR
7762	828.3819	1654.7492	1654.7475	1.09	0	(24)	0.074	1	U	F.AAPEV
7763	828.3848	1654.7550	1654.7475	4.55	0	34	0.0072	1	U	F.AAPEV

84. [2::sp|P0A7L0|RL1_ECOLI](#) Mass: 24714 Score: 83 Matches: 2(2) Sequences: 1(1)
50S ribosomal protein L1 OS=Escherichia coli (strain K12) OX=83333 GN=rp1A PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6610	736.8709	1471.7271	1471.7266	0.35	0	(74)	7.9e-07	1	U	F.TQGAN
6613	736.8733	1471.7320	1471.7266	3.66	0	83	9.1e-08	1	U	F.TQGAN

85. [2::sp|P08660|AK3_ECOLI](#) Mass: 48787 Score: 80 Matches: 4(3) Sequences: 2(2)
Lysine-sensitive aspartokinase 3 OS=Escherichia coli (strain K12) OX=83333 GN=lysC PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4268	607.3494	1212.6843	1212.6867	-1.94	0	(31)	0.0081	1	U	L.LPAVR
4269	607.3525	1212.6904	1212.6867	3.09	0	37	0.002	1	U	L.LPAVR
5946	694.3637	1386.7127	1386.7143	-1.13	2	43	0.00095	1	U	L.VALAE
5947	694.3651	1386.7157	1386.7143	0.98	2	(24)	0.088	3	U	L.VALAE

86. [2::sp|P60723|RL4_ECOLI](#) Mass: 22073 Score: 80 Matches: 5(5) Sequences: 3(3)
50S ribosomal protein L4 OS=Escherichia coli (strain K12) OX=83333 GN=rp1D PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
195	395.2388	788.4630	788.4643	-1.64	1	(25)	0.026	1	U	L.KSILSE
198	395.2396	788.4646	788.4643	0.29	1	30	0.0081	1	U	L.KSILSE
1398	472.7740	943.5335	943.5338	-0.36	1	(27)	0.021	1	U	L.VLKDAQ
1402	472.7747	943.5349	943.5338	1.12	1	28	0.016	1	U	L.VLKDAQ
2783	543.3313	1084.6480	1084.6492	-1.05	1	21	0.044	1	U	F.SVEAPK

87. [2::sp|P00490|PHSM_ECOLI](#) Mass: 90865 Score: 79 Matches: 2(2) Sequences: 2(2)
Maltodextrin phosphorylase OS=Escherichia coli (strain K12) OX=83333 GN=malP PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5083	646.3495	1290.6844	1290.6820	1.91	1	52	9.1e-05	1	U	Y.VEAQ
5689	678.8487	1355.6828	1355.7157	-24.23	0	27	0.032	1	U	L.RAEQ

88. [2::sp|P27434|RODZ_ECOLI](#) Mass: 36283 Score: 79 Matches: 4(4) Sequences: 2
 Cytoskeleton protein RodZ OS=Escherichia coli (strain K12) OX=83333 GN=rodZ PE=1 SV=
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3820	586.3257	1170.6369	1170.6357	1.08	1	(26)	0.031	1	U	L.GLSQQ
3821	586.3265	1170.6384	1170.6357	2.34	1	45	0.00038	1	U	L.GLSQQ
9116	671.3738	2011.0997	2011.0990	0.37	2	34	0.0043	1	U	L.VHIPE
9117	671.3753	2011.1041	2011.0990	2.56	2	(24)	0.037	1	U	L.VHIPE

89. [2::sp|P0AGJ9|SYU_ECOLI](#) Mass: 47896 Score: 79 Matches: 1(1) Sequences: 1(1)
 Tyrosine--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=tyrS PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
7115	772.4023	1542.7900	1542.7889	0.70	1	79	2.6e-07	1	U	L.VAQVT

90. [2::sp|P0A862|TPX_ECOLI](#) Mass: 17995 Score: 77 Matches: 1(1) Sequences: 1(1)
 Thiol peroxidase OS=Escherichia coli (strain K12) OX=83333 GN=tpx PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4951	637.8634	1273.7122	1273.7129	-0.54	2	77	2.1e-07	1	U	F.TLVAK

91. [2::sp|P0ACC7|GLMU_ECOLI](#) Mass: 49388 Score: 77 Matches: 4(4) Sequences: 2
 Bifunctional protein GlnU OS=Escherichia coli (strain K12) OX=83333 GN=glnU PE=1 SV=
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2079	504.2732	1006.5318	1006.5335	-1.68	0	(28)	0.027	1	U	F.KTIIG
2080	504.2740	1006.5334	1006.5335	-0.10	0	29	0.022	1	U	F.KTIIG
3020	554.7806	1107.5467	1107.5448	1.73	1	48	0.00034	1	U	L.TVKLD
3021	554.7807	1107.5468	1107.5448	1.84	1	(37)	0.0038	1	U	L.TVKLD

92. [2::sp|P0AG48|RL21_ECOLI](#) Mass: 11557 Score: 76 Matches: 4(4) Sequences: 2
 50S ribosomal protein L21 OS=Escherichia coli (strain K12) OX=83333 GN=rplU PE=1 SV=
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3558	576.3195	1150.6245	1150.6234	0.95	1	(32)	0.0062	1	U	W.FTDVKI

3559	576.3203	1150.6261	1150.6234	2.32	1	36	0.0024	1	U	W.FTDVKI
6827	752.3976	1502.7807	1502.7803	0.29	0	(33)	0.01	1	U	L.MIANGE
6900	760.3940	1518.7734	1518.7752	-1.19	0	40	0.0025	1	U	L.MIANGE

93. [2::sp|P0A7S9|RS13 ECOLI](#) Mass: 13148 Score: 76 Matches: 2(2) Sequences: 1
 30S ribosomal protein S13 OS=Escherichia coli (strain K12) OX=83333 GN=rpsM PE=1 SV=
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5938	693.8773	1385.7400	1385.7402	-0.15	0	76	4.7e-07	1	U	L.AAAGI
5939	693.8790	1385.7434	1385.7402	2.32	0	(61)	1.4e-05	1	U	L.AAAGI

94. [2::sp|P0ABC7|HFLK ECOLI](#) Mass: 45517 Score: 72 Matches: 3(3) Sequences: 2
 Modulator of FtsH protease HflK OS=Escherichia coli (strain K12) OX=83333 GN=hflK PE=
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
575	417.2487	832.4828	832.4694	16.0	1	23	0.031	1	U	F.AKLLP
8306	881.9260	1761.8374	1761.8381	-0.41	1	(39)	0.003	1	U	Y.SVTSP
8307	881.9296	1761.8447	1761.8381	3.76	1	52	0.00016	1	U	Y.SVTSP

95. [2::sp|P0C018|RL18 ECOLI](#) Mass: 12762 Score: 71 Matches: 4(4) Sequences: 1
 50S ribosomal protein L18 OS=Escherichia coli (strain K12) OX=83333 GN=rplR PE=1 SV=
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6254	477.2674	1428.7804	1428.7824	-1.40	0	(26)	0.034	1	U	L.VAAST
6255	715.3984	1428.7823	1428.7824	-0.04	0	(69)	1.7e-06	1	U	L.VAAST
6256	477.2686	1428.7841	1428.7824	1.22	0	(36)	0.0032	1	U	L.VAAST
6257	715.4005	1428.7865	1428.7824	2.86	0	71	1.1e-06	1	U	L.VAAST

96. [2::sp|P0AB89|PUR8 ECOLI](#) Mass: 51625 Score: 69 Matches: 5(3) Sequences: 3
 Adenylosuccinate lyase OS=Escherichia coli (strain K12) OX=83333 GN=purB PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3072	556.8243	1111.6341	1111.6349	-0.72	1	23	0.028	1	U	Y.RQLNQV
3073	556.8257	1111.6368	1111.6349	1.69	1	(23)	0.03	1	U	Y.RQLNQV
3505	574.3016	1146.5886	1146.5881	0.45	1	26	0.052	1	U	W.QRDLTD
3506	574.3018	1146.5890	1146.5881	0.78	1	(25)	0.06	1	U	W.QRDLTD
7178	518.6226	1552.8460	1552.8460	0.01	1	20	0.097	1	U	F.IDGLAL

97. [2::sp|P0A7A9|IPYR ECOLI](#) Mass: 19805 Score: 67 Matches: 3(2) Sequences: 2
 Inorganic pyrophosphatase OS=Escherichia coli (strain K12) OX=83333 GN=ppa PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3019	554.7804	1107.5462	1107.5448	1.32	1	24	0.087	1	U	Y.EIDKE
7105	771.4338	1540.8530	1540.8501	1.91	0	(43)	0.00045	1	U	Y.VVIEI
7106	771.4354	1540.8562	1540.8501	3.96	0	44	0.00036	1	U	Y.VVIEI

98. [2::sp|P00960|SYGA_ECOLI](#) Mass: 35037 Score: 67 Matches: 3(3) Sequences: 2
 Glycine--tRNA ligase alpha subunit OS=Escherichia coli (strain K12) OX=83333 GN=glyQ
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
15	380.2344	758.4543	758.4538	0.72	2	23	0.048	1	U	Y.LGSLK
8217	871.9718	1741.9290	1741.9250	2.30	1	46	0.00035	1	U	F.QVVIK
8218	871.9730	1741.9314	1741.9250	3.64	1	(27)	0.028	1	U	F.QVVIK

99. [2::sp|P0A7J3|RL10_ECOLI](#) Mass: 17757 Score: 66 Matches: 3(2) Sequences: 2
 50S ribosomal protein L10 OS=Escherichia coli (strain K12) OX=83333 GN=rplJ PE=1 SV=
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2029	501.2726	1000.5306	1000.5301	0.49	0	22	0.12	1	U	L.AAVRD
6406	724.3936	1446.7725	1446.7718	0.51	1	(33)	0.008	1	U	L.ATLPT
6407	724.3959	1446.7773	1446.7718	3.82	1	45	0.00053	1	U	L.ATLPT

100. [2::sp|P0AD61|KPYK1_ECOLI](#) Mass: 51039 Score: 63 Matches: 2(2) Sequences: 1
 Pyruvate kinase I OS=Escherichia coli (strain K12) OX=83333 GN=pykF PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
8575	915.9455	1829.8764	1829.8717	2.59	0	63	1.1e-05	1	U	F.TTDKS
8576	915.9470	1829.8795	1829.8717	4.25	0	(35)	0.0074	1	U	F.TTDKS

101. [2::sp|P37773|MPL_ECOLI](#) Mass: 50298 Score: 62 Matches: 3(2) Sequences: 2(2)
 UDP-N-acetylmuramate--L-alanyl-gamma-D-glutamyl-meso-2,6-diaminoheptandioate ligase
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2674	537.8094	1073.6043	1073.6022	2.01	2	30	0.013	1	U	F.LLQPAH
7453	534.2909	1599.8508	1599.8508	0.02	2	32	0.0091	1	U	W.EVLLDG
7454	534.2910	1599.8512	1599.8508	0.26	2	(21)	0.12	1	U	W.EVLLDG

102. [2::sp|P0A9K9|SLYD_ECOLI](#) Mass: 21182 Score: 62 Matches: 3(1) Sequences: 2
 FKBP-type peptidyl-prolyl cis-trans isomerase SlyD OS=Escherichia coli (strain K12)
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2134	507.2723	1012.5301	1012.5077	22.1	0	(21)	0.081	1	U	L.VDESP

2135	507.2723	1012.5301	1012.5077	22.2	0	22	0.072	1	U	L.VDESP
9113	1006.0218	2010.0291	2010.0270	1.09	1	40	0.0018	1	U	Y.QVRTE

103. [2::sp|P0A7V0|RS2 ECOLI](#) Mass: 26784 Score: 59 Matches: 3(3) Sequences: 2(2)
 30S ribosomal protein S2 OS=Escherichia coli (strain K12) OX=83333 GN=rpsB PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2494	528.2474	1054.4803	1054.4787	1.53	0	30	0.015	1	U	M.ATVSMR
2495	528.2482	1054.4819	1054.4787	3.03	0	(25)	0.045	1	U	M.ATVSMR
6554	732.8285	1463.6425	1463.6416	0.62	0	29	0.016	1	U	F.AIVDTN

104. [2::sp|P76373|UDG ECOLI](#) Mass: 43744 Score: 59 Matches: 3(2) Sequences: 2(1)
 UDP-glucose 6-dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=ugd PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1328	469.2547	936.4948	936.4916	3.36	0	23	0.057	1	U	L.KDVADK
5443	662.8345	1323.6544	1323.6558	-1.06	1	38	0.0033	1	U	F.TDSTEA
5444	662.8372	1323.6598	1323.6558	3.00	1	(33)	0.01	1	U	F.TDSTEA

105. [2::sp|P0A6B7|ISCS ECOLI](#) Mass: 45232 Score: 59 Matches: 4(3) Sequences: 2(1)
 Cysteine desulfurase IscS OS=Escherichia coli (strain K12) OX=83333 GN=iscS PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
202	396.2234	790.4322	790.4337	-1.88	0	(23)	0.059	1	U	L.AIKGAA
203	396.2239	790.4331	790.4337	-0.72	0	34	0.0045	1	U	L.AIKGAA
3811	586.3069	1170.5992	1170.5995	-0.21	2	25	0.045	1	U	-.MKLPIY
3812	586.3082	1170.6018	1170.5995	1.99	2	(24)	0.049	1	U	-.MKLPIY

106. [2::sp|P37652|BCSB ECOLI](#) Mass: 86140 Score: 58 Matches: 3(3) Sequences: 2(1)
 Cyclic di-GMP-binding protein OS=Escherichia coli (strain K12) OX=83333 GN=bcsB PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4932	637.3347	1272.6549	1272.6384	13.0	0	27	0.037	1	U	L.QAAKGI
4933	637.3362	1272.6578	1272.6384	15.3	0	(25)	0.058	1	U	L.QAAKGI
7534	807.9290	1613.8434	1613.8335	6.14	2	31	0.015	1	U	L.QGLLDG

107. [2::sp|P0ADR8|PPNN ECOLI](#) Mass: 51281 Score: 58 Matches: 3(3) Sequences: 2(1)
 Pyrimidine/purine nucleotide 5'-monophosphate nucleosidase OS=Escherichia coli (stra
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4810	632.8067	1263.5988	1263.5943	3.64	1	31	0.019	1	U	L.NSGSLT

5171	650.8607	1299.7069	1299.7074	-0.43	1	27	0.029	1	U	L.KLYPDQ
5172	650.8622	1299.7098	1299.7074	1.82	1	(24)	0.053	1	U	L.KLYPDQ

108. [2::sp|P0AC41|SDHA ECOLI](#) Mass: 65008 Score: 57 Matches: 2(1) Sequences: 2
 Succinate dehydrogenase flavoprotein subunit OS=Escherichia coli (strain K12) OX=833333 GN=sdhA PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4852	634.3451	1266.6756	1266.6721	2.79	1	33	0.0066	1	U	W.QFHPTG
7460	801.9251	1601.8355	1601.8301	3.40	1	25	0.077	1	U	L.TVNEKG

109. [2::sp|P0AFK0|PmbA ECOLI](#) Mass: 48625 Score: 56 Matches: 3(3) Sequences: 2
 Metalloprotease PmbA OS=Escherichia coli (strain K12) OX=833333 GN=pmbA PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
562	416.7335	831.4525	831.4636	-13.41	1	30	0.013	1	U	Y.SARKL
563	416.7336	831.4527	831.4636	-13.19	1	(25)	0.039	1	U	Y.SARKL
4119	600.8233	1199.6320	1199.6299	1.80	1	26	0.034	1	U	F.GHLVG

110. [2::sp|P36683|ACNB ECOLI](#) Mass: 94009 Score: 56 Matches: 2(2) Sequences: 1
 Aconitate hydratase B OS=Escherichia coli (strain K12) OX=833333 GN=acnB PE=1 SV=3
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5286	655.3370	1308.6595	1308.6562	2.58	0	(27)	0.034	1	U	Y.VAQVD
5287	655.3379	1308.6613	1308.6562	3.97	0	56	4.7e-05	1	U	Y.VAQVD

111. [2::sp|P0A6Y8|DnaK ECOLI](#) Mass: 69130 Score: 55 Matches: 4(2) Sequences: 2
 Chaperone protein DnaK OS=Escherichia coli (strain K12) OX=833333 GN=dnaK PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3836	587.2998	1172.5850	1172.5826	2.12	0	32	0.01	1	U	F.KIIAAD
3837	587.3003	1172.5860	1172.5826	2.95	0	(29)	0.017	1	U	F.KIIAAD
7644	818.8945	1635.7744	1635.7740	0.24	0	24	0.095	1	U	L.ENAEGD
7645	818.8950	1635.7754	1635.7740	0.84	0	(22)	0.13	1	U	L.ENAEGD

112. [2::sp|P0A717|KPRS ECOLI](#) Mass: 34425 Score: 54 Matches: 2(2) Sequences: 1
 Ribose-phosphate pyrophosphokinase OS=Escherichia coli (strain K12) OX=833333 GN=prs
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1279	466.2639	930.5132	930.5135	-0.25	0	54	6.4e-05	1	U	L.SSVGVD
1280	466.2646	930.5146	930.5135	1.26	0	(45)	0.00049	1	U	L.SSVGVD

113. [2::sp|P32131|HEMN ECOLI](#) Mass: 53209 Score: 53 Matches: 2(1) Sequences: 2
Oxygen-independent coproporphyrinogen III oxidase OS=Escherichia coli (strain K12) C
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2972	552.2900	1102.5654	1102.5659	-0.42	0	22	0.11	1	U	Y.GLPKQT
3919	591.7822	1181.5499	1181.5499	-0.00	1	30	0.018	1	U	F.NRLSMG

114. [2::sp|P0ABK5|CYSK ECOLI](#) Mass: 34525 Score: 52 Matches: 2(2) Sequences: 1
Cysteine synthase A OS=Escherichia coli (strain K12) OX=83333 GN=cysK PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
8399	891.4857	1780.9568	1780.9571	-0.17	1	(26)	0.025	1	U	L.KPGVE
8400	891.4865	1780.9585	1780.9571	0.78	1	52	6.8e-05	1	U	L.KPGVE

115. [2::sp|P15977|MALQ ECOLI](#) Mass: 79080 Score: 52 Matches: 3(2) Sequences: 2
4-alpha-glucanotransferase OS=Escherichia coli (strain K12) OX=83333 GN=malQ PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1412	473.2484	944.4821	944.4815	0.73	1	(31)	0.012	1	U	F.ADDGV
1413	473.2486	944.4826	944.4815	1.26	1	32	0.011	1	U	F.ADDGV
4303	608.8007	1215.5869	1215.6136	-21.94	1	20	0.16	1	U	W.WQLPT

116. [1::sp|cRAP104|P12081|SYHC HUMAN](#) Mass: 57944 Score: 52 Matches: 2(1) Sequences: 1
Histidine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=HARS PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
27	381.2015	760.3885	760.3901	-2.17	0	32	0.0097	1	U	-.MAERAA
6399	482.9404	1445.7993	1445.7726	18.5	0	20	0.1	1	U	L.EEKIRT

117. [2::sp|P0A6Y5|HSLO ECOLI](#) Mass: 32856 Score: 52 Matches: 4(3) Sequences: 2
33 kDa chaperonin OS=Escherichia coli (strain K12) OX=83333 GN=hs10 PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2392	521.7829	1041.5512	1041.5495	1.69	1	(24)	0.036	1	U	L.TLPANE
2393	521.7832	1041.5518	1041.5495	2.27	1	26	0.026	1	U	L.TLPANE
6543	732.3921	1462.7696	1462.7668	1.96	0	26	0.044	1	U	Y.VVITIT
6544	732.3942	1462.7739	1462.7668	4.89	0	(24)	0.07	1	U	Y.VVITIT

118. [2::sp|P03004|DNAA_ECOLI](#) Mass: 52689 Score: 51 Matches: 2(1) Sequences: 2(1)
 Chromosomal replication initiator protein DnaA OS=Escherichia coli (strain K12) OX=83333 GN=trpS PE=1 SV=3
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4608	622.3300	1242.6454	1242.6680	-18.22	1	20	0.16	3	U	L.RSNVR
5955	695.3533	1388.6921	1388.6936	-1.05	1	34	0.009	1	U	L.ARLQD

119. [2::sp|P00954|SYW_ECOLI](#) Mass: 37642 Score: 51 Matches: 2(2) Sequences: 1(1)
 Tryptophan--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=trpS PE=1 SV=3
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
7632	817.4253	1632.8361	1632.8359	0.16	1	(50)	0.00021	1	U	L.SAVTG
7633	817.4277	1632.8408	1632.8359	3.00	1	54	8.7e-05	1	U	L.SAVTG

120. [2::sp|P0AB77|KBL_ECOLI](#) Mass: 43432 Score: 51 Matches: 1(1) Sequences: 1(1)
 2-amino-3-ketobutyrate coenzyme A ligase OS=Escherichia coli (strain K12) OX=83333 GN=trpS PE=1 SV=3
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6314	718.8539	1435.6933	1435.6943	-0.68	2	51	0.00018	1	U	L.TNDLE

121. [1::sp|cRAP087|P02769|ALBU_BOVIN](#) Mass: 71244 Score: 51 Matches: 2(2) Sequences: 1(1)
 Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3904	590.8279	1179.6412	1179.6400	1.00	2	(43)	0.00052	1	U	Y.GFQNA
3905	590.8285	1179.6425	1179.6400	2.13	2	51	8.1e-05	1	U	Y.GFQNA

122. [2::sp|P27248|GCST_ECOLI](#) Mass: 40235 Score: 51 Matches: 3(2) Sequences: 2(1)
 Aminomethyltransferase OS=Escherichia coli (strain K12) OX=83333 GN=gcvT PE=1 SV=3
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1535	478.7927	955.5708	955.5702	0.65	2	28	0.0079	1	U	Y.LLANDV
1536	478.7929	955.5713	955.5702	1.11	2	(24)	0.017	1	U	Y.LLANDV
7390	397.9769	1587.8786	1587.8403	24.2	1	23	0.058	1	U	F.RLVVNS

123. [2::sp|P0A7T7|RS18_ECOLI](#) Mass: 9038 Score: 50 Matches: 2(2) Sequences: 1(1)
 30S ribosomal protein S18 OS=Escherichia coli (strain K12) OX=83333 GN=rpsR PE=1 SV=3
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
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8326	883.4482	1764.8819	1764.8781	2.14	1	(36)	0.0063	1	U	F.TAEGV
8327	883.4485	1764.8825	1764.8781	2.50	1	50	0.00022	1	U	F.TAEGV

124. [2::sp|P37177|PT1P_ECOLI](#) Mass: 84005 Score: 49 Matches: 3(3) Sequences: 2
 Phosphoenolpyruvate-dependent phosphotransferase system OS=Escherichia coli (strain
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
932	441.2631	880.5116	880.4906	23.8	1	21	0.019	1	U	L.VDPEPV
2166	508.2878	1014.5611	1014.5458	15.1	1	30	0.012	2	U	L.AQRSLE
2167	508.2879	1014.5612	1014.5458	15.2	1	(28)	0.021	2	U	L.AQRSLE

125. [2::sp|P0AA10|RL13_ECOLI](#) Mass: 16009 Score: 48 Matches: 2(2) Sequences: 1
 50S ribosomal protein L13 OS=Escherichia coli (strain K12) OX=83333 GN=rplM PE=1 SV=
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1056	452.2607	902.5069	902.5073	-0.49	0	(46)	0.00025	1	U	Y.VVDATGK
1057	452.2609	902.5073	902.5073	-0.00	0	48	0.00018	1	U	Y.VVDATGK

126. [2::sp|P69441|KAD_ECOLI](#) Mass: 23628 Score: 48 Matches: 2(1) Sequences: 2(1)
 Adenylate kinase OS=Escherichia coli (strain K12) OX=83333 GN=adk PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3992	595.3013	1188.5880	1188.5887	-0.64	0	21	0.18	1	U	L.GAPGAG
8147	863.9317	1725.8488	1725.8421	3.91	0	27	0.039	1	U	F.NPPKVE

127. [2::sp|P67910|HLDD_ECOLI](#) Mass: 34985 Score: 48 Matches: 2(2) Sequences: 1
 ADP-L-glycero-D-manno-heptose-6-epimerase OS=Escherichia coli (strain K12) OX=83333
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
7880	835.9660	1669.9174	1669.9151	1.38	0	48	0.00019	1	U	Y.VRQIL
7881	835.9679	1669.9212	1669.9151	3.65	0	(39)	0.0015	1	U	Y.VRQIL

128. [2::sp|P75831|MACB_ECOLI](#) Mass: 70829 Score: 47 Matches: 5(0) Sequences: 2
 Macrolide export ATP-binding/permease protein MacB OS=Escherichia coli (strain K12)
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
551	416.2320	830.4494	830.4320	20.9	0	(20)	0.16	1	U	L.MNGGQV
552	416.2321	830.4497	830.4320	21.3	0	24	0.061	1	U	L.MNGGQV
7292	785.4167	1568.8189	1568.8158	2.00	1	23	0.073	3	U	F.NQEQLN
7300	785.9105	1569.8064	1569.7998	4.17	1	(21)	0.14	4	U	F.NQEQLN

[7301](#) 785.9106 1569.8066 1569.7998 4.32 1 (22) 0.11 5 U F.NQEQLN

129. [2::sp|P77439|PTFX1_ECOLI](#) Mass: 92757 Score: 47 Matches: 3(1) Sequences: 2
Multiphosphoryl transfer protein 1 OS=Escherichia coli (strain K12) OX=83333 GN=fryA
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
19	380.7189	759.4232	759.4127	13.9	0	23	0.064	2	U	L.ASGVGVGT
447	410.2397	818.4648	818.4538	13.5	2	24	0.032	1	U	L.LALENIF.
448	410.2398	818.4651	818.4538	13.8	2	(20)	0.082	1	U	L.LALENIF.

130. [2::sp|P0AGI8|TRKA_ECOLI](#) Mass: 50393 Score: 46 Matches: 2(2) Sequences: 1
Trk system potassium uptake protein TrkA OS=Escherichia coli (strain K12) OX=83333 GN=trkA
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1932	496.7742	991.5338	991.5338	0.00	1	(38)	0.0019	1	U	F.ITDVERL
1933	496.7744	991.5341	991.5338	0.31	1	46	0.00027	1	U	F.ITDVERL

131. [2::sp|P77455|PAAZ_ECOLI](#) Mass: 73527 Score: 46 Matches: 3(2) Sequences: 2
Bifunctional protein PaaZ OS=Escherichia coli (strain K12) OX=83333 GN=paaZ PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1327	469.2536	936.4926	936.4739	20.0	2	21	0.1	1	U	-.MQQLASFL
1707	487.2697	972.5247	972.5128	12.3	0	(24)	0.062	2	U	W.VDIEGGIG
1708	487.2697	972.5248	972.5128	12.4	0	25	0.046	2	U	W.VDIEGGIG

132. [2::sp|P39342|YJGR_ECOLI](#) Mass: 54355 Score: 45 Matches: 2(1) Sequences: 2
Uncharacterized protein YjgR OS=Escherichia coli (strain K12) OX=83333 GN=yjgR PE=4
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2173	508.7851	1015.5556	1015.5338	21.4	2	26	0.035	4	U	L.FNDAP
7327	788.3763	1574.7381	1574.7675	-18.66	1	22	0.11	1	U	F.DTEKA

133. [2::sp|P25888|RHLE_ECOLI](#) Mass: 50016 Score: 45 Matches: 2(2) Sequences: 1
ATP-dependent RNA helicase RhIE OS=Escherichia coli (strain K12) OX=83333 GN=rhIE PE=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4529	618.3060	1234.5975	1234.5942	2.69	0	(37)	0.0047	1	U	L.AAQIGE
4530	618.3062	1234.5977	1234.5942	2.88	0	45	0.0007	1	U	L.AAQIGE

134. [2::sp|P08202|ARAA ECOLI](#) **Mass:** 56437 **Score:** 45 **Matches:** 2(0) **Sequences:** 2
L-arabinose isomerase OS=Escherichia coli (strain K12) OX=83333 GN=araA PE=1 SV=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
136	389.7089	777.4032	777.3942	11.6	1	22	0.081	1	U	W.INGLT
5199	651.8368	1301.6590	1301.6723	-10.20	2	22	0.11	1	U	W.INGLT

135. [2::sp|P77318|YDEN ECOLI](#) **Mass:** 62763 **Score:** 45 **Matches:** 3(1) **Sequences:** 2
Uncharacterized sulfatase YdeN OS=Escherichia coli (strain K12) OX=83333 GN=ydeN PE=1 SV=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
596	418.7290	835.4435	835.4327	12.9	1	25	0.045	4	U	Y.DNTIIL
598	418.7293	835.4441	835.4327	13.6	1	(20)	0.1	3	U	Y.DNTIIL
3553	576.2836	1150.5526	1150.5506	1.73	2	20	0.19	1	U	Y.TVENNQ

136. [2::sp|P0A9A6|FTSZ ECOLI](#) **Mass:** 40299 **Score:** 44 **Matches:** 2(2) **Sequences:** 1
Cell division protein FtsZ OS=Escherichia coli (strain K12) OX=83333 GN=ftsZ PE=1 SV=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1580	481.2891	960.5636	960.5644	-0.91	0	44	0.00019	1	U	L.TVAVVTK
1581	481.2900	960.5654	960.5644	1.01	0	(44)	0.00023	1	U	L.TVAVVTK

137. [2::sp|P23721|SERC ECOLI](#) **Mass:** 39986 **Score:** 44 **Matches:** 2(1) **Sequences:** 2
Phosphoserine aminotransferase OS=Escherichia coli (strain K12) OX=83333 GN=serC PE=1 SV=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3806	585.8602	1169.7059	1169.7020	3.37	1	21	0.039	1	U	L.TIVIVR
7832	831.9232	1661.8318	1661.8260	3.45	1	26	0.067	1	U	F.IQVAEE

138. [2::sp|P17854|CYSH ECOLI](#) **Mass:** 28015 **Score:** 44 **Matches:** 2(0) **Sequences:** 2
Phosphoadenosine phosphosulfate reductase OS=Escherichia coli (strain K12) OX=83333 GN=cysH PE=1 SV=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1422	473.2759	944.5373	944.5542	-17.94	2	21	0.092	1	U	L.TDKLKR
6498	729.3731	1456.7317	1456.7674	-24.52	2	23	0.1	1	U	L.EKLDAR

139. [2::sp|P0AFT5|BTSR ECOLI](#) **Mass:** 27554 **Score:** 44 **Matches:** 2(0) **Sequences:** 2
Transcriptional regulatory protein BtsR OS=Escherichia coli (strain K12) OX=83333 GN=btsR PE=1 SV=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3569	576.7888	1151.5631	1151.5719	-7.64	2	22	0.11	1	U	Y.LLQMKD
4779	630.3437	1258.6728	1258.6591	10.9	1	21	0.13	1	U	F.LDIQMP

140. [2::sp|P0AET2|HDEB_ECOLI](#) Mass: 12149 Score: 43 Matches: 2(0) Sequences: 2(0)
 Acid stress chaperone HdeB OS=Escherichia coli (strain K12) OX=83333 GN=hdeB PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
563	416.7336	831.4527	831.4524	0.31	1	20	0.13	2	U	F.MGAVAA
6371	481.9372	1442.7899	1442.7591	21.3	2	23	0.065	1	U	- <u>.MNISSL</u>

141. [2::sp|P78055|FSAA_ECOLI](#) Mass: 23096 Score: 42 Matches: 2(0) Sequences: 2(0)
 Fructose-6-phosphate aldolase 1 OS=Escherichia coli (strain K12) OX=83333 GN=fsaA PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1032	451.2404	900.4662	900.4851	-20.97	0	21	0.096	2	U	F.KTPRQ
4180	402.5361	1204.5864	1204.6010	-12.10	0	21	0.17	1	U	L.DTSDV

Proteins matching a subset of these peptides:

[2::sp|P32669|FSAB_ECOLI](#) Score: 21 Matches: 1(0) Sequences: 1(0)
 Fructose-6-phosphate aldolase 2 OS=Escherichia coli (strain K12) OX=83333 GN=fsaB PE=1 SV=1

142. [2::sp|P39321|TAMB_ECOLI](#) Mass: 136923 Score: 39 Matches: 2(0) Sequences: 2(0)
 Translocation and assembly module subunit TamB OS=Escherichia coli (strain K12) OX=83333 GN=tamB PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1837	493.2509	984.4872	984.4917	-4.49	1	22	0.067	1	U	F.QTPVGP
3805	585.8400	1169.6654	1169.6404	21.4	1	20	0.082	1	U	L.REQLEI

143. [2::sp|P0ABD5|ACCA_ECOLI](#) Mass: 35333 Score: 39 Matches: 1(1) Sequences: 1(1)
 Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha OS=Escherichia coli (strain K12) OX=83333 GN=accA PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5143	433.5858	1297.7356	1297.7354	0.19	0	39	0.00096	1	U	Y.ADDKA

144. [2::sp|P0ABD8|BCCP_ECOLI](#) Mass: 16733 Score: 38 Matches: 1(1) Sequences: 1(1)
 Biotin carboxyl carrier protein of acetyl-CoA carboxylase OS=Escherichia coli (strain K12) OX=83333 GN=bccp PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5823	686.3784	1370.7422	1370.7406	1.18	0	38	0.0025	1	U	F.IEVGQK

145. [2::sp|P77395|YBBN ECOLI](#) Mass: 31885 Score: 38 Matches: 1(1) Sequences: 1(1)
 Uncharacterized protein YbbN OS=Escherichia coli (strain K12) OX=83333 GN=ybbN PE=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5575	671.3539	1340.6933	1340.6936	-0.18	0	38	0.0021	1	U	L.KQAADT

146. [2::sp|P0A7K2|RL7 ECOLI](#) Mass: 12288 Score: 37 Matches: 2(2) Sequences: 1(1)
 50S ribosomal protein L7/L12 OS=Escherichia coli (strain K12) OX=83333 GN=rplL PE=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4790	631.3178	1260.6211	1260.6197	1.06	0	37	0.0042	1	U	L.KEGVSK
4791	631.3182	1260.6219	1260.6197	1.74	0	(34)	0.0078	1	U	L.KEGVSK

147. [2::sp|P0A763|NDK ECOLI](#) Mass: 15511 Score: 37 Matches: 1(1) Sequences: 1(1)
 Nucleoside diphosphate kinase OS=Escherichia coli (strain K12) OX=83333 GN=ndk PE=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
8779	630.3503	1888.0290	1888.0015	14.6	0	37	0.002	1	U	F.SIIKPN

148. [2::sp|P0AE12|AMN ECOLI](#) Mass: 54246 Score: 37 Matches: 2(2) Sequences: 1(1)
 AMP nucleosidase OS=Escherichia coli (strain K12) OX=83333 GN=amn PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3546	575.8265	1149.6385	1149.6394	-0.75	1	(24)	0.033	1	U	Y.TTTITR
3548	575.8273	1149.6401	1149.6394	0.63	1	37	0.0016	1	U	Y.TTTITR

149. [2::sp|P31120|GLMM ECOLI](#) Mass: 47799 Score: 36 Matches: 1(1) Sequences: 1(1)
 Phosphoglucosamine mutase OS=Escherichia coli (strain K12) OX=83333 GN=glmM PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2359	517.7799	1033.5453	1033.5444	0.85	1	36	0.0041	1	U	L.AEKADL

150. [2::sp|P0A7G6|RECA ECOLI](#) Mass: 38121 Score: 36 Matches: 2(2) Sequences: 1(1)
 Protein RecA OS=Escherichia coli (strain K12) OX=83333 GN=recA PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1746	488.7503	975.4861	975.4873	-1.25	0	36	0.0049	1	U	Y.GPESSGKT
1747	488.7506	975.4866	975.4873	-0.70	0	(33)	0.01	1	U	Y.GPESSGKT

151. [2::sp|P28912|YHHI_ECOLI](#) Mass: 43574 Score: 36 Matches: 1(1) Sequences: 1(1)
 H repeat-associated putative transposase YhhI OS=Escherichia coli (strain K12) OX=833333 GN=yhhI PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1262	465.7668	929.5190	929.5294	-11.20	0	36	0.0038	1	U	F.AVKGTQG

152. [2::sp|P05042|FUMC_ECOLI](#) Mass: 50856 Score: 36 Matches: 2(2) Sequences: 1(1)
 Fumarate hydratase class II OS=Escherichia coli (strain K12) OX=833333 GN=fumC PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1904	495.7482	989.4818	989.4818	0.04	1	36	0.0045	1	U	L.TLGQEISG
1905	495.7483	989.4821	989.4818	0.28	1	(35)	0.0051	1	U	L.TLGQEISG

153. [2::sp|P0A7X3|RS9_ECOLI](#) Mass: 14847 Score: 35 Matches: 2(2) Sequences: 1(1)
 30S ribosomal protein S9 OS=Escherichia coli (strain K12) OX=833333 GN=rpsI PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2678	538.2887	1074.5628	1074.5631	-0.22	1	(31)	0.014	1	U	L.ELVDMV
2679	538.2900	1074.5655	1074.5631	2.28	1	35	0.0054	1	U	L.ELVDMV

154. [2::sp|P0A9J6|RBSK_ECOLI](#) Mass: 32328 Score: 35 Matches: 1(1) Sequences: 1(1)
 Ribokinase OS=Escherichia coli (strain K12) OX=833333 GN=rbsK PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
8277	878.4757	1754.9369	1754.9302	3.82	1	35	0.0032	1	U	L.ALVDII

155. [2::sp|P0A6K6|DEOB_ECOLI](#) Mass: 44684 Score: 35 Matches: 1(1) Sequences: 1(1)
 Phosphopentomutase OS=Escherichia coli (strain K12) OX=833333 GN=deoB PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3733	583.2794	1164.5442	1164.5411	2.63	0	35	0.006	1	U	F.GIGATE

156. [2::sp|P04128|FIMA1_ECOLI](#) Mass: 18214 Score: 35 Matches: 1(1) Sequences: 1(1)
 Type-1 fimbrial protein, A chain OS=Escherichia coli (strain K12) OX=833333 GN=fimA PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4937	637.3718	1272.7291	1272.7549	-20.29	1	35	0.0024	1	U	M.KIKTL

157. [2::sp|P0AEI1|MIAB_ECOLI](#) Mass: 53971 Score: 34 Matches: 1(1) Sequences: 1(1)
tRNA-2-methylthio-N(6)-dimethylallyladenine synthase OS=Escherichia coli (strain K12)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3042	555.7609	1109.5072	1109.5063	0.77	0	34	0.0063	1	U	F.EGTPDM

158. [2::sp|P37653|BCSA_ECOLI](#) Mass: 100348 Score: 34 Matches: 2(2) Sequences: 1(1)
Cellulose synthase catalytic subunit [UDP-forming] OS=Escherichia coli (strain K12)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1457	475.7690	949.5233	949.5233	0.08	0	34	0.0041	1	U	L.NVVKNTIY
1460	475.7692	949.5238	949.5233	0.61	0	(27)	0.019	1	U	L.NVVKNTIY

159. [2::sp|P39160|UXUB_ECOLI](#) Mass: 54116 Score: 34 Matches: 2(1) Sequences: 1(1)
D-mannonate oxidoreductase OS=Escherichia coli (strain K12) OX=83333 GN=uxuB PE=3 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4523	617.8118	1233.6090	1233.6088	0.12	0	34	0.0097	1	U	Y.TVAEKG
4524	617.8135	1233.6124	1233.6088	2.89	0	(24)	0.093	1	U	Y.TVAEKG

160. [2::sp|P07913|TDH_ECOLI](#) Mass: 37557 Score: 33 Matches: 2(1) Sequences: 1(1)
L-threonine 3-dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=tdh PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2501	528.7539	1055.4931	1055.4924	0.72	1	33	0.0064	1	U	F.SIDDFQ
2502	528.7539	1055.4933	1055.4924	0.84	1	(23)	0.06	1	U	F.SIDDFQ

161. [2::sp|P63020|NFUA_ECOLI](#) Mass: 21212 Score: 33 Matches: 1(1) Sequences: 1(1)
Fe/S biogenesis protein NfuA OS=Escherichia coli (strain K12) OX=83333 GN=nfuA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2540	529.7963	1057.5781	1057.6019	-22.48	1	33	0.0071	1	U	L.KEGIE

162. [2::sp|P0A8J8|RHLB_ECOLI](#) Mass: 47325 Score: 33 Matches: 1(1) Sequences: 1(1)

ATP-dependent RNA helicase RhlB OS=Escherichia coli (strain K12) OX=83333 GN=rhlB PE=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
8048	853.4424	1704.8702	1704.8682	1.15	1	33	0.012	1	U	L.AVQIHA

163. [2::sp|P0A9D8|DAPD_ECOLI](#) Mass: 30044 Score: 33 Matches: 1(1) Sequences: 1(1)
2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase OS=Escherichia coli (strain K12) OX=83333 GN=dapD PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4131	601.3201	1200.6256	1200.6251	0.40	0	33	0.0098	1	U	L.RVAEKI

164. [2::sp|P77260|YDFI_ECOLI](#) Mass: 53879 Score: 32 Matches: 2(2) Sequences: 1(1)
Uncharacterized oxidoreductase YdfI OS=Escherichia coli (strain K12) OX=83333 GN=ydfI PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
684	423.7283	845.4420	845.4317	12.2	0	(27)	0.034	1	U	L.KVQGVDL
685	423.7286	845.4427	845.4317	13.0	0	32	0.0095	1	U	L.KVQGVDL

165. [2::sp|P77171|YDCI_ECOLI](#) Mass: 33552 Score: 32 Matches: 4(2) Sequences: 1(1)
Uncharacterized HTH-type transcriptional regulator YdcI OS=Escherichia coli (strain K12) OX=83333 GN=ydcI PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2159	508.2564	1014.4982	1014.5206	-22.10	0	(26)	0.031	2	U	F.ERGRQ
2160	508.2566	1014.4986	1014.5206	-21.69	0	(23)	0.061	2	U	F.ERGRQ
2161	508.2620	1014.5095	1014.5206	-10.92	0	(21)	0.093	4	U	F.ERGRQ
2162	508.2626	1014.5107	1014.5206	-9.78	0	32	0.0085	1	U	F.ERGRQ

166. [2::sp|P52643|LDHD_ECOLI](#) Mass: 36854 Score: 32 Matches: 1(1) Sequences: 1(1)
D-lactate dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=ldhA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
7877	835.8836	1669.7527	1669.7472	3.30	1	34	0.0071	1	U	F.FEDKSN

167. [2::sp|P76272|YEBT_ECOLI](#) Mass: 94912 Score: 31 Matches: 2(2) Sequences: 1(1)
Uncharacterized protein YebT OS=Escherichia coli (strain K12) OX=83333 GN=yebT PE=3 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3962	594.3230	1186.6314	1186.6445	-11.00	2	31	0.012	1	U	Y.QGLEV

[3964](#) 594.3262 1186.6379 1186.6445 -5.56 2 (24) 0.057 1 U Y.QGLEV

168. [2::sp|P0AG55|RL6_ECOLI](#) Mass: 18949 Score: 31 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L6 OS=Escherichia coli (strain K12) OX=83333 GN=rplF PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6226	713.3528	1424.6910	1424.6896	1.02	0	31	0.016	1	U	L.NDAVEV

169. [2::sp|P0A7W7|RS8_ECOLI](#) Mass: 14175 Score: 31 Matches: 2(2) Sequences: 1(1)
30S ribosomal protein S8 OS=Escherichia coli (strain K12) OX=83333 GN=rpsH PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3080	557.2579	1112.5013	1112.5026	-1.16	1	(25)	0.048	1	U	L.KEEGFI
3082	557.2585	1112.5024	1112.5026	-0.17	1	31	0.011	1	U	L.KEEGFI

170. [2::sp|P46474|YHDP_ECOLI](#) Mass: 139081 Score: 31 Matches: 2(2) Sequences: 1(1)
Uncharacterized protein YhdP OS=Escherichia coli (strain K12) OX=83333 GN=yhdP PE=3 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2401	522.2512	1042.4878	1042.4819	5.67	0	31	0.0092	1	U	L.DDPQIN
2402	522.2521	1042.4896	1042.4819	7.44	0	(25)	0.034	1	U	L.DDPQIN

171. [2::sp|P32717|YJCS_ECOLI](#) Mass: 73219 Score: 31 Matches: 2(1) Sequences: 1(1)
Putative alkyl/aryl-sulfatase YjcS OS=Escherichia coli (strain K12) OX=83333 GN=yjcS
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
7871	835.4421	1668.8696	1668.8570	7.57	0	31	0.014	1	U	L.KQVIAA
7872	835.4435	1668.8725	1668.8570	9.32	0	(21)	0.13	1	U	L.KQVIAA

172. [2::sp|P06720|AGAL_ECOLI](#) Mass: 51308 Score: 31 Matches: 2(2) Sequences: 1(1)
Alpha-galactosidase OS=Escherichia coli (strain K12) OX=83333 GN=melA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2054	502.7927	1003.5708	1003.5702	0.59	1	31	0.0063	1	U	F.VKNILG
2055	502.7928	1003.5710	1003.5702	0.79	1	(30)	0.0077	1	U	F.VKNILG

173. [2::sp|P0ADZ4|RS15_ECOLI](#) Mass: 10263 Score: 30 Matches: 1(1) Sequences: 1(1)
30S ribosomal protein S15 OS=Escherichia coli (strain K12) OX=83333 GN=rpsO PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
8223	873.4381	1744.8617	1744.8592	1.44	1	30	0.023	1	U	F.GRDAND
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174.	2::sp P0A903 BAMC ECOLI	Mass: 36877	Score: 30	Matches: 1(1)	Sequences: 1	Outer membrane protein assembly factor BamC OS=Escherichia coli (strain K12) OX=833333 Check to include this hit in error tolerant search or archive report				
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5375	659.8350	1317.6554	1317.6525	2.20	0	33	0.012	1	U	Y.TITQRD
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175.	2::sp P0ABP8 DEOD ECOLI	Mass: 26161	Score: 30	Matches: 2(2)	Sequences: 1	Purine nucleoside phosphorylase DeoD-type OS=Escherichia coli (strain K12) OX=833333 Check to include this hit in error tolerant search or archive report				
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1636	483.7611	965.5076	965.5070	0.67	1	(28)	0.022	1	U	Y.TKELITDF
1637	483.7622	965.5099	965.5070	3.01	1	30	0.014	1	U	Y.TKELITDF
<hr/>										
176.	2::sp P30176 RIBX ECOLI	Mass: 18658	Score: 30	Matches: 2(2)	Sequences: 1	N-glycosidase YbiA OS=Escherichia coli (strain K12) OX=833333 GN=ybiA PE=1 SV=1 Check to include this hit in error tolerant search or archive report				
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1191	459.7485	917.4825	917.4640	20.2	1	30	0.019	1	U	L.MELREQL.
1192	459.7487	917.4829	917.4640	20.6	1	(27)	0.036	1	U	L.MELREQL.
<hr/>										
177.	2::sp P16869 FHUE ECOLI	Mass: 81239	Score: 29	Matches: 3(1)	Sequences: 1	FhuE receptor OS=Escherichia coli (strain K12) OX=833333 GN=fhuE PE=1 SV=2 Check to include this hit in error tolerant search or archive report				
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2554	530.2875	1058.5605	1058.5682	-7.21	1	(23)	0.076	1	U	Y.QAITKP
2555	530.2876	1058.5606	1058.5682	-7.10	1	29	0.019	1	U	Y.QAITKP
2557	530.2939	1058.5733	1058.5682	4.90	1	(23)	0.072	3	U	Y.QAITKP
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178.	2::sp P28635 METQ ECOLI	Mass: 29471	Score: 29	Matches: 1(1)	Sequences: 1	D-methionine-binding lipoprotein MetQ OS=Escherichia coli (strain K12) OX=833333 GN=m Check to include this hit in error tolerant search or archive report				
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3057	556.3403	1110.6661	1110.6649	1.11	1	29	0.004	1	U	L.KDGVGL
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179.	2::sp P66948 BEPA ECOLI	Mass: 53874	Score: 29	Matches: 2(2)	Sequences: 1					

Beta-barrel assembly-enhancing protease OS=Escherichia coli (strain K12) OX=83333 GN=...
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3798	585.8127	1169.6109	1169.6292	-15.59	2	29	0.017	1	U	L.RTNPV
3799	585.8145	1169.6145	1169.6292	-12.57	2	(29)	0.018	1	U	L.RTNPV

180. [2::sp|P76251|DMLA_ECOLI](#) Mass: 40574 Score: 29 Matches: 2(2) Sequences: 1
D-malate dehydrogenase [decarboxylating] OS=Escherichia coli (strain K12) OX=83333 GN=...
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1643	484.2242	966.4339	966.4328	1.17	0	(27)	0.024	1	U	L.TSATKSN
1644	484.2244	966.4343	966.4328	1.56	0	29	0.018	1	U	L.TSATKSN

181. [2::sp|P0ABJ1|CYOA_ECOLI](#) Mass: 34946 Score: 29 Matches: 2(2) Sequences: 1
Cytochrome bo(3) ubiquinol oxidase subunit 2 OS=Escherichia coli (strain K12) OX=83333 GN=...
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
331	403.7238	805.4331	805.4334	-0.38	0	(25)	0.033	1	U	F.ADVINKF
332	403.7238	805.4331	805.4334	-0.38	0	29	0.014	1	U	F.ADVINKF

182. [2::sp|P0ACN7|CYTR_ECOLI](#) Mass: 38252 Score: 28 Matches: 2(2) Sequences: 1
HTH-type transcriptional repressor CytR OS=Escherichia coli (strain K12) OX=83333 GN=...
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2757	542.7753	1083.5360	1083.5601	-22.23	0	31	0.0095	1	U	L.DLPQP
2758	542.7763	1083.5379	1083.5601	-20.42	0	(30)	0.011	1	U	L.DLPQP

183. [2::sp|P0ACE0|MBHM_ECOLI](#) Mass: 62908 Score: 28 Matches: 1(1) Sequences: 1
Hydrogenase-2 large chain OS=Escherichia coli (strain K12) OX=83333 GN=hybC PE=1 SV=...
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2219	511.7317	1021.4488	1021.4716	-22.31	1	28	0.019	1	U	L.QDILQ

184. [2::sp|P0AC53|G6PD_ECOLI](#) Mass: 56011 Score: 28 Matches: 1(1) Sequences: 1
Glucose-6-phosphate 1-dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=zwf...
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1851	493.7854	985.5562	985.5808	-24.95	2	31	0.0087	1	U	Y.LGKETVL

185. [2::sp|P46855|YHHZ ECOLI](#) Mass: 44375 Score: 28 Matches: 2(2) Sequences: 1
Uncharacterized protein YhhZ OS=Escherichia coli (strain K12) OX=83333 GN=yhhZ PE=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
115	387.2290	772.4435	772.4331	13.5	0	(28)	0.021	1	U	L.IDKSTPL.
118	387.2293	772.4440	772.4331	14.2	0	28	0.022	1	U	L.IDKSTPL.

186. [2::sp|P62399|RL5 ECOLI](#) Mass: 20346 Score: 28 Matches: 2(2) Sequences: 1(1)
50S ribosomal protein L5 OS=Escherichia coli (strain K12) OX=83333 GN=rplE PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
954	442.7636	883.5127	883.5127	-0.03	0	(28)	0.0082	1	U	L.AAISGQKP
956	442.7637	883.5129	883.5127	0.24	0	28	0.0079	1	U	L.AAISGQKP

187. [2::sp|Q46851|GPR ECOLI](#) Mass: 38922 Score: 28 Matches: 2(2) Sequences: 1(1)
L-glyceraldehyde 3-phosphate reductase OS=Escherichia coli (strain K12) OX=83333 GN=
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1458	475.7691	949.5236	949.5233	0.40	2	28	0.015	2	U	L.AQGLLTGK
1459	475.7691	949.5237	949.5233	0.46	2	(25)	0.03	1	U	L.AQGLLTGK

188. [2::sp|P39381|YJIJ ECOLI](#) Mass: 41561 Score: 28 Matches: 1(1) Sequences: 1
Uncharacterized protein YjiJ OS=Escherichia coli (strain K12) OX=83333 GN=yjiJ PE=4
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4659	624.3167	1246.6189	1246.6095	7.54	2	28	0.038	1	U	F.SFGAFH

189. [2::sp|P37663|YHJY ECOLI](#) Mass: 25935 Score: 28 Matches: 1(1) Sequences: 1
Uncharacterized protein YhjY OS=Escherichia coli (strain K12) OX=83333 GN=yhjY PE=4
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
7076	770.8515	1539.6884	1539.6994	-7.09	2	28	0.029	1	U	L.RPWAQI

190. [2::sp|P15723|DGTP ECOLI](#) Mass: 59688 Score: 28 Matches: 3(1) Sequences: 1
Deoxyguanosinetriphosphate triphosphohydrolase OS=Escherichia coli (strain K12) OX=8
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
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1412	473.2484	944.4821	944.4967	-15.44	1	(23)	0.09	3	U	L.TWAQVGG
1413	473.2486	944.4826	944.4967	-14.91	1	28	0.029	3	U	L.TWAQVGG
1417	473.2539	944.4932	944.4967	-3.73	1	(22)	0.11	1	U	L.TWAQVGG

191. [2::sp|P0AF06|MOTB_ECOLI](#) Mass: 34165 Score: 27 Matches: 2(2) Sequences: 1
 Motility protein B OS=Escherichia coli (strain K12) OX=83333 GN=motB PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3709	582.2822	1162.5499	1162.5726	-19.55	1	27	0.034	1	U	L.MVGG
3712	582.2839	1162.5533	1162.5726	-16.60	1	(27)	0.038	1	U	L.MVGG

192. [2::sp|P08722|PTV3B_ECOLI](#) Mass: 66896 Score: 27 Matches: 1(1) Sequences: 1
 PTS system beta-glucoside-specific EIIBCA component OS=Escherichia coli (strain K12)
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5205	651.8502	1301.6859	1301.6723	10.4	1	27	0.039	1	U	L.LMPA

193. [2::sp|P62707|GPMA_ECOLI](#) Mass: 28539 Score: 27 Matches: 2(2) Sequences: 1
 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase OS=Escherichia coli (strain K12)
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3352	569.7748	1137.5350	1137.5342	0.69	2	27	0.043	1	U	Y.EFDENF
3353	569.7753	1137.5360	1137.5342	1.55	2	(26)	0.05	1	U	Y.EFDENF

194. [2::sp|P0AD10|YECJ_ECOLI](#) Mass: 9174 Score: 26 Matches: 2(1) Sequences: 1
 Uncharacterized protein YecJ OS=Escherichia coli (strain K12) OX=83333 GN=yecJ PE=4
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3106	558.2701	1114.5256	1114.5142	10.2	1	26	0.032	1	U	M.SQPLNA
3107	558.2703	1114.5261	1114.5142	10.7	1	(22)	0.078	1	U	M.SQPLNA

195. [2::sp|P23841|XAPR_ECOLI](#) Mass: 33663 Score: 26 Matches: 2(2) Sequences: 1
 HTH-type transcriptional regulator XapR OS=Escherichia coli (strain K12) OX=83333 GN=xapR
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
412	408.2344	814.4543	814.4661	-14.41	1	26	0.03	1	U	L.LERREL
413	408.2347	814.4548	814.4661	-13.82	1	(26)	0.031	1	U	L.LERREL

Proteins matching the same set of peptides:

[2::sp|Q46938|KDUI_ECOLI](#) Mass: 31341 Score: 26 Matches: 2(2) Sequences: 1(1)
4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase OS=Escherichia coli (strain K12)

196. [2::sp|P63204|GADE_ECOLI](#) Mass: 20643 Score: 26 Matches: 1(1) Sequences: 1(1)
Transcriptional regulator GadE OS=Escherichia coli (strain K12) OX=83333 GN=gadE PE=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6632	737.8990	1473.7834	1473.7537	20.2	2	26	0.042	1	U	F.SHNQFK

197. [2::sp|P0A6N4|EFP_ECOLI](#) Mass: 20635 Score: 26 Matches: 2(1) Sequences: 1(1)
Elongation factor P OS=Escherichia coli (strain K12) OX=83333 GN=efp PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
9442	738.3816	2212.1229	2212.1223	0.28	1	(21)	0.15	1	U	L.EIVDTD
9443	738.3853	2212.1341	2212.1223	5.32	1	26	0.043	1	U	L.EIVDTD

198. [2::sp|P37651|GUN_ECOLI](#) Mass: 41788 Score: 26 Matches: 2(1) Sequences: 1(1)
Endoglucanase OS=Escherichia coli (strain K12) OX=83333 GN=bcsZ PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
590	418.6997	835.3847	835.3824	2.81	0	26	0.028	1	U	L.AANDRAAF
591	418.6997	835.3849	835.3824	2.95	0	(22)	0.072	1	U	L.AANDRAAF

199. [2::sp|P77173|ZIPA_ECOLI](#) Mass: 36452 Score: 26 Matches: 2(2) Sequences: 1(1)
Cell division protein ZipA OS=Escherichia coli (strain K12) OX=83333 GN=zipA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2859	546.7879	1091.5612	1091.5499	10.4	2	26	0.048	1	U	L.LLNSIQ
2861	546.7889	1091.5633	1091.5499	12.3	2	(26)	0.048	1	U	L.LLNSIQ

200. [2::sp|P00926|SDHD_ECOLI](#) Mass: 48155 Score: 26 Matches: 1(1) Sequences: 1(1)
D-serine dehydratase OS=Escherichia coli (strain K12) OX=83333 GN=dsdA PE=1 SV=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6960	763.4173	1524.8200	1524.8147	3.49	2	26	0.033	1	U	W.LAQEEG

201. [2::sp|P45420|YHCD_ECOLI](#) Mass: 86465 Score: 26 Matches: 2(0) Sequences: 1(1)
Uncharacterized outer membrane usher protein YhcD OS=Escherichia coli (strain K12) OX=83333 GN=yhcD PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2234	511.7678	1021.5210	1021.5374	-16.08	2	(26)	0.055	1	U	-.MLKKT
2235	511.7683	1021.5220	1021.5374	-15.07	2	26	0.052	1	U	-.MLKKT

202. [2::sp|P0A9S3|GATD ECOLI](#) Mass: 37822 Score: 26 Matches: 1(1) Sequences: 1(1)
Galactitol 1-phosphate 5-dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3004	553.3062	1104.5979	1104.5927	4.64	0	26	0.036	1	U	L.AVEIAG

203. [2::sp|P0ABF6|CDD ECOLI](#) Mass: 31805 Score: 26 Matches: 2(2) Sequences: 1(1)
Cytidine deaminase OS=Escherichia coli (strain K12) OX=83333 GN=cdd PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
845	436.2467	870.4788	870.4698	10.4	1	(22)	0.041	1	U	L.QSALEPII
846	436.2480	870.4814	870.4698	13.3	1	26	0.017	1	U	L.QSALEPII

204. [1::sp|cRAP112|P00761|TRYP PIG](#) Mass: 25078 Score: 26 Matches: 2(1) Sequences: 1(1)
Trypsin OS=Sus scrofa PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4759	629.3327	1256.6508	1256.6513	-0.38	1	26	0.039	1	U	Y.VNWIQQ
4760	629.3337	1256.6529	1256.6513	1.28	1	(20)	0.15	1	U	Y.VNWIQQ

205. [2::sp|P33011|YEEA ECOLI](#) Mass: 40158 Score: 26 Matches: 2(2) Sequences: 1(1)
Inner membrane protein YeeA OS=Escherichia coli (strain K12) OX=83333 GN=yeeA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2266	513.3085	1024.6025	1024.6168	-13.97	2	(23)	0.018	1	U	L.QLELI
2267	513.3088	1024.6031	1024.6168	-13.36	2	26	0.009	1	U	L.QLELI

206. [2::sp|P0ADA3|NLPD ECOLI](#) Mass: 40181 Score: 26 Matches: 1(1) Sequences: 1(1)
Murein hydrolase activator NlpD OS=Escherichia coli (strain K12) OX=83333 GN=nlpD PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
564	416.7427	831.4707	831.4715	-0.90	1	26	0.022	1	U	L.RYLPQR.-

207. [2::sp|P65807|YGEY ECOLI](#) Mass: 45288 Score: 26 Matches: 1(1) Sequences: 1(1)

Uncharacterized protein YgeY OS=Escherichia coli (strain K12) OX=83333 GN=ygeY PE=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
774	431.6938	861.3730	861.3868	-16.11	1	26	0.023	1	U	W.GETWEGA

208. [2::sp|P0AFK9|POTD ECOLI](#) Mass: 38842 Score: 26 Matches: 2(2) Sequences: 1
Spermidine/putrescine-binding periplasmic protein OS=Escherichia coli (strain K12) OX=83333 GN=potD PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1996	500.2799	998.5452	998.5437	1.52	2	26	0.022	1	U	Y.VPPGLLEQ
1997	500.2807	998.5469	998.5437	3.23	2	(22)	0.049	1	U	Y.VPPGLLEQ

209. [2::sp|P0A7B5|PROB ECOLI](#) Mass: 39204 Score: 25 Matches: 1(1) Sequences: 1
Glutamate 5-kinase OS=Escherichia coli (strain K12) OX=83333 GN=proB PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1165	458.2969	914.5792	914.5801	-0.95	1	25	0.0044	1	U	L.VVKLGTSV

210. [2::sp|P0A9L5|PPIC ECOLI](#) Mass: 10340 Score: 25 Matches: 1(1) Sequences: 1
Peptidyl-prolyl cis-trans isomerase C OS=Escherichia coli (strain K12) OX=83333 GN=ppic PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
130	388.7126	775.4107	775.4262	-19.90	0	25	0.032	1	U	-.MAKTAAA

211. [2::sp|P0AEX7|LIVH ECOLI](#) Mass: 33074 Score: 25 Matches: 2(2) Sequences: 1
High-affinity branched-chain amino acid transport system permease protein LivH OS=Escherichia coli (strain K12) OX=83333 GN=livH PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1784	490.7684	979.5223	979.5412	-19.32	1	(26)	0.028	1	U	Y.VSFMIIA
1785	490.7688	979.5230	979.5412	-18.56	1	28	0.018	1	U	Y.VSFMIIA

212. [1::sp|cRAP008|P00722|BGAL ECOLI](#) Mass: 117321 Score: 25 Matches: 1(1) Sequences: 1
Beta-galactosidase OS=Escherichia coli (strain K12) GN=lacZ PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6598	736.3826	1470.7506	1470.7467	2.66	2	25	0.054	1	U	W.LGLGPO

Proteins matching the same set of peptides:

[2::sp|P00722|BGAL ECOLI](#) Mass: 117321 Score: 25 Matches: 1(1) Sequences: 1(1)
 Beta-galactosidase OS=Escherichia coli (strain K12) OX=83333 GN=lacZ PE=1 SV=2

213. [2::sp|P09127|HEMX ECOLI](#) Mass: 42937 Score: 25 Matches: 2(1) Sequences: 1(1)
 Protein HemX OS=Escherichia coli (strain K12) OX=83333 GN=hemX PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4154	602.3084	1202.6023	1202.6044	-1.75	1	(24)	0.089	1	U	Y.RQALEN
4165	602.8104	1203.6062	1203.5884	14.8	1	28	0.036	1	U	Y.RQALEN

214. [2::sp|P37675|YIAN ECOLI](#) Mass: 45509 Score: 25 Matches: 1(1) Sequences: 1(1)
 2,3-diketo-L-gulonate TRAP transporter large permease protein YiaN OS=Escherichia coli (strain K12) OX=83333 GN=yiaN PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3361	569.8395	1137.6645	1137.6394	22.1	2	28	0.0059	1	U	L.QPLVDS

215. [2::sp|P45758|GSPD ECOLI](#) Mass: 70826 Score: 25 Matches: 1(1) Sequences: 1(1)
 Putative type II secretion system protein D OS=Escherichia coli (strain K12) OX=83333 GN=gspD PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
300	401.7185	801.4225	801.4120	13.1	1	25	0.043	1	U	L.AEILNQL

216. [2::sp|P03959|KDPA ECOLI](#) Mass: 59492 Score: 25 Matches: 1(1) Sequences: 1(1)
 Potassium-transporting ATPase potassium-binding subunit OS=Escherichia coli (strain K12) OX=83333 GN=kdpA PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3079	557.2383	1112.4621	1112.4774	-13.77	1	25	0.027	1	U	F.VTNTN

217. [2::sp|P10906|UGPE ECOLI](#) Mass: 31536 Score: 25 Matches: 1(0) Sequences: 1(0)
 sn-glycerol-3-phosphate transport system permease protein UgpE OS=Escherichia coli (strain K12) OX=83333 GN=ugpE PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2596	532.2649	1062.5153	1062.4982	16.1	0	25	0.061	1	U	W.VNGVGT

218. [2::sp|P10378|ENTE ECOLI](#) Mass: 59588 Score: 25 Matches: 2(0) Sequences: 1(0)
 Enterobactin synthase component E OS=Escherichia coli (strain K12) OX=83333 GN=entE PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5079	646.3232	1290.6318	1290.6343	-1.93	2	(22)	0.14	1	U	L.NAYASQ
5080	646.3252	1290.6358	1290.6343	1.20	2	25	0.072	1	U	L.NAYASQ

219. [2::sp|P16686|PHNH_ECOLI](#) Mass: 21185 Score: 25 Matches: 1(1) Sequences: 1(1)
 Alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnH OS=Escherichia coli (strain K12) OX=83333 GN=phnH
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
441	409.7314	817.4482	817.4545	-7.73	0	25	0.037	1	U	L.NIATTSVL

220. [2::sp|P33235|FLGK_ECOLI](#) Mass: 57895 Score: 25 Matches: 2(2) Sequences: 1(1)
 Flagellar hook-associated protein 1 OS=Escherichia coli (strain K12) OX=83333 GN=flgK
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1400	472.7746	943.5346	943.5338	0.85	2	25	0.035	1	U	L.LNTGSLGG
1403	472.7752	943.5359	943.5338	2.21	2	(24)	0.047	1	U	L.LNTGSLGG

221. [2::sp|P75857|ELFC_ECOLI](#) Mass: 95411 Score: 25 Matches: 2(1) Sequences: 1(1)
 Probable outer membrane usher protein ElfC OS=Escherichia coli (strain K12) OX=83333 GN=elfC
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1394	472.7620	943.5094	943.4974	12.6	2	28	0.025	1	U	F.LNLNSGVN
1397	472.7631	943.5117	943.4974	15.1	2	(23)	0.078	1	U	F.LNLNSGVN

222. [2::sp|P76551|EUTA_ECOLI](#) Mass: 49853 Score: 25 Matches: 1(1) Sequences: 1(1)
 Ethanolamine utilization protein EutA OS=Escherichia coli (strain K12) OX=83333 GN=eutA
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2088	504.7768	1007.5390	1007.5539	-14.74	2	25	0.035	1	U	L.KTLIL

223. [2::sp|P0A6X1|HEM1_ECOLI](#) Mass: 46449 Score: 25 Matches: 1(1) Sequences: 1(1)
 Glutamyl-tRNA reductase OS=Escherichia coli (strain K12) OX=83333 GN=hemA PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
810	434.7657	867.5168	867.5066	11.8	1	25	0.0074	1	U	L.VLGEPOIL

224. [2::sp|P24181|ACRF_ECOLI](#) Mass: 111554 Score: 25 Matches: 1(0) Sequences: 1(0)
 Multidrug export protein AcrF OS=Escherichia coli (strain K12) OX=83333 GN=acrF PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6541	732.3784	1462.7422	1462.7490	-4.64	1	25	0.081	1	U	L.MENLAS

225. [2::sp|P77199|YAIT ECOLI](#) Mass: 104718 Score: 25 Matches: 1(1) Sequences: 1(1)
Putative uncharacterized protein YaiT OS=Escherichia coli (strain K12) OX=83333 GN=yaiT
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1326	469.2530	936.4914	936.4739	18.8	1	25	0.045	1	U	Y.AMKNNVFL

226. [2::sp|P0A8N3|SYK1 ECOLI](#) Mass: 57624 Score: 25 Matches: 1(0) Sequences: 1(0)
Lysine--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=lysS PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
8032	568.2924	1701.8553	1701.8547	0.35	0	25	0.08	1	U	L.ARRNDV

Proteins matching the same set of peptides:

[2::sp|P0A8N5|SYK2 ECOLI](#) Mass: 57847 Score: 25 Matches: 1(0) Sequences: 1(0)
Lysine--tRNA ligase, heat inducible OS=Escherichia coli (strain K12) OX=83333 GN=lysS

227. [2::sp|P23482|HYFB ECOLI](#) Mass: 73048 Score: 24 Matches: 1(1) Sequences: 1(1)
Hydrogenase-4 component B OS=Escherichia coli (strain K12) OX=83333 GN=hyfB PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2001	500.2845	998.5545	998.5437	10.8	2	24	0.028	1	U	L.LAQTGLPL

228. [2::sp|P0ABJ9|CYDA ECOLI](#) Mass: 58338 Score: 24 Matches: 1(0) Sequences: 1(0)
Cytochrome bd-I ubiquinol oxidase subunit 1 OS=Escherichia coli (strain K12) OX=83333 GN=cydA
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6069	703.8264	1405.6381	1405.6361	1.44	0	24	0.066	1	U	F.GIPDQE

229. [2::sp|P52044|YGFI ECOLI](#) Mass: 34709 Score: 24 Matches: 1(1) Sequences: 1(1)
Uncharacterized HTH-type transcriptional regulator YgfI OS=Escherichia coli (strain K12) OX=83333 GN=ygfI
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
693	424.2024	846.3902	846.3905	-0.43	0	24	0.042	1	U	L.NKAGQEL

230. [2::sp|P39401|OPGB_ECOLI](#) Mass: 85783 Score: 24 Matches: 1(1) Sequences: 1(1)
Phosphoglycerol transferase I OS=Escherichia coli (strain K12) OX=83333 GN=mdb PE=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1647	484.2399	966.4653	966.4658	-0.51	1	24	0.052	1	U	L.GDILKNSG

231. [2::sp|P0A6F1|CARA_ECOLI](#) Mass: 41633 Score: 24 Matches: 2(2) Sequences: 1(1)
Carbamoyl-phosphate synthase small chain OS=Escherichia coli (strain K12) OX=83333 GN=cpb PE=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
495	413.2632	824.5119	824.5120	-0.06	0	(21)	0.014	1	U	L.VIRDLPL.
496	413.2637	824.5129	824.5120	1.13	0	24	0.0063	1	U	L.VIRDLPL.

232. [2::sp|P0ABZ6|SURA_ECOLI](#) Mass: 47254 Score: 24 Matches: 1(1) Sequences: 1(1)
Chaperone SurA OS=Escherichia coli (strain K12) OX=83333 GN=surA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3285	565.3214	1128.6283	1128.6291	-0.77	0	24	0.046	1	U	W.GRIQEL

233. [2::sp|P77359|DJLC_ECOLI](#) Mass: 56274 Score: 24 Matches: 2(2) Sequences: 1(1)
Uncharacterized J domain-containing protein Djlc OS=Escherichia coli (strain K12) OX=83333 GN=djlc PE=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
103	386.2212	770.4279	770.4174	13.6	0	(21)	0.052	1	U	L.IPDDAKL.
104	386.2216	770.4287	770.4174	14.6	0	24	0.024	1	U	L.IPDDAKL.

234. [2::sp|Q9Z3A0|YJGW_ECOLI](#) Mass: 13248 Score: 24 Matches: 1(0) Sequences: 1(0)
Putative uncharacterized protein YjgW OS=Escherichia coli (strain K12) OX=83333 GN=yjgW PE=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3872	589.3143	1176.6141	1176.6147	-0.52	1	24	0.077	1	U	-.MIRKNK

235. [2::sp|P63284|CLPB_ECOLI](#) Mass: 95697 Score: 24 Matches: 2(2) Sequences: 1(1)
Chaperone protein ClpB OS=Escherichia coli (strain K12) OX=83333 GN=clpB PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4265	607.3295	1212.6444	1212.6350	7.73	2	27	0.029	1	U	L.LNQEKG
4266	607.3320	1212.6495	1212.6350	12.0	2	(26)	0.03	1	U	L.LNQEKG

236. [2::sp|P75906|PGAB_ECOLI](#) **Mass:** 77421 **Score:** 24 **Matches:** 1(1) **Sequences:** 1
Poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase OS=Escherichia coli (strain K12)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2128	507.2505	1012.4864	1012.4647	21.4	1	24	0.053	1	U	-. MLRNGN

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Chymotrypsin
Fixed modifications : [Carbamidomethyl \(C\)](#)
Variable modifications : [Deamidated \(NQ\)](#), [DTSSP Cross link \(K\)](#), [Oxidation \(M\)](#)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Fragment Mass Tolerance: ± 0.8 Da
Max Missed Cleavages : 2
Instrument type : ESI-TRAP
Number of queries : 9978

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