

## 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\_band3.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 11:09:44 GMT

Protein hits	: <a href="#">2::sp P02930 TOLC ECOLI</a>	Outer membrane protein TolC OS=Escherichia coli
	: <a href="#">2::sp P0A9P0 DLDH ECOLI</a>	Dihydrolipoyl dehydrogenase OS=Escherichia coli
	: <a href="#">1::sp cRAP022 P00766 CTRA BOVIN</a>	Chymotrypsinogen A OS=Bos taurus PE=1 S
	: <a href="#">2::sp P0CE47 EFTU1 ECOLI</a>	Elongation factor Tu 1 OS=Escherichia coli
	: <a href="#">2::sp P0A850 TIG ECOLI</a>	Trigger factor OS=Escherichia coli (strain ATCC 8739)
	: <a href="#">2::sp P0A6F3 GLPK ECOLI</a>	Glycerol kinase OS=Escherichia coli (strain ATCC 8739)
	: <a href="#">2::sp P0ABB4 ATPB ECOLI</a>	ATP synthase subunit beta OS=Escherichia coli
	: <a href="#">2::sp P0AE06 ACRA ECOLI</a>	Multidrug efflux pump subunit AcrA OS=Escherichia coli
	: <a href="#">2::sp P0ABB0 ATPA ECOLI</a>	ATP synthase subunit alpha OS=Escherichia coli
	: <a href="#">2::sp P0A8M0 SYN ECOLI</a>	Asparagine--tRNA ligase OS=Escherichia coli
	: <a href="#">2::sp P0A6P9 ENO ECOLI</a>	Enolase OS=Escherichia coli (strain K12)
	: <a href="#">2::sp P0A6M8 EFG ECOLI</a>	Elongation factor G OS=Escherichia coli
	: <a href="#">2::sp P04805 SYE ECOLI</a>	Glutamate--tRNA ligase OS=Escherichia coli
	: <a href="#">2::sp P0AGG8 TLDD ECOLI</a>	Metalloprotease TldD OS=Escherichia coli
	: <a href="#">2::sp P0A6H5 HSLU ECOLI</a>	ATP-dependent protease ATPase subunit H
	: <a href="#">2::sp P0C8J8 GATZ ECOLI</a>	D-tagatose-1,6-bisphosphate aldolase
	: <a href="#">2::sp P31224 ACRB ECOLI</a>	Multidrug efflux pump subunit AcrB OS=Escherichia coli
	: <a href="#">2::sp P0AFG6 ODO2 ECOLI</a>	Dihydrolipoyllysine-residue succinyltransferase
	: <a href="#">2::sp P30845 EPTA ECOLI</a>	Phosphoethanolamine transferase EptA OS=Escherichia coli
	: <a href="#">2::sp P0AG67 RS1 ECOLI</a>	30S ribosomal protein S1 OS=Escherichia coli
	: <a href="#">2::sp P00350 6PGD ECOLI</a>	6-phosphogluconate dehydrogenase, decarboxylating
	: <a href="#">2::sp P08200 IDH ECOLI</a>	Isocitrate dehydrogenase [NADP] OS=Escherichia coli
	: <a href="#">2::sp P21599 KPYK2 ECOLI</a>	Pyruvate kinase II OS=Escherichia coli
	: <a href="#">2::sp P0A6F5 CH60 ECOLI</a>	60 kDa chaperonin OS=Escherichia coli (strain ATCC 8739)
	: <a href="#">2::sp P68767 AMPA ECOLI</a>	Cytosol aminopeptidase OS=Escherichia coli
	: <a href="#">2::sp P25553 ALDA ECOLI</a>	Lactaldehyde dehydrogenase OS=Escherichia coli
	: <a href="#">2::sp P0A6E4 ASSY ECOLI</a>	Argininosuccinate synthase OS=Escherichia coli
	: <a href="#">2::sp P0AG30 RHO ECOLI</a>	Transcription termination factor Rho OS=Escherichia coli

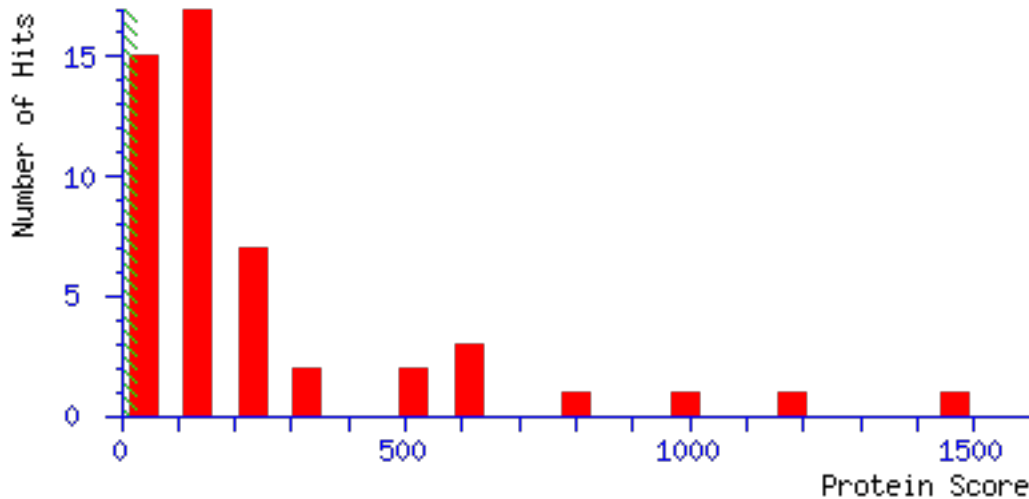
[2::sp|P0A7D4|PURA ECOLI](#)  
[2::sp|P22188|MURE ECOLI](#)  
[2::sp|P0A8L1|SYS ECOLI](#)  
[2::sp|P76403|YEGQ ECOLI](#)  
[2::sp|P76658|HLDE ECOLI](#)  
[1::sp|cRAP054|P04264|K2C1 HUMAN](#)  
[2::sp|P0A825|GLYA ECOLI](#)  
[2::sp|P21507|SRMB ECOLI](#)  
[1::sp|cRAP087|P02769|ALBU BOVIN](#)  
[2::sp|P27306|STHA ECOLI](#)  
[2::sp|P02931|OMPF ECOLI](#)  
[2::sp|P21888|SYC ECOLI](#)  
[1::sp|cRAP112|P00761|TRYP PIG](#)  
[1::sp|cRAP039|P13645|K1C10 HUMAN](#)  
[2::sp|P24182|ACCC ECOLI](#)  
[2::sp|P0AEI1|MIAB ECOLI](#)  
[2::sp|P0A6H1|CLPX ECOLI](#)  
[2::sp|P31979|NUOF ECOLI](#)  
[2::sp|P16869|FHUE ECOLI](#)  
[2::sp|P17445|BETB ECOLI](#)  
[2::sp|P0AC38|ASPA ECOLI](#)  
[2::sp|P60906|SYH ECOLI](#)  
[2::sp|P77748|YDIJ ECOLI](#)  
[2::sp|P02943|LAMB ECOLI](#)  
[2::sp|P05793|ILVC ECOLI](#)  
[2::sp|P0AD61|KPYK1 ECOLI](#)  
[2::sp|P31068|FLIH ECOLI](#)  
[2::sp|P0A9J8|PHEA ECOLI](#)  
[2::sp|P33224|AIDB ECOLI](#)  
[2::sp|P0A953|FABB ECOLI](#)  
[2::sp|P0AB89|PUR8 ECOLI](#)  
[2::sp|P25888|RHLE ECOLI](#)  
[2::sp|P0A817|METK ECOLI](#)  
[2::sp|P08722|PTV3B ECOLI](#)  
[2::sp|P09099|XYLB ECOLI](#)  
[2::sp|P0A9B2|G3P1 ECOLI](#)  
[2::sp|P28912|YHHI ECOLI](#)  
[2::sp|P24175|MANB ECOLI](#)  
[2::sp|P25552|GPPA ECOLI](#)  
[2::sp|P37652|BCSB ECOLI](#)  
[2::sp|P30863|DKGB ECOLI](#)  
[2::sp|P77171|YDCI ECOLI](#)  
[2::sp|P28305|PABC ECOLI](#)  
[2::sp|P0AEI4|RIMO ECOLI](#)  
[2::sp|P77335|HLYE ECOLI](#)  
[2::sp|P00963|ASNA ECOLI](#)  
[2::sp|P63020|NFUA ECOLI](#)  
[2::sp|P45420|YHCD ECOLI](#)

Adenylosuccinate synthetase OS=Escherichia coli  
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate  
Serine--tRNA ligase OS=Escherichia coli  
Uncharacterized protease YegQ OS=Escherichia coli  
Bifunctional protein HldE OS=Escherichia coli  
Keratin, type II cytoskeletal 1 OS=Homo sapiens  
Serine hydroxymethyltransferase OS=Escherichia coli  
ATP-dependent RNA helicase SrmB OS=Escherichia coli  
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=1  
Soluble pyridine nucleotide transhydrogenase  
Outer membrane protein F OS=Escherichia coli  
Cysteine--tRNA ligase OS=Escherichia coli  
Trypsin OS=Sus scrofa PE=1 SV=1  
Keratin, type I cytoskeletal 10 OS=Homo sapiens  
Biotin carboxylase OS=Escherichia coli  
tRNA-2-methylthio-N(6)-dimethylallyltransferase  
ATP-dependent Clp protease ATP-binding domain ClpA  
NADH-quinone oxidoreductase subunit F OXPHOS  
FhuE receptor OS=Escherichia coli (strain K12)  
NAD/NADP-dependent betaine aldehyde dehydrogenase  
Aspartate ammonia-lyase OS=Escherichia coli  
Histidine--tRNA ligase OS=Escherichia coli  
Uncharacterized protein YdiJ OS=Escherichia coli  
Maltoporin OS=Escherichia coli (strain K12)  
Ketol-acid reductoisomerase (NADP(+)) OXPHOS  
Pyruvate kinase I OS=Escherichia coli (strain K12)  
Flagellar assembly protein FliH OS=Escherichia coli  
P-protein OS=Escherichia coli (strain K12)  
Putative acyl-CoA dehydrogenase AidB OS=Escherichia coli  
3-oxoacyl-[acyl-carrier-protein] synthase 3  
Adenylosuccinate lyase OS=Escherichia coli  
ATP-dependent RNA helicase RhLE OS=Escherichia coli  
S-adenosylmethionine synthase OS=Escherichia coli  
PTS system beta-glucoside-specific EIIB  
Xylulose kinase OS=Escherichia coli (strain K12)  
Glyceraldehyde-3-phosphate dehydrogenase H repeat-associated putative transposase  
Phosphomannomutase OS=Escherichia coli  
Guanosine-5'-triphosphate, 3'-diphosphate  
Cyclic di-GMP-binding protein OS=Escherichia coli  
2,5-diketo-D-gluconic acid reductase B  
Uncharacterized HTH-type transcription factor  
Aminodeoxychorismate lyase OS=Escherichia coli  
Ribosomal protein S12 methylthiotransferase  
Hemolysin E, chromosomal OS=Escherichia coli  
Aspartate--ammonia ligase OS=Escherichia coli  
Fe/S biogenesis protein NfuA OS=Escherichia coli  
Uncharacterized outer membrane usher protein

<a href="#">1::sp cRAP008 P00722 BGAL ECOLI</a>	Beta-galactosidase OS=Escherichia coli
<a href="#">2::sp P76655 YQIG ECOLI</a>	Putative outer membrane usher protein Y
<a href="#">2::sp P0ABF6 CDD ECOLI</a>	Cytidine deaminase OS=Escherichia coli
<a href="#">2::sp P0A6A3 ACKA ECOLI</a>	Acetate kinase OS=Escherichia coli (str
<a href="#">2::sp P17115 GUTQ ECOLI</a>	Arabinose 5-phosphate isomerase GutQ OS
<a href="#">2::sp P0A915 OMPW ECOLI</a>	Outer membrane protein W OS=Escherichia
<a href="#">2::sp P25744 MDTG ECOLI</a>	Multidrug resistance protein MdtG OS=Es
<a href="#">2::sp P77416 HYFD ECOLI</a>	Hydrogenase-4 component D OS=Escherichi
<a href="#">2::sp P37909 YBGD ECOLI</a>	Uncharacterized fimbrial-like protein Y
<a href="#">2::sp P08839 PT1 ECOLI</a>	Phosphoenolpyruvate-protein phosphotran

## 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 . . . . . Mus musculus (house mouse) . . . . . Rattus . . . . . Other mammals (rodents) . . . . . Takifugu rubripes (Japanese Pufferfish) . . . . . Danio rerio (zebra fish) . . . . .				

Schizosaccharomyces pombe (fission yeast) . . . . . Pneumocystis carinii . . . . . Other Fungi . . . . . Viridiplantae  
Mycobacterium tuberculosis complex . . . . . Other Actinobacteria (class) . . . . . Firmicutes (gram-positive bacteria)  
Agrobacterium tumefaciens . . . . . Campylobacter jejuni . . . . . Escherichia coli . . . . . Neisseria meningitidis  
Species information unavailable

## Error tolerant

1. [2::sp|P02930|TOLC\\_ECOLI](#) **Mass:** 53708 **Score:** 1466 **Matches:** 83(76) **Sequences:**  
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
<a href="#">248</a>	400.7531	799.4917	799.4916	0.21	2	21	0.048	1	U	L.SLLQA
<a href="#">591</a>	433.7343	865.4540	865.4545	-0.58	1	38	0.0015	1	U	L.ILNTA
<a href="#">592</a>	433.7345	865.4544	865.4545	-0.15	1	(37)	0.0022	1	U	L.ILNTA
<a href="#">851</a>	458.7769	915.5392	915.5389	0.35	1	22	0.048	1	U	L.NIKSA
<a href="#">1006</a>	474.7353	947.4561	947.4560	0.20	1	(32)	0.011	1	U	F.SLSLQ
<a href="#">1007</a>	474.7354	947.4562	947.4560	0.26	1	36	0.0047	1	U	F.SLSLQ
<a href="#">1131</a>	482.7405	963.4665	963.4662	0.32	1	(40)	0.0015	1	U	Y.NFVGA
<a href="#">1132</a>	482.7410	963.4674	963.4662	1.28	1	46	0.00047	1	U	Y.NFVGA
<a href="#">1407</a>	501.7593	1001.5041	1001.5029	1.14	2	26	0.045	1	U	L.GTLNE
<a href="#">1409</a>	501.7595	1001.5045	1001.5029	1.56	2	(24)	0.065	1	U	L.GTLNE
<a href="#">1466</a>	507.2682	1012.5218	1012.5229	-1.09	2	(29)	0.014	1	U	L.ILNTA
<a href="#">1467</a>	507.2685	1012.5225	1012.5229	-0.44	2	33	0.0059	1	U	L.ILNTA
<a href="#">1675</a>	523.7789	1045.5432	1045.5444	-1.16	2	30	0.018	1	U	L.LPQLG
<a href="#">1676</a>	523.7802	1045.5459	1045.5444	1.40	2	(29)	0.025	1	U	L.LPQLG
<a href="#">1689</a>	526.2736	1050.5326	1050.5345	-1.88	0	(36)	0.0051	1	U	Y.TQAQK
<a href="#">1690</a>	526.2736	1050.5327	1050.5345	-1.77	0	(21)	0.17	1	U	Y.TQAQK
<a href="#">1691</a>	526.2738	1050.5330	1050.5345	-1.43	0	(25)	0.06	1	U	Y.TQAQK
<a href="#">1692</a>	526.2750	1050.5355	1050.5345	0.90	0	42	0.0012	1	U	Y.TQAQK
<a href="#">1694</a>	526.2759	1050.5373	1050.5345	2.65	0	(28)	0.032	1	U	Y.TQAQK
<a href="#">1702</a>	526.7729	1051.5312	1051.5186	12.1	0	(21)	0.11	1	U	Y.TQAQK
<a href="#">2202</a>	559.3144	1116.6143	1116.6139	0.42	0	(51)	0.0001	1	U	Y.KQAVV
<a href="#">2203</a>	559.3149	1116.6153	1116.6139	1.30	0	57	2.4e-05	1	U	Y.KQAVV
<a href="#">2586</a>	580.3375	1158.6604	1158.6609	-0.42	0	28	0.016	1	U	Y.SVGTR
<a href="#">2587</a>	580.3379	1158.6612	1158.6609	0.32	0	(25)	0.029	1	U	Y.SVGTR
<a href="#">2877</a>	599.7744	1197.5343	1197.5336	0.58	1	(26)	0.037	1	U	L.SQAEN
<a href="#">2878</a>	599.7753	1197.5361	1197.5336	2.12	1	28	0.025	1	U	L.SQAEN
<a href="#">2969</a>	605.8428	1209.6710	1209.6717	-0.61	0	43	0.00037	1	U	F.KTDKP
<a href="#">2970</a>	605.8429	1209.6712	1209.6717	-0.39	0	(38)	0.0011	1	U	F.KTDKP
<a href="#">2983</a>	606.3364	1210.6583	1210.6557	2.13	0	(21)	0.061	1	U	F.KTDKP
<a href="#">3439</a>	639.3333	1276.6519	1276.6523	-0.31	1	40	0.0018	1	U	Y.NAKQE
<a href="#">3440</a>	639.3336	1276.6527	1276.6523	0.27	1	(37)	0.0035	1	U	Y.NAKQE
<a href="#">3480</a>	642.3213	1282.6280	1282.6266	1.14	0	28	0.024	1	U	Y.SGSKT
<a href="#">3541</a>	647.2900	1292.5655	1292.5667	-0.89	0	(33)	0.0062	1	U	Y.DDSNM
<a href="#">3542</a>	647.2921	1292.5695	1292.5667	2.22	0	40	0.0011	1	U	Y.DDSNM
<a href="#">3556</a>	647.7808	1293.5471	1293.5507	-2.78	0	(22)	0.055	1	U	Y.DDSNM
<a href="#">3613</a>	651.3221	1300.6297	1300.6299	-0.13	1	34	0.0059	1	U	L.SYTQA
<a href="#">3614</a>	651.3233	1300.6320	1300.6299	1.65	1	(28)	0.026	1	U	L.SYTQA
<a href="#">3779</a>	661.8336	1321.6526	1321.6514	0.90	0	(23)	0.13	1	U	L.QEKAA
<a href="#">3780</a>	661.8336	1321.6527	1321.6514	0.99	0	47	0.00053	1	U	L.QEKAA
<a href="#">3789</a>	662.3851	1322.7557	1322.7558	-0.06	1	(36)	0.00085	1	U	F.KTDKP
<a href="#">3791</a>	662.3860	1322.7574	1322.7558	1.24	1	44	0.00012	1	U	F.KTDKP
<a href="#">4103</a>	690.8430	1379.6714	1379.6681	2.40	0	(58)	3.6e-05	1	U	F.NNINA

<a href="#">4104</a>	690.8431	1379.6716	1379.6681	2.57	0	81	1.6e-07	1	U	F.NNINA
<a href="#">4106</a>	691.3326	1380.6506	1380.6521	-1.06	0	(46)	0.00053	1	U	F.NNINA
<a href="#">4107</a>	691.3345	1380.6545	1380.6521	1.77	0	(49)	0.00025	1	U	F.NNINA
<a href="#">4424</a>	724.8780	1447.7414	1447.7419	-0.35	0	57	4.6e-05	1	U	L.VAITD
<a href="#">4425</a>	724.8793	1447.7440	1447.7419	1.42	0	(42)	0.0012	1	U	L.VAITD
<a href="#">4431</a>	725.3736	1448.7326	1448.7259	4.63	0	(45)	0.00082	1	U	L.VAITD
<a href="#">4432</a>	725.3743	1448.7341	1448.7259	5.64	0	(55)	8.5e-05	1	U	L.VAITD
<a href="#">4581</a>	743.3500	1484.6855	1484.6817	2.59	2	(44)	0.00084	1	U	F.SSLSQ
<a href="#">4582</a>	743.3502	1484.6858	1484.6817	2.75	2	55	5.8e-05	1	U	F.SSLSQ
<a href="#">4603</a>	745.8637	1489.7127	1489.7121	0.46	0	85	7.8e-08	1	U	Y.RDANG
<a href="#">4604</a>	745.8644	1489.7143	1489.7121	1.52	0	(71)	2e-06	1	U	Y.RDANG
<a href="#">4608</a>	746.3550	1490.6955	1490.6961	-0.37	0	(67)	4.9e-06	1	U	Y.RDANG
<a href="#">4609</a>	746.3565	1490.6985	1490.6961	1.61	0	(76)	5.4e-07	1	U	Y.RDANG
<a href="#">4610</a>	746.3567	1490.6988	1490.6961	1.85	0	(40)	0.002	1	U	Y.RDANG
<a href="#">4615</a>	746.8505	1491.6864	1491.6801	4.21	0	(69)	2.4e-06	1	U	Y.RDANG
<a href="#">4797</a>	768.8994	1535.7841	1535.7831	0.66	1	(52)	0.00016	1	U	L.TLQEK
<a href="#">4798</a>	768.9000	1535.7855	1535.7831	1.54	1	(42)	0.0013	1	U	L.TLQEK
<a href="#">4799</a>	768.9012	1535.7878	1535.7831	3.05	1	63	1e-05	1	U	L.TLQEK
<a href="#">4800</a>	768.9014	1535.7882	1535.7831	3.30	1	(26)	0.051	1	U	L.TLQEK
<a href="#">4801</a>	768.9019	1535.7892	1535.7831	3.93	1	(21)	0.16	1	U	L.TLQEK
<a href="#">4802</a>	769.3942	1536.7739	1536.7671	4.41	1	(40)	0.002	1	U	L.TLQEK
<a href="#">4875</a>	777.3728	1552.7310	1552.7304	0.42	0	57	4.2e-05	1	U	Y.QGGMV
<a href="#">4876</a>	777.3731	1552.7317	1552.7304	0.82	0	(29)	0.029	1	U	Y.QGGMV
<a href="#">5173</a>	804.9251	1607.8357	1607.8307	3.08	2	43	0.00083	1	U	L.RQITG
<a href="#">5174</a>	804.9251	1607.8357	1607.8307	3.08	2	(42)	0.001	1	U	L.RQITG
<a href="#">5777</a>	583.2955	1746.8646	1746.8649	-0.16	1	29	0.031	1	U	L.SNPFL
<a href="#">6031</a>	916.4877	1830.9608	1830.9588	1.09	1	(90)	1.9e-08	1	U	F.NVGLV
<a href="#">6032</a>	916.4900	1830.9654	1830.9588	3.62	1	102	1e-09	1	U	F.NVGLV
<a href="#">6100</a>	927.9518	1853.8890	1853.8829	3.29	1	(83)	1.1e-07	1	U	Y.KQAVV
<a href="#">6101</a>	927.9521	1853.8896	1853.8829	3.63	1	109	3.2e-10	1	U	Y.KQAVV
<a href="#">6134</a>	935.9464	1869.8783	1869.8778	0.24	1	(38)	0.0035	1	U	Y.KQAVV
<a href="#">6135</a>	935.9479	1869.8813	1869.8778	1.87	1	(88)	3.6e-08	1	U	Y.KQAVV
<a href="#">6136</a>	935.9489	1869.8833	1869.8778	2.91	1	(58)	3.4e-05	1	U	Y.KQAVV
<a href="#">6139</a>	935.9676	1869.9206	1869.9180	1.39	1	73	1e-06	1	U	L.ANEVT
<a href="#">6140</a>	935.9695	1869.9245	1869.9180	3.48	1	(66)	4.6e-06	1	U	L.ANEVT
<a href="#">6148</a>	936.4422	1870.8698	1870.8618	4.28	1	(53)	9.8e-05	1	U	Y.KQAVV
<a href="#">6149</a>	936.4457	1870.8768	1870.8618	8.00	1	(38)	0.0029	1	U	Y.KQAVV
<a href="#">6150</a>	936.4470	1870.8795	1870.8618	9.44	1	(39)	0.0024	1	U	Y.KQAVV
<a href="#">6151</a>	936.4619	1870.9093	1870.9020	3.86	1	(35)	0.0072	1	U	L.ANEVT
<a href="#">6251</a>	956.9334	1911.8523	1911.8558	-1.86	1	(28)	0.031	1	U	Y.SNGYR
<a href="#">6252</a>	956.9351	1911.8556	1911.8558	-0.13	1	39	0.0022	1	U	Y.SNGYR

2. [2::sp|POA9P0|DLDH\\_ECOLI](#) Mass: 50942 Score: 1185 Matches: 73(67) Sequences: Dihydropolyl 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
<a href="#">435</a>	416.1980	830.3814	830.3810	0.43	0	23	0.037	1	U	Y.TEPEV
<a href="#">622</a>	435.7557	869.4968	869.4970	-0.27	0	21	0.03	1	U	L.KEVPE
<a href="#">988</a>	473.2764	944.5382	944.5365	1.79	1	21	0.085	2	U	L.LVMGG
<a href="#">1175</a>	486.2980	970.5814	970.5811	0.30	0	25	0.015	1	U	W.KEKVI
<a href="#">1253</a>	492.2983	982.5820	982.5811	0.92	1	22	0.025	1	U	L.KEVPE

<u>1742</u>	529.7872	1057.5598	1057.5590	0.74	0	(26)	0.035	1	U	L.NVGC
<u>1743</u>	529.7873	1057.5601	1057.5590	1.08	0	32	0.01	1	U	L.NVGC
<u>2614</u>	388.2042	1161.5908	1161.5931	-1.93	0	(21)	0.2	1	U	F.IPHED
<u>2616</u>	388.2050	1161.5931	1161.5931	0.05	0	21	0.18	1	U	F.IPHED
<u>2695</u>	586.3290	1170.6435	1170.6431	0.39	1	28	0.019	1	U	L.NVGC
<u>2741</u>	589.8240	1177.6334	1177.6343	-0.75	1	49	0.00017	1	U	L.GLETV
<u>2742</u>	589.8253	1177.6360	1177.6343	1.44	1	(47)	0.00023	1	U	L.GLETV
<u>3025</u>	608.8608	1215.7071	1215.7075	-0.27	0	(35)	0.0021	1	U	M.STEIK
<u>3026</u>	608.8624	1215.7103	1215.7075	2.34	0	37	0.0012	1	U	M.STEIK
<u>3168</u>	619.3711	1236.7276	1236.7302	-2.11	0	(29)	0.0027	1	U	L.VAIGR
<u>3169</u>	619.3723	1236.7299	1236.7302	-0.24	0	(47)	4.2e-05	1	U	L.VAIGR
<u>3176</u>	619.8644	1237.7142	1237.7142	-0.03	0	(52)	2e-05	1	U	L.VAIGR
<u>3177</u>	619.8645	1237.7144	1237.7142	0.16	0	53	1.7e-05	1	U	L.VAIGR
<u>3249</u>	625.3445	1248.6744	1248.6754	-0.81	1	30	0.013	1	U	Y.FDPKV
<u>3250</u>	625.3450	1248.6755	1248.6754	0.07	1	(27)	0.027	1	U	Y.FDPKV
<u>3594</u>	650.3859	1298.7573	1298.7558	1.17	1	(61)	4.3e-06	1	U	W.KEKVI
<u>3595</u>	650.3876	1298.7607	1298.7558	3.79	1	68	8.5e-07	1	U	W.KEKVI
<u>3666</u>	436.5939	1306.7600	1306.7608	-0.68	0	34	0.0012	1	U	L.HVAKV
<u>3667</u>	436.5942	1306.7607	1306.7608	-0.10	0	(26)	0.0075	1	U	L.HVAKV
<u>4112</u>	<b>691.8619</b>	<b>1381.7093</b>	<b>1381.7089</b>	<b>0.34</b>	<b>0</b>	<b>(21)</b>	<b>0.14</b>	<b>2</b>	<b>U</b>	<b>L.TEKEA</b>
<u>4113</u>	691.8623	1381.7100	1381.7089	0.86	0	31	0.012	1	U	L.TEKEA
<u>4367</u>	718.3446	1434.6746	1434.6739	0.50	0	(52)	0.00014	1	U	L.DAGKA
<u>4368</u>	718.3448	1434.6751	1434.6739	0.85	0	78	3.3e-07	1	U	L.DAGKA
<u>4369</u>	479.2324	1434.6753	1434.6739	0.92	0	(30)	0.023	1	U	L.DAGKA
<u>4370</u>	479.2324	1434.6754	1434.6739	1.04	0	(38)	0.0038	1	U	L.DAGKA
<u>4371</u>	718.3567	1434.6988	1434.6991	-0.17	0	(40)	0.0027	1	U	L.EVEGE
<u>4372</u>	718.3583	1434.7021	1434.6991	2.13	0	(41)	0.002	1	U	L.EVEGE
<u>4374</u>	718.8492	1435.6838	1435.6831	0.51	0	(42)	0.0016	1	U	L.EVEGE
<u>4375</u>	718.8515	1435.6884	1435.6831	3.74	0	43	0.0011	1	U	L.EVEGE
<u>4495</u>	731.3560	1460.6975	1460.6970	0.35	1	(51)	0.00017	1	U	Y.HALGS
<u>4496</u>	731.3561	1460.6977	1460.6970	0.51	1	60	2.2e-05	1	U	Y.HALGS
<u>4770</u>	764.8738	1527.7331	1527.7313	1.18	1	30	0.02	1	U	L.VMGGG
<u>4909</u>	779.9169	1557.8192	1557.8151	2.63	0	60	1.7e-05	1	U	F.GEPKT
<u>4910</u>	779.9169	1557.8193	1557.8151	2.71	0	(51)	0.00013	1	U	F.GEPKT
<u>5303</u>	821.4160	1640.8175	1640.8154	1.28	2	(37)	0.0047	1	U	L.LVMGG
<u>5304</u>	821.4172	1640.8198	1640.8154	2.70	2	38	0.0037	1	U	L.LVMGG
<u>5344</u>	551.3016	1650.8829	1650.8828	0.04	1	(44)	0.00044	1	U	W.VGLTE
<u>5345</u>	551.3024	1650.8853	1650.8828	1.50	1	(28)	0.017	1	U	W.VGLTE
<u>5346</u>	551.3025	1650.8858	1650.8828	1.82	1	(38)	0.0018	1	U	W.VGLTE
<u>5347</u>	826.4509	1650.8873	1650.8828	2.72	1	(44)	0.00051	1	U	W.VGLTE
<u>5348</u>	826.4514	1650.8883	1650.8828	3.32	1	46	0.00029	1	U	W.VGLTE
<u>5374</u>	829.4615	1656.9084	1656.9087	-0.15	0	(33)	0.0065	1	U	F.DQVIP
<u>5375</u>	829.4615	1656.9084	1656.9087	-0.15	0	62	8.2e-06	1	U	F.DQVIP
<u>5376</u>	553.3104	1656.9093	1656.9087	0.35	0	(28)	0.023	1	U	F.DQVIP
<u>5377</u>	553.3105	1656.9096	1656.9087	0.58	0	(30)	0.012	1	U	F.DQVIP
<u>5379</u>	553.3116	1656.9131	1656.9087	2.68	0	(44)	0.00047	1	U	F.DQVIP
<u>5380</u>	829.4643	1656.9140	1656.9087	3.23	0	(62)	7.6e-06	1	U	F.DQVIP
<u>5504</u>	841.9648	1681.9151	1681.9151	-0.00	0	51	6.3e-05	1	U	F.DNAII
<u>5505</u>	841.9675	1681.9205	1681.9151	3.20	0	(45)	0.00029	1	U	F.DNAII
<u>5607</u>	568.9642	1703.8707	1703.8665	2.48	0	(34)	0.0093	1	U	Y.VTMEG
<u>5608</u>	568.9651	1703.8734	1703.8665	4.10	0	48	0.00032	1	U	Y.VTMEG
<u>5651</u>	574.2941	1719.8606	1719.8614	-0.47	0	(28)	0.041	1	U	Y.VTMEG
<u>5652</u>	860.9380	1719.8614	1719.8614	0.03	0	(29)	0.034	1	U	Y.VTMEG
<u>5653</u>	574.2947	1719.8624	1719.8614	0.59	0	(21)	0.19	1	U	Y.VTMEG
<u>5948</u>	897.4651	1792.9156	1792.9142	0.82	2	(39)	0.0023	1	U	F.RCADL
<u>5949</u>	897.4662	1792.9178	1792.9142	2.05	2	60	2.1e-05	1	U	F.RCADL
<u>6455</u>	996.9978	1991.9810	1991.9800	0.53	1	(48)	0.00043	1	U	F.TGANT

<a href="#">6456</a>	996.9984	1991.9823	1991.9800	1.14	1	(43)	0.0012	1	U	F.TGANT
<a href="#">6457</a>	665.0018	1991.9835	1991.9800	1.75	1	(37)	0.0053	1	U	F.TGANT
<a href="#">6458</a>	665.0031	1991.9875	1991.9800	3.77	1	(26)	0.056	1	U	F.TGANT
<a href="#">6460</a>	665.3286	1992.9640	1992.9640	-0.00	1	(29)	0.029	1	U	F.TGANT
<a href="#">6461</a>	997.4901	1992.9657	1992.9640	0.83	1	(75)	7.4e-07	1	U	F.TGANT
<a href="#">6462</a>	997.4929	1992.9712	1992.9640	3.59	1	80	2.4e-07	1	U	F.TGANT
<a href="#">6463</a>	665.3311	1992.9715	1992.9640	3.78	1	(34)	0.011	1	U	F.TGANT
<a href="#">6685</a>	708.7011	2123.0813	2123.0820	-0.31	2	(38)	0.0033	1	U	F.NLMLE
<a href="#">6686</a>	708.7016	2123.0830	2123.0820	0.46	2	(26)	0.051	1	U	F.NLMLE
<a href="#">6708</a>	714.0345	2139.0816	2139.0769	2.20	2	(29)	0.027	1	U	F.NLMLE
<a href="#">6709</a>	714.0354	2139.0844	2139.0769	3.49	2	44	0.00079	1	U	F.NLMLE

3. [1::sp|cRAP022|P00766|CTRA\\_BOVIN](#) Mass: 26220 Score: 1010 Matches: 120(101) S

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
<a href="#">125</a>	389.1708	776.3271	776.3276	-0.65	1	33	0.0031	1		F.HFCG
<a href="#">126</a>	389.1708	776.3271	776.3276	-0.58	1	(29)	0.0073	1		F.HFCG
<a href="#">389</a>	412.7288	823.4430	823.4440	-1.20	1	(26)	0.019	1	U	L.KLST
<a href="#">390</a>	412.7289	823.4433	823.4440	-0.76	1	(25)	0.022	1	U	L.KLST
<a href="#">391</a>	412.7292	823.4439	823.4440	-0.08	1	(53)	3.4e-05	1	U	L.KLST
<a href="#">392</a>	412.7292	823.4439	823.4440	-0.01	1	(53)	3.6e-05	1	U	L.KLST
<a href="#">393</a>	412.7292	823.4439	823.4440	-0.01	1	57	1.2e-05	1	U	L.KLST
<a href="#">394</a>	412.7292	823.4439	823.4440	-0.01	1	(34)	0.0026	1	U	L.KLST
<a href="#">395</a>	412.7293	823.4440	823.4440	0.07	1	(49)	8.8e-05	1	U	L.KLST
<a href="#">396</a>	412.7294	823.4442	823.4440	0.36	1	(38)	0.0012	1	U	L.KLST
<a href="#">643</a>	437.7552	873.4958	873.4960	-0.29	1	(39)	0.0018	1	U	W.TLVG
<a href="#">644</a>	437.7553	873.4961	873.4960	0.13	1	46	0.00028	1	U	W.TLVG
<a href="#">1107</a>	481.7475	961.4805	961.4804	0.15	0	(22)	0.13	1	U	L.VCKK
<a href="#">1108</a>	481.7476	961.4807	961.4804	0.34	0	28	0.026	1	U	L.VCKK
<a href="#">1109</a>	481.7481	961.4817	961.4804	1.36	0	(21)	0.16	1	U	L.VCKK
<a href="#">1121</a>	482.2383	962.4620	962.4644	-2.46	0	(28)	0.022	1	U	L.VCKK
<a href="#">1281</a>	494.2664	986.5182	986.5185	-0.38	1	(27)	0.024	1	U	L.VNWV
<a href="#">1282</a>	494.2665	986.5185	986.5185	-0.01	1	35	0.004	1	U	L.VNWV
<a href="#">1298</a>	494.7584	987.5023	987.5025	-0.20	1	(35)	0.0048	1	U	L.VNWV
<a href="#">1299</a>	494.7592	987.5038	987.5025	1.30	1	(23)	0.079	1	U	L.VNWV
<a href="#">1398</a>	501.2540	1000.4934	1000.4938	-0.37	0	(30)	0.012	1	U	Y.TNAN
<a href="#">1399</a>	501.2542	1000.4938	1000.4938	0.05	0	(25)	0.037	1	U	Y.TNAN
<a href="#">1400</a>	501.2545	1000.4944	1000.4938	0.67	0	(23)	0.069	1	U	Y.TNAN
<a href="#">1401</a>	501.2547	1000.4948	1000.4938	1.09	0	(26)	0.029	1	U	Y.TNAN
<a href="#">1402</a>	501.2549	1000.4952	1000.4938	1.45	0	(30)	0.013	1	U	Y.TNAN
<a href="#">1404</a>	501.7428	1001.4710	1001.4778	-6.77	0	(21)	0.1	1	U	Y.TNAN
<a href="#">1405</a>	501.7483	1001.4820	1001.4778	4.19	0	36	0.0039	1	U	Y.TNAN
<a href="#">1406</a>	501.7585	1001.5024	1001.4778	24.6	0	(20)	0.15	1	U	Y.TNAN
<a href="#">1495</a>	508.7843	1015.5540	1015.5550	-0.96	1	(36)	0.0038	1	U	L.TINN
<a href="#">1496</a>	508.7843	1015.5540	1015.5550	-0.96	1	(42)	0.001	1	U	L.TINN
<a href="#">1497</a>	508.7845	1015.5544	1015.5550	-0.55	1	(36)	0.0043	1	U	L.TINN
<a href="#">1498</a>	508.7845	1015.5545	1015.5550	-0.47	1	(50)	0.00018	1	U	L.TINN
<a href="#">1499</a>	508.7848	1015.5550	1015.5550	0.01	1	51	0.00011	1	U	L.TINN
<a href="#">1501</a>	508.7853	1015.5561	1015.5550	1.09	1	(47)	0.00028	1	U	L.TINN
<a href="#">1502</a>	508.7860	1015.5574	1015.5550	2.41	1	(40)	0.0013	1	U	L.TINN
<a href="#">1503</a>	508.7860	1015.5575	1015.5550	2.47	1	(50)	0.00015	1	U	L.TINN
<a href="#">1604</a>	515.2954	1028.5763	1028.5767	-0.43	1	(24)	0.037	1	U	Y.ARVT



<a href="#">1605</a>	515.2959	1028.5772	1028.5767	0.53	1	(21)	0.075	1	U	Y.ARV
<a href="#">1606</a>	515.2963	1028.5780	1028.5767	1.23	1	(25)	0.029	1	U	Y.ARV
<a href="#">1607</a>	515.2966	1028.5787	1028.5767	1.95	1	38	0.0016	1	U	Y.ARV
<a href="#">1609</a>	515.7864	1029.5582	1029.5607	-2.44	1	(22)	0.1	1	U	Y.ARV
<a href="#">1610</a>	515.7871	1029.5597	1029.5607	-1.02	1	(28)	0.024	1	U	Y.ARV
<a href="#">1711</a>	527.2927	1052.5709	1052.5689	1.92	0	23	0.039	1	U	-.CGVP
<a href="#">2236</a>	561.7927	1121.5708	1121.5717	-0.83	1	(30)	0.022	1	U	W.QVSL
<a href="#">2237</a>	561.7927	1121.5709	1121.5717	-0.72	1	(60)	2.2e-05	1	U	W.QVSL
<a href="#">2238</a>	561.7927	1121.5709	1121.5717	-0.72	1	(24)	0.074	1	U	W.QVSL
<a href="#">2240</a>	561.7930	1121.5714	1121.5717	-0.28	1	(22)	0.12	1	U	W.QVSL
<a href="#">2241</a>	561.7930	1121.5715	1121.5717	-0.17	1	64	8.2e-06	1	U	W.QVSL
<a href="#">2242</a>	561.7933	1121.5720	1121.5717	0.26	1	(35)	0.006	1	U	W.QVSL
<a href="#">2243</a>	561.7935	1121.5724	1121.5717	0.59	1	(26)	0.056	1	U	W.QVSL
<a href="#">2244</a>	561.7935	1121.5724	1121.5717	0.59	1	(21)	0.18	1	U	W.QVSL
<a href="#">2245</a>	561.7935	1121.5725	1121.5717	0.70	1	(42)	0.0013	1	U	W.QVSL
<a href="#">2246</a>	561.7935	1121.5725	1121.5717	0.70	1	(34)	0.0082	1	U	W.QVSL
<a href="#">2247</a>	561.7935	1121.5725	1121.5717	0.70	1	(22)	0.12	1	U	W.QVSL
<a href="#">2249</a>	561.7936	1121.5727	1121.5717	0.92	1	(40)	0.0018	1	U	W.QVSL
<a href="#">2250</a>	561.7937	1121.5728	1121.5717	1.02	1	(28)	0.03	1	U	W.QVSL
<a href="#">2255</a>	561.7940	1121.5735	1121.5717	1.58	1	(42)	0.0012	1	U	W.QVSL
<a href="#">2256</a>	561.7941	1121.5736	1121.5717	1.68	1	(32)	0.013	1	U	W.QVSL
<a href="#">2259</a>	561.7941	1121.5736	1121.5717	1.68	1	(32)	0.012	1	U	W.QVSL
<a href="#">2261</a>	561.7941	1121.5737	1121.5717	1.79	1	(47)	0.00039	1	U	W.QVSL
<a href="#">2262</a>	561.7941	1121.5737	1121.5717	1.79	1	(59)	2.5e-05	1	U	W.QVSL
<a href="#">2263</a>	561.7941	1121.5737	1121.5717	1.79	1	(32)	0.012	1	U	W.QVSL
<a href="#">2265</a>	561.7944	1121.5742	1121.5717	2.22	1	(52)	0.00012	1	U	W.QVSL
<a href="#">2267</a>	561.7946	1121.5747	1121.5717	2.66	1	(24)	0.078	1	U	W.QVSL
<a href="#">2277</a>	562.2893	1122.5639	1122.5557	7.34	1	(63)	9.5e-06	1	U	W.QVSL
<a href="#">2315</a>	564.2794	1126.5443	1126.5441	0.20	1	35	0.0051	1	U	L.LSNT
<a href="#">2316</a>	564.2797	1126.5448	1126.5441	0.62	1	(30)	0.014	1	U	L.LSNT
<a href="#">2509</a>	575.2534	1148.4923	1148.4921	0.21	1	(31)	0.0073	1	U	F.CGGS
<a href="#">2510</a>	575.2536	1148.4926	1148.4921	0.52	1	36	0.0022	1	U	F.CGGS
<a href="#">3027</a>	609.3223	1216.6301	1216.6299	0.16	1	40	0.0022	1	U	Y.NSLT
<a href="#">3028</a>	609.3226	1216.6307	1216.6299	0.65	1	(37)	0.0041	1	U	Y.NSLT
<a href="#">3637</a>	652.2772	1302.5398	1302.5398	-0.04	0	(23)	0.032	1	U	W.GSST
<a href="#">3638</a>	652.2790	1302.5435	1302.5398	2.86	0	25	0.024	1	U	W.GSST
<a href="#">3690</a>	655.8619	1309.7092	1309.7064	2.13	1	33	0.0048	1	U	-.CGVP
<a href="#">3740</a>	660.3426	1318.6706	1318.6728	-1.67	0	(29)	0.027	1	U	F.DQGS
<a href="#">3741</a>	660.3428	1318.6710	1318.6728	-1.40	0	(38)	0.0032	1	U	F.DQGS
<a href="#">3742</a>	660.3431	1318.6717	1318.6728	-0.84	0	(47)	0.00045	1	U	F.DQGS
<a href="#">3743</a>	660.3435	1318.6725	1318.6728	-0.28	0	(42)	0.0012	1	U	F.DQGS
<a href="#">3744</a>	660.3436	1318.6726	1318.6728	-0.19	0	(45)	0.00063	1	U	F.DQGS
<a href="#">3745</a>	660.3436	1318.6727	1318.6728	-0.10	0	(56)	5.2e-05	1	U	F.DQGS
<a href="#">3746</a>	440.5648	1318.6727	1318.6728	-0.09	0	(23)	0.095	1	U	F.DQGS
<a href="#">3751</a>	660.3440	1318.6734	1318.6728	0.45	0	(45)	0.0007	1	U	F.DQGS
<a href="#">3752</a>	440.5651	1318.6734	1318.6728	0.46	0	(22)	0.14	1	U	F.DQGS
<a href="#">3753</a>	440.5652	1318.6737	1318.6728	0.62	0	(25)	0.056	1	U	F.DQGS
<a href="#">3755</a>	660.3442	1318.6738	1318.6728	0.74	0	(50)	0.0002	1	U	F.DQGS
<a href="#">3756</a>	660.3442	1318.6739	1318.6728	0.83	0	57	4.4e-05	1	U	F.DQGS
<a href="#">3757</a>	660.3444	1318.6743	1318.6728	1.10	0	(35)	0.0061	1	U	F.DQGS
<a href="#">3758</a>	440.5654	1318.6744	1318.6728	1.16	0	(24)	0.087	1	U	F.DQGS
<a href="#">3760</a>	660.3445	1318.6745	1318.6728	1.28	0	(44)	0.00079	1	U	F.DQGS
<a href="#">3761</a>	660.3446	1318.6746	1318.6728	1.37	0	(37)	0.0041	1	U	F.DQGS
<a href="#">3765</a>	660.3473	1318.6800	1318.6728	5.45	0	(48)	0.00027	1	U	F.DQGS
<a href="#">3767</a>	660.3500	1318.6854	1318.6728	9.56	0	(39)	0.0026	1	U	F.DQGS
<a href="#">3769</a>	440.8937	1319.6593	1319.6568	1.86	0	(37)	0.0044	1	U	F.DQGS
<a href="#">3770</a>	440.8943	1319.6610	1319.6568	3.18	0	(29)	0.024	1	U	F.DQGS



<a href="#">3771</a>	660.8381	1319.6616	1319.6568	3.59	0	(46)	0.00047	1	U	F.DQGS
<a href="#">3839</a>	665.8638	1329.7131	1329.7140	-0.65	2	69	2e-06	1	U	Y.NSLT
<a href="#">3840</a>	665.8639	1329.7132	1329.7140	-0.56	2	(53)	8.7e-05	1	U	Y.NSLT
<a href="#">4355</a>	717.3151	1432.6157	1432.6194	-2.58	2	(34)	0.0036	1	U	F.HFCG
<a href="#">4356</a>	717.3170	1432.6194	1432.6194	-0.01	2	56	2.8e-05	1	U	F.HFCG
<a href="#">4357</a>	717.3173	1432.6200	1432.6194	0.41	2	(26)	0.027	1	U	F.HFCG
<a href="#">4358</a>	717.3176	1432.6207	1432.6194	0.92	2	(32)	0.0061	1	U	F.HFCG
<a href="#">5519</a>	842.3814	1682.7483	1682.7458	1.47	0	(72)	9.4e-07	1	U	F.SQTV
<a href="#">5520</a>	842.3829	1682.7513	1682.7458	3.28	0	75	4.7e-07	1	U	F.SQTV
<a href="#">5726</a>	869.9576	1737.9006	1737.9009	-0.19	1	(33)	0.0081	1	U	Y.TNAN
<a href="#">5732</a>	869.9582	1737.9018	1737.9009	0.51	1	(25)	0.049	1	U	Y.TNAN
<a href="#">5734</a>	869.9589	1737.9033	1737.9009	1.35	1	(44)	0.00063	1	U	Y.TNAN
<a href="#">5736</a>	869.9593	1737.9040	1737.9009	1.78	1	(23)	0.076	1	U	Y.TNAN
<a href="#">5741</a>	580.3094	1737.9063	1737.9009	3.11	1	(24)	0.059	1	U	Y.TNAN
<a href="#">5742</a>	869.9606	1737.9067	1737.9009	3.32	1	(25)	0.047	1	U	Y.TNAN
<a href="#">5743</a>	869.9607	1737.9068	1737.9009	3.39	1	(39)	0.0019	1	U	Y.TNAN
<a href="#">5744</a>	869.9607	1737.9069	1737.9009	3.46	1	(43)	0.00067	1	U	Y.TNAN
<a href="#">5746</a>	869.9612	1737.9078	1737.9009	3.95	1	51	0.00012	1	U	Y.TNAN
<a href="#">5751</a>	869.9634	1737.9122	1737.9009	6.48	1	(23)	0.074	1	U	Y.TNAN
<a href="#">5753</a>	870.4544	1738.8943	1738.8849	5.36	1	(38)	0.0027	1	U	Y.TNAN
<a href="#">5755</a>	870.4557	1738.8968	1738.8849	6.83	1	(36)	0.0045	1	U	Y.TNAN
<a href="#">5913</a>	892.4426	1782.8706	1782.8689	0.93	0	29	0.029	1	U	L.SRIV
<a href="#">6091</a>	926.5032	1850.9918	1850.9850	3.67	2	38	0.0016	1	U	Y.TNAN
<a href="#">6092</a>	926.5032	1850.9918	1850.9850	3.67	2	(30)	0.01	1	U	Y.TNAN
<a href="#">6501</a>	1009.9964	2017.9782	2017.9780	0.15	0	(35)	0.0072	1	U	W.VVTA
<a href="#">6502</a>	1009.9982	2017.9818	2017.9780	1.90	0	57	4e-05	1	U	W.VVTA

**Proteins matching a subset of these peptides:**

[1::sp|cRAP023|P00767|CTRB\\_BOVIN](#) Mass: 26309 Score: 147 Matches: 6(6) Sequences: 6  
 Chymotrypsinogen B OS=Bos taurus PE=1 SV=1

[1::sp|cRAP110|P00760|TRY1\\_BOVIN](#) Mass: 26453 Score: 33 Matches: 2(2) Sequences: 2  
 Cationic trypsin OS=Bos taurus PE=1 SV=3

4. [2::sp|P0CE47|EFTU1\\_ECOLI](#) Mass: 43427 Score: 773 Matches: 47(46) Sequences: 47  
 Elongation factor Tu 1 OS=Escherichia coli (strain K12) OX=83333 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
<a href="#">985</a>	473.2684	944.5222	944.5219	0.33	1	(49)	0.00017	1	U	F.LLPIE
<a href="#">986</a>	473.2685	944.5224	944.5219	0.58	1	57	2.6e-05	1	U	F.LLPIE
<a href="#">1513</a>	509.7452	1017.4758	1017.4767	-0.88	1	33	0.0072	1	U	L.KALEG
<a href="#">1514</a>	509.7462	1017.4778	1017.4767	1.11	1	(29)	0.02	1	U	L.KALEG
<a href="#">1874</a>	541.2711	1080.5277	1080.5274	0.29	0	(43)	0.00084	1	U	L.IHPIA
<a href="#">1875</a>	541.2723	1080.5301	1080.5274	2.55	0	51	0.00016	1	U	L.IHPIA
<a href="#">2000</a>	549.2700	1096.5254	1096.5223	2.80	0	(38)	0.0024	1	U	L.IHPIA
<a href="#">2001</a>	549.2703	1096.5260	1096.5223	3.35	0	(33)	0.0068	1	U	L.IHPIA
<a href="#">3013</a>	608.3012	1214.5879	1214.5891	-1.04	0	(27)	0.029	1	U	L.DEGRA
<a href="#">3014</a>	608.3030	1214.5914	1214.5891	1.88	0	42	0.0009	1	U	L.DEGRA
<a href="#">3191</a>	621.2546	1240.4947	1240.4931	1.28	0	(21)	0.044	1	U	Y.AHVDC
<a href="#">3192</a>	621.2558	1240.4970	1240.4931	3.16	0	23	0.031	1	U	Y.AHVDC
<a href="#">3226</a>	623.8219	1245.6292	1245.6275	1.44	1	50	0.00022	1	U	L.ELVEM
<a href="#">3227</a>	623.8222	1245.6298	1245.6275	1.92	1	(36)	0.0058	1	U	L.ELVEM
<a href="#">3347</a>	631.8180	1261.6214	1261.6224	-0.75	1	(33)	0.012	1	U	L.ELVEM

<a href="#">3348</a>	631.8199	1261.6252	1261.6224	2.26	1	(31)	0.019	1	U	L.ELVEM
<a href="#">3825</a>	664.8433	1327.6721	1327.6732	-0.83	1	(44)	0.00054	1	U	L.LDEGR
<a href="#">3826</a>	664.8438	1327.6729	1327.6732	-0.18	1	(48)	0.00022	1	U	L.DEGRA
<a href="#">3827</a>	664.8450	1327.6754	1327.6732	1.66	1	49	0.00019	1	U	L.DEGRA
<a href="#">3828</a>	664.8453	1327.6761	1327.6732	2.22	1	45	0.00049	1	U	L.LDEGR
<a href="#">4073</a>	688.3607	1374.7068	1374.7064	0.24	2	(31)	0.018	2	U	L.ELVEM
<a href="#">4074</a>	688.3610	1374.7075	1374.7064	0.77	2	49	0.00026	1	U	L.ELVEM
<a href="#">4194</a>	467.5717	1399.6932	1399.6918	0.95	1	44	0.00078	1	U	L.IHPIA
<a href="#">4195</a>	467.5717	1399.6932	1399.6918	1.02	1	(38)	0.0027	1	U	L.IHPIA
<a href="#">4238</a>	706.3843	1410.7540	1410.7507	2.35	0	29	0.016	1	U	Y.IPEPE
<a href="#">4398</a>	721.3863	1440.7581	1440.7572	0.62	2	46	0.00039	1	U	L.LDEGR
<a href="#">4399</a>	721.3879	1440.7612	1440.7572	2.75	2	(36)	0.0031	1	U	L.LDEGR
<a href="#">4475</a>	728.8828	1455.7511	1455.7470	2.78	1	26	0.039	1	U	Y.ILSKD
<a href="#">4913</a>	780.3892	1558.7639	1558.7628	0.73	0	(39)	0.0029	1	U	Y.DFPGD
<a href="#">4914</a>	780.3897	1558.7649	1558.7628	1.35	0	57	4e-05	1	U	Y.DFPGD
<a href="#">4915</a>	780.3910	1558.7675	1558.7628	3.07	0	(40)	0.002	1	U	Y.DFPGD
<a href="#">4916</a>	780.3914	1558.7682	1558.7628	3.47	0	(39)	0.0026	1	U	Y.DFPGD
<a href="#">5110</a>	797.3603	1592.7060	1592.7062	-0.10	2	(40)	0.0016	1	U	F.LNKCD
<a href="#">5111</a>	797.3610	1592.7075	1592.7062	0.81	2	46	0.00037	1	U	F.LNKCD
<a href="#">5176</a>	805.3589	1608.7032	1608.7011	1.32	2	(24)	0.05	1	U	F.LNKCD
<a href="#">5177</a>	805.3611	1608.7077	1608.7011	4.13	2	(41)	0.00092	1	U	F.LNKCD
<a href="#">5329</a>	824.9253	1647.8360	1647.8324	2.20	0	(37)	0.0047	1	U	Y.VKNMI
<a href="#">5330</a>	824.9288	1647.8431	1647.8324	6.50	0	46	0.00058	1	U	Y.VKNMI
<a href="#">5419</a>	832.9210	1663.8275	1663.8273	0.10	0	(35)	0.0074	1	U	Y.VKNMI
<a href="#">5420</a>	832.9222	1663.8298	1663.8273	1.50	0	(41)	0.002	1	U	Y.VKNMI
<a href="#">5685</a>	863.4845	1724.9544	1724.9533	0.66	2	24	0.042	1	U	F.RKLLD
<a href="#">5888</a>	888.9430	1775.8714	1775.8730	-0.88	1	(23)	0.12	1	U	L.DSYIP
<a href="#">5889</a>	888.9443	1775.8741	1775.8730	0.64	1	35	0.0081	1	U	L.DSYIP
<a href="#">6208</a>	630.6597	1888.9572	1888.9570	0.07	2	(27)	0.051	1	U	F.LDSYI
<a href="#">6209</a>	945.4868	1888.9590	1888.9570	1.02	2	(32)	0.016	1	U	F.LDSYI
<a href="#">6210</a>	630.6607	1888.9603	1888.9570	1.72	2	(28)	0.04	1	U	F.LDSYI
<a href="#">6211</a>	945.4885	1888.9625	1888.9570	2.89	2	33	0.012	1	U	F.LDSYI

**Proteins matching the same set of peptides:**

[2::sp|P0CE48|EFTU2\\_ECOLI](#) Mass: 43457 Score: 773 Matches: 47(46) Sequences: 1  
Elongation factor Tu 2 OS=Escherichia coli (strain K12) OX=83333 GN=tufB PE=1 SV=1

5. [2::sp|P0A850|TIG\\_ECOLI](#) Mass: 48163 Score: 647 Matches: 36(29) Sequences: 1  
Trigger factor OS=Escherichia coli (strain K12) OX=83333 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
<a href="#">861</a>	459.2518	916.4891	916.4879	1.33	0	22	0.11	1	U	L.RKQQ
<a href="#">972</a>	472.7613	943.5080	943.5087	-0.71	0	24	0.055	1	U	Y.GASV
<a href="#">973</a>	472.7617	943.5088	943.5087	0.07	0	(21)	0.1	1	U	Y.GASV
<a href="#">1115</a>	482.2123	962.4100	962.4127	-2.82	1	23	0.04	1	U	F.NELM
<a href="#">1116</a>	482.2127	962.4109	962.4127	-1.86	1	(21)	0.072	1	U	F.NELM
<a href="#">1181</a>	486.7377	971.4608	971.4600	0.80	2	(26)	0.026	1	U	Y.KLGE
<a href="#">1182</a>	486.7379	971.4612	971.4600	1.24	2	27	0.022	1	U	Y.KLGE
<a href="#">2080</a>	553.2745	1104.5344	1104.5339	0.47	0	26	0.046	1	U	Y.EDPK
<a href="#">2469</a>	572.3210	1142.6275	1142.6295	-1.74	1	25	0.037	1	U	L.LGEV
<a href="#">2816</a>	596.7966	1191.5787	1191.5806	-1.55	0	(29)	0.026	1	U	-.MQVS
<a href="#">2818</a>	596.7994	1191.5842	1191.5806	3.07	0	31	0.018	1	U	-.MQVS
<a href="#">3301</a>	628.8636	1255.7126	1255.7136	-0.76	2	55	2.6e-05	1	U	L.LLGE

<a href="#">3302</a>	628.8640	1255.7135	1255.7136	-0.09	2	(48)	0.00014	1	U	L.LLGE
<a href="#">3376</a>	634.8057	1267.5968	1267.5972	-0.35	1	48	0.00034	1	U	Y.EDPK
<a href="#">3377</a>	634.8058	1267.5971	1267.5972	-0.05	1	(36)	0.0049	1	U	Y.EDPK
<a href="#">3428</a>	638.3257	1274.6369	1274.6394	-1.96	1	(32)	0.016	1	U	F.EVYP
<a href="#">3429</a>	638.3292	1274.6439	1274.6394	3.51	1	41	0.0017	1	U	F.EVYP
<a href="#">3920</a>	676.8745	1351.7343	1351.7347	-0.27	0	49	0.00015	1	U	L.AKAK
<a href="#">3922</a>	451.5856	1351.7349	1351.7347	0.13	0	(21)	0.077	1	U	L.AKAK
<a href="#">3923</a>	676.8766	1351.7386	1351.7347	2.90	0	(41)	0.00089	1	U	L.AKAK
<a href="#">5713</a>	866.3706	1730.7267	1730.7272	-0.28	1	(41)	0.00067	1	U	F.TGSV
<a href="#">5714</a>	866.3740	1730.7335	1730.7272	3.66	1	41	0.00073	1	U	F.TGSV
<a href="#">5990</a>	909.4861	1816.9576	1816.9570	0.32	1	46	0.00044	1	U	L.KKVE
<a href="#">5995</a>	909.4895	1816.9644	1816.9570	4.08	1	(37)	0.0033	1	U	L.KKVE
<a href="#">6173</a>	627.6475	1879.9207	1879.9211	-0.17	2	(24)	0.096	1	U	Y.GASV
<a href="#">6174</a>	627.6486	1879.9240	1879.9211	1.59	2	35	0.0087	1	U	Y.GASV
<a href="#">6265</a>	641.3221	1920.9444	1920.9429	0.80	0	(37)	0.0053	1	U	W.KEKD
<a href="#">6266</a>	641.3227	1920.9462	1920.9429	1.75	0	41	0.0021	1	U	W.KEKD
<a href="#">6916</a>	1180.1311	2358.2476	2358.2471	0.25	1	(44)	0.00054	1	U	F.IDAI
<a href="#">6917</a>	787.0905	2358.2495	2358.2471	1.04	1	(22)	0.089	1	U	F.IDAI
<a href="#">6918</a>	787.0926	2358.2559	2358.2471	3.76	1	(23)	0.064	1	U	F.IDAI
<a href="#">6919</a>	1180.1361	2358.2577	2358.2471	4.49	1	48	0.00017	1	U	F.IDAI
<a href="#">7140</a>	873.1013	2616.2820	2616.2728	3.50	1	(63)	1.1e-05	1	U	L.EAIE
<a href="#">7141</a>	1309.1487	2616.2828	2616.2728	3.83	1	(62)	1.4e-05	1	U	L.EAIE
<a href="#">7142</a>	1309.1492	2616.2838	2616.2728	4.20	1	(65)	6.4e-06	1	U	L.EAIE
<a href="#">7143</a>	873.1021	2616.2845	2616.2728	4.47	1	67	4.9e-06	1	U	L.EAIE

6. [2::sp|POA6F3|GLPK\\_ECOLI](#) Mass: 56480 Score: 605 Matches: 35(30) Sequences:  
 Glycerol kinase OS=Escherichia coli (strain K12) OX=83333 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
<a href="#">15</a>	380.7187	759.4229	759.4239	-1.32	0	(28)	0.019	1	U	Y.IRSNT
<a href="#">16</a>	380.7190	759.4235	759.4239	-0.53	0	29	0.015	1	U	Y.IRSNT
<a href="#">270</a>	402.2370	802.4594	802.4589	0.67	1	33	0.0058	1	U	Y.VVPAF
<a href="#">271</a>	402.2373	802.4601	802.4589	1.52	1	(31)	0.011	1	U	Y.VVPAF
<a href="#">580</a>	432.2074	862.4002	862.4007	-0.54	0	29	0.016	1	U	F.MAGAS
<a href="#">581</a>	432.2076	862.4007	862.4007	0.02	0	(25)	0.052	1	U	F.MAGAS
<a href="#">1358</a>	498.2442	994.4738	994.4720	1.90	1	30	0.018	1	U	L.KRDGL
<a href="#">1359</a>	498.2445	994.4745	994.4720	2.59	1	(29)	0.024	1	U	L.KRDGL
<a href="#">2200</a>	559.2889	1116.5632	1116.5604	2.53	0	22	0.11	1	U	F.EQIYP
<a href="#">2213</a>	560.2825	1118.5504	1118.5469	3.14	0	24	0.072	1	U	L.RVDGG
<a href="#">2797</a>	595.7952	1189.5758	1189.5761	-0.26	0	(42)	0.0013	1	U	L.EAMQA
<a href="#">2798</a>	595.7959	1189.5772	1189.5761	0.97	0	45	0.00074	1	U	L.EAMQA
<a href="#">2808</a>	596.3242	1190.6338	1190.6336	0.16	2	23	0.077	1	U	Y.VVPAF
<a href="#">2841</a>	597.8099	1193.6052	1193.6040	0.97	0	55	6.1e-05	1	U	F.ATKVQ
<a href="#">2842</a>	597.8102	1193.6059	1193.6040	1.57	0	(48)	0.00028	1	U	F.ATKVQ
<a href="#">2848</a>	598.3046	1194.5947	1194.5881	5.57	0	(27)	0.037	1	U	F.ATKVQ
<a href="#">2933</a>	603.7929	1205.5713	1205.5710	0.21	0	(31)	0.018	1	U	L.EAMQA
<a href="#">2934</a>	603.7942	1205.5738	1205.5710	2.33	0	(37)	0.0041	1	U	L.EAMQA
<a href="#">3447</a>	640.2977	1278.5808	1278.5802	0.46	2	(29)	0.022	1	U	L.DWDDK
<a href="#">3448</a>	640.2981	1278.5816	1278.5802	1.13	2	30	0.018	1	U	L.DWDDK
<a href="#">3861</a>	668.3376	1334.6606	1334.6579	2.08	0	(20)	0.22	1	U	F.RPGIE
<a href="#">3862</a>	668.3380	1334.6615	1334.6579	2.71	0	32	0.016	1	U	F.RPGIE
<a href="#">3900</a>	674.3676	1346.7205	1346.7194	0.85	1	39	0.002	1	U	Y.IRSNT
<a href="#">3901</a>	674.3688	1346.7231	1346.7194	2.76	1	(35)	0.0055	1	U	Y.IRSNT

<a href="#">4110</a>	691.8166	1381.6187	1381.6184	0.26	0	(50)	0.00015	1	U	L.TTIAC
<a href="#">4111</a>	691.8184	1381.6222	1381.6184	2.73	0	63	8.2e-06	1	U	L.TTIAC
<a href="#">5166</a>	803.9083	1605.8021	1605.8032	-0.68	1	30	0.029	1	U	L.MNTGE
<a href="#">5167</a>	803.9095	1605.8044	1605.8032	0.76	1	(26)	0.063	1	U	L.MNTGE
<a href="#">6367</a>	654.3371	1959.9895	1959.9901	-0.33	2	(44)	0.001	1	U	W.QNLDE
<a href="#">6368</a>	654.3373	1959.9902	1959.9901	0.03	2	(52)	0.00017	1	U	W.QNLDE
<a href="#">6369</a>	981.0031	1959.9917	1959.9901	0.79	2	56	7.1e-05	1	U	W.QNLDE
<a href="#">6370</a>	981.0060	1959.9974	1959.9901	3.71	2	(52)	0.00016	1	U	W.QNLDE
<a href="#">7056</a>	827.4465	2479.3178	2479.3143	1.40	0	49	0.00012	1	U	Y.GQTNI
<a href="#">7057</a>	827.4482	2479.3229	2479.3143	3.47	0	(49)	0.00012	1	U	Y.GQTNI
<a href="#">7150</a>	876.4714	2626.3923	2626.3827	3.64	1	23	0.051	1	U	Y.GQTNI

7. [2::sp|P0ABB4|ATPB\\_ECOLI](#) Mass: 50351 Score: 582 Matches: 30(27) 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
<a href="#">436</a>	416.2031	830.3916	830.3923	-0.78	0	(21)	0.062	1	U	L.VVGQE
<a href="#">437</a>	416.2035	830.3924	830.3923	0.19	0	22	0.051	1	U	L.VVGQE
<a href="#">1055</a>	478.7740	955.5335	955.5338	-0.31	1	37	0.0014	1	U	L.VLEVQ
<a href="#">1056</a>	478.7753	955.5360	955.5338	2.24	1	(25)	0.023	1	U	L.VLEVQ
<a href="#">1102</a>	481.2637	960.5129	960.5128	0.14	1	(24)	0.068	1	U	Y.TLAGT
<a href="#">1103</a>	481.2642	960.5139	960.5128	1.16	1	24	0.062	1	U	Y.TLAGT
<a href="#">1464</a>	507.2523	1012.4901	1012.4899	0.22	1	(35)	0.004	1	U	L.TGLTM
<a href="#">1465</a>	507.2525	1012.4904	1012.4899	0.51	1	36	0.0028	1	U	L.TGLTM
<a href="#">1833</a>	537.8057	1073.5968	1073.5968	-0.06	2	37	0.003	1	U	Y.TLAGT
<a href="#">2033</a>	550.8316	1099.6486	1099.6489	-0.20	1	25	0.023	1	U	L.LETGI
<a href="#">2210</a>	560.2590	1118.5035	1118.5033	0.22	1	30	0.014	1	U	Y.DHLPE
<a href="#">2375</a>	568.3265	1134.6384	1134.6397	-1.15	1	(20)	0.076	1	U	Y.VSLKD
<a href="#">2376</a>	568.3268	1134.6390	1134.6397	-0.62	1	33	0.0045	1	U	Y.VSLKD
<a href="#">3354</a>	633.2820	1264.5494	1264.5493	0.11	1	(39)	0.0014	1	U	L.GMDEL
<a href="#">3355</a>	633.2823	1264.5501	1264.5493	0.69	1	39	0.0014	1	U	L.GMDEL
<a href="#">3963</a>	679.3406	1356.6666	1356.6633	2.42	1	(37)	0.0034	1	U	Y.DALEV
<a href="#">3964</a>	679.3414	1356.6683	1356.6633	3.67	1	55	4.4e-05	1	U	Y.DALEV
<a href="#">4099</a>	690.3377	1378.6609	1378.6585	1.73	0	(38)	0.0033	1	U	F.GGAGV
<a href="#">4157</a>	698.3339	1394.6533	1394.6534	-0.08	0	56	6.1e-05	1	U	F.GGAGV
<a href="#">4158</a>	698.3344	1394.6543	1394.6534	0.62	0	(53)	0.00012	1	U	F.GGAGV
<a href="#">4859</a>	773.8682	1545.7218	1545.7199	1.21	1	(26)	0.044	1	U	Y.VPADD
<a href="#">4860</a>	773.8702	1545.7258	1545.7199	3.83	1	29	0.024	1	U	Y.VPADD
<a href="#">5011</a>	785.4155	1568.8165	1568.8158	0.44	2	(46)	0.00035	1	U	Y.DALEV
<a href="#">5012</a>	785.4173	1568.8200	1568.8158	2.70	2	(53)	7.4e-05	1	U	Y.DALEV
<a href="#">5015</a>	785.9088	1569.8029	1569.7998	1.99	2	(48)	0.00028	1	U	Y.DALEV
<a href="#">5016</a>	785.9088	1569.8031	1569.7998	2.07	2	57	3.4e-05	1	U	Y.DALEV
<a href="#">5715</a>	866.4501	1730.8857	1730.8839	1.04	1	(45)	0.00066	1	U	L.GIYPA
<a href="#">5716</a>	866.4504	1730.8862	1730.8839	1.33	1	64	8.8e-06	1	U	L.GIYPA
<a href="#">6363</a>	654.0292	1959.0657	1959.0677	-1.02	1	(34)	0.0054	1	U	L.DVKDL
<a href="#">6364</a>	654.0301	1959.0684	1959.0677	0.38	1	39	0.0013	1	U	L.DVKDL

8. [2::sp|P0AE06|ACRA\\_ECOLI](#) Mass: 42228 Score: 520 Matches: 36(33) 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
<a href="#">739</a>	450.2876	898.5606	898.5600	0.69	2	20	0.033	1	U	F.LRLK
<a href="#">755</a>	451.2401	900.4657	900.4665	-0.92	0	23	0.051	1	U	L.VQNG
<a href="#">1197</a>	487.2691	972.5236	972.5240	-0.41	1	(36)	0.0037	1	U	L.KQEL
<a href="#">1198</a>	487.2696	972.5247	972.5240	0.72	1	43	0.00086	1	U	L.KQEL
<a href="#">1211</a>	487.7618	973.5091	973.5080	1.16	1	(24)	0.074	1	U	L.KQEL
<a href="#">1212</a>	487.7622	973.5098	973.5080	1.86	1	(38)	0.0029	1	U	L.KQEL
<a href="#">2184</a>	557.8328	1113.6510	1113.6506	0.33	0	(37)	0.0017	1	U	L.KAGD
<a href="#">2185</a>	557.8335	1113.6524	1113.6506	1.66	0	39	0.00098	1	U	L.KAGD
<a href="#">3203</a>	621.8624	1241.7103	1241.7092	0.93	2	(27)	0.019	1	U	L.RLKQ
<a href="#">3204</a>	621.8636	1241.7126	1241.7092	2.80	2	35	0.0029	1	U	L.RLKQ
<a href="#">3210</a>	622.3552	1242.6958	1242.6932	2.10	2	(20)	0.1	1	U	L.RLKQ
<a href="#">4020</a>	684.3381	1366.6616	1366.6616	-0.01	1	(24)	0.078	1	U	F.KEGS
<a href="#">4021</a>	684.3381	1366.6617	1366.6616	0.07	1	(30)	0.023	1	U	F.KEGS
<a href="#">4022</a>	684.3384	1366.6622	1366.6616	0.44	1	49	0.00028	1	U	F.KEGS
<a href="#">4023</a>	684.3395	1366.6645	1366.6616	2.14	1	(29)	0.023	1	U	F.KEGS
<a href="#">4024</a>	684.3397	1366.6648	1366.6616	2.31	1	(38)	0.0032	1	U	F.KEGS
<a href="#">4025</a>	684.3401	1366.6656	1366.6616	2.94	1	(48)	0.00034	1	U	F.KEGS
<a href="#">4376</a>	718.8726	1435.7306	1435.7307	-0.09	0	50	0.00022	1	U	L.QITT
<a href="#">4377</a>	718.8741	1435.7337	1435.7307	2.12	0	(36)	0.0057	1	U	L.QITT
<a href="#">4611</a>	746.3889	1490.7633	1490.7617	1.07	0	(44)	0.0009	1	U	L.ITSD
<a href="#">4612</a>	746.3909	1490.7672	1490.7617	3.69	0	56	6.1e-05	1	U	L.ITSD
<a href="#">4872</a>	775.9730	1549.9315	1549.9304	0.71	0	(23)	0.0062	1	U	Y.RIAE
<a href="#">4873</a>	517.6515	1549.9326	1549.9304	1.45	0	(23)	0.0067	1	U	Y.RIAE
<a href="#">4874</a>	775.9750	1549.9354	1549.9304	3.24	0	28	0.0018	1	U	Y.RIAE
<a href="#">5849</a>	884.4423	1766.8700	1766.8727	-1.54	1	(35)	0.0069	1	U	L.ITSD
<a href="#">5850</a>	884.4468	1766.8790	1766.8727	3.57	1	73	1.2e-06	1	U	L.ITSD
<a href="#">6109</a>	928.4966	1854.9786	1854.9799	-0.69	1	(47)	0.00029	1	U	Y.DSAK
<a href="#">6110</a>	619.3339	1854.9799	1854.9799	0.02	1	(25)	0.051	1	U	Y.DSAK
<a href="#">6111</a>	928.4975	1854.9804	1854.9799	0.30	1	49	0.00017	1	U	Y.DSAK
<a href="#">6112</a>	619.3355	1854.9845	1854.9799	2.50	1	(31)	0.011	1	U	Y.DSAK
<a href="#">7028</a>	1227.6536	2453.2926	2453.2914	0.46	0	(51)	0.00011	1	U	L.VVGA
<a href="#">7029</a>	818.7722	2453.2947	2453.2914	1.31	0	(32)	0.0087	1	U	L.VVGA
<a href="#">7030</a>	818.7723	2453.2952	2453.2914	1.53	0	(38)	0.0019	1	U	L.VVGA
<a href="#">7032</a>	1227.6575	2453.3004	2453.2914	3.65	0	(57)	2.1e-05	1	U	L.VVGA
<a href="#">7033</a>	819.0978	2454.2717	2454.2755	-1.53	0	58	2.5e-05	1	U	L.VVGA
<a href="#">7035</a>	819.1023	2454.2850	2454.2755	3.91	0	(41)	0.001	1	U	L.VVGA

9. [2::sp|P0ABB0|ATPA\\_ECOLI](#) Mass: 55416 Score: 491 Matches: 28 (23) 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
<a href="#">129</a>	390.2182	778.4218	778.4225	-0.92	1	30	0.01	1	U	L.KGIL
<a href="#">130</a>	390.2186	778.4227	778.4225	0.27	1	(29)	0.011	1	U	L.KGIL
<a href="#">2117</a>	555.2773	1108.5401	1108.5400	0.08	1	(23)	0.11	1	U	Y.DDLS
<a href="#">2118</a>	555.2778	1108.5411	1108.5400	0.96	1	24	0.082	1	U	Y.DDLS
<a href="#">2553</a>	578.7907	1155.5669	1155.5673	-0.34	1	21	0.11	1	U	L.AYVD
<a href="#">2916</a>	402.2342	1203.6808	1203.6823	-1.22	0	(21)	0.062	1	U	F.TKGE
<a href="#">2918</a>	602.8485	1203.6825	1203.6823	0.14	0	(29)	0.011	1	U	F.TKGE
<a href="#">2919</a>	602.8500	1203.6855	1203.6823	2.68	0	33	0.0035	1	U	F.TKGE
<a href="#">3408</a>	636.8684	1271.7223	1271.7197	1.99	0	29	0.012	1	U	L.IIGD
<a href="#">3409</a>	636.8688	1271.7230	1271.7197	2.55	0	(26)	0.022	1	U	L.IIGD
<a href="#">3443</a>	639.8519	1277.6892	1277.6867	1.94	2	67	2.3e-06	1	U	Y.LADV

<a href="#">3444</a>	639.8522	1277.6899	1277.6867	2.51	2	(61)	9.2e-06	1	U	Y.LADV
<a href="#">3845</a>	666.8425	1331.6704	1331.6681	1.72	1	52	0.00015	1	U	F.ASDL
<a href="#">3846</a>	666.8435	1331.6725	1331.6681	3.29	1	(51)	0.00015	1	U	F.ASDL
<a href="#">4630</a>	748.3643	1494.7140	1494.7103	2.44	1	31	0.021	1	U	L.GAPI
<a href="#">4631</a>	748.3655	1494.7164	1494.7103	4.07	1	(29)	0.027	1	U	L.GAPI
<a href="#">5164</a>	803.8997	1605.7849	1605.7821	1.74	1	(48)	0.00048	1	U	L.NLER
<a href="#">5165</a>	803.9007	1605.7868	1605.7821	2.96	1	55	8e-05	1	U	L.NLER
<a href="#">5234</a>	811.8970	1621.7795	1621.7770	1.54	1	(43)	0.0012	1	U	L.NLER
<a href="#">5235</a>	811.8981	1621.7816	1621.7770	2.82	1	(43)	0.0014	1	U	L.NLER
<a href="#">5415</a>	555.2819	1662.8238	1662.8213	1.48	2	(25)	0.086	1	U	F.RDRG
<a href="#">5416</a>	555.2820	1662.8241	1662.8213	1.70	2	31	0.023	1	U	F.RDRG
<a href="#">6518</a>	1019.9773	2037.9400	2037.9313	4.28	1	(58)	3.9e-05	1	U	L.MQEI
<a href="#">6553</a>	1027.9739	2053.9332	2053.9262	3.40	1	(61)	1.4e-05	1	U	L.MQEI
<a href="#">6554</a>	1027.9746	2053.9347	2053.9262	4.11	1	79	2.6e-07	1	U	L.MQEI
<a href="#">7068</a>	838.7676	2513.2809	2513.2762	1.88	0	(37)	0.003	1	U	F.SAVE
<a href="#">7069</a>	838.7682	2513.2829	2513.2762	2.68	0	39	0.0018	1	U	F.SAVE
<a href="#">7070</a>	1257.6499	2513.2852	2513.2762	3.61	0	(30)	0.014	1	U	F.SAVE

10. [2::sp|POA8M0|SYN ECOLI](#) Mass: 52766 Score: 303 Matches: 13(13) Sequences: 7  
 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
<a href="#">729</a>	449.7660	897.5174	897.5172	0.31	0	32	0.003	1	U	M.SVVPV
<a href="#">1576</a>	513.7482	1025.4819	1025.4818	0.11	1	24	0.059	1	U	L.ERFIE
<a href="#">2668</a>	584.7786	1167.5427	1167.5408	1.65	1	(27)	0.034	1	U	L.TVSGQ
<a href="#">2669</a>	584.7796	1167.5446	1167.5408	3.31	1	42	0.001	1	U	L.TVSGQ
<a href="#">3524</a>	646.2997	1290.5848	1290.5840	0.60	1	(56)	3.8e-05	1	U	W.GVDLS
<a href="#">3525</a>	646.3000	1290.5854	1290.5840	1.08	1	(58)	2.8e-05	1	U	W.GVDLS
<a href="#">3526</a>	646.3008	1290.5871	1290.5840	2.40	1	(56)	4e-05	1	U	W.GVDLS
<a href="#">3527</a>	646.3013	1290.5880	1290.5840	3.07	1	58	2.5e-05	1	U	W.GVDLS
<a href="#">3724</a>	658.8455	1315.6764	1315.6772	-0.63	0	(62)	1.2e-05	1	U	F.EIQAS
<a href="#">3725</a>	658.8477	1315.6808	1315.6772	2.71	0	66	5.9e-06	1	U	F.EIQAS
<a href="#">3895</a>	672.7867	1343.5589	1343.5551	2.84	0	41	0.00061	1	U	L.ITASD
<a href="#">4959</a>	784.3937	1566.7729	1566.7712	1.13	1	(34)	0.0085	1	U	F.KAVLE
<a href="#">4961</a>	784.3960	1566.7774	1566.7712	4.01	1	41	0.002	1	U	F.KAVLE

11. [2::sp|POA6P9|ENO ECOLI](#) Mass: 45683 Score: 282 Matches: 14(12) Sequences: 7  
 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	Peptide
<a href="#">1415</a>	503.2715	1004.5285	1004.5291	-0.61	1	35	0.0059	1	U	Y.VLAGE
<a href="#">1834</a>	538.2854	1074.5562	1074.5557	0.51	1	(33)	0.011	1	U	F.NQIGS
<a href="#">1835</a>	538.2861	1074.5576	1074.5557	1.76	1	40	0.002	1	U	F.NQIGS
<a href="#">2040</a>	551.3037	1100.5929	1100.5938	-0.83	0	26	0.038	1	U	Y.NGRKE
<a href="#">2622</a>	581.8279	1161.6412	1161.6393	1.61	0	(55)	4.1e-05	1	U	L.AVIAE
<a href="#">2623</a>	581.8284	1161.6423	1161.6393	2.55	0	68	1.7e-06	1	U	L.AVIAE
<a href="#">3764</a>	660.3469	1318.6792	1318.6769	1.72	2	33	0.0089	1	U	L.GDKIQ
<a href="#">3766</a>	660.3487	1318.6828	1318.6769	4.50	2	(20)	0.19	1	U	L.GDKIQ
<a href="#">4593</a>	496.9412	1487.8018	1487.7983	2.35	1	(23)	0.089	1	U	L.IRIEE
<a href="#">4594</a>	496.9413	1487.8021	1487.7983	2.53	1	26	0.044	1	U	L.IRIEE

<a href="#">6064</a>	922.4976	1842.9806	1842.9839	-1.81	2	(40)	0.0015	1	U	Y.NQLIR
<a href="#">6065</a>	922.4986	1842.9826	1842.9839	-0.68	2	54	6.7e-05	1	U	Y.NQLIR
<a href="#">6066</a>	615.3353	1842.9842	1842.9839	0.14	2	(41)	0.0013	1	U	Y.NQLIR
<a href="#">6067</a>	615.3369	1842.9889	1842.9839	2.71	2	(36)	0.0037	1	U	Y.NQLIR

12. [2::sp|P0A6M8|EFG ECOLI](#) Mass: 77704 Score: 276 Matches: 11(10) Sequences: 6  
 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
<a href="#">160</a>	396.2183	790.4220	790.4225	-0.60	0	(31)	0.011	1	U	F.KIATD
<a href="#">161</a>	396.2185	790.4225	790.4225	0.03	0	39	0.0015	1	U	F.KIATD
<a href="#">2174</a>	557.7795	1113.5445	1113.5455	-0.83	1	37	0.0029	1	U	L.QLAIG
<a href="#">2175</a>	557.7811	1113.5476	1113.5455	1.91	1	(22)	0.095	1	U	L.QLAIG
<a href="#">2712</a>	587.8251	1173.6356	1173.6394	-3.23	1	(37)	0.0031	1	U	F.KIATD
<a href="#">2713</a>	587.8267	1173.6389	1173.6394	-0.41	1	47	0.00029	1	U	F.KIATD
<a href="#">4139</a>	694.8640	1387.7135	1387.7096	2.81	0	36	0.0051	1	U	F.NVEAN
<a href="#">4776</a>	765.4074	1528.8003	1528.7984	1.21	2	67	3.1e-06	1	U	Y.LGGEE
<a href="#">4777</a>	765.4075	1528.8005	1528.7984	1.37	2	(65)	5.1e-06	1	U	Y.LGGEE
<a href="#">6331</a>	972.4856	1942.9566	1942.9558	0.45	1	(29)	0.033	1	U	L.KDVTT
<a href="#">6332</a>	972.4870	1942.9594	1942.9558	1.89	1	49	0.00028	1	U	L.KDVTT

13. [2::sp|P04805|SYE ECOLI](#) Mass: 54181 Score: 263 Matches: 12(10) Sequences: 8  
 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	Peptide
<a href="#">2791</a>	595.2964	1188.5782	1188.5775	0.61	0	(40)	0.002	1	U	F.DDQ
<a href="#">2792</a>	595.2968	1188.5791	1188.5775	1.32	0	57	3.4e-05	1	U	F.DDQ
<a href="#">2849</a>	598.3188	1194.6230	1194.6244	-1.18	1	35	0.0041	1	U	F.TLN
<a href="#">3131</a>	411.5374	1231.5904	1231.5907	-0.23	1	31	0.014	1	U	F.TRE
<a href="#">3132</a>	411.5375	1231.5906	1231.5907	-0.06	1	(24)	0.069	1	U	F.TRE
<a href="#">3245</a>	625.2947	1248.5749	1248.5735	1.18	1	(36)	0.0055	1	U	L.DFI
<a href="#">3246</a>	625.2955	1248.5765	1248.5735	2.44	1	38	0.0035	1	U	L.DFI
<a href="#">3343</a>	631.3248	1260.6350	1260.6350	-0.01	2	25	0.067	1	U	Y.RDD
<a href="#">4381</a>	719.3899	1436.7652	1436.7663	-0.78	1	27	0.027	1	U	Y.INA
<a href="#">5003</a>	785.3587	1568.7028	1568.7028	0.02	1	25	0.052	1	U	Y.NAV
<a href="#">7314</a>	1012.7928	3035.3565	3035.4216	-21.42	2	30	0.0093	1	U	F.VLR
<a href="#">7315</a>	1012.7929	3035.3567	3035.4216	-21.36	2	(28)	0.016	1	U	F.VLR

14. [2::sp|P0AGG8|TLDD ECOLI](#) Mass: 51446 Score: 241 Matches: 9(6) Sequences: 5  
 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
<a href="#">1264</a>	492.7898	983.5650	983.5651	-0.10	1	27	0.011	1	U	Y.NVLIE
<a href="#">1346</a>	497.2650	992.5155	992.5178	-2.31	2	(24)	0.078	1	U	F.AYADQ
<a href="#">1347</a>	497.2661	992.5177	992.5178	-0.17	2	33	0.0086	1	U	F.AYADQ
<a href="#">4334</a>	715.8495	1429.6844	1429.6837	0.48	2	64	7.1e-06	1	U	F.LADLD
<a href="#">4335</a>	715.8503	1429.6860	1429.6837	1.58	2	(59)	2.3e-05	1	U	F.LADLD



<a href="#">5118</a>	797.8970	1593.7795	1593.7787	0.48	1	98	4.5e-09	1	U	Y.APNFG
<a href="#">5119</a>	797.8996	1593.7846	1593.7787	3.70	1	(88)	3.9e-08	1	U	Y.APNFG
<a href="#">6297</a>	968.9833	1935.9521	1935.9499	1.14	0	22	0.16	1	U	Y.MLPKG
<a href="#">6298</a>	968.9851	1935.9557	1935.9499	2.97	0	(21)	0.2	1	U	Y.MLPKG

15. [2::sp|P0A6H5|HSLU\\_ECOLI](#) Mass: 49677 Score: 232 Matches: 10(10) Sequences: 1  
 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
<a href="#">440</a>	416.2394	830.4643	830.4650	-0.82	1	(45)	0.00039	1	U	L.AKLAN
<a href="#">441</a>	416.2399	830.4652	830.4650	0.21	1	50	0.00013	1	U	L.AKLAN
<a href="#">915</a>	468.2816	934.5487	934.5488	-0.07	0	(31)	0.0026	1	U	F.IKVEA
<a href="#">916</a>	468.2821	934.5496	934.5488	0.96	0	38	0.00042	1	U	F.IKVEA
<a href="#">1491</a>	508.2871	1014.5595	1014.5597	-0.13	1	49	0.00018	1	U	L.LIEEE
<a href="#">1492</a>	508.2873	1014.5600	1014.5597	0.35	1	(39)	0.0015	1	U	L.LIEEE
<a href="#">3912</a>	675.8300	1349.6455	1349.6463	-0.60	2	38	0.0036	1	U	L.DALVA
<a href="#">3914</a>	675.8320	1349.6495	1349.6463	2.38	2	(35)	0.0075	1	U	L.DALVA
<a href="#">5451</a>	835.4315	1668.8484	1668.8471	0.74	0	(53)	9.4e-05	1	U	L.KQDAI
<a href="#">5452</a>	835.4315	1668.8485	1668.8471	0.81	0	57	4.2e-05	1	U	L.KQDAI

16. [2::sp|P0C8J8|GATZ\\_ECOLI](#) Mass: 47535 Score: 210 Matches: 9(9) Sequences: 5  
 D-tagatose-1,6-bisphosphate aldolase subunit GatZ 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
<a href="#">444</a>	416.7499	831.4852	831.4854	-0.28	1	31	0.0041	1	U	L.KVGPA
<a href="#">445</a>	416.7500	831.4854	831.4854	0.01	1	(29)	0.0059	1	U	L.KVGPA
<a href="#">903</a>	466.2459	930.4773	930.4770	0.25	0	(35)	0.005	1	U	F.ERIQS
<a href="#">904</a>	466.2460	930.4774	930.4770	0.44	0	39	0.002	1	U	F.ERIQS
<a href="#">1476</a>	507.7766	1013.5387	1013.5393	-0.61	1	41	0.00075	1	U	F.ALAQI
<a href="#">1477</a>	507.7769	1013.5392	1013.5393	-0.06	1	(39)	0.0014	1	U	F.ALAQI
<a href="#">3075</a>	613.8404	1225.6662	1225.6666	-0.32	0	54	3.9e-05	1	U	L.APETV
<a href="#">3076</a>	613.8419	1225.6692	1225.6666	2.07	0	(40)	0.00091	1	U	L.APETV
<a href="#">3252</a>	625.8052	1249.5958	1249.5939	1.55	0	45	0.00069	1	U	L.IEATS

Proteins matching a subset of these peptides:

- [2::sp|P0C8K0|KBAZ\\_ECOLI](#) Mass: 47562 Score: 31 Matches: 2(2) Sequences: 1  
 D-tagatose-1,6-bisphosphate aldolase subunit KbaZ OS=Escherichia coli (strain K12) OX=83333

17. [2::sp|P31224|ACRB\\_ECOLI](#) Mass: 113615 Score: 203 Matches: 7(7) Sequences: 4  
 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
<a href="#">1334</a>	496.7743	991.5340	991.5338	0.19	0	(34)	0.0048	1	U	L.ASKLP
<a href="#">1336</a>	496.7749	991.5353	991.5338	1.48	0	51	9.6e-05	1	U	L.ASKLP
<a href="#">2497</a>	573.8043	1145.5940	1145.5928	1.00	0	(29)	0.025	1	U	L.GVSIN
<a href="#">2498</a>	573.8046	1145.5947	1145.5928	1.65	0	42	0.0013	1	U	L.GVSIN

<a href="#">4049</a>	686.3791	1370.7436	1370.7405	2.28	0	(33)	0.0077	1	U	F.KIDID
<a href="#">4050</a>	686.3797	1370.7448	1370.7405	3.17	0	45	0.00046	1	U	F.KIDID
<a href="#">5257</a>	814.9332	1627.8519	1627.8529	-0.61	1	65	4.6e-06	1	U	L.ATGAN

18. [2::sp|P0AFG6|ODO2\\_ECOLI](#) Mass: 43984 Score: 184 Matches: 8(8) Sequences: 5  
 Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex  
 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
<a href="#">351</a>	408.2649	814.5153	814.5164	-1.28	1	21	0.031	1	U	F.LVTIK
<a href="#">422</a>	414.7629	827.5113	827.5116	-0.45	0	51	4e-05	1	U	Y.VKAVV
<a href="#">423</a>	414.7630	827.5114	827.5116	-0.31	0	(45)	0.00014	1	U	Y.VKAVV
<a href="#">1325</a>	496.2945	990.5744	990.5750	-0.54	1	32	0.0051	1	U	F.YVKAV
<a href="#">3091</a>	614.3510	1226.6873	1226.6871	0.22	1	(25)	0.029	1	U	L.VTPVL
<a href="#">3092</a>	614.3515	1226.6884	1226.6871	1.12	1	27	0.021	1	U	L.VTPVL
<a href="#">6310</a>	970.4750	1938.9354	1938.9323	1.60	0	(35)	0.0086	1	U	L.KRYPE
<a href="#">6312</a>	970.4768	1938.9389	1938.9323	3.42	0	56	5.8e-05	1	U	L.KRYPE

19. [2::sp|P30845|EPTA\\_ECOLI](#) Mass: 62369 Score: 163 Matches: 7(7) Sequences: 4  
 Phosphoethanolamine transferase EptA OS=Escherichia coli (strain K12) OX=83333 GN=ep  
 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
<a href="#">1703</a>	526.7917	1051.5689	1051.5702	-1.21	2	22	0.052	1	U	F.ILVGA
<a href="#">3051</a>	611.8067	1221.5988	1221.5990	-0.09	0	(46)	0.00059	1	U	L.IVGET
<a href="#">3052</a>	611.8070	1221.5995	1221.5990	0.42	0	48	0.00032	1	U	L.IVGET
<a href="#">3287</a>	627.8565	1253.6985	1253.6980	0.41	1	38	0.0012	1	U	Y.INNLQ
<a href="#">3288</a>	627.8576	1253.7006	1253.6980	2.15	1	(35)	0.002	1	U	Y.INNLQ
<a href="#">4543</a>	737.8992	1473.7839	1473.7827	0.80	1	58	2.8e-05	1	U	L.VKSLs
<a href="#">4544</a>	737.8997	1473.7848	1473.7827	1.38	1	(33)	0.0092	1	U	L.VKSLs

20. [2::sp|P0AG67|RS1\\_ECOLI](#) Mass: 61235 Score: 161 Matches: 8(7) Sequences: 4(4)  
 30S ribosomal protein S1 OS=Escherichia coli (strain K12) OX=83333 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
<a href="#">2451</a>	571.7961	1141.5777	1141.5768	0.84	2	43	0.00056	1	U	L.GLKQL
<a href="#">2452</a>	571.7971	1141.5797	1141.5768	2.56	2	(39)	0.0015	1	U	L.GLKQL
<a href="#">2935</a>	603.8056	1205.5966	1205.5928	3.20	0	(22)	0.15	1	U	L.KSESA
<a href="#">2936</a>	603.8057	1205.5968	1205.5928	3.30	0	27	0.041	1	U	L.KSESA
<a href="#">3159</a>	618.7971	1235.5797	1235.5782	1.20	0	(46)	0.00057	1	U	W.NVAGE
<a href="#">3160</a>	618.7976	1235.5807	1235.5782	2.00	0	51	0.00015	1	U	W.NVAGE
<a href="#">3537</a>	646.8399	1291.6652	1291.6660	-0.57	1	(38)	0.0032	1	U	L.VLSVG
<a href="#">3539</a>	646.8413	1291.6681	1291.6660	1.61	1	39	0.0023	1	U	L.VLSVG

21. [2::sp|P00350|6PGD\\_ECOLI](#) Mass: 51563 Score: 158 Matches: 7(6) Sequences: 4  
 6-phosphogluconate dehydrogenase, decarboxylating OS=Escherichia coli (strain K12) OX=83333 GN=6PGD 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
<a href="#">1015</a>	476.2611	950.5075	950.5073	0.28	1	34	0.0038	1	U	F.LQKIT
<a href="#">1383</a>	500.2423	998.4700	998.4709	-0.89	1	41	0.00078	1	U	Y.FKQIA
<a href="#">1384</a>	500.2425	998.4704	998.4709	-0.47	1	(27)	0.02	1	U	Y.FKQIA
<a href="#">1537</a>	511.7661	1021.5177	1021.5192	-1.53	1	30	0.018	1	U	L.ALNIE
<a href="#">1538</a>	511.7669	1021.5192	1021.5192	-0.02	1	(23)	0.11	1	U	L.ALNIE
<a href="#">4559</a>	739.3813	1476.7480	1476.7460	1.35	1	53	0.00011	1	U	Y.LDKGD
<a href="#">4560</a>	739.3824	1476.7502	1476.7460	2.84	1	(42)	0.0013	1	U	Y.LDKGD

22. [2::sp|P08200|IDH\\_ECOLI](#) Mass: 46070 Score: 148 Matches: 7(7) Sequences: 4(4)  
 Isocitrate dehydrogenase [NADP] OS=Escherichia coli (strain K12) OX=83333 GN=icd 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
<a href="#">563</a>	427.2850	852.5555	852.5545	1.18	0	(20)	0.012	1	U	Y.RVAIK
<a href="#">564</a>	427.2854	852.5562	852.5545	2.05	0	24	0.0046	1	U	Y.RVAIK
<a href="#">2825</a>	596.8328	1191.6510	1191.6499	0.88	0	(48)	0.00018	1	U	L.KVVDA
<a href="#">2826</a>	596.8334	1191.6522	1191.6499	1.90	0	57	2.5e-05	1	U	L.KVVDA
<a href="#">3706</a>	656.3675	1310.7204	1310.7194	0.78	0	39	0.001	1	U	Y.AGQDK
<a href="#">3707</a>	656.3683	1310.7221	1310.7194	2.09	0	(36)	0.0022	1	U	Y.AGQDK
<a href="#">4658</a>	751.8751	1501.7356	1501.7334	1.42	0	28	0.035	1	U	Y.IEGDG

23. [2::sp|P21599|KPYK2\\_ECOLI](#) Mass: 51553 Score: 138 Matches: 7(5) Sequences: 4  
 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
<a href="#">281</a>	403.7243	805.4341	805.4334	0.89	1	20	0.092	1	U	F.LNIGD
<a href="#">3552</a>	647.3740	1292.7335	1292.7340	-0.40	0	43	0.00028	1	U	Y.KGLPA
<a href="#">3553</a>	647.3757	1292.7369	1292.7340	2.24	0	(33)	0.0023	1	U	Y.KGLPA
<a href="#">4207</a>	702.3917	1402.7689	1402.7667	1.54	0	(25)	0.044	1	U	L.TEKDK
<a href="#">4208</a>	702.3921	1402.7696	1402.7667	2.07	0	34	0.005	1	U	L.TEKDK
<a href="#">4660</a>	752.3479	1502.6812	1502.6849	-2.40	0	(24)	0.073	1	U	F.DSAND
<a href="#">4661</a>	752.3492	1502.6839	1502.6849	-0.62	0	46	0.00042	1	U	F.DSAND

24. [2::sp|P0A6F5|CH60\\_ECOLI](#) Mass: 57464 Score: 134 Matches: 6(6) Sequences: 3  
 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
<a href="#">5277</a>	815.9199	1629.8253	1629.8250	0.19	1	(34)	0.0077	1	U	F.INKPE
<a href="#">5278</a>	815.9201	1629.8256	1629.8250	0.41	1	36	0.0057	1	U	F.INKPE
<a href="#">5897</a>	889.4544	1776.8943	1776.8934	0.49	2	(53)	0.00011	1	U	Y.FINKP
<a href="#">5898</a>	889.4553	1776.8961	1776.8934	1.51	2	55	8.8e-05	1	U	Y.FINKP
<a href="#">6313</a>	647.3447	1939.0124	1939.0123	0.04	1	(35)	0.0055	1	U	L.ADLRG
<a href="#">6314</a>	647.3462	1939.0167	1939.0123	2.30	1	44	0.00062	1	U	L.ADLRG

25. [2::sp|P68767|AMPA\\_ECOLI](#) Mass: 55358 Score: 124 Matches: 5(4) Sequences: 3  
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
<a href="#">3515</a>	645.8068	1289.5990	1289.6000	-0.80	0	36	0.0043	1	U	L.IAASE
<a href="#">3518</a>	645.8093	1289.6040	1289.6000	3.09	0	(23)	0.089	1	U	L.IAASE
<a href="#">4489</a>	730.8727	1459.7309	1459.7307	0.17	2	(26)	0.052	1	U	W.RLPLG
<a href="#">4490</a>	730.8755	1459.7365	1459.7307	4.02	2	37	0.0044	1	U	W.RLPLG
<a href="#">4796</a>	768.3851	1534.7557	1534.7515	2.75	1	50	0.00023	1	U	L.SPIAE

26. [2::sp|P25553|ALDA\\_ECOLI](#) Mass: 52411 Score: 118 Matches: 6(6) Sequences: 3  
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
<a href="#">3318</a>	629.3430	1256.6714	1256.6725	-0.88	1	36	0.004	1	U	L.VLGRG
<a href="#">3319</a>	629.3439	1256.6733	1256.6725	0.67	1	(28)	0.02	1	U	L.VLGRG
<a href="#">3655</a>	653.3562	1304.6978	1304.6976	0.18	0	(51)	0.00014	1	U	L.TGNTI
<a href="#">3656</a>	653.3563	1304.6981	1304.6976	0.36	0	51	0.00012	1	U	L.TGNTI
<a href="#">5447</a>	835.4257	1668.8369	1668.8318	3.02	0	34	0.0079	1	U	Y.EGEII
<a href="#">5448</a>	835.4262	1668.8377	1668.8318	3.54	0	(32)	0.012	1	U	Y.EGEII

27. [2::sp|P0A6E4|ASSY\\_ECOLI](#) Mass: 50038 Score: 111 Matches: 5(5) Sequences: 3  
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
<a href="#">1390</a>	500.7564	999.4983	999.4985	-0.25	0	32	0.0066	1	U	F.SPDDR
<a href="#">1391</a>	500.7565	999.4984	999.4985	-0.07	0	(28)	0.018	1	U	F.SPDDR
<a href="#">4280</a>	710.3210	1418.6274	1418.6314	-2.80	0	33	0.0063	1	U	L.TGIHN
<a href="#">6238</a>	951.4656	1900.9167	1900.9126	2.16	1	46	0.00053	1	U	L.SSSAA
<a href="#">6239</a>	951.4680	1900.9215	1900.9126	4.66	1	(39)	0.0024	1	U	L.SSSAA

28. [2::sp|P0AG30|RHO\\_ECOLI](#) Mass: 47032 Score: 101 Matches: 6(6) Sequences: 2(2)  
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
<a href="#">1898</a>	542.8215	1083.6285	1083.6288	-0.28	0	(33)	0.0033	1	U	Y.NTVVP
<a href="#">1899</a>	542.8226	1083.6306	1083.6288	1.64	0	44	0.0003	1	U	Y.NTVVP
<a href="#">5874</a>	888.4078	1774.8010	1774.7971	2.19	1	(26)	0.041	1	U	L.IDTGS
<a href="#">5875</a>	888.4081	1774.8016	1774.7971	2.53	1	57	3.4e-05	1	U	L.IDTGS
<a href="#">5935</a>	896.4063	1790.7981	1790.7920	3.37	1	(50)	0.00016	1	U	L.IDTGS
<a href="#">5936</a>	896.4067	1790.7988	1790.7920	3.78	1	(41)	0.0012	1	U	L.IDTGS

29. [2::sp|P0A7D4|PURA\\_ECOLI](#) Mass: 47543 Score: 98 Matches: 6(5) Sequences: 4

Adenylosuccinate synthetase OS=Escherichia coli (strain K12) OX=83333 GN=purA 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
<a href="#">3099</a>	614.8624	1227.7102	1227.7074	2.24	2	21	0.063	1	U	L.DVLDG
<a href="#">4521</a>	735.9212	1469.8278	1469.8202	5.21	0	25	0.032	1	U	L.RENVT
<a href="#">4863</a>	774.4020	1546.7895	1546.7913	-1.12	1	(26)	0.055	1	U	Y.QKVLD
<a href="#">4864</a>	774.4040	1546.7935	1546.7913	1.48	1	28	0.038	1	U	Y.QKVLD
<a href="#">6591</a>	1037.4840	2072.9535	2072.9401	6.44	2	27	0.033	1	U	W.KGVEP
<a href="#">6592</a>	1037.4840	2072.9535	2072.9401	6.44	2	(26)	0.045	1	U	W.KGVEP

30. [2::sp|P22188|MURE\\_ECOLI](#) Mass: 53766 Score: 97 Matches: 5(5) Sequences: 3(3)  
 UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase OS=Escherichia coli (strain K12) OX=83333 GN=murG 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
<a href="#">1188</a>	486.7773	971.5401	971.5400	0.11	2	32	0.0078	1	U	Y.LSQLNE
<a href="#">1189</a>	486.7779	971.5413	971.5400	1.36	2	(29)	0.018	1	U	Y.LSQLNE
<a href="#">1222</a>	488.2301	974.4457	974.4458	-0.05	0	(29)	0.014	1	U	L.VAGKGH
<a href="#">1223</a>	488.2304	974.4463	974.4458	0.59	0	35	0.003	1	U	L.VAGKGH
<a href="#">2926</a>	603.3191	1204.6236	1204.6200	2.99	1	29	0.022	1	U	Y.QIVGNQ

31. [2::sp|P0A8L1|SYS\\_ECOLI](#) Mass: 48669 Score: 96 Matches: 3(2) Sequences: 3(3)  
 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
<a href="#">1550</a>	512.3080	1022.6015	1022.6012	0.34	1	42	0.00019	1	U	Y.ALIPT
<a href="#">3915</a>	675.8554	1349.6963	1349.6980	-1.26	2	31	0.013	1	U	Y.GTGQL
<a href="#">4455</a>	727.3865	1452.7585	1452.7572	0.88	0	22	0.08	1	U	Y.QQADG

32. [2::sp|P76403|YEQQ\\_ECOLI](#) Mass: 51446 Score: 94 Matches: 5(4) Sequences: 3(3)  
 Uncharacterized protease YegQ OS=Escherichia coli (strain K12) OX=83333 GN=yegQ 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
<a href="#">1146</a>	483.7359	965.4573	965.4567	0.67	0	21	0.15	1	U	Y.SVSDR
<a href="#">3871</a>	669.8053	1337.5960	1337.5921	2.93	0	(43)	0.0009	1	U	F.MIEEA
<a href="#">3872</a>	669.8054	1337.5963	1337.5921	3.11	0	46	0.00049	1	U	F.MIEEA
<a href="#">3979</a>	453.9167	1358.7283	1358.7306	-1.68	0	27	0.033	1	U	Y.RKAID
<a href="#">3980</a>	453.9172	1358.7297	1358.7306	-0.67	0	(26)	0.041	1	U	Y.RKAID

33. [2::sp|P76658|HLDE\\_ECOLI](#) Mass: 51247 Score: 91 Matches: 4(4) Sequences: 2(2)  
 Bifunctional protein HldE OS=Escherichia coli (strain K12) OX=83333 GN=hldE 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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<a href="#">3019</a>	608.8250	1215.6355	1215.6347	0.62	0	39	0.0024	1	U	Y.DVTGA
<a href="#">3020</a>	608.8254	1215.6363	1215.6347	1.32	0	(30)	0.019	1	U	Y.DVTGA
<a href="#">4283</a>	710.3580	1418.7014	1418.7042	-1.96	1	52	0.00014	1	U	W.VVSFE
<a href="#">4284</a>	710.3605	1418.7065	1418.7042	1.65	1	(42)	0.0016	1	U	W.VVSFE

34. [1::sp|cRAP054|P04264|K2C1\\_HUMAN](#) Mass: 66170 Score: 90 Matches: 4(3) Sequences: 3  
 Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6  
 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
<a href="#">2954</a>	604.8307	1207.6468	1207.6449	1.64	0	27	0.025	1	U	F.VTIKK
<a href="#">3438</a>	639.3213	1276.6280	1276.6259	1.68	1	21	0.18	2	U	L.KSDQS
<a href="#">4690</a>	757.7994	1513.5842	1513.5819	1.55	1	(33)	0.0011	1	U	Y.GSGGG
<a href="#">4691</a>	757.8008	1513.5871	1513.5819	3.48	1	43	0.00013	1	U	Y.GSGGG

35. [2::sp|P0A825|GLYA\\_ECOLI](#) Mass: 45459 Score: 90 Matches: 6(4) Sequences: 3  
 Serine hydroxymethyltransferase OS=Escherichia coli (strain K12) OX=83333 GN=glyA PE=1 SV=6  
 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
<a href="#">1594</a>	514.8032	1027.5918	1027.5914	0.40	2	30	0.0098	1	U	F.LVDLVD
<a href="#">1595</a>	514.8039	1027.5932	1027.5914	1.82	2	(28)	0.014	1	U	F.LVDLVD
<a href="#">2747</a>	590.3163	1178.6180	1178.6183	-0.22	2	32	0.0094	1	U	L.ILAKGG
<a href="#">2748</a>	590.3175	1178.6204	1178.6183	1.85	2	(23)	0.088	1	U	L.ILAKGG
<a href="#">3414</a>	637.3312	1272.6479	1272.6463	1.30	1	(25)	0.072	1	U	Y.KVVS GG
<a href="#">3415</a>	637.3317	1272.6488	1272.6463	1.98	1	27	0.039	1	U	Y.KVVS GG

36. [2::sp|P21507|SRMB\\_ECOLI](#) Mass: 49998 Score: 88 Matches: 4(4) Sequences: 2  
 ATP-dependent RNA helicase SrmB OS=Escherichia coli (strain K12) OX=83333 GN=srmB PE=1 SV=6  
 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
<a href="#">792</a>	454.2294	906.4442	906.4447	-0.48	1	(27)	0.038	1	U	L.EALQDK
<a href="#">793</a>	454.2294	906.4442	906.4447	-0.48	1	34	0.0066	1	U	L.EALQDK
<a href="#">2759</a>	591.2935	1180.5725	1180.5724	0.06	0	53	0.0001	1	U	L.GSAPTG
<a href="#">2760</a>	591.2939	1180.5732	1180.5724	0.67	0	(29)	0.024	1	U	L.GSAPTG

37. [1::sp|cRAP087|P02769|ALBU\\_BOVIN](#) Mass: 71244 Score: 78 Matches: 3(3) Sequences: 3  
 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
<a href="#">2753</a>	590.8274	1179.6403	1179.6400	0.27	2	55	3e-05	1	U	Y.GFQNA
<a href="#">2754</a>	590.8291	1179.6436	1179.6400	3.07	2	(53)	4.3e-05	1	U	Y.GFQNA
<a href="#">5078</a>	792.4566	1582.8986	1582.8930	3.55	2	22	0.039	1	U	F.AVEGP

38. [2::sp|P27306|STHA\\_ECOLI](#) Mass: 51984 Score: 78 Matches: 3(3) Sequences: 2  
 Soluble pyridine nucleotide transhydrogenase 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
<a href="#">5195</a>	807.9261	1613.8376	1613.8373	0.22	2	37	0.0036	1	U	L.ALQNI
<a href="#">5267</a>	815.4388	1628.8631	1628.8621	0.63	0	(37)	0.0035	1	U	Y.TIPEIS
<a href="#">5268</a>	815.4392	1628.8639	1628.8621	1.08	0	40	0.0015	1	U	Y.TIPEIS

39. [2::sp|P02931|OMPF\\_ECOLI](#) Mass: 39309 Score: 70 Matches: 4(4) Sequences: 2  
 Outer membrane protein F OS=Escherichia coli (strain K12) OX=833333 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	Peptide
<a href="#">3404</a>	636.8448	1271.6750	1271.6721	2.30	0	43	0.00091	1	U	Y.IINQI
<a href="#">3405</a>	636.8456	1271.6766	1271.6721	3.54	0	(30)	0.016	1	U	Y.IINQI
<a href="#">4575</a>	742.3797	1482.7448	1482.7426	1.49	1	27	0.031	1	U	Y.GAADR
<a href="#">4576</a>	742.3798	1482.7451	1482.7426	1.65	1	(27)	0.035	1	U	Y.GAADR

40. [2::sp|P21888|SYC\\_ECOLI](#) Mass: 52454 Score: 68 Matches: 3(3) Sequences: 2  
 Cysteine--tRNA ligase OS=Escherichia coli (strain K12) OX=833333 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
<a href="#">2349</a>	566.7798	1131.5450	1131.5448	0.21	2	27	0.031	1	U	L.GLLEQE
<a href="#">4549</a>	738.8760	1475.7374	1475.7369	0.37	0	(30)	0.025	1	U	L.RGTDKT
<a href="#">4550</a>	738.8777	1475.7408	1475.7369	2.69	0	41	0.0019	1	U	L.RGTDKT

41. [1::sp|cRAP112|P00761|TRYP\\_PIG](#) Mass: 25078 Score: 63 Matches: 3(3) Sequences: 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
<a href="#">892</a>	465.2874	928.5603	928.5593	1.12	1	26	0.016	1	U	L.IKLSSP
<a href="#">3316</a>	629.3329	1256.6513	1256.6513	0.02	1	38	0.0025	1	U	Y.VNWIQQ
<a href="#">3317</a>	629.3345	1256.6545	1256.6513	2.54	1	(33)	0.0077	1	U	Y.VNWIQQ

42. [1::sp|cRAP039|P13645|K1C10\\_HUMAN](#) Mass: 59020 Score: 62 Matches: 4(2) Sequences: 1  
 Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6  
 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
<a href="#">372</a>	410.2275	818.4405	818.4385	2.38	0	20	0.17	1	U	Y.KSEITE
<a href="#">3932</a>	677.7684	1353.5222	1353.5182	2.96	0	22	0.015	1	U	Y.GGGSSS
<a href="#">3933</a>	677.7684	1353.5223	1353.5182	3.04	0	(21)	0.02	1	U	Y.GGGSSS
<a href="#">5527</a>	843.4578	1684.9011	1684.8995	0.93	2	22	0.1	1	U	L.KNQILN



43. [2::sp|P24182|ACCC\\_ECOLI](#) Mass: 49745 Score: 52 Matches: 2(2) Sequences: 1  
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
<a href="#">1535</a>	511.7482	1021.4818	1021.4829	-1.05	0	(49)	0.00026	1	U	F.AEQVE
<a href="#">1536</a>	511.7486	1021.4827	1021.4829	-0.15	0	54	8.4e-05	1	U	F.AEQVE

44. [2::sp|P0AEI1|MIAB\\_ECOLI](#) Mass: 53971 Score: 51 Matches: 3(1) Sequences: 2  
tRNA-2-methylthio-N(6)-dimethylallyladenosine synthase 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
<a href="#">2129</a>	555.7608	1109.5070	1109.5063	0.66	0	31	0.013	1	U	F.EGTPDM
<a href="#">2130</a>	555.7608	1109.5070	1109.5063	0.66	0	(21)	0.11	1	U	F.EGTPDM
<a href="#">2695</a>	586.3290	1170.6435	1170.6244	16.3	1	20	0.12	2	U	L.AAQGVR

45. [2::sp|P0A6H1|CLPX\\_ECOLI](#) Mass: 46726 Score: 50 Matches: 3(2) Sequences: 2  
ATP-dependent Clp protease ATP-binding subunit ClpX 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
<a href="#">1178</a>	486.2987	970.5827	970.5811	1.70	1	22	0.028	1	U	L.RSIVEA
<a href="#">3503</a>	644.8446	1287.6746	1287.6711	2.79	1	(24)	0.092	1	U	L.AQVEPE
<a href="#">3504</a>	644.8453	1287.6761	1287.6711	3.94	1	28	0.034	1	U	L.AQVEPE

46. [2::sp|P31979|NUOF\\_ECOLI](#) Mass: 49774 Score: 48 Matches: 3(1) Sequences: 2  
NADH-quinone oxidoreductase subunit F 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
<a href="#">1708</a>	527.2711	1052.5277	1052.5291	-1.33	2	(23)	0.077	1	U	L.VRNLEE
<a href="#">1709</a>	527.2721	1052.5296	1052.5291	0.52	2	29	0.022	1	U	L.VRNLEE
<a href="#">4686</a>	757.3712	1512.7279	1512.7209	4.63	2	24	0.065	1	U	W.QPGGAG

47. [2::sp|P16869|FHUE\\_ECOLI](#) Mass: 81239 Score: 47 Matches: 3(1) Sequences: 2  
FhuE receptor OS=Escherichia coli (strain K12) OX=83333 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
<a href="#">1755</a>	530.2936	1058.5727	1058.5682	4.31	1	27	0.034	1	U	Y.QAITK
<a href="#">1756</a>	530.2941	1058.5737	1058.5682	5.24	1	(21)	0.13	2	U	Y.QAITK
<a href="#">1945</a>	544.8006	1087.5866	1087.5985	-10.94	0	21	0.16	1	U	W.NSGKR

48. [2::sp|P17445|BETB\\_ECOLI](#) **Mass:** 53163 **Score:** 45 **Matches:** 2(2) **Sequences:** 1(1)  
NAD/NADP-dependent betaine aldehyde dehydrogenase 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
<a href="#">4090</a>	689.3677	1376.7208	1376.7122	6.26	1	45	0.00052	1	U	W.KSAPA
<a href="#">4091</a>	689.3682	1376.7218	1376.7122	6.96	1	(34)	0.0065	1	U	W.KSAPA

49. [2::sp|P0AC38|ASPA\\_ECOLI](#) **Mass:** 52950 **Score:** 45 **Matches:** 2(2) **Sequences:** 1(1)  
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
<a href="#">3717</a>	658.3463	1314.6779	1314.6779	0.03	1	45	0.00054	1	U	M.SNNIR
<a href="#">3718</a>	658.3475	1314.6804	1314.6779	1.89	1	(28)	0.025	1	U	M.SNNIR

50. [2::sp|P60906|SYH\\_ECOLI](#) **Mass:** 47285 **Score:** 41 **Matches:** 2(2) **Sequences:** 1(1)  
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
<a href="#">4626</a>	747.9306	1493.8466	1493.8453	0.89	0	(33)	0.0027	1	U	Y.SEIRL
<a href="#">4627</a>	747.9321	1493.8497	1493.8453	2.94	0	41	0.00046	1	U	Y.SEIRL

51. [2::sp|P77748|YDIJ\\_ECOLI](#) **Mass:** 114259 **Score:** 40 **Matches:** 2(2) **Sequences:** 2(2)  
Uncharacterized protein YdiJ OS=Escherichia coli (strain K12) OX=83333 GN=ydiJ PE=4 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
<a href="#">3874</a>	669.8725	1337.7304	1337.7013	21.8	0	22	0.051	1	U	L.SEKHIG
<a href="#">4445</a>	726.4171	1450.8195	1450.7854	23.6	1	21	0.038	1	U	L.SEKHIG

52. [2::sp|P02943|LAMB\\_ECOLI](#) **Mass:** 49995 **Score:** 40 **Matches:** 1(1) **Sequences:** 1(1)  
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
<a href="#">2978</a>	606.2841	1210.5536	1210.5500	2.97	0	40	0.0017	1	U	Y.ATDSMT

53. [2::sp|P05793|ILVC\\_ECOLI](#) **Mass:** 54376 **Score:** 37 **Matches:** 2(2) **Sequences:** 1(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
<a href="#">6194</a>	944.9369	1887.8592	1887.8526	3.49	2	40	0.0018	1	U	F.ETAPQY

[6195](#) 944.9377 1887.8609 1887.8526 4.39 2 (32) 0.0099 1 U F.ETAPQY

54. [2::sp|P0AD61|KPYK1 ECOLI](#) Mass: 51039 Score: 36 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
<a href="#">6029</a>	915.9451	1829.8756	1829.8717	2.12	0	36	0.0051	1	U	F.TTDKSV
<a href="#">6030</a>	915.9452	1829.8758	1829.8717	2.25	0	(33)	0.0097	1	U	F.TTDKSV

55. [2::sp|P31068|FLIH ECOLI](#) Mass: 25149 Score: 34 Matches: 2(2) Sequences: 1  
Flagellar assembly protein FliH OS=Escherichia coli (strain K12) OX=83333 GN=fliH 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
<a href="#">628</a>	436.2719	870.5293	870.5174	13.6	0	(27)	0.0091	1	U	L.IKQIQQL
<a href="#">629</a>	436.2720	870.5295	870.5174	13.9	0	34	0.0016	1	U	L.IKQIQQL

56. [2::sp|P0A9J8|PHEA ECOLI](#) Mass: 43312 Score: 34 Matches: 2(2) Sequences: 1  
P-protein OS=Escherichia coli (strain K12) OX=83333 GN=pheA 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
<a href="#">4535</a>	736.9085	1471.8025	1471.7704	21.8	2	(33)	0.0069	1	U	L.LMATGQ
<a href="#">4536</a>	736.9094	1471.8042	1471.7704	22.9	2	36	0.0034	1	U	L.LMATGQ

57. [2::sp|P33224|AIDB ECOLI](#) Mass: 61235 Score: 33 Matches: 1(1) Sequences: 1  
Putative acyl-CoA dehydrogenase AidB OS=Escherichia coli (strain K12) OX=83333 GN=aidB 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
<a href="#">2482</a>	572.8206	1143.6267	1143.5996	23.7	0	33	0.0068	1	U	W.DRRADA

58. [2::sp|P0A953|FABB ECOLI](#) Mass: 42928 Score: 32 Matches: 2(2) Sequences: 1  
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
<a href="#">3519</a>	645.8331	1289.6516	1289.6463	4.10	0	32	0.014	1	U	L.NIVTET
<a href="#">3520</a>	645.8359	1289.6573	1289.6463	8.55	0	(27)	0.048	1	U	L.NIVTET

59. [2::sp|P0AB89|PUR8 ECOLI](#) Mass: 51625 Score: 31 Matches: 2(2) Sequences: 1  
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
<a href="#">11</a>	380.2434	758.4723	758.4538	24.5	1	(22)	0.038	2	U	Y.EKLKEL.T
<a href="#">12</a>	380.2436	758.4726	758.4538	24.8	1	31	0.0046	1	U	Y.EKLKEL.T

60. [2::sp|P25888|RHLE\\_ECOLI](#) Mass: 50016 Score: 31 Matches: 2(2) Sequences: 1(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
<a href="#">3150</a>	618.3060	1234.5975	1234.5942	2.69	0	31	0.019	1	U	L.AAQIGE
<a href="#">3151</a>	618.3060	1234.5975	1234.5942	2.69	0	(28)	0.04	1	U	L.AAQIGE

61. [2::sp|P0A817|METK\\_ECOLI](#) Mass: 42153 Score: 30 Matches: 1(1) Sequences: 1(1)  
 S-adenosylmethionine synthase OS=Escherichia coli (strain K12) OX=83333 GN=metK 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
<a href="#">5148</a>	802.9318	1603.8491	1603.8457	2.08	1	30	0.019	1	U	F.QYDDGK

62. [2::sp|P08722|PTV3B\\_ECOLI](#) Mass: 66896 Score: 29 Matches: 1(1) Sequences: 1(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
<a href="#">3636</a>	651.8489	1301.6832	1301.6723	8.38	1	29	0.022	1	U	L.LMPAIM

63. [2::sp|P09099|XYLB\\_ECOLI](#) Mass: 52927 Score: 29 Matches: 1(1) Sequences: 1(1)  
 Xylulose kinase OS=Escherichia coli (strain K12) OX=83333 GN=xylB 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
<a href="#">4085</a>	688.8568	1375.6989	1375.6765	16.3	1	29	0.028	1	U	W.RQMLAD

64. [2::sp|P0A9B2|G3P1\\_ECOLI](#) Mass: 35681 Score: 29 Matches: 2(1) Sequences: 1(1)  
 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
<a href="#">3240</a>	624.8162	1247.6178	1247.6146	2.54	1	(22)	0.14	1	U	F.DAKAGI
<a href="#">3241</a>	624.8168	1247.6191	1247.6146	3.62	1	29	0.031	1	U	F.DAKAGI

65. [2::sp|P28912|YHHI\\_ECOLI](#) Mass: 43574 Score: 29 Matches: 2(2) Sequences: 1(1)

H repeat-associated putative transposase YhhI OS=Escherichia coli (strain K12) OX=833333 GN=yhhI 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
<a href="#">897</a>	465.7670	929.5195	929.5294	-10.66	0	29	0.019	1	U	F.AVKGTQG
<a href="#">898</a>	465.7673	929.5200	929.5294	-10.15	0	(27)	0.029	1	U	F.AVKGTQG

66. [2::sp|P24175|MANB\\_ECOLI](#) Mass: 50716 Score: 29 Matches: 2(2) Sequences: 1(1)  
 Phosphomannomutase OS=Escherichia coli (strain K12) OX=833333 GN=manB 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
<a href="#">2029</a>	550.7999	1099.5852	1099.5947	-8.66	1	29	0.019	1	U	Y.INVKNL
<a href="#">2030</a>	550.8004	1099.5863	1099.5947	-7.66	1	(25)	0.046	1	U	Y.INVKNL

67. [2::sp|P25552|GPPA\\_ECOLI](#) Mass: 55293 Score: 28 Matches: 1(1) Sequences: 1(1)  
 Guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase OS=Escherichia coli (strain K12) OX=833333 GN=gppA 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
<a href="#">3500</a>	644.8319	1287.6491	1287.6459	2.53	0	31	0.017	1	U	L.GKEIIA

68. [2::sp|P37652|BCSB\\_ECOLI](#) Mass: 86140 Score: 27 Matches: 1(1) Sequences: 1(1)  
 Cyclic di-GMP-binding protein OS=Escherichia coli (strain K12) OX=833333 GN=bcsB 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
<a href="#">3416</a>	637.3353	1272.6561	1272.6384	14.0	0	27	0.037	1	U	L.QAAKGI

69. [2::sp|P30863|DKGB\\_ECOLI](#) Mass: 29475 Score: 27 Matches: 2(1) Sequences: 1(1)  
 2,5-diketo-D-gluconic acid reductase B OS=Escherichia coli (strain K12) OX=833333 GN=dkgB 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
<a href="#">517</a>	423.2576	844.5007	844.5018	-1.28	1	(21)	0.075	1	U	L.KESLQKL
<a href="#">518</a>	423.2582	844.5019	844.5018	0.17	1	27	0.014	1	U	L.KESLQKL

70. [2::sp|P77171|YDCI\\_ECOLI](#) Mass: 33552 Score: 27 Matches: 2(2) Sequences: 1(1)  
 Uncharacterized HTH-type transcriptional regulator YdcI OS=Escherichia coli (strain K12) OX=833333 GN=ydcI 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
<a href="#">1486</a>	508.2567	1014.4988	1014.5206	-21.51	0	(26)	0.029	1	U	F.ERGRQ
<a href="#">1487</a>	508.2568	1014.4991	1014.5206	-21.25	0	27	0.023	1	U	F.ERGRQ

71. [2::sp|P28305|PABC ECOLI](#) **Mass:** 30266 **Score:** 27 **Matches:** 1(1) **Sequences:** 1  
Aminodeoxychorismate lyase OS=Escherichia coli (strain K12) OX=83333 GN=pabC 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
<a href="#">264</a>	401.7186	801.4226	801.4344	-14.80	0	27	0.028	1	U	L.RNEGITL

72. [2::sp|P0AEI4|RIMO ECOLI](#) **Mass:** 50064 **Score:** 27 **Matches:** 2(2) **Sequences:** 1  
Ribosomal protein S12 methylthiotransferase RimO OS=Escherichia coli (strain K12) OX=83333 GN=rmo 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
<a href="#">2769</a>	591.8585	1181.7025	1181.7020	0.44	2	(24)	0.012	1	U	F.LSLVPE
<a href="#">2770</a>	591.8594	1181.7042	1181.7020	1.90	2	27	0.0063	1	U	F.LSLVPE

73. [2::sp|P77335|HLYE ECOLI](#) **Mass:** 33852 **Score:** 27 **Matches:** 1(1) **Sequences:** 1  
Hemolysin E, chromosomal OS=Escherichia coli (strain K12) OX=83333 GN=hlyE 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
<a href="#">4352</a>	716.8865	1431.7584	1431.7391	13.5	0	27	0.04	1	U	Y.NEKKAS

74. [2::sp|P00963|ASNA ECOLI](#) **Mass:** 36742 **Score:** 26 **Matches:** 1(1) **Sequences:** 1  
Aspartate--ammonia ligase OS=Escherichia coli (strain K12) OX=83333 GN=asnA 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
<a href="#">2604</a>	581.2923	1160.5700	1160.5422	24.0	0	26	0.051	1	U	L.SRVGDG

75. [2::sp|P63020|NFUA ECOLI](#) **Mass:** 21212 **Score:** 26 **Matches:** 2(2) **Sequences:** 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
<a href="#">1746</a>	529.7956	1057.5766	1057.6019	-23.88	1	26	0.035	1	U	L.KEGIE
<a href="#">1747</a>	529.7961	1057.5777	1057.6019	-22.84	1	(25)	0.051	1	U	L.KEGIE

76. [2::sp|P45420|YHCD ECOLI](#) **Mass:** 86465 **Score:** 26 **Matches:** 2(1) **Sequences:** 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
<a href="#">1539</a>	511.7671	1021.5197	1021.5374	-17.34	2	26	0.05	1	U	-.MLKKT
<a href="#">1540</a>	511.7679	1021.5211	1021.5374	-15.91	2	(23)	0.095	1	U	-.MLKKT

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77. [1::sp|cRAP008|P00722|BGAL ECOLI](#) Mass: 117321 Score: 25 Matches: 1(0) Sequences: 1(0)  
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
<a href="#">2370</a>	568.2722	1134.5299	1134.5305	-0.58	0	25	0.056	1	U	Y.GQDSRL

**Proteins matching the same set of peptides:**

[2::sp|P00722|BGAL ECOLI](#) Mass: 117321 Score: 25 Matches: 1(0) Sequences: 1(0)  
Beta-galactosidase OS=Escherichia coli (strain K12) OX=83333 GN=lacZ PE=1 SV=2

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78. [2::sp|P76655|YQIG ECOLI](#) Mass: 92021 Score: 25 Matches: 1(1) Sequences: 1(1)  
Putative outer membrane usher protein YqiG 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
<a href="#">388</a>	412.7111	823.4076	823.4076	0.06	2	28	0.024	1	U	L.NSLGSLSF

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79. [2::sp|P0ABF6|CDD ECOLI](#) Mass: 31805 Score: 25 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
<a href="#">626</a>	436.2469	870.4792	870.4698	10.7	1	(24)	0.023	1	U	L.QSALEPIL
<a href="#">627</a>	436.2474	870.4803	870.4698	12.1	1	25	0.02	1	U	L.QSALEPIL

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80. [2::sp|P0A6A3|ACKA ECOLI](#) Mass: 43605 Score: 25 Matches: 2(1) Sequences: 1(1)  
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
<a href="#">1187</a>	486.7771	971.5397	971.5400	-0.28	0	25	0.039	1	U	L.VIAQDASR
<a href="#">1196</a>	487.2679	972.5212	972.5240	-2.86	0	(21)	0.13	1	U	L.VIAQDASR

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81. [2::sp|P17115|GUTQ ECOLI](#) Mass: 34181 Score: 24 Matches: 2(1) Sequences: 1(1)  
Arabinose 5-phosphate isomerase GutQ OS=Escherichia coli (strain K12) OX=83333 GN=gu  
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
<a href="#">987</a>	473.2758	944.5370	944.5291	8.35	2	(22)	0.079	1	U	L.ELSRTGLG
<a href="#">988</a>	473.2764	944.5382	944.5291	9.64	2	24	0.041	1	U	L.ELSRTGLG

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82. [2::sp|P0A915|OMPW ECOLI](#) Mass: 22913 Score: 24 Matches: 1(0) Sequences: 1(0)  
 Outer membrane protein W OS=Escherichia coli (strain K12) OX=83333 GN=ompW 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
<a href="#">2404</a>	570.2636	1138.5127	1138.5142	-1.38	1	24	0.064	1	U	L.GGFSVTV

83. [2::sp|P25744|MDTG ECOLI](#) Mass: 44067 Score: 24 Matches: 1(1) Sequences: 1(1)  
 Multidrug resistance protein MdtG OS=Escherichia coli (strain K12) OX=83333 GN=mdtG 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
<a href="#">1882</a>	541.3386	1080.6627	1080.6543	7.76	2	24	0.005	1	U	Y.VQTPLQ

84. [2::sp|P77416|HYFD ECOLI](#) Mass: 51949 Score: 24 Matches: 1(0) Sequences: 1(0)  
 Hydrogenase-4 component D OS=Escherichia coli (strain K12) OX=83333 GN=hyfD 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
<a href="#">2507</a>	574.8048	1147.5949	1147.6125	-15.30	2	24	0.071	1	U	L.TLVNV

85. [2::sp|P37909|YBGD ECOLI](#) Mass: 19940 Score: 24 Matches: 1(1) Sequences: 1(1)  
 Uncharacterized fimbrial-like protein YbgD OS=Escherichia coli (strain K12) OX=83333 GN=ybgD 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
<a href="#">1508</a>	509.2959	1016.5773	1016.5688	8.34	1	24	0.046	1	U	F.KGQKTL

86. [2::sp|P08839|PT1 ECOLI](#) Mass: 63750 Score: 24 Matches: 2(0) Sequences: 1(0)  
 Phosphoenolpyruvate-protein phosphotransferase OS=Escherichia coli (strain K12) OX=83333 GN=pt1 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
<a href="#">6202</a>	630.6514	1888.9325	1888.9425	-5.32	0	(20)	0.25	1	U	F.ITDAGG
<a href="#">6203</a>	630.6514	1888.9325	1888.9425	-5.32	0	24	0.098	1	U	F.ITDAGG

## 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 :  $\pm$  25 ppm  
Fragment Mass Tolerance:  $\pm$  0.8 Da  
Max Missed Cleavages : 2  
Instrument type : ESI-TRAP  
Number of queries : 7342

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