

## 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\_band6.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 11:12:31 GMT

Protein hits	: <a href="#">2::sp P02930 TOLC ECOLI</a>	Outer membrane protein TolC OS=Escherichia coli
	: <a href="#">2::sp P0ABB4 ATPB ECOLI</a>	ATP synthase subunit beta OS=Escherichia coli
	: <a href="#">2::sp P0A850 TIG ECOLI</a>	Trigger factor OS=Escherichia coli (strain ATCC 8739)
	: <a href="#">1::sp cRAP022 P00766 CTRA BOVIN</a>	Chymotrypsinogen A OS=Bos taurus PE=1 SV=1
	: <a href="#">2::sp P0A9P0 DLDH ECOLI</a>	Dihydrolipoyl dehydrogenase OS=Escherichia coli
	: <a href="#">2::sp P00350 6PGD ECOLI</a>	6-phosphogluconate dehydrogenase, decarboxylating OS=Escherichia coli
	: <a href="#">2::sp P0AFG6 ODO2 ECOLI</a>	Dihydrolipoyllysine-residue succinyltransferase OS=Escherichia coli
	: <a href="#">2::sp P0AE06 ACRA ECOLI</a>	Multidrug efflux pump subunit AcrA OS=Escherichia coli
	: <a href="#">2::sp P0CE47 EFTU1 ECOLI</a>	Elongation factor Tu 1 OS=Escherichia coli
	: <a href="#">2::sp P0A6P9 ENO ECOLI</a>	Enolase OS=Escherichia coli (strain K12)
	: <a href="#">2::sp P0A6H5 HSLU ECOLI</a>	ATP-dependent protease ATPase subunit H OS=Escherichia coli
	: <a href="#">2::sp P0A6E4 ASSY ECOLI</a>	Argininosuccinate synthase OS=Escherichia coli
	: <a href="#">2::sp P0A8M0 SYN ECOLI</a>	Asparagine--tRNA ligase OS=Escherichia coli
	: <a href="#">2::sp P0AGD7 SRP54 ECOLI</a>	Signal recognition particle protein OS=Escherichia coli
	: <a href="#">2::sp P0AGG8 TLDD ECOLI</a>	Metalloprotease TldD OS=Escherichia coli
	: <a href="#">2::sp P0A6F3 GLPK ECOLI</a>	Glycerol kinase OS=Escherichia coli (strain ATCC 8739)
	: <a href="#">2::sp P0A8L1 SYS ECOLI</a>	Serine--tRNA ligase OS=Escherichia coli
	: <a href="#">1::sp cRAP087 P02769 ALBU BOVIN</a>	Serum albumin OS=Bos taurus GN=ALB PE=1 SV=1
	: <a href="#">2::sp P0A7D4 PURA ECOLI</a>	Adenylosuccinate synthetase OS=Escherichia coli
	: <a href="#">2::sp P0A910 OMPA ECOLI</a>	Outer membrane protein A OS=Escherichia coli
	: <a href="#">2::sp P0AG30 RHO ECOLI</a>	Transcription termination factor Rho OS=Escherichia coli
	: <a href="#">2::sp P0C0V0 DEGP ECOLI</a>	Periplasmic serine endoprotease DegP OS=Escherichia coli
	: <a href="#">1::sp cRAP039 P13645 K1C10 HUMAN</a>	Keratin, type I cytoskeletal 10 OS=Homo sapiens
	: <a href="#">2::sp P0A825 GLYA ECOLI</a>	Serine hydroxymethyltransferase OS=Escherichia coli
	: <a href="#">2::sp P25553 ALDA ECOLI</a>	Lactaldehyde dehydrogenase OS=Escherichia coli
	: <a href="#">2::sp P02931 OMPF ECOLI</a>	Outer membrane protein F OS=Escherichia coli
	: <a href="#">2::sp P08200 IDH ECOLI</a>	Isocitrate dehydrogenase [NADP] OS=Escherichia coli
	: <a href="#">2::sp P21888 SYC ECOLI</a>	Cysteine--tRNA ligase OS=Escherichia coli

[2::sp|P24182|ACCC ECOLI](#)  
[2::sp|P0A9B2|G3P1 ECOLI](#)  
[2::sp|P06715|GSHR ECOLI](#)  
[2::sp|P0ABB0|ATPA ECOLI](#)  
[2::sp|P04805|SYE ECOLI](#)  
[1::sp|cRAP112|P00761|TRYP PIG](#)  
[2::sp|P25522|MNME ECOLI](#)  
[2::sp|P0ACC7|GLMU ECOLI](#)  
[2::sp|P0A6P1|EFTS ECOLI](#)  
[2::sp|P0AEX9|MALE ECOLI](#)  
[2::sp|P0AD61|KPYK1 ECOLI](#)  
[1::sp|cRAP054|P04264|K2C1 HUMAN](#)  
[2::sp|P21165|PEPQ ECOLI](#)  
[2::sp|P0A6H1|CLPX ECOLI](#)  
[2::sp|P15034|AMPP ECOLI](#)  
[2::sp|P27306|STHA ECOLI](#)  
[2::sp|P21599|KPYK2 ECOLI](#)  
[2::sp|Q46808|YQEB ECOLI](#)  
[2::sp|P77748|YDIJ ECOLI](#)  
[2::sp|P11447|ARLY ECOLI](#)  
[2::sp|P0C8J8|GATZ ECOLI](#)  
[1::sp|cRAP041|P35527|K1C9 HUMAN](#)  
[2::sp|P0A6F5|CH60 ECOLI](#)  
[2::sp|P37177|PT1P ECOLI](#)  
[2::sp|P76403|YEQQ ECOLI](#)  
[2::sp|P60906|SYH ECOLI](#)  
[2::sp|P0A6Y8|DNAK ECOLI](#)  
[2::sp|P60422|RL2 ECOLI](#)  
[2::sp|P04982|RBSD ECOLI](#)  
[2::sp|P76658|HLDE ECOLI](#)  
[2::sp|P0A953|FABB ECOLI](#)  
[2::sp|P00490|PHSM ECOLI](#)  
[2::sp|P76251|DMLA ECOLI](#)  
[2::sp|P32664|NUDC ECOLI](#)  
[2::sp|P0A9J8|PHEA ECOLI](#)  
[2::sp|P37651|GUN ECOLI](#)  
[2::sp|P77260|YDFI ECOLI](#)  
[2::sp|P42591|YGJJ ECOLI](#)  
[2::sp|P0A817|METK ECOLI](#)  
[2::sp|P31068|FLIH ECOLI](#)  
[2::sp|P37652|BCSB ECOLI](#)  
[2::sp|P68187|MALK ECOLI](#)  
[2::sp|P0ABH7|CISY ECOLI](#)  
[2::sp|P76272|YEBT ECOLI](#)  
[2::sp|P0A870|TALB ECOLI](#)  
[2::sp|P75990|BLUF ECOLI](#)  
[2::sp|P24175|MANB ECOLI](#)  
[2::sp|Q46814|XDHD ECOLI](#)

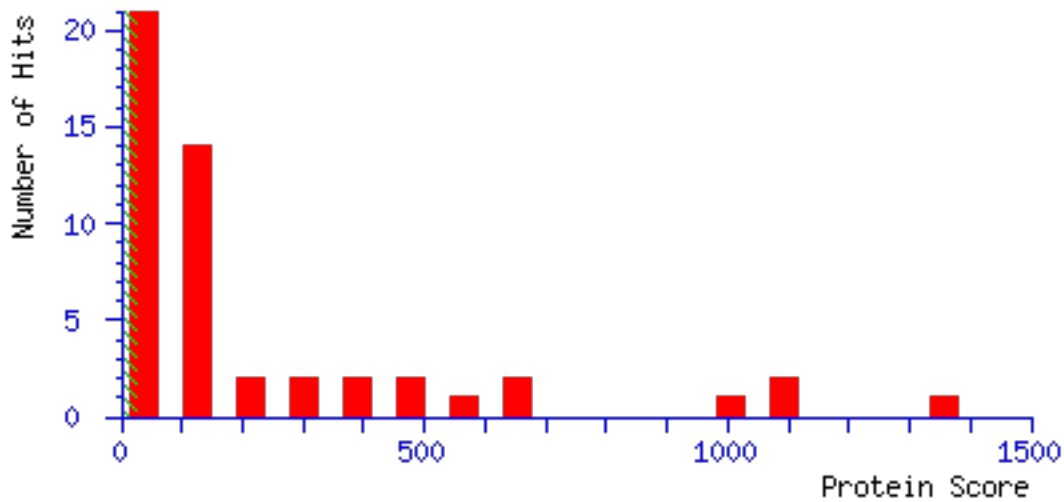
Biotin carboxylase OS=Escherichia coli  
Glyceraldehyde-3-phosphate dehydrogenas  
Glutathione reductase OS=Escherichia co  
ATP synthase subunit alpha OS=Escherich  
Glutamate--tRNA ligase OS=Escherichiac  
Trypsin OS=Sus scrofa PE=1 SV=1  
tRNA modification GTPase MnmE OS=Escher  
Bifunctional protein GlmU OS=Escherichi  
Elongation factor Ts OS=Escherichia col  
Maltose-binding periplasmic protein OS=  
Pyruvate kinase I OS=Escherichia coli (  
Keratin, type II cytoskeletal 1 OS=Homo  
Xaa-Pro dipeptidase OS=Escherichiacoli  
ATP-dependent Clp protease ATP-binding  
Xaa-Pro aminopeptidase OS=Escherichia c  
Soluble pyridine nucleotide transhydrog  
Pyruvate kinase II OS=Escherichia coli  
Uncharacterized protein YqeB OS=Escheri  
Uncharacterized protein YdiJ OS=Escheri  
Argininosuccinate lyase OS=Escherichia  
D-tagatose-1,6-bisphosphate aldolase su  
Keratin, type I cytoskeletal 9 OS=Homo  
60 kDa chaperonin OS=Escherichia coli (  
Phosphoenolpyruvate-dependent phosphotr  
Uncharacterized protease YegQ OS=Escher  
Histidine--tRNA ligase OS=Escherichia c  
Chaperone protein DnaK OS=Escherichia c  
50S ribosomal protein L2 OS=Escherichia  
D-ribose pyranase OS=Escherichia coli (  
Bifunctional protein HldE OS=Escherichi  
3-oxoacyl-[acyl-carrier-protein] syntha  
Maltodextrin phosphorylase OS=Escherich  
D-malate dehydrogenase [decarboxylating  
NADH pyrophosphatase OS=Escherichia col  
P-protein OS=Escherichia coli (strain K  
Endoglucanase OS=Escherichia coli (stra  
Uncharacterized oxidoreductase YdfI OS=  
Uncharacterized protein YgjJ OS=Escheri  
S-adenosylmethionine synthase OS=Escher  
Flagellar assembly protein FliH OS=Esch  
Cyclic di-GMP-binding protein OS=Escher  
Maltose/maltodextrin import ATP-binding  
Citrate synthase OS=Escherichia coli (s  
Uncharacterized protein YebT OS=Escheri  
Transaldolase B OS=Escherichia coli (st  
Blue light- and temperature-regulated a  
Phosphomannomutase OS=Escherichia coli  
Probable hypoxanthine oxidase XdhD OS=E

[2::sp|P0A763|NDK ECOLI](#)  
[2::sp|P77504|YBBP ECOLI](#)

Nucleoside diphosphate kinase OS=Escher  
 Uncharacterized ABC transporter permeas

## 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 (alveo and relatives) . . . . . bony vertebrates . . . . . lobe-finned fish and tetrapod clade . . . . . Mam				
Mus . . . . . Mus musculus (house mouse) . . . . . Rattus . . . . . Oth				
fishes) . . . . . Takifugu rubripes (Japanese Pufferfish) . . . . . Danio rerio (zebra fish) . . . . .				
Schizosaccharomyces pombe (fission yeast) . . . . . Pneumocystis carinii . . . . . Other Fungi . . . . . Viridiplant				
Mycobacterium tuberculosis complex . . . . . Other Actinobacteria (class) . . . . . Firmicutes (gram-positive bac				
Agrobacterium tumefaciens . . . . . Campylobacter jejuni . . . . . Escherichia coli . . . . . Neisseria meningitidis				
Species information unavailable				

### Error tolerant

1. [2::sp|P02930|TOLC ECOLI](#) **Mass:** 53708 **Score:** 1355 **Matches:** 71 (66) **Sequences:**

Outer membrane protein TolC OS=Escherichia coli (strain K12) OX=83333 GN=tolC 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="#">233</a>	400.7525	799.4904	799.4916	-1.47	2	24	0.025	1	U	L.SLLQA
<a href="#">546</a>	433.7343	865.4540	865.4545	-0.58	1	(24)	0.041	1	U	L.ILNTA
<a href="#">547</a>	433.7345	865.4544	865.4545	-0.15	1	27	0.022	1	U	L.ILNTA
<a href="#">1022</a>	482.7408	963.4671	963.4662	0.95	1	(36)	0.004	1	U	Y.NFVGA
<a href="#">1023</a>	482.7410	963.4675	963.4662	1.40	1	44	0.00074	1	U	Y.NFVGA
<a href="#">1293</a>	501.7589	1001.5032	1001.5029	0.28	2	32	0.012	1	U	L.GTLNE
<a href="#">1294</a>	501.7593	1001.5040	1001.5029	1.08	2	(30)	0.018	1	U	L.GTLNE
<a href="#">1351</a>	507.2681	1012.5216	1012.5229	-1.33	2	29	0.014	1	U	L.ILNTA
<a href="#">1352</a>	507.2684	1012.5223	1012.5229	-0.62	2	(25)	0.038	1	U	L.ILNTA
<a href="#">1543</a>	523.7788	1045.5431	1045.5444	-1.28	2	(24)	0.083	1	U	L.LPQLG
<a href="#">1544</a>	523.7799	1045.5453	1045.5444	0.83	2	32	0.013	1	U	L.LPQLG
<a href="#">1566</a>	526.2742	1050.5339	1050.5345	-0.61	0	(20)	0.19	1	U	Y.TQAQK
<a href="#">1567</a>	526.2752	1050.5359	1050.5345	1.26	0	(36)	0.0053	1	U	Y.TQAQK
<a href="#">1568</a>	526.2753	1050.5360	1050.5345	1.37	0	38	0.0032	1	U	Y.TQAQK
<a href="#">2042</a>	559.3144	1116.6143	1116.6139	0.42	0	(49)	0.00017	1	U	Y.KQAVV
<a href="#">2043</a>	559.3149	1116.6152	1116.6139	1.19	0	62	8.2e-06	1	U	Y.KQAVV
<a href="#">2398</a>	578.8184	1155.6223	1155.6247	-2.12	0	(52)	7.7e-05	1	U	F.EKINE
<a href="#">2400</a>	578.8192	1155.6237	1155.6247	-0.86	0	57	2.3e-05	1	U	F.EKINE
<a href="#">2423</a>	580.3373	1158.6601	1158.6609	-0.63	0	34	0.004	1	U	Y.SVGTR
<a href="#">2424</a>	580.3374	1158.6602	1158.6609	-0.53	0	(27)	0.019	1	U	Y.SVGTR
<a href="#">2790</a>	605.8424	1209.6701	1209.6717	-1.30	0	45	0.00023	1	U	F.KTDKP
<a href="#">2793</a>	605.8442	1209.6738	1209.6717	1.72	0	(41)	0.00052	1	U	F.KTDKP
<a href="#">3227</a>	639.3324	1276.6502	1276.6523	-1.64	1	25	0.057	1	U	Y.NAKQE
<a href="#">3261</a>	642.3206	1282.6267	1282.6266	0.09	0	28	0.024	1	U	Y.SGSKT
<a href="#">3317</a>	647.2900	1292.5654	1292.5667	-0.98	0	(43)	0.00059	1	U	Y.DDSNM
<a href="#">3318</a>	647.2906	1292.5666	1292.5667	-0.04	0	44	0.00045	1	U	Y.DDSNM
<a href="#">3385</a>	651.3220	1300.6294	1300.6299	-0.41	1	34	0.0066	1	U	L.SYTOA
<a href="#">3386</a>	651.3226	1300.6307	1300.6299	0.62	1	(26)	0.041	1	U	L.SYTOA
<a href="#">3536</a>	661.8319	1321.6493	1321.6514	-1.60	0	51	0.00021	1	U	L.QEKAA
<a href="#">3537</a>	661.8331	1321.6516	1321.6514	0.16	0	(46)	0.00061	1	U	L.QEKAA
<a href="#">3546</a>	662.3857	1322.7569	1322.7558	0.87	1	(34)	0.0012	1	U	F.KTDKP
<a href="#">3548</a>	662.3872	1322.7597	1322.7558	3.00	1	35	0.001	1	U	F.KTDKP
<a href="#">3839</a>	690.8415	1379.6684	1379.6681	0.27	0	(52)	0.00015	1	U	F.NNINA
<a href="#">3840</a>	690.8429	1379.6712	1379.6681	2.31	0	59	2.6e-05	1	U	F.NNINA
<a href="#">3841</a>	691.3342	1380.6538	1380.6521	1.25	0	(38)	0.003	1	U	F.NNINA
<a href="#">4154</a>	724.8775	1447.7404	1447.7419	-1.02	0	61	1.9e-05	1	U	L.VAITD
<a href="#">4155</a>	724.8803	1447.7461	1447.7419	2.86	0	(40)	0.0021	1	U	L.VAITD
<a href="#">4160</a>	725.3729	1448.7312	1448.7259	3.61	0	(55)	7.3e-05	1	U	L.VAITD
<a href="#">4161</a>	725.3751	1448.7357	1448.7259	6.73	0	(44)	0.00092	1	U	L.VAITD
<a href="#">4309</a>	743.3501	1484.6856	1484.6817	2.67	2	(45)	0.00055	1	U	F.SLSQ
<a href="#">4310</a>	743.3502	1484.6858	1484.6817	2.75	2	45	0.00055	1	U	F.SLSQ
<a href="#">4329</a>	745.8635	1489.7124	1489.7121	0.20	0	(66)	6.1e-06	1	U	Y.RDANG
<a href="#">4330</a>	745.8635	1489.7124	1489.7121	0.20	0	(60)	2.2e-05	1	U	Y.RDANG
<a href="#">4333</a>	746.3567	1490.6988	1490.6961	1.85	0	(69)	2.7e-06	1	U	Y.RDANG
<a href="#">4334</a>	746.3568	1490.6991	1490.6961	2.01	0	70	2.3e-06	1	U	Y.RDANG
<a href="#">4509</a>	768.8991	1535.7837	1535.7831	0.35	1	(42)	0.0014	1	U	L.TLQEK
<a href="#">4510</a>	768.8993	1535.7840	1535.7831	0.59	1	63	1.2e-05	1	U	L.TLQEK
<a href="#">4511</a>	768.8995	1535.7845	1535.7831	0.91	1	(34)	0.0082	1	U	L.TLQEK
<a href="#">4512</a>	768.9005	1535.7865	1535.7831	2.18	1	(50)	0.00021	1	U	L.TLQEK
<a href="#">4513</a>	768.9017	1535.7888	1535.7831	3.69	1	(32)	0.012	1	U	L.TLQEK
<a href="#">4586</a>	777.3734	1552.7323	1552.7304	1.21	0	55	8.2e-05	1	U	Y.QGMV
<a href="#">4587</a>	777.3735	1552.7325	1552.7304	1.38	0	(42)	0.0015	1	U	Y.QGMV

<a href="#">4590</a>	777.8658	1553.7170	1553.7144	1.68	0	(46)	0.00047	1	U	Y.QGGMV
<a href="#">4591</a>	777.8672	1553.7198	1553.7144	3.49	0	(23)	0.12	1	U	Y.QGGMV
<a href="#">4876</a>	804.9230	1607.8315	1607.8307	0.49	2	43	0.00093	1	U	L.RQITG
<a href="#">4877</a>	804.9232	1607.8319	1607.8307	0.73	2	(41)	0.0015	1	U	L.RQITG
<a href="#">5384</a>	583.2964	1746.8673	1746.8649	1.42	1	30	0.022	1	U	L.SNPGL
<a href="#">5616</a>	916.4874	1830.9602	1830.9588	0.76	1	97	3.5e-09	1	U	F.NVGLV
<a href="#">5617</a>	916.4887	1830.9629	1830.9588	2.22	1	(89)	2.1e-08	1	U	F.NVGLV
<a href="#">5678</a>	927.9495	1853.8845	1853.8829	0.85	1	97	4.8e-09	1	U	Y.KQAVV
<a href="#">5679</a>	927.9514	1853.8881	1853.8829	2.83	1	(92)	1.5e-08	1	U	Y.KQAVV
<a href="#">5712</a>	935.9476	1869.8807	1869.8778	1.54	1	(81)	1.5e-07	1	U	Y.KQAVV
<a href="#">5713</a>	935.9493	1869.8841	1869.8778	3.37	1	(93)	9.7e-09	1	U	Y.KQAVV
<a href="#">5714</a>	935.9657	1869.9168	1869.9180	-0.63	1	63	1.2e-05	1	U	L.ANEVT
<a href="#">5717</a>	935.9697	1869.9249	1869.9180	3.68	1	(56)	5.1e-05	1	U	L.ANEVT
<a href="#">5724</a>	936.4614	1870.9083	1870.9020	3.35	1	(45)	0.00059	1	U	L.ANEVT
<a href="#">5725</a>	936.4631	1870.9117	1870.9020	5.17	1	(55)	5.9e-05	1	U	L.ANEVT
<a href="#">5820</a>	956.9334	1911.8521	1911.8558	-1.92	1	(24)	0.078	1	U	Y.SNGYR
<a href="#">5821</a>	956.9355	1911.8564	1911.8558	0.32	1	(42)	0.0012	1	U	Y.SNGYR
<a href="#">5822</a>	956.9394	1911.8643	1911.8558	4.46	1	45	0.00061	1	U	Y.SNGYR
<a href="#">5825</a>	957.4306	1912.8466	1912.8398	3.57	1	(25)	0.048	1	U	Y.SNGYR

2. [2::sp|P0ABB4|ATPB\\_ECOLI](#) Mass: 50351 Score: 1123 Matches: 65(59) 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="#">414</a>	416.2032	830.3919	830.3923	-0.46	0	(25)	0.025	1	U	L.VVGQE
<a href="#">415</a>	416.2033	830.3919	830.3923	-0.39	0	29	0.01	1	U	L.VVGQE
<a href="#">808</a>	469.2317	936.4488	936.4487	0.10	0	(28)	0.026	1	U	L.GRMPS
<a href="#">819</a>	469.7689	937.5233	937.5233	0.00	1	24	0.021	1	U	F.AHLDA
<a href="#">921</a>	477.2303	952.4460	952.4436	2.43	0	30	0.017	1	U	L.GRMPS
<a href="#">922</a>	477.2318	952.4490	952.4436	5.63	0	(24)	0.062	1	U	L.GRMPS
<a href="#">951</a>	478.7268	955.4391	955.4399	-0.85	0	(23)	0.055	1	U	Y.DHLPE
<a href="#">952</a>	478.7275	955.4404	955.4399	0.49	0	24	0.039	1	U	Y.DHLPE
<a href="#">953</a>	478.7743	955.5340	955.5338	0.13	1	27	0.014	1	U	L.VLEVQ
<a href="#">954</a>	478.7743	955.5341	955.5338	0.26	1	(25)	0.019	1	U	L.VLEVQ
<a href="#">1003</a>	481.2633	960.5121	960.5128	-0.67	1	(22)	0.098	1	U	Y.TLAGT
<a href="#">1004</a>	481.2636	960.5125	960.5128	-0.23	1	39	0.002	1	U	Y.TLAGT
<a href="#">1349</a>	507.2523	1012.4901	1012.4899	0.22	1	(39)	0.0015	1	U	L.TGLTM
<a href="#">1350</a>	507.2530	1012.4914	1012.4899	1.42	1	47	0.00023	1	U	L.TGLTM
<a href="#">1630</a>	530.2940	1058.5735	1058.5720	1.37	0	(22)	0.11	1	U	Y.DTARG
<a href="#">1632</a>	530.2950	1058.5755	1058.5720	3.31	0	24	0.068	2	U	Y.DTARG
<a href="#">1688</a>	533.7714	1065.5282	1065.5277	0.43	1	28	0.028	1	U	L.LGRMP
<a href="#">1707</a>	537.8058	1073.5971	1073.5968	0.29	2	(42)	0.00086	1	U	Y.TLAGT
<a href="#">1708</a>	537.8064	1073.5982	1073.5968	1.32	2	49	0.00018	1	U	Y.TLAGT
<a href="#">1887</a>	550.8309	1099.6472	1099.6489	-1.53	1	51	5.2e-05	1	U	L.LETGI
<a href="#">1888</a>	550.8322	1099.6499	1099.6489	0.91	1	(33)	0.0034	1	U	L.LETGI
<a href="#">2052</a>	560.2595	1118.5045	1118.5033	1.09	1	29	0.015	1	U	Y.DHLPE
<a href="#">2053</a>	560.2596	1118.5047	1118.5033	1.31	1	(24)	0.047	1	U	Y.DHLPE
<a href="#">2214</a>	568.3276	1134.6406	1134.6397	0.79	1	(32)	0.0047	1	U	Y.VSLKD
<a href="#">2215</a>	568.3280	1134.6414	1134.6397	1.53	1	36	0.0019	1	U	Y.VSLKD
<a href="#">2387</a>	578.3534	1154.6922	1154.6910	1.03	1	33	0.0023	1	U	Y.QELKD
<a href="#">2388</a>	578.3535	1154.6925	1154.6910	1.25	1	(21)	0.034	2	U	Y.QELKD

<a href="#">2809</a>	606.7936	1211.5726	1211.5717	0.76	0	(31)	0.013	1	U	Y.GQMNE
<a href="#">2900</a>	614.7889	1227.5633	1227.5666	-2.67	0	(22)	0.077	1	U	Y.GQMNE
<a href="#">2902</a>	614.7909	1227.5673	1227.5666	0.61	0	(33)	0.0074	1	U	Y.GQMNE
<a href="#">2903</a>	614.7915	1227.5684	1227.5666	1.50	0	47	0.00028	1	U	Y.GQMNE
<a href="#">2904</a>	614.7920	1227.5694	1227.5666	2.30	0	(26)	0.036	1	U	Y.GQMNE
<a href="#">3133</a>	633.2816	1264.5487	1264.5493	-0.46	1	44	0.00042	1	U	L.GMDEL
<a href="#">3134</a>	633.2834	1264.5522	1264.5493	2.34	1	(38)	0.0019	1	U	L.GMDEL
<a href="#">3190</a>	424.8951	1271.6636	1271.6622	1.09	0	(31)	0.013	1	U	L.IRNIA
<a href="#">3191</a>	636.8391	1271.6637	1271.6622	1.15	0	35	0.005	1	U	L.IRNIA
<a href="#">3192</a>	424.8952	1271.6637	1271.6622	1.16	0	(34)	0.0069	1	U	L.IRNIA
<a href="#">3193</a>	636.8406	1271.6667	1271.6622	3.56	0	(31)	0.014	1	U	L.IRNIA
<a href="#">3712</a>	679.3405	1356.6665	1356.6633	2.33	1	(46)	0.00039	1	U	Y.DALEV
<a href="#">3713</a>	679.3415	1356.6685	1356.6633	3.85	1	60	1.5e-05	1	U	Y.DALEV
<a href="#">3714</a>	679.8307	1357.6469	1357.6473	-0.29	1	(55)	5.1e-05	1	U	Y.DALEV
<a href="#">3716</a>	679.8323	1357.6501	1357.6473	2.05	1	(54)	6.6e-05	1	U	Y.DALEV
<a href="#">3837</a>	690.3373	1378.6600	1378.6585	1.11	0	(45)	0.00073	1	U	F.GGAGV
<a href="#">3838</a>	690.3383	1378.6620	1378.6585	2.53	0	(36)	0.0054	1	U	F.GGAGV
<a href="#">3886</a>	698.3340	1394.6534	1394.6534	0.01	0	(61)	2e-05	1	U	F.GGAGV
<a href="#">3887</a>	698.3358	1394.6571	1394.6534	2.65	0	64	9e-06	1	U	F.GGAGV
<a href="#">4516</a>	769.8840	1537.7535	1537.7520	0.95	1	39	0.003	1	U	L.ETGIK
<a href="#">4517</a>	769.8842	1537.7539	1537.7520	1.20	1	(33)	0.014	1	U	L.ETGIK
<a href="#">4564</a>	773.8683	1545.7221	1545.7199	1.46	1	36	0.0044	1	U	Y.VPADD
<a href="#">4715</a>	785.4159	1568.8173	1568.8158	0.98	2	(41)	0.0013	1	U	Y.DALEV
<a href="#">4716</a>	785.4164	1568.8183	1568.8158	1.60	2	(57)	3e-05	1	U	Y.DALEV
<a href="#">4720</a>	785.9078	1569.8011	1569.7998	0.83	2	(35)	0.0056	1	U	Y.DALEV
<a href="#">4721</a>	785.9102	1569.8059	1569.7998	3.87	2	63	8.4e-06	1	U	Y.DALEV
<a href="#">4722</a>	785.9119	1569.8093	1569.7998	6.04	2	(49)	0.0002	1	U	Y.DALEV
<a href="#">4843</a>	802.3874	1602.7603	1602.7559	2.75	0	42	0.0015	1	U	Y.HEMTD
<a href="#">5008</a>	824.4539	1646.8933	1646.8913	1.23	0	(32)	0.01	1	U	Y.MVGS
<a href="#">5009</a>	824.4551	1646.8957	1646.8913	2.71	0	69	1.6e-06	1	U	Y.MVGS
<a href="#">5325</a>	866.4498	1730.8851	1730.8839	0.69	1	(34)	0.0091	1	U	L.GIYPA
<a href="#">5326</a>	866.4499	1730.8853	1730.8839	0.83	1	50	0.00021	1	U	L.GIYPA
<a href="#">5908</a>	654.0289	1959.0650	1959.0677	-1.39	1	(60)	1.3e-05	1	U	L.DVKDL
<a href="#">5909</a>	980.5403	1959.0661	1959.0677	-0.80	1	(33)	0.0062	1	U	L.DVKDL
<a href="#">5910</a>	654.0295	1959.0668	1959.0677	-0.46	1	(58)	2e-05	1	U	L.DVKDL
<a href="#">5911</a>	980.5441	1959.0737	1959.0677	3.07	1	62	7e-06	1	U	L.DVKDL
<a href="#">6565</a>	892.7640	2675.2701	2675.2683	0.67	1	(41)	0.0016	1	U	L.GRIMN
<a href="#">6566</a>	892.7642	2675.2707	2675.2683	0.88	1	45	0.00065	1	U	L.GRIMN

3. [2::sp|P0A850|TIG ECOLI](#) Mass: 48163 Score: 1049 Matches: 63 (57) Sequences: 2  
 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="#">691</a>	452.2502	902.4859	902.4861	-0.24	1	22	0.1	1	U	L.ELPR
<a href="#">866</a>	472.7617	943.5088	943.5087	0.14	0	(25)	0.048	1	U	Y.GASV
<a href="#">867</a>	472.7618	943.5090	943.5087	0.33	0	27	0.029	1	U	Y.GASV
<a href="#">1001</a>	481.2275	960.4404	960.4400	0.41	0	(48)	0.00021	1	U	F.GVED
<a href="#">1002</a>	481.2277	960.4408	960.4400	0.78	0	55	3.5e-05	1	U	F.GVED
<a href="#">1011</a>	482.2132	962.4118	962.4127	-0.97	1	28	0.018	1	U	F.NELM
<a href="#">1012</a>	482.2139	962.4132	962.4127	0.55	1	(21)	0.078	1	U	F.NELM
<a href="#">1085</a>	486.7370	971.4594	971.4600	-0.64	2	(22)	0.067	1	U	Y.KLGE
<a href="#">1086</a>	486.7376	971.4607	971.4600	0.68	2	23	0.049	1	U	Y.KLGE
<a href="#">1926</a>	553.2742	1104.5339	1104.5339	0.02	0	(34)	0.0076	1	U	Y.EDPK

<u>1928</u>	553.2745	1104.5345	1104.5339	0.58	0	40	0.002	1	U	Y.EDPK
<u>2299</u>	572.3207	1142.6268	1142.6295	-2.37	1	35	0.0042	1	U	L.LGEV
<u>2300</u>	572.3212	1142.6278	1142.6295	-1.51	1	(32)	0.0078	1	U	L.LGEV
<u>2314</u>	572.8192	1143.6239	1143.6248	-0.78	0	25	0.042	1	U	L.KADE
<u>2316</u>	<b>572.8199</b>	<b>1143.6252</b>	<b>1143.6248</b>	<b>0.41</b>	<b>0</b>	<b>(25)</b>	<b>0.046</b>	<b>2</b>	<b>U</b>	<b>L.KADE</b>
<u>2647</u>	596.7977	1191.5809	1191.5806	0.30	0	54	8.8e-05	1	U	-.MQVS
<u>2648</u>	596.7983	1191.5821	1191.5806	1.32	0	(48)	0.00032	1	U	-.MQVS
<u>2769</u>	604.7950	1207.5755	1207.5755	0.05	0	(39)	0.0025	1	U	-.MQVS
<u>2770</u>	604.7964	1207.5782	1207.5755	2.28	0	(44)	0.0008	1	U	-.MQVS
<u>2772</u>	604.8036	1207.5926	1207.5755	14.2	0	(33)	0.0096	1	U	-.MQVS
<u>2815</u>	607.2845	1212.5544	1212.5550	-0.52	0	(47)	0.0003	1	U	F.TIDV
<u>2816</u>	607.2846	1212.5547	1212.5550	-0.31	0	53	6.8e-05	1	U	F.TIDV
<u>2865</u>	613.3420	1224.6695	1224.6714	-1.52	0	32	0.0056	1	U	L.VKAN
<u>2868</u>	613.3441	1224.6736	1224.6714	1.78	0	(28)	0.012	1	U	L.VKAN
<u>2915</u>	615.3274	1228.6403	1228.6412	-0.67	1	39	0.0022	1	U	Y.GASV
<u>3089</u>	628.8657	1255.7168	1255.7136	2.54	2	(47)	0.00018	1	U	L.LLGE
<u>3090</u>	628.8657	1255.7169	1255.7136	2.64	2	47	0.00017	1	U	L.LLGE
<u>3159</u>	634.8052	1267.5959	1267.5972	-1.01	1	41	0.0014	1	U	Y.EDPK
<u>3160</u>	634.8071	1267.5997	1267.5972	1.97	1	(37)	0.0037	1	U	Y.EDPK
<u>3214</u>	638.3275	1274.6405	1274.6394	0.82	1	(47)	0.00047	1	U	F.EVYP
<u>3215</u>	638.3290	1274.6434	1274.6394	3.13	1	52	0.00016	1	U	F.EVYP
<u>3683</u>	676.8750	1351.7354	1351.7347	0.55	0	(33)	0.0054	1	U	L.AKAK
<u>3684</u>	676.8752	1351.7358	1351.7347	0.81	0	39	0.0014	1	U	L.AKAK
<u>5323</u>	866.3735	1730.7324	1730.7272	3.02	1	(75)	3e-07	1	U	F.TGSV
<u>5324</u>	866.3745	1730.7345	1730.7272	4.22	1	94	4.1e-09	1	U	F.TGSV
<u>5562</u>	907.5090	1813.0035	1812.9985	2.76	0	46	0.00023	1	U	F.IDAI
<u>5563</u>	907.5093	1813.0041	1812.9985	3.10	0	(45)	0.00031	1	U	F.IDAI
<u>5575</u>	606.6594	1816.9563	1816.9570	-0.43	1	(23)	0.097	1	U	L.KKVE
<u>5576</u>	909.4854	1816.9563	1816.9570	-0.42	1	52	0.00013	1	U	L.KKVE
<u>5578</u>	909.4871	1816.9597	1816.9570	1.46	1	(37)	0.0033	1	U	L.KKVE
<u>5749</u>	627.6486	1879.9239	1879.9211	1.49	2	46	0.00066	1	U	Y.GASV
<u>5751</u>	627.6494	1879.9262	1879.9211	2.75	2	(27)	0.052	1	U	Y.GASV
<u>5833</u>	641.3205	1920.9397	1920.9429	-1.67	0	(44)	0.00096	1	U	W.KEKD
<u>5836</u>	641.3215	1920.9428	1920.9429	-0.06	0	45	0.00092	1	U	W.KEKD
<u>5837</u>	641.3222	1920.9448	1920.9429	0.99	0	(24)	0.1	1	U	W.KEKD
<u>5838</u>	641.3224	1920.9453	1920.9429	1.29	0	(27)	0.052	1	U	W.KEKD
<u>5839</u>	641.3228	1920.9466	1920.9429	1.94	0	(27)	0.048	1	U	W.KEKD
<u>5840</u>	641.3231	1920.9475	1920.9429	2.43	0	(31)	0.021	1	U	W.KEKD
<u>6080</u>	685.6732	2053.9978	2053.9990	-0.55	1	(25)	0.076	1	U	L.KADE
<u>6082</u>	685.6751	2054.0033	2053.9990	2.12	1	26	0.054	1	U	L.KADE
<u>6371</u>	1180.1279	2358.2413	2358.2471	-2.44	1	(50)	0.00016	1	U	F.IDAI
<u>6372</u>	787.0894	2358.2463	2358.2471	-0.35	1	(26)	0.037	1	U	F.IDAI
<u>6373</u>	787.0908	2358.2505	2358.2471	1.43	1	(42)	0.00082	1	U	F.IDAI
<u>6374</u>	1180.1362	2358.2579	2358.2471	4.60	1	54	4.8e-05	1	U	F.IDAI
<u>6514</u>	1309.1427	2616.2708	2616.2728	-0.74	1	(67)	4.8e-06	1	U	L.EAIE
<u>6515</u>	1309.1432	2616.2718	2616.2728	-0.37	1	81	2e-07	1	U	L.EAIE
<u>6516</u>	1309.1433	2616.2721	2616.2728	-0.28	1	(64)	8.9e-06	1	U	L.EAIE
<u>6517</u>	873.0997	2616.2774	2616.2728	1.74	1	(72)	1.4e-06	1	U	L.EAIE
<u>6518</u>	873.0998	2616.2775	2616.2728	1.81	1	(65)	7.2e-06	1	U	L.EAIE
<u>6519</u>	1309.1489	2616.2833	2616.2728	4.02	1	(56)	5.8e-05	1	U	L.EAIE
<u>6520</u>	873.1020	2616.2841	2616.2728	4.34	1	(39)	0.0026	1	U	L.EAIE
<u>6521</u>	1309.1503	2616.2860	2616.2728	5.04	1	(53)	0.00011	1	U	L.EAIE
<u>6522</u>	873.1027	2616.2862	2616.2728	5.10	1	(53)	0.00012	1	U	L.EAIE

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="#">367</a>	412.7289	823.4433	823.4440	-0.83	1	(34)	0.0032	1	U	L.KLST
<a href="#">368</a>	412.7292	823.4439	823.4440	-0.01	1	(50)	7.2e-05	1	U	L.KLST
<a href="#">369</a>	412.7294	823.4442	823.4440	0.28	1	(55)	2.1e-05	1	U	L.KLST
<a href="#">370</a>	412.7294	823.4442	823.4440	0.28	1	(35)	0.0019	1	U	L.KLST
<a href="#">371</a>	412.7295	823.4445	823.4440	0.65	1	56	1.8e-05	1	U	L.KLST
<a href="#">372</a>	412.7295	823.4445	823.4440	0.65	1	(55)	2e-05	1	U	L.KLST
<a href="#">592</a>	437.7550	873.4955	873.4960	-0.56	1	(46)	0.00032	1	U	W.TLVG
<a href="#">593</a>	437.7556	873.4965	873.4960	0.61	1	47	0.00025	1	U	W.TLVG
<a href="#">686</a>	452.2424	902.4703	902.4709	-0.66	0	(37)	0.0033	2	U	L.TINN
<a href="#">687</a>	452.2428	902.4710	902.4709	0.16	0	40	0.0019	2	U	L.TINN
<a href="#">1005</a>	481.7476	961.4806	961.4804	0.21	0	23	0.085	1	U	L.VCKK
<a href="#">1006</a>	481.7476	961.4807	961.4804	0.34	0	(23)	0.096	1	U	L.VCKK
<a href="#">1177</a>	494.2661	986.5177	986.5185	-0.82	1	(30)	0.013	1	U	L.VNWW
<a href="#">1178</a>	494.2665	986.5185	986.5185	-0.07	1	35	0.0039	1	U	L.VNWW
<a href="#">1195</a>	494.7580	987.5015	987.5025	-1.05	1	(29)	0.018	1	U	L.VNWW
<a href="#">1285</a>	501.2538	1000.4929	1000.4938	-0.81	0	(27)	0.022	1	U	Y.TNAN
<a href="#">1286</a>	501.2541	1000.4936	1000.4938	-0.13	0	(24)	0.046	1	U	Y.TNAN
<a href="#">1287</a>	501.2543	1000.4940	1000.4938	0.23	0	(29)	0.016	1	U	Y.TNAN
<a href="#">1288</a>	501.2544	1000.4942	1000.4938	0.41	0	30	0.014	1	U	Y.TNAN
<a href="#">1289</a>	501.2544	1000.4943	1000.4938	0.55	0	(24)	0.056	1	U	Y.TNAN
<a href="#">1290</a>	501.2546	1000.4947	1000.4938	0.91	0	(24)	0.047	1	U	Y.TNAN
<a href="#">1291</a>	501.2548	1000.4951	1000.4938	1.33	0	(23)	0.063	1	U	Y.TNAN
<a href="#">1371</a>	508.7846	1015.5545	1015.5550	-0.41	1	(47)	0.00033	1	U	L.TINN
<a href="#">1372</a>	508.7846	1015.5547	1015.5550	-0.23	1	(42)	0.00099	1	U	L.TINN
<a href="#">1373</a>	508.7847	1015.5548	1015.5550	-0.17	1	(45)	0.00052	1	U	L.TINN
<a href="#">1374</a>	508.7848	1015.5550	1015.5550	0.01	1	(53)	8.4e-05	1	U	L.TINN
<a href="#">1375</a>	508.7853	1015.5560	1015.5550	1.03	1	(39)	0.0018	1	U	L.TINN
<a href="#">1377</a>	508.7860	1015.5575	1015.5550	2.47	1	56	3.8e-05	1	U	L.TINN
<a href="#">1481</a>	515.2953	1028.5760	1028.5767	-0.66	1	26	0.025	1	U	Y.ARVV
<a href="#">1482</a>	515.2962	1028.5778	1028.5767	1.11	1	(21)	0.087	1	U	Y.ARVV
<a href="#">1483</a>	515.2964	1028.5782	1028.5767	1.48	1	(25)	0.035	1	U	Y.ARVV
<a href="#">1486</a>	515.7871	1029.5595	1029.5607	-1.13	1	(26)	0.041	1	U	Y.ARVV
<a href="#">1487</a>	515.7876	1029.5606	1029.5607	-0.07	1	(24)	0.063	1	U	Y.ARVV
<a href="#">1581</a>	527.2910	1052.5675	1052.5689	-1.31	0	23	0.041	1	U	-.CGVP
<a href="#">2072</a>	561.7925	1121.5704	1121.5717	-1.15	1	(23)	0.11	1	U	W.QVSL
<a href="#">2073</a>	561.7925	1121.5705	1121.5717	-1.05	1	(57)	4.7e-05	1	U	W.QVSL
<a href="#">2077</a>	561.7927	1121.5709	1121.5717	-0.72	1	(29)	0.023	1	U	W.QVSL
<a href="#">2078</a>	561.7928	1121.5710	1121.5717	-0.60	1	(54)	7.6e-05	1	U	W.QVSL
<a href="#">2079</a>	561.7929	1121.5713	1121.5717	-0.39	1	(26)	0.05	1	U	W.QVSL
<a href="#">2080</a>	561.7929	1121.5713	1121.5717	-0.39	1	(31)	0.017	1	U	W.QVSL
<a href="#">2081</a>	561.7931	1121.5716	1121.5717	-0.07	1	(27)	0.037	1	U	W.QVSL
<a href="#">2083</a>	561.7932	1121.5719	1121.5717	0.15	1	(47)	0.00039	1	U	W.QVSL
<a href="#">2084</a>	561.7932	1121.5719	1121.5717	0.15	1	(61)	1.6e-05	1	U	W.QVSL
<a href="#">2085</a>	561.7933	1121.5720	1121.5717	0.26	1	(25)	0.062	1	U	W.QVSL
<a href="#">2086</a>	561.7933	1121.5721	1121.5717	0.36	1	(36)	0.0056	1	U	W.QVSL
<a href="#">2087</a>	561.7934	1121.5722	1121.5717	0.49	1	(22)	0.13	1	U	W.QVSL
<a href="#">2092</a>	561.7937	1121.5728	1121.5717	1.02	1	(56)	4.7e-05	1	U	W.QVSL
<a href="#">2096</a>	561.7941	1121.5737	1121.5717	1.79	1	(25)	0.072	1	U	W.QVSL
<a href="#">2097</a>	561.7942	1121.5738	1121.5717	1.90	1	(57)	4.4e-05	1	U	W.QVSL
<a href="#">2102</a>	561.7945	1121.5744	1121.5717	2.43	1	70	2.1e-06	1	U	W.QVSL
<a href="#">2104</a>	561.7951	1121.5756	1121.5717	3.52	1	(42)	0.0013	1	U	W.QVSL
<a href="#">2151</a>	564.2790	1126.5435	1126.5441	-0.46	1	(21)	0.1	1	U	L.LSNT



<a href="#">2152</a>	564.2797	1126.5448	1126.5441	0.62	1	36	0.0033	1	U	L.LSNT
<a href="#">2153</a>	564.2801	1126.5456	1126.5441	1.39	1	(36)	0.0037	1	U	L.LSNT
<a href="#">2332</a>	575.2536	1148.4926	1148.4921	0.52	1	(36)	0.0024	1	U	F.CGGS
<a href="#">2333</a>	575.2548	1148.4951	1148.4921	2.65	1	36	0.002	1	U	F.CGGS
<a href="#">2841</a>	609.3220	1216.6294	1216.6299	-0.45	1	(34)	0.0079	1	U	Y.NSLT
<a href="#">2842</a>	609.3238	1216.6330	1216.6299	2.56	1	54	6.8e-05	1	U	Y.NSLT
<a href="#">3409</a>	652.2785	1302.5424	1302.5398	2.01	0	28	0.011	1	U	W.GSST
<a href="#">3410</a>	652.2793	1302.5440	1302.5398	3.24	0	(21)	0.053	1	U	W.GSST
<a href="#">3453</a>	655.8597	1309.7048	1309.7064	-1.23	1	23	0.059	1	U	-.CGVP
<a href="#">3507</a>	660.3424	1318.6701	1318.6728	-2.04	0	(36)	0.0055	1	U	F.DQGS
<a href="#">3508</a>	660.3434	1318.6723	1318.6728	-0.39	0	(52)	0.00013	1	U	F.DQGS
<a href="#">3509</a>	660.3437	1318.6728	1318.6728	-0.01	0	(51)	0.00017	1	U	F.DQGS
<a href="#">3510</a>	660.3441	1318.6736	1318.6728	0.56	0	(44)	0.00075	1	U	F.DQGS
<a href="#">3511</a>	440.5652	1318.6737	1318.6728	0.62	0	(20)	0.17	1	U	F.DQGS
<a href="#">3513</a>	440.5652	1318.6739	1318.6728	0.82	0	(22)	0.11	1	U	F.DQGS
<a href="#">3514</a>	660.3444	1318.6743	1318.6728	1.10	0	(30)	0.022	1	U	F.DQGS
<a href="#">3515</a>	440.5655	1318.6747	1318.6728	1.44	0	(24)	0.074	1	U	F.DQGS
<a href="#">3517</a>	660.3447	1318.6748	1318.6728	1.48	0	(46)	0.0005	1	U	F.DQGS
<a href="#">3518</a>	660.3453	1318.6760	1318.6728	2.41	0	(53)	9.7e-05	1	U	F.DQGS
<a href="#">3519</a>	660.3455	1318.6764	1318.6728	2.68	0	62	1.1e-05	1	U	F.DQGS
<a href="#">3525</a>	660.8351	1319.6556	1319.6568	-0.94	0	(58)	3.8e-05	1	U	F.DQGS
<a href="#">3526</a>	440.8927	1319.6563	1319.6568	-0.43	0	(25)	0.07	1	U	F.DQGS
<a href="#">3527</a>	660.8364	1319.6582	1319.6568	1.00	0	(60)	2.1e-05	1	U	F.DQGS
<a href="#">3595</a>	665.8646	1329.7146	1329.7140	0.45	2	43	0.00081	1	U	Y.NSLT
<a href="#">3596</a>	665.8660	1329.7175	1329.7140	2.66	2	(31)	0.012	1	U	Y.NSLT
<a href="#">4081</a>	717.3149	1432.6153	1432.6194	-2.83	2	(42)	0.00057	1	U	F.HFCG
<a href="#">4082</a>	717.3172	1432.6198	1432.6194	0.32	2	47	0.0002	1	U	F.HFCG
<a href="#">4085</a>	717.8151	1433.6156	1433.6034	8.55	2	(32)	0.0061	1	U	F.HFCG
<a href="#">5180</a>	842.3804	1682.7462	1682.7458	0.24	0	81	1.3e-07	1	U	F.SQTV
<a href="#">5181</a>	842.3827	1682.7509	1682.7458	3.07	0	(75)	4.7e-07	1	U	F.SQTV
<a href="#">5335</a>	869.9573	1737.9001	1737.9009	-0.47	1	(27)	0.036	1	U	Y.TNAN
<a href="#">5336</a>	869.9574	1737.9002	1737.9009	-0.40	1	(28)	0.028	1	U	Y.TNAN
<a href="#">5340</a>	869.9578	1737.9010	1737.9009	0.02	1	(42)	0.00096	1	U	Y.TNAN
<a href="#">5342</a>	869.9583	1737.9019	1737.9009	0.58	1	(36)	0.0039	1	U	Y.TNAN
<a href="#">5343</a>	869.9587	1737.9028	1737.9009	1.07	1	(34)	0.007	1	U	Y.TNAN
<a href="#">5348</a>	869.9609	1737.9072	1737.9009	3.61	1	(30)	0.013	1	U	Y.TNAN
<a href="#">5349</a>	869.9611	1737.9076	1737.9009	3.81	1	50	0.00015	1	U	Y.TNAN
<a href="#">5350</a>	869.9611	1737.9076	1737.9009	3.81	1	(44)	0.00057	1	U	Y.TNAN
<a href="#">5355</a>	869.9615	1737.9085	1737.9009	4.38	1	(29)	0.018	1	U	Y.TNAN
<a href="#">5356</a>	870.4542	1738.8939	1738.8849	5.14	1	(33)	0.0089	1	U	Y.TNAN
<a href="#">5357</a>	870.4543	1738.8940	1738.8849	5.21	1	(45)	0.00052	1	U	Y.TNAN
<a href="#">5513</a>	892.4426	1782.8707	1782.8689	1.00	0	(37)	0.0038	1	U	L.SRIV
<a href="#">5514</a>	892.4451	1782.8757	1782.8689	3.80	0	49	0.00029	1	U	L.SRIV
<a href="#">5669</a>	926.5005	1850.9864	1850.9850	0.77	2	(30)	0.013	1	U	Y.TNAN
<a href="#">5670</a>	926.5005	1850.9864	1850.9850	0.77	2	40	0.0011	1	U	Y.TNAN
<a href="#">5673</a>	926.9977	1851.9809	1851.9690	6.44	2	(22)	0.068	1	U	Y.TNAN
<a href="#">6035</a>	1009.9965	2017.9785	2017.9780	0.27	0	51	0.00019	1	U	W.VVTA
<a href="#">6036</a>	1009.9976	2017.9806	2017.9780	1.30	0	(38)	0.0039	1	U	W.VVTA

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

[1::sp|cRAP023|P00767|CTRB\\_BOVIN](#) Mass: 26309 Score: 96 Matches: 4(3) Sequences: 4

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

5. [2::sp|P0A9P0|DLDH\\_ECOLI](#) Mass: 50942 Score: 685 Matches: 43(40) Sequences: 43

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

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1082</a>	486.2979	970.5813	970.5811	0.17	0	25	0.015	1	U	W.KEKVI
<a href="#">1083</a>	486.2980	970.5814	970.5811	0.30	0	(24)	0.019	1	U	W.KEKVI
<a href="#">2531</a>	586.3303	1170.6460	1170.6431	2.48	1	27	0.024	1	U	L.NVGC
<a href="#">2577</a>	589.8242	1177.6338	1177.6343	-0.43	1	(49)	0.00017	1	U	L.GLETV
<a href="#">2578</a>	589.8247	1177.6349	1177.6343	0.50	1	56	3.1e-05	1	U	L.GLETV
<a href="#">2839</a>	608.8607	1215.7068	1215.7075	-0.57	0	30	0.0066	1	U	M.STEIK
<a href="#">2840</a>	608.8609	1215.7072	1215.7075	-0.17	0	(30)	0.007	1	U	M.STEIK
<a href="#">2977</a>	619.3704	1236.7263	1236.7302	-3.20	0	(35)	0.00067	1	U	L.VAIGR
<a href="#">2978</a>	619.3733	1236.7320	1236.7302	1.45	0	52	1.3e-05	1	U	L.VAIGR
<a href="#">2986</a>	619.8638	1237.7131	1237.7142	-0.92	0	(33)	0.0015	1	U	L.VAIGR
<a href="#">2989</a>	619.8659	1237.7173	1237.7142	2.44	0	(39)	0.0004	1	U	L.VAIGR
<a href="#">3044</a>	625.3441	1248.6737	1248.6754	-1.38	1	37	0.0029	1	U	Y.FDPKV
<a href="#">3045</a>	625.3444	1248.6743	1248.6754	-0.90	1	(22)	0.078	1	U	Y.FDPKV
<a href="#">4093</a>	479.2320	1434.6741	1434.6739	0.14	0	(33)	0.011	1	U	L.DAGKA
<a href="#">4094</a>	718.3445	1434.6744	1434.6739	0.33	0	(56)	6.1e-05	1	U	L.DAGKA
<a href="#">4095</a>	479.2321	1434.6746	1434.6739	0.48	0	(28)	0.034	1	U	L.DAGKA
<a href="#">4096</a>	718.3450	1434.6754	1434.6739	1.01	0	65	7.3e-06	1	U	L.DAGKA
<a href="#">4097</a>	718.3564	1434.6983	1434.6991	-0.50	0	(35)	0.0075	1	U	L.EVEGE
<a href="#">4098</a>	718.3567	1434.6988	1434.6739	17.4	0	(44)	0.0011	1	U	L.DAGKA
<a href="#">4099</a>	718.3569	1434.6992	1434.6991	0.09	0	(38)	0.0043	1	U	L.EVEGE
<a href="#">4100</a>	718.8489	1435.6833	1435.6831	0.18	0	39	0.0027	1	U	L.EVEGE
<a href="#">4101</a>	718.8499	1435.6853	1435.6831	1.53	0	(27)	0.049	1	U	L.EVEGE
<a href="#">4228</a>	731.3554	1460.6963	1460.6970	-0.48	1	59	2.6e-05	1	U	Y.HALGS
<a href="#">4229</a>	731.3557	1460.6969	1460.6970	-0.07	1	(53)	9.9e-05	1	U	Y.HALGS
<a href="#">4475</a>	764.8727	1527.7309	1527.7313	-0.26	1	(20)	0.17	1	U	L.VMGGG
<a href="#">4476</a>	764.8731	1527.7315	1527.7313	0.15	1	33	0.0098	1	U	L.VMGGG
<a href="#">4608</a>	779.9174	1557.8203	1557.8151	3.33	0	(38)	0.0028	1	U	F.GEPKT
<a href="#">4609</a>	779.9179	1557.8211	1557.8151	3.89	0	48	0.00026	1	U	F.GEPKT
<a href="#">4993</a>	821.4162	1640.8178	1640.8154	1.50	2	22	0.15	1	U	L.LVMGG
<a href="#">5027</a>	826.4476	1650.8807	1650.8828	-1.28	1	(36)	0.0029	1	U	W.VGLTE
<a href="#">5029</a>	551.3013	1650.8820	1650.8828	-0.50	1	38	0.0019	1	U	W.VGLTE
<a href="#">5031</a>	551.3018	1650.8835	1650.8828	0.39	1	(38)	0.0021	1	U	W.VGLTE
<a href="#">5032</a>	826.4508	1650.8871	1650.8828	2.58	1	(30)	0.013	1	U	W.VGLTE
<a href="#">5033</a>	826.4528	1650.8910	1650.8828	4.94	1	(32)	0.0068	1	U	W.VGLTE
<a href="#">5059</a>	553.3098	1656.9076	1656.9087	-0.65	0	(25)	0.043	1	U	F.DQVIP
<a href="#">5060</a>	553.3102	1656.9087	1656.9087	0.02	0	(29)	0.016	1	U	F.DQVIP
<a href="#">5061</a>	829.4625	1656.9104	1656.9087	1.02	0	59	1.6e-05	1	U	F.DQVIP
<a href="#">5062</a>	829.4631	1656.9117	1656.9087	1.83	0	(46)	0.00031	1	U	F.DQVIP
<a href="#">5280</a>	574.2945	1719.8616	1719.8614	0.16	0	41	0.0021	1	U	Y.VTMEG
<a href="#">5281</a>	574.2954	1719.8644	1719.8614	1.76	0	(28)	0.036	1	U	Y.VTMEG
<a href="#">5998</a>	996.9974	1991.9802	1991.9800	0.11	1	(50)	0.00028	1	U	F.TGANT
<a href="#">5999</a>	996.9976	1991.9806	1991.9800	0.29	1	63	1.4e-05	1	U	F.TGANT
<a href="#">6003</a>	997.4905	1992.9664	1992.9640	1.21	1	(37)	0.0048	1	U	F.TGANT

6. [2::sp|P00350|6PGD\\_ECOLI](#) Mass: 51563 Score: 668 Matches: 30(28) Sequences:  
 6-phosphogluconate dehydrogenase, decarboxylating OS=Escherichia coli (strain K12) C  
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">536</a>	430.6995	859.3845	859.3824	2.39	0	(20)	0.082	1	U	Y.IGADG

<u>537</u>	430.6997	859.3847	859.3824	2.70	0	25	0.029	1	U	Y.IGADG
<u>768</u>	462.7851	923.5556	923.5552	0.37	0	(29)	0.0024	1	U	Y.RAAVL
<u>769</u>	462.7853	923.5561	923.5552	0.92	0	35	0.00062	1	U	Y.RAAVL
<u>842</u>	471.7678	941.5211	941.5222	-1.18	2	28	0.013	1	U	L.YLGKI
<u>909</u>	476.2605	950.5065	950.5073	-0.81	1	(35)	0.0031	1	U	F.LQKIT
<u>910</u>	476.2611	950.5076	950.5073	0.35	1	35	0.0029	1	U	F.LQKIT
<u>1065</u>	485.2530	968.4915	968.4927	-1.23	0	(35)	0.0032	1	U	Y.AENPO
<u>1066</u>	485.2533	968.4920	968.4927	-0.65	0	38	0.0015	1	U	Y.AENPO
<u>1273</u>	500.2421	998.4696	998.4709	-1.25	1	51	8.9e-05	1	U	Y.FKQIA
<u>1274</u>	500.2434	998.4723	998.4709	1.37	1	(44)	0.00045	1	U	Y.FKQIA
<u>1421</u>	511.7666	1021.5186	1021.5192	-0.62	1	(28)	0.032	1	U	L.ALNIE
<u>1422</u>	511.7668	1021.5191	1021.5192	-0.08	1	33	0.011	1	U	L.ALNIE
<u>1726</u>	539.3137	1076.6129	1076.6118	1.05	1	29	0.011	1	U	Y.LIDIT
<u>1750</u>	541.7966	1081.5786	1081.5767	1.71	1	30	0.0092	1	U	Y.AENPO
<u>1751</u>	541.7967	1081.5788	1081.5767	1.93	1	(29)	0.01	1	U	Y.AENPO
<u>2298</u>	572.3066	1142.5986	1142.5972	1.25	0	20	0.13	1	U	Y.AVQNG
<u>3308</u>	646.8294	1291.6443	1291.6408	2.68	1	44	0.00088	1	U	F.KQIAD
<u>3309</u>	646.8296	1291.6446	1291.6408	2.96	1	(36)	0.0054	1	U	F.KQIAD
<u>4292</u>	739.3803	1476.7461	1476.7460	0.02	1	(50)	0.00023	1	U	Y.LDKGD
<u>4293</u>	739.3809	1476.7472	1476.7460	0.77	1	(55)	7.8e-05	1	U	Y.LDKGD
<u>4294</u>	739.3810	1476.7474	1476.7460	0.93	1	80	2.6e-07	1	U	Y.LDKGD
<u>4295</u>	493.5813	1477.7222	1477.7235	-0.90	0	26	0.054	1	U	L.KGPSI
<u>4296</u>	493.5818	1477.7235	1477.7235	-0.03	0	(26)	0.06	1	U	L.KGPSI
<u>5609</u>	610.3319	1827.9739	1827.9731	0.46	2	(32)	0.01	1	U	Y.LVDVI
<u>5610</u>	914.9959	1827.9771	1827.9731	2.24	2	(55)	5.2e-05	1	U	Y.LVDVI
<u>5611</u>	914.9966	1827.9787	1827.9731	3.10	2	67	3.3e-06	1	U	Y.LVDVI
<u>6507</u>	869.4322	2605.2747	2605.2694	2.06	1	63	1.1e-05	1	U	F.IGTGV
<u>6684</u>	956.4650	2866.3733	2866.3807	-2.60	2	(27)	0.039	1	U	F.NFIGT
<u>6685</u>	956.4669	2866.3789	2866.3807	-0.62	2	69	2.6e-06	1	U	F.NFIGT

7. [2::sp|P0AFG6|ODO2\\_ECOLI](#) Mass: 43984 Score: 566 Matches: 34(31) Sequences:  
 Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase  
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<u>329</u>	408.2652	814.5158	814.5164	-0.74	1	31	0.003	1	U	F.LVTIK
<u>330</u>	408.2654	814.5163	814.5164	-0.07	1	(23)	0.018	1	U	F.LVTIK
<u>397</u>	414.7629	827.5113	827.5116	-0.45	0	52	3.2e-05	1	U	Y.VKAVV
<u>398</u>	414.7630	827.5115	827.5116	-0.16	0	(48)	8.5e-05	1	U	Y.VKAVV
<u>1212</u>	496.2937	990.5728	990.5750	-2.14	1	34	0.0034	1	U	F.YVKAV
<u>1213</u>	496.2940	990.5734	990.5750	-1.57	1	(31)	0.0063	1	U	F.YVKAV
<u>1214</u>	496.2943	990.5740	990.5750	-0.97	1	(31)	0.0057	1	U	F.YVKAV
<u>1572</u>	526.7478	1051.4810	1051.4822	-1.12	1	(46)	0.00039	1	U	L.TVEDL
<u>1573</u>	526.7479	1051.4813	1051.4822	-0.89	1	58	2.4e-05	1	U	L.TVEDL
<u>1842</u>	547.2805	1092.5465	1092.5485	-1.82	1	(42)	0.0013	1	U	L.LEAKN
<u>1843</u>	547.2820	1092.5494	1092.5485	0.85	1	44	0.00086	1	U	L.LEAKN
<u>2897</u>	614.3505	1226.6864	1226.6871	-0.57	1	(29)	0.013	1	U	L.VTPVL
<u>2898</u>	614.3520	1226.6895	1226.6871	2.02	1	38	0.0014	1	U	L.VTPVL
<u>3388</u>	434.5768	1300.7087	1300.7099	-0.94	0	(35)	0.0054	1	U	L.DASAI
<u>3389</u>	434.5771	1300.7094	1300.7099	-0.36	0	(24)	0.066	1	U	L.DASAI
<u>3390</u>	651.3633	1300.7121	1300.7099	1.70	0	(46)	0.00038	1	U	L.DASAI
<u>3391</u>	651.3638	1300.7131	1300.7099	2.45	0	63	6.8e-06	1	U	L.DASAI
<u>3412</u>	652.3229	1302.6313	1302.6312	0.13	0	(51)	0.00016	1	U	F.NEVNM
<u>3413</u>	652.3243	1302.6341	1302.6312	2.27	0	58	3.3e-05	1	U	F.NEVNM

<a href="#">3502</a>	660.3185	1318.6225	1318.6261	-2.70	0	(30)	0.019	1	U	F.NEVNM
<a href="#">3503</a>	660.3207	1318.6268	1318.6261	0.55	0	(38)	0.003	1	U	F.NEVNM
<a href="#">3504</a>	660.3214	1318.6283	1318.6261	1.66	0	(30)	0.019	1	U	F.NEVNM
<a href="#">3619</a>	668.3174	1334.6203	1334.6210	-0.51	0	(35)	0.0054	1	U	F.NEVNM
<a href="#">3620</a>	668.3178	1334.6211	1334.6210	0.05	0	(45)	0.00066	1	U	F.NEVNM
<a href="#">3873</a>	695.8837	1389.7528	1389.7537	-0.66	0	(25)	0.047	1	U	L.GMADI
<a href="#">3874</a>	695.8845	1389.7545	1389.7537	0.56	0	25	0.04	1	U	L.GMADI
<a href="#">4374</a>	500.9237	1499.7493	1499.7481	0.81	1	23	0.097	1	U	Y.DHRLI
<a href="#">5412</a>	877.9722	1753.9298	1753.9284	0.79	1	26	0.032	1	U	F.GSLMS
<a href="#">5876</a>	970.4739	1938.9332	1938.9323	0.46	0	(44)	0.0011	1	U	L.KRYPE
<a href="#">5877</a>	970.4765	1938.9384	1938.9323	3.16	0	67	4.6e-06	1	U	L.KRYPE
<a href="#">5966</a>	495.5218	1978.0581	1978.0596	-0.77	2	(22)	0.078	1	U	L.LAEHN
<a href="#">5967</a>	495.5221	1978.0591	1978.0596	-0.22	2	(25)	0.04	1	U	L.LAEHN
<a href="#">5968</a>	660.3613	1978.0622	1978.0596	1.31	2	(41)	0.0011	1	U	L.LAEHN
<a href="#">5969</a>	660.3631	1978.0675	1978.0596	3.99	2	55	3.1e-05	1	U	L.LAEHN

8. [2::sp|P0AE06|ACRA\\_ECOLI](#) Mass: 42228 Score: 521 Matches: 27 (23) 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	Peptide
<a href="#">59</a>	384.1998	766.3850	766.3861	-1.36	0	20	0.094	1	U	Y.ISKQE
<a href="#">903</a>	475.7690	949.5235	949.5233	0.27	2	27	0.017	1	U	Y.QKLLG
<a href="#">1097</a>	487.2689	972.5232	972.5240	-0.84	1	37	0.003	1	U	L.KQELA
<a href="#">1098</a>	487.2693	972.5241	972.5240	0.10	1	(36)	0.0038	1	U	L.KQELA
<a href="#">1109</a>	487.7621	973.5097	973.5080	1.74	1	(29)	0.024	1	U	L.KQELA
<a href="#">1110</a>	487.7625	973.5104	973.5080	2.48	1	(35)	0.0063	1	U	L.KQELA
<a href="#">2021</a>	557.8325	1113.6505	1113.6506	-0.10	0	(43)	0.00044	1	U	L.KAGDR
<a href="#">2022</a>	557.8336	1113.6526	1113.6506	1.76	0	45	0.00029	1	U	L.KAGDR
<a href="#">2735</a>	602.8060	1203.5974	1203.5983	-0.74	0	(25)	0.065	1	U	F.KEGSD
<a href="#">2736</a>	602.8065	1203.5985	1203.5983	0.17	0	40	0.0024	1	U	F.KEGSD
<a href="#">3016</a>	622.3558	1242.6971	1242.6932	3.18	2	21	0.087	1	U	L.RLKQE
<a href="#">3763</a>	684.3368	1366.6590	1366.6616	-1.89	1	(30)	0.02	1	U	F.KEGSD
<a href="#">3764</a>	684.3384	1366.6623	1366.6616	0.53	1	(48)	0.00037	1	U	F.KEGSD
<a href="#">3765</a>	684.3392	1366.6639	1366.6616	1.68	1	(27)	0.046	1	U	F.KEGSD
<a href="#">3766</a>	684.3395	1366.6644	1366.6616	2.05	1	(26)	0.058	1	U	F.KEGSD
<a href="#">3767</a>	684.3400	1366.6654	1366.6616	2.77	1	48	0.00035	1	U	F.KEGSD
<a href="#">4104</a>	718.8731	1435.7317	1435.7307	0.68	0	30	0.022	1	U	L.QITTE
<a href="#">4335</a>	746.3887	1490.7628	1490.7617	0.74	0	60	2.2e-05	1	U	L.ITSDG
<a href="#">4336</a>	746.3896	1490.7647	1490.7617	2.05	0	(40)	0.0023	1	U	L.ITSDG
<a href="#">4583</a>	775.9728	1549.9310	1549.9304	0.40	0	38	0.0002	1	U	Y.RIAEV
<a href="#">4585</a>	775.9731	1549.9317	1549.9304	0.86	0	(38)	0.00021	1	U	Y.RIAEV
<a href="#">5456</a>	884.4467	1766.8789	1766.8727	3.50	1	69	2.7e-06	1	U	L.ITSDG
<a href="#">5457</a>	884.4473	1766.8801	1766.8727	4.19	1	(43)	0.0011	1	U	L.ITSDG
<a href="#">5689</a>	928.4967	1854.9788	1854.9799	-0.56	1	47	0.00032	1	U	Y.DSAKG
<a href="#">5690</a>	928.4977	1854.9809	1854.9799	0.56	1	(42)	0.00083	1	U	Y.DSAKG
<a href="#">6448</a>	818.7730	2453.2972	2453.2914	2.35	0	41	0.001	1	U	L.VVGAD
<a href="#">6449</a>	818.7730	2453.2972	2453.2914	2.35	0	(38)	0.0018	1	U	L.VVGAD

9. [2::sp|P0CE47|EFTU1\\_ECOLI](#) Mass: 43427 Score: 491 Matches: 33 (27) Sequences:  
 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="#">880</a>	473.2685	944.5225	944.5219	0.64	1	52	9e-05	1	U	F.LLPPIE
<a href="#">881</a>	473.2686	944.5225	944.5219	0.71	1	(39)	0.0019	1	U	F.LLPPIE
<a href="#">1392</a>	509.7456	1017.4767	1017.4767	-0.03	1	33	0.0084	1	U	L.KALEG
<a href="#">1393</a>	509.7460	1017.4774	1017.4767	0.68	1	(31)	0.011	1	U	L.KALEG
<a href="#">1744</a>	541.2708	1080.5271	1080.5274	-0.28	0	39	0.0023	1	U	L.IHPIA
<a href="#">1859</a>	549.2701	1096.5257	1096.5223	3.13	0	(34)	0.0061	1	U	L.IHPIA
<a href="#">1860</a>	549.2701	1096.5257	1096.5223	3.13	0	(35)	0.0044	1	U	L.IHPIA
<a href="#">2999</a>	621.2532	1240.4919	1240.4931	-0.99	0	22	0.036	1	U	Y.AHVDC
<a href="#">3024</a>	623.8218	1245.6290	1245.6275	1.25	1	40	0.0019	1	U	L.ELVEM
<a href="#">3025</a>	623.8232	1245.6319	1245.6275	3.59	1	(26)	0.051	1	U	L.ELVEM
<a href="#">3124</a>	631.8182	1261.6218	1261.6224	-0.45	1	(37)	0.0041	1	U	L.ELVEM
<a href="#">3125</a>	631.8187	1261.6229	1261.6224	0.42	1	(27)	0.041	1	U	L.ELVEM
<a href="#">3580</a>	664.8433	1327.6720	1327.6732	-0.92	1	(39)	0.002	1	U	L.LDEGR
<a href="#">3581</a>	664.8437	1327.6728	1327.6732	-0.27	1	57	3.3e-05	1	U	L.LDEGR
<a href="#">3814</a>	688.3604	1374.7063	1374.7064	-0.12	2	(22)	0.12	1	U	L.ELVEM
<a href="#">3815</a>	688.3638	1374.7131	1374.7064	4.85	2	25	0.063	1	U	L.ELVEM
<a href="#">4129</a>	721.3876	1440.7607	1440.7572	2.40	2	38	0.002	1	U	L.LDEGR
<a href="#">4130</a>	721.3876	1440.7607	1440.7572	2.40	2	(33)	0.0066	1	U	L.LDEGR
<a href="#">4612</a>	780.3899	1558.7653	1558.7628	1.66	0	(28)	0.034	1	U	Y.DFPGD
<a href="#">4613</a>	780.3903	1558.7660	1558.7628	2.06	0	(30)	0.02	1	U	Y.DFPGD
<a href="#">4614</a>	780.3904	1558.7662	1558.7628	2.21	0	52	0.00012	1	U	Y.DFPGD
<a href="#">4615</a>	780.3906	1558.7666	1558.7628	2.45	0	(44)	0.00078	1	U	Y.DFPGD
<a href="#">4815</a>	797.3597	1592.7048	1592.7062	-0.87	2	(48)	0.00024	1	U	F.LNKCD
<a href="#">4816</a>	797.3612	1592.7079	1592.7062	1.05	2	(41)	0.0013	1	U	F.LNKCD
<a href="#">4878</a>	805.3588	1608.7031	1608.7011	1.24	2	(25)	0.037	1	U	F.LNKCD
<a href="#">4879</a>	805.3603	1608.7060	1608.7011	3.06	2	49	0.00016	1	U	F.LNKCD
<a href="#">5014</a>	824.9242	1647.8338	1647.8324	0.87	0	(20)	0.23	1	U	Y.VKNMI
<a href="#">5015</a>	824.9270	1647.8394	1647.8324	4.28	0	(36)	0.0068	1	U	Y.VKNMI
<a href="#">5102</a>	832.9210	1663.8274	1663.8273	0.03	0	(24)	0.099	1	U	Y.VKNMI
<a href="#">5103</a>	832.9233	1663.8320	1663.8273	2.82	0	42	0.0017	1	U	Y.VKNMI
<a href="#">5494</a>	888.9423	1775.8701	1775.8730	-1.63	1	23	0.12	1	U	L.DSYIP
<a href="#">5778</a>	630.6605	1888.9597	1888.9570	1.42	2	27	0.043	1	U	F.LDSYI
<a href="#">5779</a>	945.4902	1888.9658	1888.9570	4.63	2	(21)	0.18	1	U	F.LDSYI

Proteins matching the same set of peptides:

[2::sp|P0CE48|EFTU2\\_ECOLI](#) Mass: 43457 Score: 491 Matches: 33(27) Sequences: 1  
Elongation factor Tu 2 OS=Escherichia coli (strain K12) OX=83333 GN=tufB PE=1 SV=1

10. [2::sp|P0A6P9|ENO\\_ECOLI](#) Mass: 45683 Score: 403 Matches: 21(20) Sequences: 1  
Enolase OS=Escherichia coli (strain K12) OX=83333 GN=eno PE=1 SV=2  
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1302</a>	503.2719	1004.5292	1004.5291	0.12	1	41	0.0012	1	U	Y.VLAGE
<a href="#">1303</a>	503.2721	1004.5296	1004.5291	0.54	1	(38)	0.0024	1	U	Y.VLAGE
<a href="#">1711</a>	538.2848	1074.5550	1074.5557	-0.62	1	56	4.3e-05	1	U	F.NQIGS
<a href="#">1712</a>	538.2848	1074.5550	1074.5557	-0.62	1	(48)	0.0003	1	U	F.NQIGS
<a href="#">2371</a>	577.7965	1153.5783	1153.5801	-1.53	0	50	0.00014	1	U	L.AAIKM
<a href="#">2374</a>	577.7982	1153.5819	1153.5801	1.54	0	(29)	0.017	1	U	L.AAIKM
<a href="#">2451</a>	581.8297	1161.6449	1161.6393	4.76	0	49	0.00013	1	U	L.AVIAE
<a href="#">2452</a>	581.8299	1161.6452	1161.6393	5.08	0	(44)	0.00041	1	U	L.AVIAE

<a href="#">3520</a>	660.3458	1318.6770	1318.6769	0.06	2	37	0.0037	1	U	L.GDKIQ
<a href="#">3521</a>	660.3459	1318.6772	1318.6769	0.25	2	(36)	0.005	1	U	L.GDKIQ
<a href="#">4320</a>	496.9413	1487.8020	1487.7983	2.47	1	38	0.0027	1	U	L.IRIEE
<a href="#">4321</a>	496.9414	1487.8024	1487.7983	2.73	1	(30)	0.018	1	U	L.IRIEE
<a href="#">4408</a>	757.3532	1512.6919	1512.6879	2.66	0	29	0.022	1	U	L.KAKGM
<a href="#">5012</a>	824.9046	1647.7946	1647.7886	3.66	0	37	0.0048	1	U	F.VGMAA
<a href="#">5013</a>	824.9054	1647.7962	1647.7886	4.63	0	(34)	0.0091	1	U	F.VGMAA
<a href="#">5643</a>	922.4988	1842.9831	1842.9839	-0.42	2	(25)	0.048	1	U	Y.NQLIR
<a href="#">5644</a>	615.3364	1842.9873	1842.9839	1.82	2	(38)	0.0025	1	U	Y.NQLIR
<a href="#">5645</a>	922.5014	1842.9882	1842.9839	2.36	2	(30)	0.015	1	U	Y.NQLIR
<a href="#">5646</a>	615.3371	1842.9895	1842.9839	3.02	2	39	0.0018	1	U	Y.NQLIR
<a href="#">5764</a>	943.9308	1885.8471	1885.8438	1.80	2	25	0.054	1	U	Y.ELGKD
<a href="#">5765</a>	943.9334	1885.8523	1885.8438	4.52	2	(25)	0.062	1	U	Y.ELGKD

11. [2::sp|P0A6H5|HSLU\\_ECOLI](#) Mass: 49677 Score: 348 Matches: 19(15) Sequences:  
 ATP-dependent protease ATPase subunit HslU OS=Escherichia coli (strain K12) OX=83333  
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">418</a>	416.2395	830.4644	830.4650	-0.68	1	(41)	0.0009	1	U	L.AKLAN
<a href="#">419</a>	416.2397	830.4648	830.4650	-0.22	1	42	0.00089	1	U	L.AKLAN
<a href="#">802</a>	468.2820	934.5494	934.5488	0.70	0	37	0.00053	1	U	F.IKVEA
<a href="#">803</a>	468.2823	934.5501	934.5488	1.43	0	(33)	0.0014	1	U	F.IKVEA
<a href="#">1367</a>	508.2871	1014.5597	1014.5597	0.05	1	35	0.0041	1	U	L.LIEEE
<a href="#">1368</a>	508.2872	1014.5599	1014.5597	0.23	1	(35)	0.0044	1	U	L.LIEEE
<a href="#">1745</a>	541.2793	1080.5440	1080.5451	-1.01	1	(23)	0.086	1	U	L.TTSDF
<a href="#">1746</a>	541.2799	1080.5453	1080.5451	0.12	1	28	0.025	1	U	L.TTSDF
<a href="#">1973</a>	555.7613	1109.5080	1109.5063	1.56	0	31	0.012	1	U	L.MATEG
<a href="#">2138</a>	563.7573	1125.5001	1125.5012	-1.01	0	(24)	0.044	1	U	L.MATEG
<a href="#">2603</a>	593.2767	1184.5389	1184.5383	0.51	1	28	0.019	1	U	L.ERLME
<a href="#">2680</a>	598.7756	1195.5366	1195.5357	0.75	0	23	0.071	1	U	L.SGQNI
<a href="#">3583</a>	664.8614	1327.7083	1327.7095	-0.88	1	29	0.016	1	U	Y.RAEEL
<a href="#">3671</a>	675.8318	1349.6490	1349.6463	2.02	2	(31)	0.017	1	U	L.DALVA
<a href="#">3672</a>	675.8321	1349.6496	1349.6463	2.47	2	33	0.013	1	U	L.DALVA
<a href="#">3945</a>	703.8415	1405.6685	1405.6759	-5.21	0	25	0.07	1	U	M.SEMTP
<a href="#">3946</a>	703.8431	1405.6716	1405.6759	-3.03	0	(24)	0.11	1	U	M.SEMTP
<a href="#">5131</a>	835.4333	1668.8520	1668.8471	2.93	0	(29)	0.023	1	U	L.KQDAI
<a href="#">5132</a>	835.4340	1668.8534	1668.8471	3.73	0	35	0.0062	1	U	L.KQDAI

12. [2::sp|P0A6E4|ASSY\\_ECOLI](#) Mass: 50038 Score: 322 Matches: 14(14) Sequences:  
 Argininosuccinate synthase OS=Escherichia coli (strain K12) OX=83333 GN=argG 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="#">945</a>	478.2489	954.4832	954.4844	-1.23	0	25	0.033	1	U	Y.KMSVE
<a href="#">1279</a>	500.7568	999.4991	999.4985	0.55	0	(33)	0.0056	1	U	F.SPDDR
<a href="#">1280</a>	500.7569	999.4992	999.4985	0.73	0	35	0.0038	1	U	F.SPDDR
<a href="#">1819</a>	545.2936	1088.5727	1088.5713	1.28	1	27	0.033	1	U	Y.SILNT
<a href="#">2974</a>	619.3264	1236.6381	1236.6350	2.54	1	29	0.025	1	U	L.DITDT
<a href="#">3679</a>	676.2873	1350.5600	1350.5575	1.84	1	25	0.017	1	U	Y.TANLG
<a href="#">4012</a>	710.3247	1418.6349	1418.6314	2.46	0	(24)	0.054	3	U	L.TGIHN
<a href="#">4013</a>	710.3257	1418.6368	1418.6314	3.83	0	35	0.0052	1	U	L.TGIHN

<a href="#">5273</a>	573.6367	1717.8882	1717.8887	-0.29	0	(27)	0.042	1	U	W.DESVK
<a href="#">5274</a>	573.6375	1717.8907	1717.8887	1.19	0	32	0.013	1	U	W.DESVK
<a href="#">5804</a>	951.4644	1900.9142	1900.9126	0.81	1	63	1e-05	1	U	L.SSSAA
<a href="#">5805</a>	951.4678	1900.9211	1900.9126	4.46	1	(39)	0.0025	1	U	L.SSSAA
<a href="#">5812</a>	635.6633	1903.9680	1903.9680	0.01	1	52	0.00013	1	U	F.WDESV
<a href="#">5813</a>	635.6636	1903.9691	1903.9680	0.59	1	(46)	0.00056	1	U	F.WDESV

13. [2::sp|POA8M0|SYN\\_ECOLI](#) Mass: 52766 Score: 312 Matches: 12(10) 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="#">159</a>	396.2242	790.4337	790.4337	0.02	2	23	0.051	1	U	F.GLGFE
<a href="#">160</a>	396.2242	790.4339	790.4337	0.17	2	(21)	0.088	1	U	F.GLGFE
<a href="#">1456</a>	513.7475	1025.4804	1025.4818	-1.31	1	30	0.018	1	U	L.ERFIE
<a href="#">1457</a>	513.7482	1025.4819	1025.4818	0.11	1	(28)	0.024	1	U	L.ERFIE
<a href="#">2497</a>	584.7794	1167.5442	1167.5408	2.90	1	(33)	0.0089	1	U	L.TVSGQ
<a href="#">2498</a>	584.7796	1167.5446	1167.5408	3.31	1	47	0.0003	1	U	L.TVSGQ
<a href="#">3298</a>	646.2995	1290.5844	1290.5840	0.32	1	(55)	4.7e-05	1	U	W.GVDLS
<a href="#">3299</a>	646.3010	1290.5875	1290.5840	2.69	1	69	1.8e-06	1	U	W.GVDLS
<a href="#">3485</a>	658.8459	1315.6772	1315.6772	0.02	0	(68)	3.6e-06	1	U	F.EIQAS
<a href="#">3486</a>	658.8462	1315.6778	1315.6772	0.48	0	75	6.2e-07	1	U	F.EIQAS
<a href="#">3722</a>	453.5842	1357.7308	1357.7314	-0.43	0	22	0.1	1	U	F.AERVD
<a href="#">4648</a>	784.3923	1566.7700	1566.7712	-0.75	1	45	0.00073	1	U	F.KAVLE

14. [2::sp|P0AGD7|SRP54\\_ECOLI](#) Mass: 49812 Score: 214 Matches: 10(8) Sequences: 7  
 Signal recognition particle protein OS=Escherichia coli (strain K12) OX=83333 GN=ffh  
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">470</a>	422.7476	843.4807	843.4814	-0.86	1	(22)	0.086	1	U	L.LVDTA
<a href="#">471</a>	422.7479	843.4812	843.4814	-0.29	1	22	0.079	1	U	L.LVDTA
<a href="#">1837</a>	546.8241	1091.6336	1091.6339	-0.21	1	50	4.3e-05	1	U	L.NLAAQ
<a href="#">1838</a>	546.8242	1091.6339	1091.6339	0.01	1	(36)	0.0012	1	U	L.NLAAQ
<a href="#">3656</a>	672.8617	1343.7088	1343.7085	0.24	0	(39)	0.0028	1	U	L.EADVA
<a href="#">3657</a>	672.8635	1343.7125	1343.7085	2.97	0	39	0.0024	1	U	L.EADVA
<a href="#">5294</a>	863.4111	1724.8077	1724.8040	2.18	0	64	8.9e-06	1	U	F.VVDAM
<a href="#">5295</a>	863.4114	1724.8083	1724.8040	2.54	0	(36)	0.0056	1	U	F.VVDAM
<a href="#">6059</a>	682.0363	2043.0871	2043.0847	1.17	1	(34)	0.0055	1	U	L.SLIED
<a href="#">6060</a>	682.0366	2043.0880	2043.0847	1.61	1	44	0.0006	1	U	L.SLIED

15. [2::sp|P0AGG8|TLDD\\_ECOLI](#) Mass: 51446 Score: 212 Matches: 7(6) Sequences: 4  
 Metalloprotease TldD OS=Escherichia coli (strain K12) OX=83333 GN=tldD PE=1 SV=1  
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1231</a>	497.2666	992.5186	992.5178	0.82	2	30	0.016	1	U	F.AYADQ
<a href="#">4060</a>	715.8495	1429.6844	1429.6837	0.48	2	(63)	1e-05	1	U	F.LADLD
<a href="#">4061</a>	715.8516	1429.6886	1429.6837	3.37	2	72	1.1e-06	1	U	F.LADLD
<a href="#">4821</a>	797.8966	1593.7785	1593.7787	-0.13	1	(66)	6.5e-06	1	U	Y.APNFG

<a href="#">4822</a>	797.8967	1593.7788	1593.7787	0.03	1	82	1.7e-07	1	U	Y.APNFG
<a href="#">5867</a>	968.9828	1935.9510	1935.9499	0.57	0	(23)	0.13	1	U	Y.MLPKG
<a href="#">5868</a>	968.9873	1935.9600	1935.9499	5.23	0	30	0.025	1	U	Y.MLPKG

16. [2::sp|P0A6F3|GLPK ECOLI](#) Mass: 56480 Score: 170 Matches: 10(6) Sequences: 5  
 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>	380.7189	759.4232	759.4239	-0.84	0	32	0.0087	1	U	Y.IRSNT
<a href="#">17</a>	380.7190	759.4234	759.4239	-0.69	0	(27)	0.024	1	U	Y.IRSNT
<a href="#">2668</a>	597.8116	1193.6087	1193.6040	3.94	0	40	0.0019	1	U	F.ATKVO
<a href="#">2669</a>	597.8120	1193.6093	1193.6040	4.44	0	(36)	0.0048	1	U	F.ATKVO
<a href="#">3623</a>	668.3361	1334.6577	1334.6579	-0.12	0	(21)	0.17	1	U	F.RPGIE
<a href="#">3624</a>	668.3365	1334.6585	1334.6579	0.52	0	28	0.037	1	U	F.RPGIE
<a href="#">3666</a>	674.3675	1346.7204	1346.7194	0.76	1	(23)	0.086	1	U	Y.IRSNT
<a href="#">3667</a>	674.3684	1346.7223	1346.7194	2.13	1	23	0.083	1	U	Y.IRSNT
<a href="#">5912</a>	654.3365	1959.9876	1959.9901	-1.27	2	48	0.00045	1	U	W.QNLDE
<a href="#">5914</a>	654.3367	1959.9882	1959.9901	-0.99	2	(27)	0.057	1	U	W.QNLDE

17. [2::sp|P0A8L1|SYS ECOLI](#) Mass: 48669 Score: 161 Matches: 8(8) Sequences: 4(4)  
 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="#">1432</a>	512.3076	1022.6006	1022.6012	-0.60	1	(36)	0.0008	1	U	Y.ALIPT
<a href="#">1433</a>	512.3080	1022.6015	1022.6012	0.34	1	50	3.5e-05	1	U	Y.ALIPT
<a href="#">3675</a>	675.8560	1349.6975	1349.6980	-0.36	2	(29)	0.025	1	U	Y.GTGQL
<a href="#">3676</a>	675.8572	1349.6999	1349.6980	1.45	2	32	0.01	1	U	Y.GTGQL
<a href="#">4186</a>	727.3859	1452.7572	1452.7572	-0.06	0	35	0.0046	1	U	Y.QQADG
<a href="#">4187</a>	727.3863	1452.7581	1452.7572	0.62	0	(26)	0.031	1	U	Y.QQADG
<a href="#">5083</a>	831.3745	1660.7345	1660.7329	0.97	1	(39)	0.0014	1	U	F.HTRPL
<a href="#">5084</a>	831.3762	1660.7378	1660.7329	2.95	1	44	0.00058	1	U	F.HTRPL

18. [1::sp|cRAP087|P02769|ALBU BOVIN](#) Mass: 71244 Score: 160 Matches: 7(6) Sequences: 5(5)  
 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="#">831</a>	470.7606	939.5066	939.5066	0.01	2	25	0.022	1	U	L.VLIAF
<a href="#">1130</a>	488.7825	975.5504	975.5501	0.25	1	21	0.068	1	U	F.QNALI
<a href="#">2585</a>	590.8279	1179.6412	1179.6400	1.00	2	(44)	0.00038	1	U	Y.GFQNA
<a href="#">2586</a>	590.8281	1179.6417	1179.6400	1.42	2	52	6.5e-05	1	U	Y.GFQNA
<a href="#">4778</a>	792.4559	1582.8973	1582.8930	2.71	2	(24)	0.029	1	U	F.AVEGP
<a href="#">4779</a>	792.4561	1582.8975	1582.8930	2.86	2	31	0.0059	1	U	F.AVEGP
<a href="#">5392</a>	584.3287	1749.9644	1749.9665	-1.21	1	32	0.0053	1	U	L.SQKFP

19. [2::sp|P0A7D4|PURA ECOLI](#) Mass: 47543 Score: 159 Matches: 7(5) Sequences: 5(5)



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="#">1090</a>	486.7903	971.5659	971.5651	0.83	0	24	0.038	1	U	L.VING
<a href="#">2909</a>	614.8628	1227.7111	1227.7074	3.02	2	21	0.062	1	U	L.DVLD
<a href="#">4264</a>	735.9189	1469.8233	1469.8202	2.15	0	35	0.0034	1	U	L.RENV
<a href="#">4569</a>	774.4029	1546.7912	1546.7913	-0.02	1	38	0.0033	1	U	Y.QKVL
<a href="#">4570</a>	774.4042	1546.7938	1546.7913	1.63	1	(31)	0.019	1	U	Y.QKVL
<a href="#">6116</a>	1037.4794	2072.9442	2072.9401	1.97	2	44	0.00066	1	U	W.KGVE
<a href="#">6117</a>	1037.4810	2072.9474	2072.9401	3.50	2	(25)	0.058	1	U	W.KGVE

20. [2::sp|P0A910|OMPA\\_ECOLI](#) Mass: 37292 Score: 158 Matches: 7(6) Sequences: 5(3)  
 Outer membrane protein A OS=Escherichia coli (strain K12) OX=83333 GN=ompA PE=1 SV=1  
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1762</a>	542.8217	1083.6288	1083.6288	-0.01	0	37	0.0015	1	U	Y.AITPEI
<a href="#">1764</a>	542.8227	1083.6308	1083.6288	1.89	0	(32)	0.0037	1	U	Y.AITPEI
<a href="#">3265</a>	642.8033	1283.5921	1283.5921	-0.02	1	27	0.034	1	U	L.GYPITD
<a href="#">3649</a>	671.8662	1341.7179	1341.7140	2.88	1	41	0.001	1	U	L.SNLDPK
<a href="#">5135</a>	835.9515	1669.8885	1669.8887	-0.09	2	33	0.0069	1	U	Y.SQLSNL
<a href="#">5136</a>	835.9535	1669.8925	1669.8887	2.32	2	(32)	0.0076	1	U	Y.SQLSNL
<a href="#">5408</a>	877.4171	1752.8197	1752.8179	0.98	1	23	0.13	1	U	F.INNNGP

21. [2::sp|P0AG30|RHO\\_ECOLI](#) Mass: 47032 Score: 138 Matches: 8(7) Sequences: 4(3)  
 Transcription termination factor Rho OS=Escherichia coli (strain K12) OX=83333 GN=rhoA 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="#">1761</a>	542.8213	1083.6280	1083.6288	-0.73	0	55	2.2e-05	1	U	Y.NTVVP
<a href="#">1763</a>	542.8220	1083.6295	1083.6288	0.62	0	(42)	0.00044	1	U	Y.NTVVP
<a href="#">2740</a>	603.2606	1204.5066	1204.5070	-0.40	1	23	0.038	1	U	L.AMTKT
<a href="#">5481</a>	888.4059	1774.7972	1774.7971	0.05	1	(26)	0.048	1	U	L.IDTGS
<a href="#">5482</a>	888.4087	1774.8028	1774.7971	3.22	1	(30)	0.017	1	U	L.IDTGS
<a href="#">5534</a>	896.4000	1790.7855	1790.7920	-3.66	1	(27)	0.028	1	U	L.IDTGS
<a href="#">5535</a>	896.4065	1790.7984	1790.7920	3.57	1	39	0.0019	1	U	L.IDTGS
<a href="#">5729</a>	625.3187	1872.9344	1872.9251	4.95	1	23	0.11	1	U	L.LIDER

22. [2::sp|P0C0V0|DEGP\\_ECOLI](#) Mass: 49438 Score: 124 Matches: 5(4) Sequences: 3(3)  
 Periplasmic serine endoprotease DegP OS=Escherichia coli (strain K12) OX=83333 GN=degP 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="#">3673</a>	675.8548	1349.6950	1349.6939	0.84	1	(27)	0.038	1	U	L.ALNIQ
<a href="#">3674</a>	675.8559	1349.6972	1349.6939	2.47	1	29	0.022	1	U	L.ALNIQ
<a href="#">3726</a>	680.3743	1358.7341	1358.7340	0.06	0	20	0.17	1	U	L.RAQVG
<a href="#">4458</a>	763.3819	1524.7492	1524.7494	-0.09	1	75	6.6e-07	1	U	F.MALGS
<a href="#">4459</a>	763.3824	1524.7503	1524.7494	0.63	1	(67)	4.1e-06	1	U	F.MALGS

23. [1::sp|cRAP039|P13645|K1C10 HUMAN](#) Mass: 59020 Score: 121 Matches: 6(5) 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="#">1238</a>	497.7633	993.5121	993.5131	-0.96	1	22	0.099	1	U	W.FNEKSK
<a href="#">3688</a>	677.7671	1353.5196	1353.5182	1.06	0	(30)	0.0017	1	U	Y.GGGSSS
<a href="#">3689</a>	677.7674	1353.5202	1353.5182	1.52	0	32	0.0013	1	U	Y.GGGSSS
<a href="#">4231</a>	731.3754	1460.7363	1460.7259	7.10	2	28	0.034	1	U	L.LQIDNA
<a href="#">4943</a>	813.8784	1625.7423	1625.7420	0.16	0	39	0.0026	1	U	L.TTEIDN
<a href="#">4944</a>	813.8808	1625.7470	1625.7420	3.08	0	(33)	0.012	1	U	L.TTEIDN

24. [2::sp|P0A825|GLYA ECOLI](#) Mass: 45459 Score: 116 Matches: 7(6) Sequences: 4  
 Serine hydroxymethyltransferase OS=Escherichia coli (strain K12) OX=83333 GN=glyA PE=1 SV=1  
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1474</a>	514.8030	1027.5915	1027.5914	0.17	2	26	0.023	1	U	F.LVDLVD
<a href="#">2158</a>	564.8108	1127.6071	1127.6074	-0.23	2	(21)	0.09	1	U	Y.TALLEP
<a href="#">2159</a>	564.8110	1127.6075	1127.6074	0.11	2	25	0.033	1	U	Y.TALLEP
<a href="#">2581</a>	590.3164	1178.6181	1178.6183	-0.10	2	(28)	0.024	1	U	L.ILAKGG
<a href="#">2582</a>	590.3173	1178.6201	1178.6183	1.54	2	36	0.0047	1	U	L.ILAKGG
<a href="#">3202</a>	637.3296	1272.6446	1272.6463	-1.29	1	(28)	0.03	1	U	Y.KVVS GG
<a href="#">3203</a>	637.3306	1272.6467	1272.6463	0.34	1	28	0.029	1	U	Y.KVVS GG

25. [2::sp|P25553|ALDA ECOLI](#) Mass: 52411 Score: 111 Matches: 4(2) 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="#">3104</a>	629.3455	1256.6765	1256.6725	3.20	1	24	0.057	1	U	L.VLGRGE
<a href="#">3428</a>	653.3556	1304.6967	1304.6976	-0.67	0	54	6e-05	1	U	L.TGNTIV
<a href="#">5127</a>	835.4257	1668.8368	1668.8318	2.95	0	(23)	0.095	1	U	Y.EGEIIQ
<a href="#">5128</a>	835.4262	1668.8377	1668.8318	3.54	0	35	0.0063	1	U	Y.EGEIIQ

26. [2::sp|P02931|OMP F ECOLI](#) Mass: 39309 Score: 102 Matches: 5(3) Sequences: 3  
 Outer membrane protein F OS=Escherichia coli (strain K12) OX=83333 GN=ompF PE=1 SV=1  
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2477</a>	583.2971	1164.5796	1164.5775	1.79	1	20	0.2	1	U	Y.NKDG N
<a href="#">3194</a>	636.8436	1271.6726	1271.6721	0.38	0	50	0.00018	1	U	Y.IINQI
<a href="#">3195</a>	636.8457	1271.6768	1271.6721	3.73	0	(26)	0.037	1	U	Y.IINQI
<a href="#">4303</a>	742.3796	1482.7446	1482.7426	1.32	1	(24)	0.071	1	U	Y.GAADR
<a href="#">4304</a>	742.3810	1482.7474	1482.7426	3.21	1	33	0.0082	1	U	Y.GAADR

27. [2::sp|P08200|IDH ECOLI](#) **Mass:** 46070 **Score:** 101 **Matches:** 5(4) **Sequences:** 2(2)  
Isocitrate dehydrogenase [NADP] OS=Escherichia coli (strain K12) OX=83333 GN=icd 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="#">2653</a>	398.2230	1191.6471	1191.6499	-2.33	0	(20)	0.13	1	U	L.KVVDA
<a href="#">2654</a>	596.8329	1191.6513	1191.6499	1.20	0	(50)	0.00013	1	U	L.KVVDA
<a href="#">2655</a>	596.8336	1191.6526	1191.6499	2.22	0	57	2.7e-05	1	U	L.KVVDA
<a href="#">3463</a>	656.3669	1310.7192	1310.7194	-0.15	0	45	0.00029	1	U	Y.AGQDK
<a href="#">3464</a>	656.3684	1310.7223	1310.7194	2.18	0	(35)	0.0026	1	U	Y.AGQDK

28. [2::sp|P21888|SYC ECOLI](#) **Mass:** 52454 **Score:** 93 **Matches:** 3(3) **Sequences:** 2(2)  
Cysteine--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=cysS PE=1 SV=2  
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2192</a>	566.7794	1131.5443	1131.5448	-0.44	2	36	0.0041	1	U	L.GLLEQ
<a href="#">4287</a>	738.8778	1475.7411	1475.7369	2.85	0	57	4.9e-05	1	U	L.RGTDK
<a href="#">4288</a>	738.8779	1475.7413	1475.7369	3.01	0	(47)	0.00047	1	U	L.RGTDK

29. [2::sp|P24182|ACCC ECOLI](#) **Mass:** 49745 **Score:** 86 **Matches:** 3(3) **Sequences:** 2(2)  
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="#">1261</a>	499.7330	997.4515	997.4505	1.01	2	32	0.0099	1	U	Y.GFLSE
<a href="#">1417</a>	511.7487	1021.4828	1021.4829	-0.09	0	(47)	0.00047	1	U	F.AEQVE
<a href="#">1419</a>	511.7490	1021.4834	1021.4829	0.49	0	57	4.3e-05	1	U	F.AEQVE

30. [2::sp|P0A9B2|G3P1 ECOLI](#) **Mass:** 35681 **Score:** 80 **Matches:** 4(4) **Sequences:** 2(2)  
Glyceraldehyde-3-phosphate dehydrogenase A OS=Escherichia coli (strain K12) OX=83333 GN=g3p1 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="#">3033</a>	624.8151	1247.6157	1247.6146	0.88	1	41	0.0021	1	U	F.DAKAGI
<a href="#">3034</a>	624.8156	1247.6167	1247.6146	1.66	1	(34)	0.0093	1	U	F.DAKAGI
<a href="#">3339</a>	648.3699	1294.7253	1294.7245	0.61	0	(36)	0.0017	1	U	F.RVPTPN
<a href="#">3340</a>	648.3706	1294.7267	1294.7245	1.66	0	39	0.0008	1	U	F.RVPTPN

31. [2::sp|P06715|GSHR ECOLI](#) **Mass:** 49084 **Score:** 76 **Matches:** 4(2) **Sequences:** 2(2)  
Glutathione reductase OS=Escherichia coli (strain K12) OX=83333 GN=gor PE=1 SV=1  
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">3888</a>	698.8630	1395.7115	1395.7106	0.66	0	24	0.06	1	U	W.AIGRE
<a href="#">3889</a>	698.8637	1395.7127	1395.7106	1.54	0	(24)	0.07	1	U	W.AIGRE

<a href="#">4769</a>	791.9512	1581.8879	1581.8879	0.03	0	(37)	0.0014	1	U	F.ALPA
<a href="#">4770</a>	791.9522	1581.8899	1581.8879	1.27	0	52	5.1e-05	1	U	F.ALPA

32. [2::sp|P0ABB0|ATPA\\_ECOLI](#) Mass: 55416 Score: 74 Matches: 4(4) Sequences: 2  
 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	Peptide
<a href="#">4870</a>	803.8989	1605.7832	1605.7821	0.67	1	(39)	0.0038	1	U	L.NLERN
<a href="#">4933</a>	811.8962	1621.7778	1621.7770	0.49	1	47	0.00055	1	U	L.NLERN
<a href="#">4934</a>	811.8973	1621.7800	1621.7770	1.85	1	(43)	0.0012	1	U	L.NLERN
<a href="#">6471</a>	838.7675	2513.2806	2513.2762	1.74	0	28	0.025	1	U	F.SAVEA

33. [2::sp|P04805|SYE\\_ECOLI](#) Mass: 54181 Score: 70 Matches: 4(4) Sequences: 2  
 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="#">2625</a>	595.2960	1188.5775	1188.5775	-0.01	0	31	0.014	1	U	F.DDQIRG
<a href="#">2626</a>	595.2964	1188.5782	1188.5775	0.61	0	(31)	0.016	1	U	F.DDQIRG
<a href="#">3040</a>	625.2950	1248.5754	1248.5735	1.56	1	39	0.0026	1	U	L.DFIAER
<a href="#">3041</a>	625.2955	1248.5765	1248.5735	2.44	1	(36)	0.0046	1	U	L.DFIAER

34. [1::sp|cRAP112|P00761|TRYP\\_PIG](#) Mass: 25078 Score: 70 Matches: 5(5) 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="#">779</a>	465.2868	928.5590	928.5593	-0.35	1	(25)	0.02	1	U	L.IKLSS
<a href="#">782</a>	465.2872	928.5598	928.5593	0.58	1	27	0.012	1	U	L.IKLSS
<a href="#">3101</a>	629.3322	1256.6499	1256.6513	-1.16	1	43	0.00073	1	U	Y.VNWIQ
<a href="#">3102</a>	629.3325	1256.6505	1256.6513	-0.66	1	(41)	0.0012	1	U	Y.VNWIQ
<a href="#">3103</a>	629.3344	1256.6543	1256.6513	2.35	1	(37)	0.003	1	U	Y.VNWIQ

35. [2::sp|P25522|MNME\\_ECOLI](#) Mass: 49258 Score: 62 Matches: 3(2) Sequences: 2  
 tRNA modification GTPase MnmE OS=Escherichia coli (strain K12) OX=83333 GN=mnmE 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="#">3664</a>	674.3498	1346.6850	1346.6830	1.50	1	30	0.022	1	U	W.QEIEQA
<a href="#">4859</a>	803.4153	1604.8161	1604.8158	0.20	2	(24)	0.094	1	U	L.RLAQQN
<a href="#">4860</a>	803.4158	1604.8170	1604.8158	0.73	2	32	0.014	1	U	L.RLAQQN

36. [2::sp|P0ACC7|GLMU\\_ECOLI](#) Mass: 49388 Score: 59 Matches: 2(2) Sequences: 2  
 Bifunctional protein GlmU OS=Escherichia coli (strain K12) OX=83333 GN=glmU 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="#">100</a>	386.2338	770.4531	770.4538	-0.89	0	22	0.046	1	U	Y.SDLPKV
<a href="#">1952</a>	554.7811	1107.5477	1107.5448	2.61	1	37	0.0042	1	U	L.TVKLDD

37. [2::sp|P0A6P1|EFTS ECOLI](#) Mass: 30518 Score: 58 Matches: 2(2) Sequences: 1  
 Elongation factor Ts OS=Escherichia coli (strain K12) OX=83333 GN=tsf PE=1 SV=2  
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">4170</a>	726.3482	1450.6819	1450.6828	-0.61	0	(40)	0.0026	1	U	F.EVGE
<a href="#">4171</a>	726.3487	1450.6829	1450.6828	0.13	0	58	4.3e-05	1	U	F.EVGE

38. [2::sp|P0AEX9|MALE ECOLI](#) Mass: 43360 Score: 53 Matches: 2(1) Sequences: 2  
 Maltose-binding periplasmic protein OS=Escherichia coli (strain K12) OX=83333 GN=mal  
 Check 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="#">1656</a>	531.8013	1061.5880	1061.5869	1.00	1	22	0.073	1	U	Y.NGLAEV
<a href="#">2264</a>	570.7817	1139.5489	1139.5459	2.70	0	31	0.011	1	U	W.SNIDTS

39. [2::sp|P0AD61|KPYK1 ECOLI](#) Mass: 51039 Score: 52 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="#">5614</a>	915.9432	1829.8719	1829.8717	0.12	0	(39)	0.0023	1	U	F.TTDKS
<a href="#">5615</a>	915.9459	1829.8772	1829.8717	2.99	0	52	0.00014	1	U	F.TTDKS

40. [1::sp|cRAP054|P04264|K2C1 HUMAN](#) Mass: 66170 Score: 51 Matches: 3(3) Sequences: 1  
 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="#">2774</a>	604.8300	1207.6455	1207.6449	0.53	0	24	0.044	1	U	F.VTIKDD
<a href="#">4409</a>	757.8001	1513.5855	1513.5819	2.43	1	26	0.0052	1	U	Y.GSGGGS
<a href="#">4410</a>	757.8012	1513.5879	1513.5819	3.97	1	(24)	0.011	1	U	Y.GSGGGS

41. [2::sp|P21165|PEPQ ECOLI](#) Mass: 50315 Score: 50 Matches: 3(2) Sequences: 2  
 Xaa-Pro dipeptidase OS=Escherichia coli (strain K12) OX=83333 GN=pepQ PE=1 SV=2  
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2798</a>	606.2819	1210.5493	1210.5466	2.25	1	30	0.018	1	U	W.SAKSDN
<a href="#">2799</a>	606.2820	1210.5494	1210.5466	2.34	1	(27)	0.029	1	U	W.SAKSDN

[3745](#) 682.3207 1362.6269 1362.6245 1.81 2 21 0.17 1 U F.NVFLDD

42. [2::sp|P0A6H1|CLPX\\_ECOLI](#) Mass: 46726 Score: 48 Matches: 2(1) Sequences: 2  
ATP-dependent Clp protease ATP-binding subunit ClpX OS=Escherichia coli (strain K12)  
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1377</a>	508.7860	1015.5575	1015.5437	13.6	1	26	0.037	4	U	L.SEEALI
<a href="#">3280</a>	644.8436	1287.6727	1287.6711	1.29	1	22	0.13	1	U	L.AQVEPE

43. [2::sp|P15034|AMPP\\_ECOLI](#) Mass: 50012 Score: 46 Matches: 3(0) Sequences: 2  
Xaa-Pro aminopeptidase OS=Escherichia coli (strain K12) OX=83333 GN=pepP PE=1 SV=2  
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1619</a>	529.7897	1057.5649	1057.5655	-0.59	1	23	0.067	1	U	L.GILKGD
<a href="#">5041</a>	828.3808	1654.7470	1654.7475	-0.24	0	(22)	0.11	1	U	F.AAPEVT
<a href="#">5042</a>	828.3809	1654.7473	1654.7475	-0.10	0	23	0.086	1	U	F.AAPEVT

44. [2::sp|P27306|STHA\\_ECOLI](#) Mass: 51984 Score: 45 Matches: 2(2) Sequences: 1  
Soluble pyridine nucleotide transhydrogenase 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="#">4959</a>	815.4401	1628.8656	1628.8621	2.13	0	45	0.00048	1	U	Y.TIPEI
<a href="#">4960</a>	815.4407	1628.8668	1628.8621	2.87	0	(31)	0.014	1	U	Y.TIPEI

45. [2::sp|P21599|KPYK2\\_ECOLI](#) Mass: 51553 Score: 45 Matches: 2(2) Sequences: 1  
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="#">3325</a>	647.3737	1292.7329	1292.7340	-0.87	0	48	8.9e-05	1	U	Y.KGLPA
<a href="#">3326</a>	647.3742	1292.7339	1292.7340	-0.11	0	(23)	0.025	1	U	Y.KGLPA

46. [2::sp|Q46808|YQE\\_B\\_ECOLI](#) Mass: 58044 Score: 44 Matches: 2(1) Sequences: 1  
Uncharacterized protein YqeB OS=Escherichia coli (strain K12) OX=83333 GN=yqeB PE=4  
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1650</a>	531.7859	1061.5572	1061.5393	16.9	2	(25)	0.055	1	U	L.LNDGL
<a href="#">1651</a>	531.7862	1061.5579	1061.5393	17.5	2	44	0.00068	1	U	L.LNDGL

47. [2::sp|P77748|YDIJ\\_ECOLI](#) Mass: 114259 Score: 43 Matches: 2(1) Sequences: 2

Uncharacterized protein YdiJ OS=Escherichia coli (strain K12) OX=83333 GN=ydiJ PE=4  
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">3630</a>	669.8723	1337.7301	1337.7013	21.5	0	21	0.061	2	U	L.SEKHIG
<a href="#">4174</a>	726.4155	1450.8165	1450.7854	21.5	1	24	0.021	1	U	L.SEKHIG

48. [2::sp|P11447|ARLY\\_ECOLI](#) Mass: 50686 Score: 41 Matches: 1(1) Sequences: 1  
Argininosuccinate lyase OS=Escherichia coli (strain K12) OX=83333 GN=argH PE=1 SV=3  
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">4140</a>	722.3846	1442.7546	1442.7518	1.97	1	43	0.00079	1	U	Y.RLAEQ

49. [2::sp|POC8J8|GATZ\\_ECOLI](#) Mass: 47535 Score: 41 Matches: 2(2) Sequences: 1  
D-tagatose-1,6-bisphosphate aldolase subunit GatZ OS=Escherichia coli (strain K12) OX=83333 GN=gatZ 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="#">2879</a>	613.8412	1225.6679	1225.6666	1.08	0	(28)	0.017	1	U	L.APETV
<a href="#">2880</a>	613.8422	1225.6698	1225.6666	2.56	0	41	0.00075	1	U	L.APETV

50. [1::sp|cRAP041|P35527|K1C9\\_HUMAN](#) Mass: 62255 Score: 39 Matches: 2(0) Sequences: 1  
Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 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="#">2280</a>	571.7451	1141.4757	1141.4749	0.73	0	21	0.064	1	U	Y.GGGSGS
<a href="#">3055</a>	626.2976	1250.5807	1250.5812	-0.46	0	21	0.18	1	U	L.TANEKS

51. [2::sp|P0A6F5|CH60\\_ECOLI](#) Mass: 57464 Score: 39 Matches: 2(2) Sequences: 1  
60 kDa chaperonin OS=Escherichia coli (strain K12) OX=83333 GN=groL PE=1 SV=2  
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">5499</a>	889.4540	1776.8934	1776.8934	0.00	2	(39)	0.0034	1	U	Y.FINKPE
<a href="#">5500</a>	889.4545	1776.8945	1776.8934	0.62	2	39	0.0031	1	U	Y.FINKPE

52. [2::sp|P37177|PT1P\\_ECOLI](#) Mass: 84005 Score: 39 Matches: 2(1) Sequences: 2  
Phosphoenolpyruvate-dependent phosphotransferase system OS=Escherichia coli (strain K12) OX=83333 GN=pta 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="#">628</a>	441.2635	880.5124	880.4906	24.8	1	20	0.025	1	U	L.VDPEPV
<a href="#">1368</a>	508.2872	1014.5599	1014.5458	13.9	1	21	0.1	2	U	L.AQRSLE

53. [2::sp|P76403|YEQQ\\_ECOLI](#) Mass: 51446 Score: 38 Matches: 2(2) Sequences: 1(1)  
Uncharacterized protease YegQ OS=Escherichia coli (strain K12) OX=83333 GN=yegQ PE=3  
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">3627</a>	669.8036	1337.5927	1337.5921	0.46	0	38	0.0024	1	U	F.MIEEQAQ
<a href="#">3628</a>	669.8049	1337.5953	1337.5921	2.37	0	(34)	0.0068	1	U	F.MIEEQAQ

54. [2::sp|P60906|SYH\\_ECOLI](#) Mass: 47285 Score: 37 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="#">4342</a>	747.9293	1493.8441	1493.8453	-0.83	0	(32)	0.0033	1	U	Y.SEIRLPL
<a href="#">4343</a>	747.9313	1493.8481	1493.8453	1.88	0	37	0.001	1	U	Y.SEIRLPL

55. [2::sp|P0A6Y8|DNAK\\_ECOLI](#) Mass: 69130 Score: 35 Matches: 1(1) Sequences: 1(1)  
Chaperone protein DnaK OS=Escherichia coli (strain K12) OX=83333 GN=dnaK PE=1 SV=2  
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">4972</a>	818.8950	1635.7755	1635.7740	0.91	0	35	0.0062	1	U	L.ENAEGD

56. [2::sp|P60422|RL2\\_ECOLI](#) Mass: 29956 Score: 34 Matches: 1(1) Sequences: 1(1)  
50S ribosomal protein L2 OS=Escherichia coli (strain K12) OX=83333 GN=rplB PE=1 SV=2  
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1827</a>	546.2976	1090.5807	1090.5771	3.27	0	34	0.0055	1	U	Y.VQIVAR

57. [2::sp|P04982|RBSD\\_ECOLI](#) Mass: 15454 Score: 34 Matches: 1(1) Sequences: 1(1)  
D-ribose pyranase OS=Escherichia coli (strain K12) OX=83333 GN=rbsD 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="#">2638</a>	596.3001	1190.5855	1190.6143	-24.11	0	34	0.0084	1	U	L.NSDIS

58. [2::sp|P76658|HLDE\\_ECOLI](#) Mass: 51247 Score: 33 Matches: 2(2) Sequences: 1(1)  
Bifunctional protein HldE OS=Escherichia coli (strain K12) OX=83333 GN=hldE PE=1 SV=3  
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
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<a href="#">2833</a>	608.8250	1215.6355	1215.6347	0.62	0	33	0.009	1	U	Y.DVTGAG
<a href="#">2834</a>	608.8265	1215.6385	1215.6347	3.13	0	(33)	0.01	1	U	Y.DVTGAG

59. [2::sp|P0A953|FABB ECOLI](#) Mass: 42928 Score: 32 Matches: 2(2) Sequences: 1(1)  
 3-oxoacyl-[acyl-carrier-protein] synthase 1 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="#">3292</a>	645.8328	1289.6510	1289.6463	3.62	0	32	0.014	1	U	L.NIVTET
<a href="#">3293</a>	645.8350	1289.6554	1289.6463	7.03	0	(26)	0.061	1	U	L.NIVTET

60. [2::sp|P00490|PHSM ECOLI](#) Mass: 90865 Score: 32 Matches: 1(1) Sequences: 1(1)  
 Maltodextrin phosphorylase OS=Escherichia coli (strain K12) OX=833333 GN=malP PE=1 SV=1  
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">3701</a>	678.8488	1355.6831	1355.7157	-24.04	0	32	0.0091	1	U	L.RAEQQ

61. [2::sp|P76251|DMLA ECOLI](#) Mass: 40574 Score: 31 Matches: 2(2) Sequences: 1(1)  
 D-malate dehydrogenase [decarboxylating] OS=Escherichia coli (strain K12) OX=833333 GN=malE 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="#">1050</a>	484.2232	966.4319	966.4328	-0.90	0	(27)	0.025	1	U	L.TSATKSNGL
<a href="#">1051</a>	484.2234	966.4322	966.4328	-0.59	0	31	0.012	1	U	L.TSATKSNGL

62. [2::sp|P32664|NUDC ECOLI](#) Mass: 30012 Score: 30 Matches: 1(1) Sequences: 1(1)  
 NADH pyrophosphatase OS=Escherichia coli (strain K12) OX=833333 GN=nudC 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="#">1551</a>	524.7643	1047.5140	1047.5349	-19.94	1	30	0.021	1	U	L.AGRGV

63. [2::sp|P0A9J8|PHEA ECOLI](#) Mass: 43312 Score: 29 Matches: 1(1) Sequences: 1(1)  
 P-protein OS=Escherichia coli (strain K12) OX=833333 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="#">4275</a>	736.9091	1471.8036	1471.7704	22.5	2	32	0.0098	1	U	L.LMATGQ

64. [2::sp|P37651|GUN ECOLI](#) Mass: 41788 Score: 29 Matches: 2(2) Sequences: 1(1)  
 Endoglucanase OS=Escherichia coli (strain K12) OX=833333 GN=bcsZ PE=1 SV=1  
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">429</a>	418.6984	835.3823	835.3824	-0.11	0	(24)	0.044	1	U	L.AANDRAAF
<a href="#">430</a>	418.6988	835.3831	835.3824	0.89	0	29	0.015	1	U	L.AANDRAAF

65. [2::sp|P77260|YDFI\\_ECOLI](#) Mass: 53879 Score: 28 Matches: 1(1) Sequences: 1  
 Uncharacterized oxidoreductase YdfI OS=Escherichia coli (strain K12) OX=83333 GN=ydfI  
 Check 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="#">493</a>	423.7286	845.4427	845.4317	13.0	0	28	0.027	1	U	L.KVQGVDL

66. [2::sp|P42591|YGJJ\\_ECOLI](#) Mass: 40188 Score: 28 Matches: 2(2) Sequences: 1  
 Uncharacterized protein YgjJ OS=Escherichia coli (strain K12) OX=83333 GN=ygjJ PE=3  
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">129</a>	390.2237	778.4329	778.4225	13.4	1	(22)	0.045	1	U	Y.EALKGVY
<a href="#">130</a>	390.2237	778.4329	778.4225	13.4	1	28	0.013	1	U	Y.EALKGVY

67. [2::sp|P0A817|METK\\_ECOLI](#) Mass: 42153 Score: 28 Matches: 1(1) Sequences: 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="#">4850</a>	802.9330	1603.8514	1603.8457	3.53	1	28	0.032	1	U	F.QYDDGK

68. [2::sp|P31068|FLIH\\_ECOLI](#) Mass: 25149 Score: 27 Matches: 2(2) Sequences: 1  
 Flagellar assembly protein FliH OS=Escherichia coli (strain K12) OX=83333 GN=fliH 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="#">578</a>	436.2716	870.5286	870.5174	12.8	0	27	0.0082	1	U	L.IKQIQQL
<a href="#">579</a>	436.2718	870.5291	870.5174	13.4	0	(23)	0.022	1	U	L.IKQIQQL

69. [2::sp|P37652|BCSB\\_ECOLI](#) Mass: 86140 Score: 27 Matches: 1(1) Sequences: 1  
 Cyclic di-GMP-binding protein OS=Escherichia coli (strain K12) OX=83333 GN=bcsB 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="#">3205</a>	637.3350	1272.6554	1272.6384	13.4	0	27	0.038	1	U	L.QAAKGI

70. [2::sp|P68187|MALK\\_ECOLI](#) Mass: 41136 Score: 27 Matches: 1(1) Sequences: 1  
 Maltose/maltodextrin import ATP-binding protein MalK 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="#">2165</a>	565.2770	1128.5395	1128.5663	-23.69	0	27	0.027	1	U	L.EGEVQ

71. [2::sp|P0ABH7|CISY\\_ECOLI](#) Mass: 48383 Score: 26 Matches: 1(1) Sequences: 1(1)  
Citrate synthase OS=Escherichia coli (strain K12) OX=83333 GN=gltA 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="#">1506</a>	516.7692	1031.5239	1031.5135	10.1	1	26	0.041	1	U	L.TLNGDT

72. [2::sp|P76272|YEBT\\_ECOLI](#) Mass: 94912 Score: 26 Matches: 1(1) Sequences: 1(1)  
Uncharacterized protein YebT OS=Escherichia coli (strain K12) OX=83333 GN=yebT PE=3 SV=1  
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2611</a>	594.3180	1186.6215	1186.6445	-19.34	2	26	0.041	1	U	Y.QGLEV

73. [2::sp|P0A870|TALB\\_ECOLI](#) Mass: 35368 Score: 26 Matches: 1(1) Sequences: 1(1)  
Transaldolase B OS=Escherichia coli (strain K12) OX=83333 GN=talB PE=1 SV=2  
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">3932</a>	467.2318	1398.6737	1398.6878	-10.10	1	26	0.054	1	U	Y.QPQDA

74. [2::sp|P75990|BLUF\\_ECOLI](#) Mass: 45551 Score: 25 Matches: 1(1) Sequences: 1(1)  
Blue light- and temperature-regulated antirepressor BluF OS=Escherichia coli (strain K12) OX=83333 GN=bluF 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="#">1880</a>	550.3293	1098.6441	1098.6284	14.3	2	25	0.018	1	U	F.LLNEIK

75. [2::sp|P24175|MANB\\_ECOLI](#) Mass: 50716 Score: 25 Matches: 1(1) Sequences: 1(1)  
Phosphomannomutase OS=Escherichia coli (strain K12) OX=83333 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="#">1883</a>	550.8018	1099.5890	1099.5947	-5.22	1	25	0.042	1	U	Y.INVKNL

76. [2::sp|Q46814|XDHD\\_ECOLI](#) Mass: 104366 Score: 25 Matches: 2(2) Sequences: 1(1)  
Probable hypoxanthine oxidase XdhD OS=Escherichia coli (strain K12) OX=83333 GN=xdhD 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="#">3630</a>	669.8723	1337.7301	1337.7013	21.5	1	(26)	0.023	1	U	L.TVPCNG
<a href="#">3633</a>	670.3638	1338.7130	1338.6853	20.7	1	28	0.018	1	U	L.TVPCNG

77. [2::sp|P0A763|NDK ECOLI](#) Mass: 15511 Score: 24 Matches: 1(1) Sequences: 1(1)  
 Nucleoside diphosphate kinase OS=Escherichia coli (strain K12) OX=83333 GN=ndk PE=1  
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">5770</a>	630.3503	1888.0290	1888.0015	14.6	0	24	0.038	1	U	F.SIIKPN

78. [2::sp|P77504|YBBP ECOLI](#) Mass: 89617 Score: 24 Matches: 1(1) Sequences: 1(1)  
 Uncharacterized ABC transporter permease YbbP OS=Escherichia coli (strain K12) OX=83333 GN=ybbp 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="#">2512</a>	585.3229	1168.6312	1168.6339	-2.33	0	24	0.031	1	U	L.INIATE

## Search Parameters

Type of search : MS/MS Ion Search  
 Enzyme : Chymotrypsin  
 Fixed modifications : [Carbamidomethyl \(C\)](#)  
 Variable modifications : [Deamidated \(NQ\)](#), [DTSSP Cross link \(K\)](#), [Oxidation \(M\)](#)  
 Mass values : Monoisotopic  
 Protein Mass : Unrestricted  
 Peptide Mass Tolerance : ± 25 ppm  
 Fragment Mass Tolerance: ± 0.8 Da  
 Max Missed Cleavages : 2  
 Instrument type : ESI-TRAP  
 Number of queries : 6735

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