

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_band4.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 11:10:32 GMT

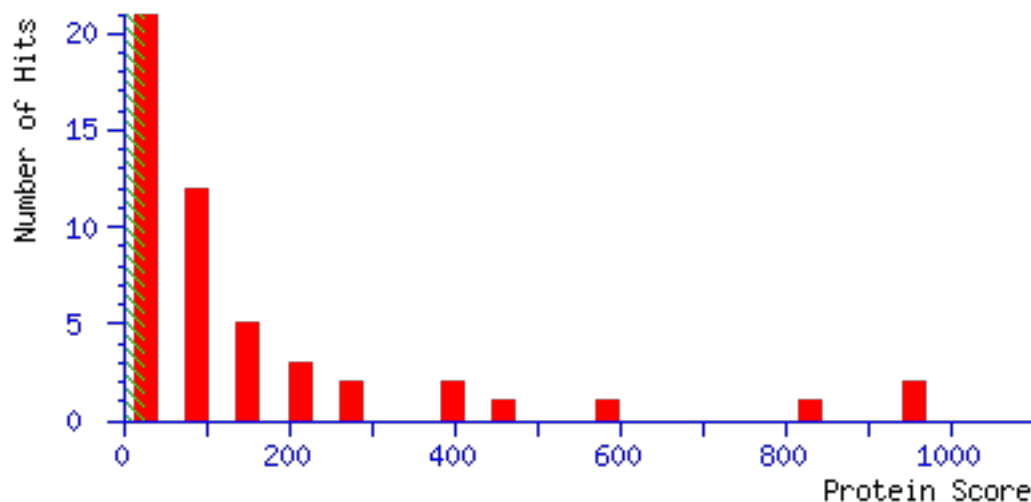
Protein hits	: 2::sp P0AE06 ACRA ECOLI	Multidrug efflux pump subunit AcrA OS=Escherichia coli
	: 2::sp P0CE47 EFTU1 ECOLI	Elongation factor Tu 1 OS=Escherichia coli
	: 1::sp cRAP022 P00766 CTRA BOVIN	Chymotrypsinogen A OS=Bos taurus PE=1 SV=1
	: 2::sp P0C8J8 GATZ ECOLI	D-tagatose-1,6-bisphosphate aldolase subunit OS=Escherichia coli
	: 2::sp P0AAI5 FABF ECOLI	3-oxoacyl-[acyl-carrier-protein] synthase class 1 OS=Escherichia coli
	: 2::sp P0A6A3 ACKA ECOLI	Acetate kinase OS=Escherichia coli (strain ATCC 25962)
	: 2::sp P02931 OMPF ECOLI	Outer membrane protein F OS=Escherichia coli
	: 2::sp P0A953 FABB ECOLI	3-oxoacyl-[acyl-carrier-protein] synthase class 2 OS=Escherichia coli
	: 2::sp P08200 IDH ECOLI	Isocitrate dehydrogenase [NADP] OS=Escherichia coli
	: 2::sp P0ABH7 CISY ECOLI	Citrate synthase OS=Escherichia coli (strain ATCC 25962)
	: 2::sp P0A749 MURA ECOLI	UDP-N-acetylglucosamine 1-carboxyvinyltransferase OS=Escherichia coli
	: 2::sp P31979 NUOF ECOLI	NADH-quinone oxidoreductase subunit F OS=Escherichia coli
	: 2::sp P0AG67 RS1 ECOLI	30S ribosomal protein S1 OS=Escherichia coli
	: 2::sp P0A855 TOLB ECOLI	Tol-Pal system protein TolB OS=Escherichia coli
	: 2::sp P0AGJ9 SYY ECOLI	Tyrosine--tRNA ligase OS=Escherichia coli
	: 2::sp P0A817 METHK ECOLI	S-adenosylmethionine synthase OS=Escherichia coli
	: 2::sp P31224 ACRB ECOLI	Multidrug efflux pump subunit AcrB OS=Escherichia coli
	: 2::sp P0A9B2 G3P1 ECOLI	Glyceraldehyde-3-phosphate dehydrogenase class 1 OS=Escherichia coli
	: 2::sp P24180 ACRE ECOLI	Multidrug export protein AcrE OS=Escherichia coli
	: 2::sp P0A6B7 ISCS ECOLI	Cysteine desulfurase IscS OS=Escherichia coli
	: 2::sp P07004 PROA ECOLI	Gamma-glutamyl phosphate reductase OS=Escherichia coli
	: 2::sp P0A836 SUCC ECOLI	Succinate--CoA ligase [ADP-forming] subunit OS=Escherichia coli
	: 2::sp P76373 UDG ECOLI	UDP-glucose 6-dehydrogenase OS=Escherichia coli
	: 2::sp P0A9T0 SERA ECOLI	D-3-phosphoglycerate dehydrogenase OS=Escherichia coli
	: 2::sp P00509 AAT ECOLI	Aspartate aminotransferase OS=Escherichia coli
	: 1::sp cRAP087 P02769 ALBU BOVIN	Serum albumin OS=Bos taurus GN=ALB PE=1 SV=1
	: 2::sp P0AB71 ALF ECOLI	Fructose-bisphosphate aldolase class 2 OS=Escherichia coli
	: 1::sp cRAP112 P00761 TRYP PIG	Trypsin OS=Sus scrofa PE=1 SV=1

[2::sp|P0AFG3|ODO1_ECOLI](#)
[2::sp|P0AEX9|MALE_ECOLI](#)
[2::sp|P0A799|PGK_ECOLI](#)
[1::sp|cRAP054|P04264|K2C1_HUMAN](#)
[2::sp|P02920|LACY_ECOLI](#)
[2::sp|P0A6K6|DEOB_ECOLI](#)
[2::sp|P77398|ARNA_ECOLI](#)
[2::sp|P30176|RIBX_ECOLI](#)
[2::sp|P36672|PTTBC_ECOLI](#)
[2::sp|P69924|RIR2_ECOLI](#)
[2::sp|P0A825|GLYA_ECOLI](#)
[2::sp|Q47142|HCAT_ECOLI](#)
[2::sp|P02930|TOLC_ECOLI](#)
[2::sp|P0A7Z4|RPOA_ECOLI](#)
[2::sp|P0AC53|G6PD_ECOLI](#)
[2::sp|P0ABZ1|FLIG_ECOLI](#)
[2::sp|P0A9J8|PHEA_ECOLI](#)
[2::sp|P0A940|BAMA_ECOLI](#)
[2::sp|P0AD99|BRNQ_ECOLI](#)
[2::sp|P60906|SYH_ECOLI](#)
[2::sp|P37095|PEPB_ECOLI](#)
[2::sp|P0AAT4|YBDG_ECOLI](#)
[2::sp|P77789|YDES_ECOLI](#)
[2::sp|P46474|YHDP_ECOLI](#)
[2::sp|P31548|THIQ_ECOLI](#)
[2::sp|P36683|ACNB_ECOLI](#)
[2::sp|P77768|RPNB_ECOLI](#)
[2::sp|Q2MB16|YOBH_ECOLI](#)
[2::sp|P52612|FLII_ECOLI](#)
[2::sp|P77515|STFQ_ECOLI](#)
[2::sp|P0A877|TRPA_ECOLI](#)
[2::sp|P31448|YIDK_ECOLI](#)
[2::sp|P75898|RUTA_ECOLI](#)
[2::sp|P31433|YICH_ECOLI](#)
[2::sp|P07012|RF2_ECOLI](#)

2-oxoglutarate dehydrogenase E1 componen
 Maltose-binding periplasmic protein OS=E
 Phosphoglycerate kinase OS=Escherichia c
 Keratin, type II cytoskeletal 1 OS=Homo
 Lactose permease OS=Escherichia coli (st
 Phosphopentomutase OS=Escherichia coli (
 Bifunctional polymyxin resistance protei
 N-glycosidase YbiA OS=Escherichia coli (
 PTS system trehalose-specific EIIBC comp
 Ribonucleoside-diphosphate reductase 1 s
 Serine hydroxymethyltransferase OS=Esche
 Probable 3-phenylpropionic acid transpor
 Outer membrane protein TolC OS=Escherich
 DNA-directed RNA polymerase subunit alph
 Glucose-6-phosphate 1-dehydrogenase OS=E
 Flagellar motor switch protein FliG OS=E
 P-protein OS=Escherichia coli (strain K1
 Outer membrane protein assembly factor B
 Branched-chain amino acid transport syst
 Histidine--tRNA ligase OS=Escherichia co
 Peptidase B OS=Escherichia coli (strain
 Miniconductance mechanosensitive channel
 Uncharacterized fimbrial-like protein Yd
 Uncharacterized protein YhdP OS=Escheric
 Thiamine import ATP-binding protein ThiQ
 Aconitate hydratase B OS=Escherichia col
 Recombination-promoting nuclease RpnB OS
 Uncharacterized protein YobH OS=Escheric
 Flagellum-specific ATP synthase OS=Esche
 Prophage side tail fiber protein homolog
 Tryptophan synthase alpha chain OS=Esche
 Uncharacterized symporter YidK OS=Escher
 Pyrimidine monooxygenase RutA OS=Escheri
 AsmA family protein YicH OS=Escherichia
 Peptide chain release factor RF2 OS=Esch

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 meningit Species information unavailable				

Error tolerant

- [2::sp|P0AE06|ACRA ECOLI](#) **Mass:** 42228 **Score:** 956 **Matches:** 74(64) **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
35	384.1991	766.3837	766.3861	-3.11	0	36	0.0025	1	U	Y.ISKQ
37	384.1997	766.3848	766.3861	-1.68	0	(21)	0.072	1	U	Y.ISKQ
38	384.1997	766.3849	766.3861	-1.52	0	(31)	0.0071	1	U	Y.ISKQ
39	384.1998	766.3850	766.3861	-1.36	0	(20)	0.089	1	U	Y.ISKQ
40	384.1999	766.3852	766.3861	-1.21	0	(24)	0.044	1	U	Y.ISKQ
271	404.1984	806.3823	806.3810	1.59	0	21	0.13	1		Y.QIDP
696	450.2871	898.5597	898.5600	-0.27	2	(22)	0.02	1	U	F.LRLK

<u>697</u>	450.2874	898.5603	898.5600	0.42	2	24	0.013	1	U	F.LRLK
<u>712</u>	451.2401	900.4657	900.4665	-0.85	0	(25)	0.036	1	U	L.VQNG
<u>717</u>	451.7321	901.4496	901.4505	-1.03	0	28	0.019	1	U	L.VQNG
<u>718</u>	451.7324	901.4502	901.4505	-0.37	0	(21)	0.11	2	U	L.VQNG
<u>976</u>	475.7690	949.5234	949.5233	0.15	2	35	0.0033	1	U	Y.QKLL
<u>977</u>	475.7693	949.5241	949.5233	0.86	2	(31)	0.0085	2	U	Y.QKLL
<u>1133</u>	487.2695	972.5244	972.5240	0.47	1	(47)	0.00028	1	U	L.KQEL
<u>1134</u>	487.2698	972.5251	972.5240	1.11	1	55	6e-05	1	U	L.KQEL
<u>1143</u>	487.7620	973.5094	973.5080	1.41	1	(44)	0.0007	1	U	L.KQEL
<u>1144</u>	487.7620	973.5095	973.5080	1.53	1	(54)	7.3e-05	1	U	L.KQEL
<u>2001</u>	557.8329	1113.6513	1113.6506	0.67	0	(21)	0.072	1	U	L.KAGD
<u>2002</u>	557.8336	1113.6527	1113.6506	1.87	0	31	0.0066	1	U	L.KAGD
<u>2400</u>	585.3350	1168.6555	1168.6564	-0.76	0	(57)	1.4e-05	1	U	L.AKAQ
<u>2401</u>	585.3357	1168.6568	1168.6564	0.39	0	57	1.3e-05	1	U	L.AKAQ
<u>2545</u>	597.8045	1193.5944	1193.5928	1.39	1	(24)	0.081	1	U	Y.ISKQ
<u>2546</u>	597.8046	1193.5946	1193.5928	1.51	1	41	0.0017	1	U	Y.ISKQ
<u>2547</u>	597.8051	1193.5957	1193.5928	2.41	1	(29)	0.025	1	U	Y.ISKQ
<u>2548</u>	597.8054	1193.5962	1193.5928	2.83	1	(36)	0.0049	1	U	Y.ISKQ
<u>2613</u>	401.5624	1201.6653	1201.6666	-1.08	0	23	0.061	1	U	L.KQEN
<u>2619</u>	602.8062	1203.5977	1203.5983	-0.44	0	(29)	0.029	1	U	F.KEGS
<u>2620</u>	602.8062	1203.5979	1203.5983	-0.34	0	30	0.022	1	U	F.KEGS
<u>2837</u>	621.8633	1241.7120	1241.7092	2.30	2	(38)	0.0013	1	U	L.RLKQ
<u>2838</u>	621.8635	1241.7125	1241.7092	2.70	2	(34)	0.0031	1	U	L.RLKQ
<u>2843</u>	622.3539	1242.6933	1242.6932	0.13	2	40	0.0011	1	U	L.RLKQ
<u>2844</u>	622.3542	1242.6938	1242.6932	0.54	2	(26)	0.034	1	U	L.RLKQ
<u>2845</u>	622.3547	1242.6949	1242.6932	1.42	2	(31)	0.011	1	U	L.RLKQ
<u>3489</u>	684.3376	1366.6606	1366.6616	-0.72	1	(47)	0.00046	1	U	F.KEGS
<u>3492</u>	684.3387	1366.6628	1366.6616	0.88	1	(48)	0.00035	1	U	F.KEGS
<u>3493</u>	684.3389	1366.6632	1366.6616	1.16	1	(44)	0.00077	1	U	F.KEGS
<u>3494</u>	684.3400	1366.6654	1366.6616	2.77	1	(47)	0.0004	1	U	F.KEGS
<u>3495</u>	684.3401	1366.6656	1366.6616	2.94	1	(31)	0.017	1	U	F.KEGS
<u>3496</u>	684.3402	1366.6659	1366.6616	3.12	1	52	0.00014	1	U	F.KEGS
<u>3788</u>	718.8723	1435.7299	1435.7307	-0.52	0	(44)	0.00086	1	U	L.QITT
<u>3789</u>	718.8726	1435.7306	1435.7307	-0.09	0	45	0.00069	1	U	L.QITT
<u>4003</u>	746.3881	1490.7616	1490.7617	-0.08	0	71	1.9e-06	1	U	L.ITSD
<u>4004</u>	746.3887	1490.7629	1490.7617	0.82	0	(64)	8.9e-06	1	U	L.ITSD
<u>4005</u>	746.3898	1490.7651	1490.7617	2.29	0	(53)	0.00011	1	U	L.ITSD
<u>4006</u>	746.3912	1490.7679	1490.7617	4.19	0	(43)	0.0011	1	U	L.ITSD
<u>4256</u>	775.9751	1549.9356	1549.9304	3.39	0	(25)	0.0031	1	U	Y.RIAE
<u>4257</u>	775.9752	1549.9358	1549.9304	3.47	0	(32)	0.00077	1	U	Y.RIAE
<u>4260</u>	776.4653	1550.9160	1550.9144	1.03	0	36	0.00062	1	U	Y.RIAE
<u>4261</u>	776.4667	1550.9188	1550.9144	2.83	0	(28)	0.0026	1	U	Y.RIAE
<u>4958</u>	576.3410	1726.0012	1725.9989	1.32	2	28	0.0047	1	U	W.LVTE
<u>5057</u>	884.4443	1766.8741	1766.8727	0.81	1	48	0.00039	1	U	L.ITSD
<u>5058</u>	884.4462	1766.8778	1766.8727	2.88	1	(42)	0.0013	1	U	L.ITSD
<u>5261</u>	921.4735	1840.9325	1840.9294	1.65	1	(42)	0.0013	1	U	L.RAIF
<u>5265</u>	921.4771	1840.9397	1840.9294	5.56	1	49	0.00024	1	U	L.RAIF
<u>5299</u>	928.4966	1854.9786	1854.9799	-0.69	1	58	2.4e-05	1	U	Y.DSAK
<u>5300</u>	619.3338	1854.9796	1854.9799	-0.17	1	(33)	0.008	1	U	Y.DSAK
<u>5301</u>	619.3351	1854.9834	1854.9799	1.90	1	(27)	0.026	1	U	Y.DSAK
<u>5302</u>	928.4992	1854.9839	1854.9799	2.15	1	(48)	0.00021	1	U	Y.DSAK
<u>5808</u>	1120.5375	2239.0604	2239.0645	-1.82	2	71	2e-06	1		L.ATVQ
<u>5809</u>	1120.5413	2239.0680	2239.0645	1.56	2	(33)	0.012	1		L.ATVQ
<u>5810</u>	747.3642	2239.0708	2239.0645	2.81	2	(34)	0.0093	1		L.ATVQ
<u>5811</u>	747.3654	2239.0743	2239.0645	4.36	2	(24)	0.086	1		L.ATVQ
<u>5913</u>	1227.6512	2453.2879	2453.2914	-1.42	0	(50)	0.00014	1	U	L.VVGA

5915	1227.6539	2453.2933	2453.2914	0.76	0	(45)	0.00039	1	U	L.VVGA
5916	818.7725	2453.2956	2453.2914	1.67	0	(32)	0.0073	1	U	L.VVGA
5917	818.7728	2453.2967	2453.2914	2.13	0	(44)	0.00052	1	U	L.VVGA
5921	819.1011	2454.2814	2454.2755	2.42	0	(43)	0.00074	1	U	L.VVGA
5922	819.1026	2454.2860	2454.2755	4.29	0	51	0.00012	1	U	L.VVGA
6152	1160.2575	3477.7505	3477.7560	-1.58	0	(23)	0.066	1	U	L.QKVR
6154	1160.2595	3477.7567	3477.7560	0.21	0	(33)	0.0059	1	U	L.QKVR
6155	870.4484	3477.7643	3477.7560	2.39	0	(26)	0.031	1	U	L.QKVR
6157	870.4485	3477.7651	3477.7560	2.61	0	(20)	0.11	1	U	L.QKVR
6162	1160.2642	3477.7707	3477.7560	4.21	0	34	0.0047	1	U	L.QKVR
6163	1160.2675	3477.7806	3477.7560	7.06	0	(29)	0.014	1	U	L.QKVR

2. [2::sp|POCE47|EFTU1_ECOLI](#) Mass: 43427 Score: 951 Matches: 85(69) 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
939	473.2686	944.5227	944.5219	0.85	1	(44)	0.00056	1	U	F.LLPIE
940	473.2691	944.5236	944.5219	1.87	1	47	0.00028	1	U	F.LLPIE
1423	509.7452	1017.4757	1017.4767	-0.94	1	(23)	0.068	1	U	L.KALEG
1424	509.7452	1017.4759	1017.4767	-0.76	1	(25)	0.045	1	U	L.KALEG
1425	509.7459	1017.4773	1017.4767	0.56	1	27	0.031	1	U	L.KALEG
1426	509.7463	1017.4780	1017.4767	1.29	1	(20)	0.15	1	U	L.KALEG
1442	510.7560	1019.4975	1019.4957	1.77	0	25	0.061	1	U	L.VEMEV
1443	510.7564	1019.4982	1019.4957	2.43	0	(23)	0.088	1	U	L.VEMEV
1725	541.2705	1080.5265	1080.5274	-0.84	0	(52)	0.00012	1	U	L.IHPIA
1726	541.2707	1080.5268	1080.5274	-0.51	0	62	1.3e-05	1	U	L.IHPIA
1841	549.2676	1096.5206	1096.5223	-1.54	0	(35)	0.0044	1	U	L.IHPIA
1842	549.2687	1096.5229	1096.5223	0.58	0	(42)	0.00085	1	U	L.IHPIA
1843	549.2688	1096.5230	1096.5223	0.69	0	(46)	0.00035	1	U	L.IHPIA
1844	549.2695	1096.5245	1096.5223	2.02	0	(47)	0.00031	1	U	L.IHPIA
2684	608.3019	1214.5893	1214.5891	0.17	0	57	2.9e-05	1	U	L.DEGRA
2685	608.3029	1214.5912	1214.5891	1.68	0	(52)	9.8e-05	1	U	L.DEGRA
2769	615.7968	1229.5791	1229.5789	0.13	0	23	0.084	1	U	L.SKDEG
2828	621.2540	1240.4934	1240.4931	0.20	0	(26)	0.012	1	U	Y.AHVDC
2829	621.2551	1240.4957	1240.4931	2.07	0	33	0.003	1	U	Y.AHVDC
2854	623.8220	1245.6295	1245.6275	1.63	1	58	3.1e-05	1	U	L.ELVEM
2855	623.8223	1245.6301	1245.6275	2.13	1	(56)	5.6e-05	1	U	L.ELVEM
2945	631.8177	1261.6208	1261.6224	-1.23	1	(33)	0.011	1	U	L.ELVEM
2946	631.8180	1261.6214	1261.6224	-0.75	1	(37)	0.0048	1	U	L.ELVEM
2947	631.8182	1261.6218	1261.6224	-0.45	1	(28)	0.037	1	U	L.ELVEM
2948	631.8188	1261.6230	1261.6224	0.52	1	(31)	0.017	1	U	L.ELVEM
2949	631.8195	1261.6244	1261.6224	1.58	1	(46)	0.00059	1	U	L.ELVEM
3339	664.8436	1327.6727	1327.6732	-0.36	1	56	4.2e-05	1	U	L.LDEGR
3340	664.8450	1327.6754	1327.6732	1.66	1	(49)	0.00017	1	U	L.LDEGR
3341	664.8456	1327.6766	1327.6732	2.58	1	(56)	4.4e-05	1	U	L.DEGRA
3342	664.8457	1327.6768	1327.6732	2.76	1	56	3.9e-05	1	U	L.DEGRA
3536	688.3609	1374.7072	1374.7064	0.59	2	33	0.0098	2	U	L.ELVEM
3537	688.3626	1374.7107	1374.7064	3.08	2	(27)	0.044	2	U	L.ELVEM
3555	462.2397	1383.6972	1383.6969	0.25	1	44	0.00063	1	U	L.IHPIA
3556	462.2397	1383.6977	1383.6969	0.60	1	(32)	0.01	1	U	L.IHPIA
3557	462.2399	1383.6979	1383.6969	0.70	1	(44)	0.00072	1	U	L.IHPIA

3558	692.8569	1383.6993	1383.6969	1.74	1	(27)	0.037	1	U	L.IHP
3634	700.8525	1399.6904	1399.6918	-1.01	1	(33)	0.0087	1	U	L.IHP
3635	467.5710	1399.6912	1399.6918	-0.44	1	(39)	0.0025	1	U	L.IHP
3636	467.5715	1399.6927	1399.6918	0.61	1	(37)	0.0039	1	U	L.IHP
3637	700.8549	1399.6952	1399.6918	2.39	1	(39)	0.0024	1	U	L.IHP
3665	706.3835	1410.7524	1410.7507	1.22	0	(24)	0.051	1	U	Y.IPEPE
3666	706.3852	1410.7558	1410.7507	3.64	0	30	0.012	1	U	Y.IPEPE
3809	721.3860	1440.7574	1440.7572	0.12	2	(40)	0.0016	1	U	L.LDEGR
3810	721.3867	1440.7589	1440.7572	1.14	2	65	4.5e-06	1	U	L.LDEGR
3869	486.2554	1455.7445	1455.7470	-1.76	1	(21)	0.12	1	U	Y.ILSKD
3870	486.2564	1455.7473	1455.7470	0.20	1	(22)	0.11	1	U	Y.ILSKD
3872	728.8812	1455.7478	1455.7470	0.51	1	34	0.0066	1	U	Y.ILSKD
3875	728.8822	1455.7498	1455.7470	1.94	1	(32)	0.012	1	U	Y.ILSKD
3876	728.8827	1455.7508	1455.7470	2.61	1	(30)	0.017	1	U	Y.ILSKD
3877	728.8835	1455.7524	1455.7470	3.70	1	(30)	0.016	1	U	Y.ILSKD
3960	740.8198	1479.6250	1479.6221	1.92	1	(37)	0.0018	1	U	L.NKCDM
3961	740.8198	1479.6251	1479.6221	2.00	1	(28)	0.015	1	U	L.NKCDM
4024	748.8160	1495.6174	1495.6171	0.24	1	(37)	0.0016	1	U	L.NKCDM
4025	748.8178	1495.6211	1495.6171	2.69	1	37	0.0014	1	U	L.NKCDM
4291	780.3888	1558.7630	1558.7628	0.17	0	(50)	0.00022	1	U	Y.DFPGD
4292	780.3889	1558.7633	1558.7628	0.34	0	(47)	0.00043	1	U	Y.DFPGD
4293	780.3894	1558.7642	1558.7628	0.96	0	70	2.1e-06	1	U	Y.DFPGD
4294	780.3895	1558.7644	1558.7628	1.05	0	(64)	8.6e-06	1	U	Y.DFPGD
4295	780.3896	1558.7646	1558.7628	1.20	0	(54)	9.3e-05	1	U	Y.DFPGD
4296	780.3915	1558.7684	1558.7628	3.63	0	(39)	0.0024	1	U	Y.DFPGD
4447	797.3605	1592.7064	1592.7062	0.12	2	(48)	0.00025	1	U	F.LNKCD
4448	797.3608	1592.7070	1592.7062	0.51	2	(58)	2.6e-05	1	U	F.LNKCD
4516	805.3591	1608.7036	1608.7011	1.54	2	(37)	0.0023	1	U	F.LNKCD
4517	805.3592	1608.7039	1608.7011	1.76	2	(24)	0.05	1	U	F.LNKCD
4518	805.3593	1608.7041	1608.7011	1.84	2	(39)	0.0016	1	U	F.LNKCD
4519	805.3600	1608.7054	1608.7011	2.68	2	59	1.5e-05	1	U	F.LNKCD
4520	805.3604	1608.7061	1608.7011	3.13	2	(27)	0.026	1	U	F.LNKCD
4597	816.9262	1631.8377	1631.8375	0.16	0	53	0.00011	1	U	Y.VKNMI
4598	816.9285	1631.8424	1631.8375	3.01	0	(40)	0.0024	1	U	Y.VKNMI
4649	824.9239	1647.8333	1647.8324	0.58	0	(40)	0.0022	1	U	Y.VKNMI
4650	824.9243	1647.8341	1647.8324	1.03	0	(35)	0.0069	1	U	Y.VKNMI
4733	832.9212	1663.8278	1663.8273	0.32	0	(29)	0.034	1	U	Y.VKNMI
4736	832.9217	1663.8288	1663.8273	0.91	0	(25)	0.079	1	U	Y.VKNMI
4737	832.9219	1663.8292	1663.8273	1.14	0	(24)	0.09	1	U	Y.VKNMI
4739	832.9227	1663.8309	1663.8273	2.16	0	(46)	0.00058	1	U	Y.VKNMI
4944	863.4851	1724.9555	1724.9533	1.30	2	44	0.00039	1	U	F.RKLLD
4946	863.4869	1724.9592	1724.9533	3.42	2	(25)	0.031	1	U	F.RKLLD
5096	888.9431	1775.8717	1775.8730	-0.73	1	24	0.1	1	U	L.DSYIP
5097	888.9431	1775.8717	1775.8730	-0.73	1	(23)	0.14	1	U	L.DSYIP
5364	630.6599	1888.9579	1888.9570	0.45	2	(20)	0.23	1	U	F.LDSYI
5365	630.6600	1888.9583	1888.9570	0.64	2	(21)	0.17	1	U	F.LDSYI
5366	945.4868	1888.9590	1888.9570	1.02	2	27	0.049	1	U	F.LDSYI
5367	630.6603	1888.9592	1888.9570	1.14	2	(22)	0.13	1	U	F.LDSYI
5368	945.4891	1888.9636	1888.9570	3.46	2	(22)	0.13	1	U	F.LDSYI
5369	630.6622	1888.9649	1888.9570	4.14	2	(21)	0.19	1	U	F.LDSYI

Proteins matching the same set of peptides:

[2::sp|P0CE48|EFTU2_ECOLI](#) Mass: 43457 Score: 951 Matches: 85(69) Sequences:
Elongation factor Tu 2 OS=Escherichia coli (strain K12) OX=83333 GN=tufB PE=1 SV=1

3. [1::sp|cRAP022|P00766|CTRA_BOVIN](#) Mass: 26220 Score: 863 Matches: 71 (64) Seq

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

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

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
365	412.7289	823.4433	823.4440	-0.76	1	(30)	0.0068	1	U	L.KLST
366	412.7290	823.4434	823.4440	-0.61	1	(29)	0.009	1	U	L.KLST
367	412.7292	823.4438	823.4440	-0.23	1	55	1.9e-05	1	U	L.KLST
368	412.7295	823.4444	823.4440	0.50	1	(50)	5.9e-05	1	U	L.KLST
369	412.7298	823.4450	823.4440	1.33	1	(52)	4.1e-05	1	U	L.KLST
370	412.7298	823.4451	823.4440	1.40	1	(50)	7.2e-05	1	U	L.KLST
579	437.7554	873.4963	873.4960	0.33	1	(42)	0.0008	1	U	W.TLVG
580	437.7557	873.4968	873.4960	0.91	1	57	2.6e-05	1	U	W.TLVG
725	452.2427	902.4709	902.4709	-0.04	0	42	0.0011	1	U	L.TINN
726	452.2427	902.4709	902.4709	0.03	0	(36)	0.0047	1	U	L.TINN
1067	482.2378	962.4611	962.4644	-3.41	0	23	0.071	1	U	L.VCKK
1225	494.2670	986.5194	986.5185	0.92	1	(29)	0.018	1	U	L.VNWW
1226	494.2674	986.5203	986.5185	1.79	1	(21)	0.11	1	U	L.VNWW
1238	494.7583	987.5020	987.5025	-0.57	1	(28)	0.023	1	U	L.VNWW
1239	494.7584	987.5023	987.5025	-0.26	1	31	0.012	1	U	L.VNWW
1322	501.2545	1000.4944	1000.4938	0.67	0	(26)	0.029	1	U	Y.TNAN
1323	501.2545	1000.4944	1000.4938	0.67	0	(26)	0.029	1	U	Y.TNAN
1326	501.2548	1000.4950	1000.4938	1.21	0	(28)	0.021	1	U	Y.TNAN
1327	501.2552	1000.4959	1000.4938	2.19	0	30	0.014	1	U	Y.TNAN
1405	508.7845	1015.5544	1015.5550	-0.55	1	50	0.00015	1	U	L.TINN
1406	508.7849	1015.5551	1015.5550	0.18	1	(50)	0.00016	1	U	L.TINN
1407	508.7852	1015.5559	1015.5550	0.91	1	(25)	0.039	1	U	L.TINN
1408	508.7856	1015.5566	1015.5550	1.62	1	(40)	0.0015	1	U	L.TINN
1409	508.7858	1015.5571	1015.5550	2.11	1	(40)	0.0013	1	U	L.TINN
1410	508.7860	1015.5575	1015.5550	2.47	1	(46)	0.00037	1	U	L.TINN
1502	515.2960	1028.5774	1028.5767	0.64	1	26	0.027	1	U	Y.ARVV
1503	515.2961	1028.5776	1028.5767	0.88	1	(23)	0.049	1	U	Y.ARVV
2042	561.7925	1121.5704	1121.5717	-1.15	1	83	1e-07	1	U	W.QVSL
2043	561.7927	1121.5708	1121.5717	-0.83	1	(56)	4.6e-05	1	U	W.QVSL
2044	561.7927	1121.5708	1121.5717	-0.83	1	(43)	0.00098	1	U	W.QVSL
2046	561.7929	1121.5713	1121.5717	-0.39	1	(56)	5e-05	1	U	W.QVSL
2047	561.7930	1121.5714	1121.5717	-0.28	1	(37)	0.0046	1	U	W.QVSL
2051	561.7938	1121.5731	1121.5717	1.24	1	(56)	4.8e-05	1	U	W.QVSL
2052	561.7939	1121.5733	1121.5717	1.47	1	(40)	0.0021	1	U	W.QVSL
2102	564.2795	1126.5444	1126.5441	0.30	1	29	0.017	1	U	L.LSNT
2251	575.2539	1148.4933	1148.4921	1.06	1	30	0.0099	1	U	F.CGGS
2252	575.2539	1148.4933	1148.4921	1.06	1	(24)	0.035	1	U	F.CGGS
3184	652.2777	1302.5409	1302.5398	0.80	0	(24)	0.025	1	U	W.GSST
3185	652.2786	1302.5427	1302.5398	2.21	0	29	0.008	1	U	W.GSST
3270	660.3437	1318.6728	1318.6728	-0.01	0	(26)	0.047	1	U	F.DQGS
3271	440.5649	1318.6729	1318.6728	0.05	0	(30)	0.019	1	U	F.DQGS
3273	660.3438	1318.6729	1318.6728	0.08	0	69	2.5e-06	1	U	F.DQGS
3274	660.3438	1318.6731	1318.6728	0.18	0	(49)	0.00025	1	U	F.DQGS
3276	660.3440	1318.6734	1318.6728	0.45	0	(55)	6.7e-05	1	U	F.DQGS
3277	440.5653	1318.6742	1318.6728	1.03	0	(24)	0.076	1	U	F.DQGS
3278	660.3447	1318.6748	1318.6728	1.48	0	(49)	0.00026	1	U	F.DQGS
3279	660.3451	1318.6757	1318.6728	2.21	0	(39)	0.0027	1	U	F.DQGS
3280	660.3452	1318.6759	1318.6728	2.30	0	(45)	0.00059	1	U	F.DQGS
3281	660.3454	1318.6762	1318.6728	2.59	0	(38)	0.0033	1	U	F.DQGS
3282	660.3467	1318.6788	1318.6728	4.53	0	(26)	0.052	1	U	F.DQGS
3283	440.8924	1319.6555	1319.6568	-1.05	0	(22)	0.13	1	U	F.DQGS

3284	660.8365	1319.6584	1319.6568	1.20	0	(39)	0.0026	1	U	F.DQGS
3352	665.8641	1329.7136	1329.7140	-0.29	2	79	1.9e-07	1	U	Y.NSLT
3353	665.8650	1329.7154	1329.7140	1.09	2	(48)	0.00028	1	U	Y.NSLT
3774	717.3181	1432.6217	1432.6194	1.61	2	(33)	0.0054	1	U	F.HFCG
3775	717.3197	1432.6248	1432.6194	3.81	2	38	0.0019	1	U	F.HFCG
4827	842.3810	1682.7474	1682.7458	0.96	0	46	0.00036	1	U	F.SQTV
4828	842.3821	1682.7496	1682.7458	2.27	0	(30)	0.016	1	U	F.SQTV
4974	869.9580	1737.9015	1737.9009	0.30	1	(26)	0.045	1	U	Y.TNAN
4975	869.9581	1737.9016	1737.9009	0.37	1	47	0.00032	1	U	Y.TNAN
4976	869.9583	1737.9021	1737.9009	0.65	1	(20)	0.15	1	U	Y.TNAN
4977	869.9587	1737.9028	1737.9009	1.07	1	(42)	0.0011	1	U	Y.TNAN
4979	869.9591	1737.9037	1737.9009	1.57	1	(27)	0.03	1	U	Y.TNAN
4980	869.9596	1737.9046	1737.9009	2.12	1	(21)	0.12	1	U	Y.TNAN
4985	869.9612	1737.9078	1737.9009	3.95	1	(37)	0.0029	1	U	Y.TNAN
4987	870.4553	1738.8961	1738.8849	6.41	1	(40)	0.0017	1	U	Y.TNAN
4988	870.4570	1738.8995	1738.8849	8.37	1	(30)	0.015	1	U	Y.TNAN
5112	892.4427	1782.8708	1782.8689	1.07	0	37	0.0045	1	U	L.SRIV
5285	926.5011	1850.9876	1850.9850	1.43	2	24	0.056	1	U	Y.TNAN
5621	1009.9998	2017.9851	2017.9780	3.54	0	40	0.0021	1	U	W.VVTA
5622	1009.9999	2017.9853	2017.9780	3.66	0	(23)	0.12	1	U	W.VVTA

Proteins matching a subset of these peptides:

[1::sp|cRAP023|P00767|CTRB_BOVIN](#) Mass: 26309 Score: 40 Matches: 2 (1) Sequences: 1
 Chymotrypsinogen B OS=Bos taurus PE=1 SV=1

4. [2::sp|P0C8J8|GATZ_ECOLI](#) Mass: 47535 Score: 614 Matches: 30 (29) Sequences: 30
 D-tagatose-1,6-bisphosphate aldolase subunit GatZ 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
118	391.7090	781.4033	781.4044	-1.33	0	(23)	0.052	1	U	L.IMDKI
119	391.7091	781.4036	781.4044	-1.00	0	(22)	0.061	1	U	L.IMDKI
215	399.7065	797.3985	797.3993	-0.98	0	32	0.0057	1	U	L.IMDKI
216	399.7068	797.3991	797.3993	-0.27	0	(26)	0.023	1	U	L.IMDKI
348	410.2396	818.4646	818.4650	-0.47	1	35	0.0027	1	U	F.ALREA
349	410.2397	818.4648	818.4650	-0.22	1	(30)	0.0085	1	U	F.ALREA
407	416.7491	831.4837	831.4854	-2.13	1	(33)	0.003	1		L.KVGPA
408	416.7498	831.4850	831.4854	-0.57	1	44	0.00021	1		L.KVGPA
504	425.7368	849.4591	849.4596	-0.63	0	35	0.0032	1	U	F.TIADK
505	425.7370	849.4594	849.4596	-0.28	0	(29)	0.014	1	U	F.TIADK
819	458.2374	914.4603	914.4610	-0.77	1	25	0.032	1	U	W.ELVRD
820	458.2376	914.4606	914.4610	-0.44	1	(25)	0.035	1	U	W.ELVRD
879	466.2456	930.4766	930.4770	-0.48	0	(25)	0.046	1	U	F.ERIQS
880	466.2459	930.4771	930.4770	0.12	0	35	0.005	1	U	F.ERIQS
1298	499.7383	997.4620	997.4617	0.28	0	20	0.14	1	U	F.DHSNI
1398	507.7771	1013.5397	1013.5393	0.41	1	(49)	0.00012	1	U	F.ALAQI
1399	507.7776	1013.5407	1013.5393	1.38	1	54	3.9e-05	1	U	F.ALAQI
1452	511.7672	1021.5199	1021.5193	0.60	2	(26)	0.048	1	U	Y.RTGFN
1453	511.7676	1021.5207	1021.5193	1.44	2	36	0.0047	1	U	Y.RTGFN
1536	521.2555	1040.4964	1040.4961	0.35	0	34	0.0058	1	U	W.IENTR
2734	613.8397	1225.6649	1225.6666	-1.42	0	(45)	0.00035	1	U	L.APETV
2735	613.8402	1225.6659	1225.6666	-0.62	0	55	3.1e-05	1	U	L.APETV
2876	625.8051	1249.5955	1249.5939	1.34	0	65	6.9e-06	1	U	L.IEATS
2877	625.8052	1249.5958	1249.5939	1.55	0	(50)	0.00022	1	U	L.IEATS

3083	644.2885	1286.5625	1286.5602	1.80	1	24	0.049	1	U	Y.TGMT
4383	789.3674	1576.7202	1576.7151	3.22	0	(46)	0.00052	1	U	F.AAESV
4384	789.3674	1576.7203	1576.7151	3.29	0	63	8.9e-06	1	U	F.AAESV
4727	831.8865	1661.7585	1661.7566	1.15	0	(54)	7.9e-05	1	U	W.QQENA
4778	839.8850	1677.7553	1677.7515	2.27	0	(58)	3.2e-05	1	U	W.QQENA
4779	839.8861	1677.7577	1677.7515	3.65	0	58	2.9e-05	1	U	W.QQENA

5. [2::sp|P0AAI5|FABF_ECOLI](#) Mass: 43247 Score: 462 Matches: 23(21) Sequences:
 3-oxoacyl-[acyl-carrier-protein] synthase 2 OS=Escherichia coli (strain K12) OX=83333
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
245	401.7241	801.4337	801.4344	-0.95	0	(29)	0.018	1	U	F.GEAA
246	401.7242	801.4337	801.4344	-0.87	0	30	0.014	1	U	F.GEAA
1981	556.7828	1111.5510	1111.5509	0.07	1	42	0.00075	1	U	L.GLIE
1982	556.7828	1111.5511	1111.5509	0.17	1	(32)	0.0084	1	U	L.GLIE
2846	622.8164	1243.6181	1243.6197	-1.25	1	(38)	0.0024	1	U	L.AGQS
2847	622.8178	1243.6211	1243.6197	1.10	1	55	5.8e-05	1	U	L.AGQS
3034	640.3179	1278.6212	1278.6204	0.61	0	(33)	0.012	1	U	L.RDAG
3035	640.3193	1278.6240	1278.6204	2.80	0	41	0.0016	1	U	L.RDAG
3451	679.3593	1356.7041	1356.7038	0.22	2	83	8.9e-08	1	U	L.LAGQ
3452	679.3611	1356.7076	1356.7038	2.83	2	(70)	1.6e-06	1	U	L.LAGQ
3507	684.8150	1367.6154	1367.6140	1.09	0	(47)	0.00032	1	U	Y.HMTS
3508	684.8159	1367.6172	1367.6140	2.35	0	(33)	0.0098	1	U	Y.HMTS
3509	684.8164	1367.6183	1367.6140	3.16	0	61	1.5e-05	1	U	Y.HMTS
3951	739.3561	1476.6976	1476.6919	3.87	1	43	0.0012	1	U	L.GMLS
4007	747.3517	1492.6888	1492.6868	1.34	1	(33)	0.011	1	U	L.GMLS
4008	747.3530	1492.6915	1492.6868	3.15	1	(23)	0.1	1	U	L.GMLS
4464	533.9253	1598.7540	1598.7549	-0.56	0	(26)	0.051	1	U	L.STRN
4465	800.3856	1598.7566	1598.7549	1.02	0	(30)	0.021	1	U	L.STRN
4466	533.9262	1598.7566	1598.7549	1.05	0	34	0.0079	1	U	L.STRN
4467	800.3883	1598.7621	1598.7549	4.46	0	(30)	0.019	1	U	L.STRN
4872	852.9092	1703.8039	1703.8036	0.18	0	40	0.0025	1	U	Y.GDAD
4873	852.9101	1703.8056	1703.8036	1.19	0	(28)	0.032	1	U	Y.GDAD
5907	1212.0801	2422.1456	2422.1434	0.89	2	37	0.0045	1	U	L.ALRD

6. [2::sp|P0A6A3|ACKA_ECOLI](#) Mass: 43605 Score: 386 Matches: 23(19) Sequences:
 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
135	393.7576	785.5007	785.5011	-0.48	2	23	0.015	1	U	L.SLGKL
652	442.2178	882.4210	882.4195	1.66	0	(41)	0.0011	1	U	L.GAGAA
653	442.2183	882.4220	882.4195	2.77	0	42	0.00078	1	U	L.GAGAA
1128	486.7775	971.5405	971.5400	0.55	0	41	0.00096	1	U	L.VIAQD
1129	486.7776	971.5406	971.5400	0.67	0	(40)	0.0012	1	U	L.VIAQD
1346	503.7654	1005.5162	1005.5165	-0.25	0	(40)	0.0016	1	U	Y.VTQEA
1347	503.7654	1005.5162	1005.5165	-0.25	0	40	0.0016	1	U	Y.VTQEA
1373	506.2462	1010.4779	1010.4781	-0.21	0	21	0.11	1	U	F.EVDHE
1743	542.8032	1083.5918	1083.5924	-0.58	1	33	0.0039	1	U	L.AQKPE
1744	542.8044	1083.5942	1083.5924	1.68	1	(33)	0.0041	1	U	L.AQKPE
2157	569.2278	1136.4411	1136.4444	-2.90	0	28	0.0042	1	U	F.HQTMP

2158	569.2288	1136.4430	1136.4444	-1.28	0	(28)	0.0048	1	U	F.HQTMP
2159	569.2301	1136.4456	1136.4444	1.07	0	(24)	0.015	1	U	F.HQTMP
2396	585.2976	1168.5805	1168.5798	0.65	1	33	0.006	1	U	F.YVTQE
2397	585.2993	1168.5841	1168.5798	3.68	1	(31)	0.0098	1	U	F.YVTQE
3170	650.7974	1299.5802	1299.5765	2.80	1	(42)	0.00071	1	U	L.GLTEV
3171	650.7976	1299.5807	1299.5765	3.19	1	55	4.3e-05	1	U	L.GLTEV
3724	712.3660	1422.7175	1422.7177	-0.14	2	39	0.0028	1	U	Y.TALMD
3725	712.3675	1422.7204	1422.7177	1.91	2	(24)	0.086	1	U	Y.TALMD
5546	660.6962	1979.0669	1979.0687	-0.94	0	(23)	0.062	1	U	F.INKEG
5547	660.6973	1979.0700	1979.0687	0.63	0	(29)	0.014	1	U	F.INKEG
5548	990.5435	1979.0725	1979.0687	1.90	0	33	0.0049	1	U	F.INKEG
5549	990.5439	1979.0732	1979.0687	2.26	0	(20)	0.1	1	U	F.INKEG

7. [2::sp|P02931|OMP_F_ECOLI](#) Mass: 39309 Score: 376 Matches: 18(18) Sequences:
 Outer membrane protein F OS=Escherichia coli (strain K12) OX=83333 GN=ompF PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
599	438.7507	875.4869	875.4865	0.49	1	23	0.044	1	U	F.GLRPS
1175	489.7717	977.5289	977.5294	-0.55	0	(27)	0.023	1	U	F.VGRVG
1176	489.7718	977.5290	977.5294	-0.43	0	39	0.0016	1	U	F.VGRVG
1884	551.7440	1101.4734	1101.4727	0.62	1	(25)	0.027	1	U	Y.FSKGN
1885	551.7445	1101.4745	1101.4727	1.62	1	36	0.002	1	U	Y.FSKGN
2373	583.2955	1164.5764	1164.5775	-0.94	1	30	0.018	1	U	Y.NKDG
2376	583.2962	1164.5778	1164.5775	0.31	1	(29)	0.023	1	U	Y.NKDG
3009	636.8442	1271.6739	1271.6721	1.43	0	64	5.9e-06	1	U	Y.IINQI
3010	636.8450	1271.6755	1271.6721	2.68	0	(46)	0.00044	1	U	Y.IINQI
3730	713.3461	1424.6777	1424.6783	-0.44	1	45	0.00061	1	U	F.KGETQ
3731	713.3476	1424.6806	1424.6783	1.63	1	(35)	0.0066	1	U	F.KGETQ
3766	716.8007	1431.5868	1431.5864	0.24	1	70	6.2e-07	1	U	Y.TDMLP
3767	716.8025	1431.5905	1431.5864	2.88	1	(44)	0.00031	1	U	Y.TDMLP
3966	742.3794	1482.7442	1482.7426	1.07	1	(35)	0.0049	1	U	Y.GAADR
3967	742.3804	1482.7463	1482.7426	2.47	1	(32)	0.01	1	U	Y.GAADR
3972	742.8715	1483.7284	1483.7267	1.16	1	(34)	0.0065	1	U	Y.GAADR
3973	742.8727	1483.7308	1483.7267	2.80	1	37	0.0038	1	U	Y.GAADR
5312	620.9646	1859.8720	1859.8722	-0.10	0	31	0.016	1	U	F.QGNNS

8. [2::sp|P0A953|FABF_ECOLI](#) Mass: 42928 Score: 305 Matches: 15(13) Sequences:
 3-oxoacyl-[acyl-carrier-protein] synthase 1 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
257	403.2318	804.4491	804.4494	-0.38	0	(34)	0.0037	1	U	L.AAIRE
258	403.2319	804.4492	804.4494	-0.15	0	36	0.0022	1	U	L.AAIRE
3056	641.3060	1280.5974	1280.5997	-1.78	0	(27)	0.045	1	U	Y.NDTPE
3057	641.3084	1280.6021	1280.5997	1.94	0	32	0.014	1	U	Y.NDTPE
3110	645.8332	1289.6518	1289.6463	4.29	0	39	0.0028	1	U	L.NIVTE
3111	645.8348	1289.6551	1289.6463	6.84	0	(25)	0.07	1	U	L.NIVTE
3660	705.3626	1408.7105	1408.7054	3.63	0	36	0.0049	1	U	Y.VVTKA
3884	729.3857	1456.7568	1456.7522	3.19	0	42	0.0011	1	U	L.GIVSS
3885	729.3865	1456.7585	1456.7522	4.37	0	(35)	0.0061	1	U	L.GIVSS
4202	514.2571	1539.7496	1539.7529	-2.16	0	21	0.18	1	U	L.NSHGT

4669	551.9535	1652.8388	1652.8370	1.12	1	(40)	0.0018	1	U	Y.LNSHG
4670	551.9537	1652.8392	1652.8370	1.34	1	(32)	0.011	1	U	Y.LNSHG
4671	827.4273	1652.8401	1652.8370	1.87	1	68	2.9e-06	1	U	Y.LNSHG
4672	827.4278	1652.8410	1652.8370	2.46	1	(53)	9.7e-05	1	U	Y.LNSHG
4749	834.8758	1667.7370	1667.7348	1.32	1	30	0.018	1	U	L.SMEQA

9. [2::sp|P08200|IDH_ECOLI](#) Mass: 46070 Score: 280 Matches: 13(13) Sequences: 6
 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
988	477.2221	952.4295	952.4290	0.53	1	(27)	0.028	1	U	F.TEGAF
989	477.2224	952.4301	952.4290	1.16	1	29	0.019	1	U	F.TEGAF
2285	578.3088	1154.6031	1154.5972	5.17	0	30	0.012	1	U	L.NVPEN
2431	587.8071	1173.5996	1173.5990	0.54	0	(30)	0.022	1	U	Y.AIAND
2432	587.8071	1173.5997	1173.5990	0.64	0	35	0.0062	1	U	Y.AIAND
2535	398.2236	1191.6489	1191.6499	-0.87	0	(48)	0.0002	1	U	L.KVVDA
2536	398.2238	1191.6496	1191.6499	-0.24	0	(27)	0.025	1	U	L.KVVDA
2537	596.8328	1191.6510	1191.6499	0.88	0	(52)	8.4e-05	1	U	L.KVVDA
2538	596.8330	1191.6515	1191.6499	1.30	0	71	1e-06	1	U	L.KVVDA
3232	656.3663	1310.7181	1310.7194	-0.99	0	59	1.1e-05	1	U	Y.AGQDK
3233	656.3688	1310.7230	1310.7194	2.73	0	(50)	8.1e-05	1	U	Y.AGQDK
3714	711.3859	1420.7573	1420.7562	0.80	0	57	3.1e-05	1	U	W.KADSA
3715	711.3867	1420.7588	1420.7562	1.83	0	(49)	0.00017	1	U	W.KADSA

10. [2::sp|P0ABH7|CISY_ECOLI](#) Mass: 48383 Score: 244 Matches: 14(13) Sequences: 6
 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
1661	532.7597	1063.5048	1063.5047	0.18	0	22	0.13	1	U	W.GPAHG
1864	550.7603	1099.5059	1099.5042	1.59	0	30	0.014	1	U	L.KAMGI
2539	597.2753	1192.5361	1192.5360	0.08	0	28	0.029	1	U	L.NGEKP
2540	597.2758	1192.5370	1192.5360	0.80	0	(25)	0.048	1	U	L.NGEKP
2544	597.7701	1193.5256	1193.5200	4.68	0	(25)	0.046	1	U	L.NGEKP
3829	725.3590	1448.7033	1448.7068	-2.42	2	(40)	0.003	1	U	L.GTKDD
3830	725.3628	1448.7111	1448.7068	2.97	2	52	0.00019	1	U	L.GTKDD
4152	510.2943	1527.8611	1527.8621	-0.63	1	38	0.0016	1	U	L.KGTLG
4153	510.2943	1527.8612	1527.8621	-0.57	1	(36)	0.0026	1	U	L.KGTLG
4182	767.3942	1532.7738	1532.7722	1.03	2	(39)	0.003	1	U	Y.ILLNG
4183	767.3944	1532.7743	1532.7722	1.35	2	40	0.0025	1	U	Y.ILLNG
4410	792.8454	1583.6762	1583.6740	1.44	1	(30)	0.013	1	U	L.NGEKP
4411	792.8461	1583.6776	1583.6740	2.29	1	35	0.0036	1	U	L.NGEKP
4418	793.3384	1584.6622	1584.6580	2.67	1	(34)	0.0032	1	U	L.NGEKP

11. [2::sp|P0A749|MURA_ECOLI](#) Mass: 45132 Score: 241 Matches: 13(10) Sequences: 6
 UDP-N-acetylglucosamine 1-carboxyvinyltransferase 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
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685	449.7762	897.5379	897.5396	-1.93	0	36	0.00094	1	U	F.RVQG
1694	536.7913	1071.5681	1071.5672	0.79	0	25	0.04	1	U	L.GANI
3642	702.3851	1402.7556	1402.7569	-0.91	0	(25)	0.056	1	U	Y.RVLP
3643	702.3865	1402.7585	1402.7569	1.18	0	27	0.033	1	U	Y.RVLP
4993	582.2880	1743.8421	1743.8428	-0.40	1	46	0.00058	1	U	L.AKLR
4994	872.9305	1743.8464	1743.8428	2.09	1	(42)	0.0014	1	U	L.AKLR
4995	582.2895	1743.8468	1743.8428	2.33	1	(24)	0.092	1	U	L.AKLR
4996	872.9337	1743.8529	1743.8428	5.81	1	(41)	0.0018	1	U	L.AKLR
5239	918.9821	1835.9496	1835.9451	2.41	1	(52)	0.00013	1	U	L.VLAG
5240	918.9826	1835.9506	1835.9451	3.00	1	64	9.1e-06	1	U	L.VLAG
5867	787.7256	2360.1551	2360.1496	2.36	0	(25)	0.071	1	U	L.AEGT
5868	787.7269	2360.1588	2360.1496	3.91	0	(32)	0.014	1	U	L.AEGT
5869	1181.0869	2360.1593	2360.1496	4.12	0	46	0.00058	1	U	L.AEGT

12. [2::sp|P31979|NUOF_ECOLI](#) Mass: 49774 Score: 186 Matches: 10(9) Sequences: 6
 NADH-quinone oxidoreductase subunit F OS=Escherichia coli (strain K12) OX=83333 GN=r
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
160	396.6867	791.3589	791.3596	-0.84	0	24	0.037	1	U	Y.AGGMR
161	396.6868	791.3590	791.3596	-0.76	0	(24)	0.044	1	U	Y.AGGMR
162	396.6874	791.3602	791.3596	0.78	0	(24)	0.044	1	U	Y.AGGMR
1579	527.2723	1052.5300	1052.5291	0.88	2	36	0.0044	1	U	L.VRNLE
3401	674.3670	1346.7194	1346.7194	0.05	2	24	0.065	1	U	F.LRGEY
3632	700.8369	1399.6593	1399.6579	0.96	0	27	0.037	1	U	L.EREGE
4076	757.3701	1512.7256	1512.7209	3.10	2	28	0.029	1	U	W.QPGGA
5071	885.9289	1769.8432	1769.8432	0.04	1	(43)	0.0013	1	U	L.EREGE
5072	885.9304	1769.8463	1769.8432	1.77	1	51	0.00018	1	U	L.EREGE
5073	885.9335	1769.8525	1769.8432	5.28	1	(45)	0.00069	1	U	L.EREGE

13. [2::sp|P0AG67|RS1_ECOLI](#) Mass: 61235 Score: 143 Matches: 6(6) Sequences: 3(3)
 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
2217	571.7971	1141.5796	1141.5768	2.45	2	(43)	0.00057	1	U	L.GLKQL
2218	571.7971	1141.5796	1141.5768	2.45	2	45	0.00041	1	U	L.GLKQL
2805	618.7976	1235.5807	1235.5782	2.00	0	51	0.00017	1	U	W.NVAGE
2806	618.7979	1235.5813	1235.5782	2.48	0	(30)	0.024	1	U	W.NVAGE
3123	646.8412	1291.6678	1291.6660	1.43	1	(44)	0.00073	1	U	L.VLSVG
3124	646.8422	1291.6699	1291.6660	3.02	1	48	0.0003	1	U	L.VLSVG

14. [2::sp|P0A855|TOLB_ECOLI](#) Mass: 45927 Score: 139 Matches: 5(4) Sequences: 3(3)
 Tol-Pal system protein TolB OS=Escherichia coli (strain K12) OX=83333 GN=tolB PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2641	605.3002	1208.5858	1208.5826	2.63	0	23	0.11	1	U	Y.VVQTN
2705	611.2967	1220.5788	1220.5786	0.21	0	41	0.0016	1	U	F.TSDQA
2706	611.2967	1220.5788	1220.5786	0.21	0	(41)	0.0018	1	U	F.TSDQA

4825	842.3586	1682.7026	1682.7020	0.36	0	(65)	2.7e-06	1	U	W.EGSQ
4826	842.3598	1682.7050	1682.7020	1.81	0	75	3e-07	1	U	W.EGSQ

15. [2::sp|P0AGJ9|SYY ECOLI](#) Mass: 47896 Score: 127 Matches: 5(4) Sequences: 3(3)
 Tyrosine--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=tyrS PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1180	490.7745	979.5344	979.5338	0.58	0	(29)	0.011	1	U	L.ITKAD
1181	490.7745	979.5345	979.5338	0.70	0	29	0.0097	1	U	L.ITKAD
1556	524.7877	1047.5608	1047.5600	0.69	1	(24)	0.064	1	U	W.LDPKK
1557	524.7883	1047.5620	1047.5600	1.86	1	29	0.019	1	U	W.LDPKK
4222	772.4018	1542.7890	1542.7889	0.07	1	72	1.3e-06	1	U	L.VAQVT

16. [2::sp|P0A817|METK ECOLI](#) Mass: 42153 Score: 126 Matches: 8(3) Sequences: 5(3)
 S-adenosylmethionine synthase OS=Escherichia coli (strain K12) OX=83333 GN=metK 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
463	422.2553	842.4960	842.4974	-1.62	2	23	0.038	1	U	L.LRDAAG
464	422.2556	842.4967	842.4974	-0.82	2	(23)	0.04	1	U	L.LRDAAG
1771	544.2852	1086.5559	1086.5557	0.18	0	23	0.072	1	U	F.GTEKVP
1773	544.2867	1086.5588	1086.5557	2.87	0	(20)	0.15	1	U	F.GTEKVP
2942	631.3487	1260.6828	1260.6826	0.16	1	23	0.073	1	U	W.LRPDAK
4394	790.8980	1579.7813	1579.7804	0.62	0	25	0.082	1	U	Y.AIGVAE
4494	802.9324	1603.8502	1603.8457	2.77	1	(20)	0.18	1	U	F.QYDDGK
4495	802.9327	1603.8508	1603.8457	3.15	1	31	0.013	1	U	F.QYDDGK

17. [2::sp|P31224|ACRB ECOLI](#) Mass: 113615 Score: 124 Matches: 6(5) Sequences: 4(3)
 Multidrug efflux pump subunit AcrB OS=Escherichia coli (strain K12) OX=83333 GN=acrB 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
457	422.1993	842.3839	842.3844	-0.52	0	31	0.0072	1	U	Y.VMSEAK
458	422.1997	842.3847	842.3844	0.43	0	(29)	0.01	1	U	Y.VMSEAK
1592	527.7668	1053.5190	1053.5165	2.40	0	24	0.054	1	U	F.SQIKDA
1807	546.2824	1090.5503	1090.5520	-1.55	0	26	0.042	1	U	F.AGRGQN
2243	573.8047	1145.5948	1145.5928	1.75	0	(37)	0.0042	1	U	L.GVSIND
2244	573.8051	1145.5957	1145.5928	2.49	0	43	0.001	1	U	L.GVSIND

18. [2::sp|P0A9B2|G3P1 ECOLI](#) Mass: 35681 Score: 120 Matches: 6(6) Sequences: 3(3)
 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
962	474.7794	947.5442	947.5440	0.15	0	(24)	0.024	1	U	M.TIKVG
963	474.7796	947.5447	947.5440	0.72	0	28	0.01	1	U	M.TIKVG
2867	624.8141	1247.6136	1247.6146	-0.77	1	(41)	0.0018	1	U	F.DAKAG

2868	624.8142	1247.6139	1247.6146	-0.58	1	44	0.00092	1	U	F.DAKAG
3141	648.3708	1294.7270	1294.7245	1.94	0	48	9.1e-05	1	U	F.RVPTP
3142	648.3708	1294.7270	1294.7245	1.94	0	(47)	0.00014	1	U	F.RVPTP

19. [2::sp|P24180|ACRE_ECOLI](#) Mass: 41350 Score: 112 Matches: 7(3) Sequences: 3
 Multidrug export protein AcrE OS=Escherichia coli (strain K12) OX=83333 GN=acrE 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
271	404.1984	806.3823	806.3810	1.59	0	21	0.13	1		Y.QIDPA
5262	614.6526	1840.9361	1840.9294	3.64	1	23	0.096	1	U	L.RAVFP
5265	921.4771	1840.9397	1840.9294	5.56	1	(21)	0.15	2	U	L.RAVFP
5808	1120.5375	2239.0604	2239.0645	-1.82	2	71	2e-06	1		L.ATVQQ
5809	1120.5413	2239.0680	2239.0645	1.56	2	(33)	0.012	1		L.ATVQQ
5810	747.3642	2239.0708	2239.0645	2.81	2	(34)	0.0093	1		L.ATVQQ
5811	747.3654	2239.0743	2239.0645	4.36	2	(24)	0.086	1		L.ATVQQ

20. [2::sp|P0A6B7|ISCS_ECOLI](#) Mass: 45232 Score: 112 Matches: 6(6) Sequences: 3
 Cysteine desulfurase IscS OS=Escherichia coli (strain K12) OX=83333 GN=iscS 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
156	396.2230	790.4315	790.4337	-2.82	0	(36)	0.003	1	U	L.AIKGAA
157	396.2239	790.4333	790.4337	-0.49	0	38	0.0016	1	U	L.AIKGAA
2410	586.3077	1170.6008	1170.5995	1.15	2	(32)	0.0086	1	U	- .MKLPIY
2411	586.3078	1170.6010	1170.5995	1.36	2	38	0.0019	1	U	- .MKLPIY
3092	644.8321	1287.6497	1287.6459	2.98	1	(33)	0.0097	1	U	Y.KQGVDL
3093	644.8322	1287.6499	1287.6459	3.08	1	38	0.0036	1	U	Y.KQGVDL

21. [2::sp|P07004|PROA_ECOLI](#) Mass: 45001 Score: 110 Matches: 4(3) Sequences: 3
 Gamma-glutamyl phosphate reductase OS=Escherichia coli (strain K12) OX=83333 GN=proA
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2446	588.7999	1175.5852	1175.6042	-16.21	1	22	0.17	2	U	L.CLKTKG
3512	685.8679	1369.7213	1369.7201	0.84	0	61	1e-05	1	U	Y.EARPNI
3513	685.8693	1369.7241	1369.7201	2.88	0	(51)	0.0001	1	U	Y.EARPNI
4868	850.9523	1699.8901	1699.8879	1.28	1	30	0.016	2	U	L.EKIAD

22. [2::sp|P0A836|SUCC_ECOLI](#) Mass: 41652 Score: 93 Matches: 3(2) Sequences: 3
 Succinate--CoA ligase [ADP-forming] subunit beta OS=Escherichia coli (strain K12) OX=83333 GN=sucC
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2317	580.3158	1158.6170	1158.6132	3.33	0	22	0.12	1	U	L.VEAATD
3289	661.8476	1321.6806	1321.6765	3.13	1	40	0.0017	1	U	L.VEAATD

[4656](#) 550.6224 1648.8455 1648.8421 2.08 1 31 0.021 1 U F.LDVGGG

23. [2::sp|P76373|UDG_ECOLI](#) Mass: 43744 Score: 91 Matches: 5(5) Sequences: 3(3)
UDP-glucose 6-dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=ugd 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
1818	547.3038	1092.5930	1092.5927	0.22	0	24	0.046	1	U	L.IAQNHE
2249	573.8353	1145.6560	1145.6557	0.26	0	(27)	0.016	1	U	L.SRKPOV
2250	573.8367	1145.6589	1145.6557	2.81	0	28	0.011	1	U	L.SRKPOV
3306	662.8350	1323.6554	1323.6558	-0.32	1	41	0.0016	1	U	F.TDSTEA
3307	662.8390	1323.6634	1323.6558	5.77	1	(35)	0.0072	1	U	F.TDSTEA

24. [2::sp|P0A9T0|SERA_ECOLI](#) Mass: 44376 Score: 81 Matches: 3(2) Sequences: 2(1)
D-3-phosphoglycerate dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=serA 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
282	404.7131	807.4116	807.4126	-1.31	1	23	0.069	1	U	W.NKLAA
4962	864.9491	1727.8836	1727.8829	0.44	0	60	1.9e-05	1	U	Y.VVIDI
4963	864.9524	1727.8903	1727.8829	4.32	0	(38)	0.0032	1	U	Y.VVIDI

25. [2::sp|P00509|AAT_ECOLI](#) Mass: 43831 Score: 80 Matches: 3(2) Sequences: 2(1)
Aspartate aminotransferase OS=Escherichia coli (strain K12) OX=83333 GN=aspC PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2719	612.8107	1223.6069	1223.6033	2.91	2	20	0.17	1	U	Y.LLENE
3046	640.8091	1279.6037	1279.6044	-0.56	0	(47)	0.00039	1	U	L.VAADS
3047	640.8104	1279.6062	1279.6044	1.35	0	62	1.4e-05	1	U	L.VAADS

26. [1::sp|cRAP087|P02769|ALBU_BOVIN](#) Mass: 71244 Score: 76 Matches: 3(3) Sequences: 3(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
2474	590.8279	1179.6413	1179.6400	1.10	2	(49)	0.00013	1	U	Y.GFQNA
2475	590.8292	1179.6439	1179.6400	3.27	2	54	4e-05	1	U	Y.GFQNA
4406	792.4543	1582.8940	1582.8930	0.62	2	23	0.039	1	U	F.AVEGP

27. [2::sp|P0AB71|ALF_ECOLI](#) Mass: 39351 Score: 71 Matches: 3(2) Sequences: 3(2)
Fructose-bisphosphate aldolase class 2 OS=Escherichia coli (strain K12) OX=83333 GN=ald
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2887	626.3887	1250.7629	1250.7598	2.46	1	24	0.0045	1	U	Y.KPGNVV

4569	541.9866	1622.9381	1622.9355	1.55	0	21	0.028	1	U	F.IAGKGV
4932	861.9006	1721.7866	1721.7857	0.54	0	25	0.063	1	U	F.HGSGS

28. [1::sp|cRAP112|P00761|TRYP_PIG](#) Mass: 25078 Score: 63 Matches: 3(2) Sequences: 2
 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
870	465.2564	928.4983	928.5052	-7.44	1	21	0.087	1	U	L.QCLKAP
2924	629.3333	1256.6521	1256.6513	0.59	1	42	0.001	1	U	Y.VNWIQQ
2925	629.3347	1256.6548	1256.6513	2.74	1	(41)	0.0012	1	U	Y.VNWIQQ

29. [2::sp|P0AFG3|ODO1_ECOLI](#) Mass: 105566 Score: 59 Matches: 3(3) Sequences: 2
 2-oxoglutarate dehydrogenase E1 component 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
1382	506.7212	1011.4278	1011.4258	1.98	0	25	0.029	1	U	L.SGEDSG
3064	641.8701	1281.7256	1281.7292	-2.87	1	34	0.0024	1	U	Y.ATLVDE
3065	641.8702	1281.7259	1281.7292	-2.59	1	(32)	0.0036	1	U	Y.ATLVDE

30. [2::sp|P0AEX9|MALE_ECOLI](#) Mass: 43360 Score: 56 Matches: 3(3) Sequences: 2
 Maltose-binding periplasmic protein OS=Escherichia coli (strain K12) OX=83333 GN=malt
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2997	636.3343	1270.6540	1270.6517	1.84	0	31	0.011	1	U	L.SAGINA
2998	636.3347	1270.6548	1270.6517	2.42	0	(28)	0.025	1	U	L.SAGINA
4220	514.9434	1541.8084	1541.8049	2.27	0	25	0.053	1	U	Y.DIKDVG

31. [2::sp|P0A799|PGK_ECOLI](#) Mass: 41264 Score: 53 Matches: 3(1) Sequences: 2(1)
 Phosphoglycerate kinase OS=Escherichia coli (strain K12) OX=83333 GN=pgk PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
532	433.7339	865.4533	865.4545	-1.35	0	22	0.065	1	U	F.GIADKI
533	433.7353	865.4561	865.4545	1.89	0	(21)	0.084	1	U	F.GIADKI
5923	820.0850	2457.2332	2457.2234	3.98	1	31	0.016	1	U	L.KSVNDV

32. [1::sp|cRAP054|P04264|K2C1_HUMAN](#) Mass: 66170 Score: 53 Matches: 2(2) Sequences: 2
 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
4086	757.7989	1513.5833	1513.5819	0.98	1	(34)	0.00082	1	U	Y.GSGGG
4087	757.8008	1513.5870	1513.5819	3.40	1	53	1.2e-05	1	U	Y.GSGGG

33. [2::sp|P02920|LACY_ECOLI](#) **Mass:** 46928 **Score:** 45 **Matches:** 2(2) **Sequences:** 2
 Lactose permease OS=Escherichia coli (strain K12) OX=83333 GN=lacY 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
3975	742.9202	1483.8258	1483.8432	-11.72	2	24	0.04	1	U	L.IINRI
4664	551.3326	1650.9759	1650.9491	16.3	2	21	0.018	1	U	F.APLII

34. [2::sp|P0A6K6|DEOB_ECOLI](#) **Mass:** 44684 **Score:** 45 **Matches:** 2(2) **Sequences:** 1
 Phosphopentomutase OS=Escherichia coli (strain K12) OX=83333 GN=deoB PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2371	583.2787	1164.5429	1164.5411	1.58	0	45	0.00064	1	U	F.GIGAT
2372	583.2790	1164.5434	1164.5411	1.99	0	(34)	0.0077	1	U	F.GIGAT

35. [2::sp|P77398|ARNA_ECOLI](#) **Mass:** 74869 **Score:** 45 **Matches:** 2(2) **Sequences:** 1
 Bifunctional polymyxin resistance protein ArnA OS=Escherichia coli (strain K12) OX=83333 GN=arnA 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
2878	625.8223	1249.6300	1249.6303	-0.22	1	45	0.0007	1	U	Y.GLDIGS
2879	625.8228	1249.6311	1249.6303	0.64	1	(38)	0.0029	1	U	Y.GLDIGS

36. [2::sp|P30176|RIBX_ECOLI](#) **Mass:** 18658 **Score:** 40 **Matches:** 1(1) **Sequences:** 1
 N-glycosidase YbiA OS=Escherichia coli (strain K12) OX=83333 GN=ybiA PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
843	459.7476	917.4807	917.4640	18.2	1	40	0.0016	1	U	L.MELREQ.

37. [2::sp|P36672|PTTBC_ECOLI](#) **Mass:** 51389 **Score:** 40 **Matches:** 1(1) **Sequences:** 1
 PTS system trehalose-specific EIIBC component OS=Escherichia coli (strain K12) OX=83333 GN=pttBC 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
4595	815.9174	1629.8203	1629.8145	3.58	0	40	0.0022	1	U	F.RNVIGD

38. [2::sp|P69924|RIR2_ECOLI](#) **Mass:** 43775 **Score:** 40 **Matches:** 2(2) **Sequences:** 1
 Ribonucleoside-diphosphate reductase 1 subunit beta OS=Escherichia coli (strain K12) OX=83333 GN=rir2 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
4258	776.3574	1550.7003	1550.7001	0.11	1	40	0.0016	1	U	F.VQAAQQ
4259	776.3602	1550.7059	1550.7001	3.73	1	(37)	0.0032	1	U	F.VQAAQQ

39. [2::sp|P0A825|GLYA ECOLI](#) Mass: 45459 Score: 37 Matches: 2(2) Sequences: 1(1)
 Serine hydroxymethyltransferase OS=Escherichia coli (strain K12) OX=83333 GN=glyA 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
1492	514.8025	1027.5905	1027.5914	-0.78	2	37	0.0018	1	U	F.LVDLVD
1493	514.8032	1027.5918	1027.5914	0.40	2	(26)	0.024	1	U	F.LVDLVD

40. [2::sp|Q47142|HCAT ECOLI](#) Mass: 41964 Score: 35 Matches: 2(2) Sequences: 1(1)
 Probable 3-phenylpropionic acid transporter OS=Escherichia coli (strain K12) OX=83333 GN=hcat 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
1465	513.3033	1024.5920	1024.5805	11.3	2	35	0.0013	1	U	F.SPLVPL
1466	513.3040	1024.5935	1024.5805	12.7	2	(22)	0.025	1	U	F.SPLVPL

41. [2::sp|P02930|TOLC ECOLI](#) Mass: 53708 Score: 33 Matches: 1(1) Sequences: 1(1)
 Outer membrane protein TolC OS=Escherichia coli (strain K12) OX=83333 GN=tolC PE=1 S=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
4190	768.9003	1535.7861	1535.7831	1.94	1	36	0.0056	1	U	L.TLQEK

42. [2::sp|P0A7Z4|RPOA ECOLI](#) Mass: 36717 Score: 33 Matches: 1(1) Sequences: 1(1)
 DNA-directed RNA polymerase subunit alpha OS=Escherichia coli (strain K12) OX=83333 GN=rpoA 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
3974	742.9200	1483.8254	1483.8246	0.54	2	33	0.0052	1	U	Y.IGDLVQ

43. [2::sp|P0AC53|G6PD ECOLI](#) Mass: 56011 Score: 30 Matches: 1(1) Sequences: 1(1)
 Glucose-6-phosphate 1-dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=zwf 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
1220	493.7854	985.5562	985.5808	-24.89	2	33	0.0057	1	U	Y.LGKETVL

44. [2::sp|P0ABZ1|FLIG ECOLI](#) Mass: 36753 Score: 29 Matches: 1(1) Sequences: 1(1)
 Flagellar motor switch protein FliG OS=Escherichia coli (strain K12) OX=83333 GN=fliG 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
	3439	678.8997	1355.7849	1355.7772	5.65	2	29	0.0083	1	U	L.VKALGE
45.	2::sp P0A9J8 PHEA_ECOLI			Mass: 43312			Score: 29		Matches: 1(1)		Sequences: 1(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										
	3938	736.9094	1471.8042	1471.7704	22.9	2	32	0.0096	1	U	L.LMATGQ
46.	2::sp P0A940 BAMA_ECOLI			Mass: 90611			Score: 29		Matches: 1(1)		Sequences: 1(1)
	Outer membrane protein assembly factor BamA OS=Escherichia coli (strain K12) OX=83333 GN=bamA PE=1 SV=1 Check to include this hit in error tolerant search or archive report										
	5032	880.3965	1758.7784	1758.7705	4.48	1	29	0.019	1	U	Y.VHNSLS
47.	2::sp P0AD99 BRNQ_ECOLI			Mass: 46464			Score: 29		Matches: 1(1)		Sequences: 1(1)
	Branched-chain amino acid transport system 2 carrier protein OS=Escherichia coli (strain K12) OX=83333 GN=brnQ PE=1 SV=1 Check to include this hit in error tolerant search or archive report										
	3842	726.8942	1451.7738	1451.7872	-9.21	1	31	0.0094	1	U	F.EVGIAF
48.	2::sp P60906 SYH_ECOLI			Mass: 47285			Score: 29		Matches: 1(1)		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										
	4018	747.9310	1493.8475	1493.8453	1.46	0	29	0.0073	1	U	Y.SEIRLP
49.	2::sp P37095 PEPB_ECOLI			Mass: 46436			Score: 28		Matches: 1(1)		Sequences: 1(1)
	Peptidase B OS=Escherichia coli (strain K12) OX=83333 GN=pepB PE=1 SV=2 Check to include this hit in error tolerant search or archive report										
	5169	905.4728	1808.9311	1808.9268	2.38	1	28	0.031	1	U	W.VRDTIN
50.	2::sp P0AAT4 YBDG_ECOLI			Mass: 46630			Score: 28		Matches: 1(1)		Sequences: 1(1)
	Miniconductance mechanosensitive channel YbdG OS=Escherichia coli (strain K12) OX=83333 GN=ybdG 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
225	400.2256	798.4366	798.4487	-15.19	0	28	0.0071	1	U	L.IGQSPA

51. [2::sp|P77789|YDES ECOLI](#) Mass: 19108 Score: 27 Matches: 1(1) Sequences: 1(1)
 Uncharacterized fimbrial-like protein YdeS 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
3029	640.2944	1278.5742	1278.5762	-1.55	1	27	0.03	1	U	L.KLDEGS

52. [2::sp|P46474|YHDP ECOLI](#) Mass: 139081 Score: 27 Matches: 2(2) Sequences: 1(1)
 Uncharacterized protein YhdP OS=Escherichia coli (strain K12) OX=833333 GN=yhdP 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
1544	522.2507	1042.4869	1042.4819	4.85	0	(27)	0.022	1	U	L.DDPQIN
1545	522.2517	1042.4889	1042.4819	6.73	0	27	0.02	1	U	L.DDPQIN

53. [2::sp|P31548|THIQ ECOLI](#) Mass: 25097 Score: 27 Matches: 2(2) Sequences: 1(1)
 Thiamine import ATP-binding protein ThiQ OS=Escherichia coli (strain K12) OX=833333 GN=thiQ
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1731	541.3397	1080.6648	1080.6543	9.72	2	(25)	0.004	1	U	L.VREQPI
1732	541.3406	1080.6666	1080.6543	11.4	2	27	0.0027	1	U	L.VREQPI

54. [2::sp|P36683|ACNB ECOLI](#) Mass: 94009 Score: 27 Matches: 1(1) Sequences: 1(1)
 Aconitate hydratase B OS=Escherichia coli (strain K12) OX=833333 GN=acnB PE=1 SV=3
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3213	655.3348	1308.6550	1308.6562	-0.88	0	27	0.04	1	U	Y.VAQVDR

55. [2::sp|P77768|RPNB ECOLI](#) Mass: 34329 Score: 27 Matches: 1(1) Sequences: 1(1)
 Recombination-promoting nuclease RpnB OS=Escherichia coli (strain K12) OX=833333 GN=rpnB
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2779	616.3024	1230.5902	1230.6204	-24.57	1	27	0.034	1	U	L.LVTGN

56. [2::sp|Q2MB16|YOBH ECOLI](#) Mass: 8623 Score: 26 Matches: 1(1) Sequences: 1(1)
 Uncharacterized protein YobH OS=Escherichia coli (strain K12) OX=833333 GN=yobH 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
	3749	714.4351	1426.8556	1426.8734	-12.50	2	26	0.009	1	U	F.IIRTV
57.	2::sp P52612 FLII_ECOLI			Mass: 49342		Score: 25	Matches: 1(1)	Sequences: 1(1)			
				Flagellum-specific ATP synthase OS=Escherichia coli (strain K12) OX=83333 GN=fliI PE=1							
				Check to include this hit in error tolerant search or archive report							
	3661	705.3915	1408.7685	1408.7748	-4.46	2	25	0.026	1	U	L.QSGKQL
58.	2::sp P77515 STFQ_ECOLI			Mass: 32882		Score: 25	Matches: 1(1)	Sequences: 1(1)			
				Prophage side tail fiber protein homolog StfQ OS=Escherichia coli (strain K12) OX=83333 GN=stfQ PE=1							
				Check to include this hit in error tolerant search or archive report							
	5280	926.4215	1850.8285	1850.8455	-9.20	2	25	0.058	1	U	-.MNTAL
59.	2::sp P0A877 TRPA_ECOLI			Mass: 28877		Score: 25	Matches: 2(1)	Sequences: 1(1)			
				Tryptophan synthase alpha chain OS=Escherichia coli (strain K12) OX=83333 GN=trpA PE=1							
				Check to include this hit in error tolerant search or archive report							
	1874	551.2664	1100.5182	1100.5350	-15.26	0	25	0.044	1	U	L.ADGPT
	1875	551.2664	1100.5183	1100.5350	-15.15	0	(22)	0.085	1	U	L.ADGPT
60.	2::sp P31448 YIDK_ECOLI			Mass: 62329		Score: 25	Matches: 1(1)	Sequences: 1(1)			
				Uncharacterized symporter YidK OS=Escherichia coli (strain K12) OX=83333 GN=yidK PE=1							
				Check to include this hit in error tolerant search or archive report							
	1168	488.7784	975.5423	975.5497	-7.60	2	25	0.031	1	U	L.LTAVLKML
61.	2::sp P75898 RUTA_ECOLI			Mass: 42420		Score: 24	Matches: 2(1)	Sequences: 1(1)			
				Pyrimidine monooxygenase RutA OS=Escherichia coli (strain K12) OX=83333 GN=rutA PE=1							
				Check to include this hit in error tolerant search or archive report							
	712	451.2401	900.4657	900.4487	18.9	0	24	0.041	2	U	-.MQDAAPRL
	713	451.2403	900.4661	900.4487	19.3	0	(21)	0.09	1	U	-.MQDAAPRL
62.	2::sp P31433 YICH_ECOLI			Mass: 62234		Score: 24	Matches: 2(0)	Sequences: 1(0)			
				AsmA family protein YicH OS=Escherichia coli (strain K12) OX=83333 GN=yicH PE=3 SV=2							

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3298	662.3190	1322.6235	1322.5925	23.4	1	(20)	0.2	1	U	W.EGGMVR
3300	662.3194	1322.6242	1322.5925	24.0	1	24	0.083	1	U	W.EGGMVR

63. [2::sp|P07012|RF2 ECOLI](#) Mass: 41339 Score: 24 Matches: 1(1) Sequences: 1(1)
Peptide chain release factor RF2 OS=Escherichia coli (strain K12) OX=83333 GN=prfB
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2118	565.3077	1128.6008	1128.6026	-1.60	2	24	0.049	1	U	L.DALEEK

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 : 6172

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