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_band1.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 11:07:42 GMT

                 2::sp|P0CE47|EFTU1_ECOLI      Elongation factor Tu 1 OS=Escherichia co
Protein hits   :
                 2::sp|P02931|OMPF_ECOLI       Outer membrane protein F OS=Escherichia
                 2::sp|P0AE06|ACRA_ECOLI       Multidrug efflux pump subunit AcrA OS=Es
                 2::sp|P0A799|PGK_ECOLI        Phosphoglycerate kinase OS=Escherichia c
                 1::sp|cRAP022|P00766|CTRA_BOVIN Chymotrypsinogen A OS=Bos taurus PE=1 SV
                 2::sp|P0A817|METK_ECOLI       S-adenosylmethionine synthase OS=Escheri
                 2::sp|P0A910|OMPA_ECOLI       Outer membrane protein A OS=Escherichia
                 2::sp|P08200|IDH_ECOLI        Isocitrate dehydrogenase [NADP] OS=Esche
                 2::sp|P0AAI5|FABF_ECOLI       3-oxoacyl-[acyl-carrier-protein] synthas
                 2::sp|P0AEX9|MALE_ECOLI       Maltose-binding periplasmic protein OS=E
                 2::sp|P0C8J8|GATZ_ECOLI       D-tagatose-1,6-bisphosphate aldolase sub
                 2::sp|P0ABH7|CISY_ECOLI       Citrate synthase OS=Escherichia coli (st
                 2::sp|P0A836|SUCC_ECOLI       Succinate--CoA ligase [ADP-forming] subu
                 2::sp|P0A6P1|EFTS_ECOLI       Elongation factor Ts OS=Escherichia coli
                 2::sp|P0A6A3|ACKA_ECOLI       Acetate kinase OS=Escherichia coli (stra
                 2::sp|P0A953|FABB_ECOLI       3-oxoacyl-[acyl-carrier-protein] synthas
                 2::sp|P0A9B2|G3P1_ECOLI       Glyceraldehyde-3-phosphate dehydrogenase
                 2::sp|P02925|RBSB_ECOLI       Ribose import binding protein RbsB OS=Es
                 2::sp|P0AB71|ALF_ECOLI        Fructose-bisphosphate aldolase class 2 O
                 2::sp|P0A9A6|FTSZ_ECOLI       Cell division protein FtsZ OS=Escherichi
                 2::sp|P23893|GSA_ECOLI        Glutamate-1-semialdehyde 2,1-aminomutase
                 2::sp|P61889|MDH_ECOLI        Malate dehydrogenase OS=Escherichia coli
                 2::sp|P02930|TOLC_ECOLI       Outer membrane protein TolC OS=Escherich
                 2::sp|P76373|UDG_ECOLI        UDP-glucose 6-dehydrogenase OS=Escherich
                 2::sp|P0AE08|AHPC_ECOLI       Alkyl hydroperoxide reductase C OS=Esche
                 2::sp|P0A855|TOLB_ECOLI       Tol-Pal system protein TolB OS=Escherich
                 2::sp|P0A7Z4|RPOA_ECOLI       DNA-directed RNA polymerase subunit alph
                 2::sp|P0A870|TALB_ECOLI       Transaldolase B OS=Escherichia coli (str
```

2::sp|P0AGJ9|SYY_ECOLI	Tyrosine--tRNA ligase OS=Escherichia col
2::sp|P0AGE9|SUCD_ECOLI	Succinate--CoA ligase [ADP-forming] subu
2::sp|P23721|SERC_ECOLI	Phosphoserine aminotransferase OS=Escher
2::sp|P0A6K6|DEOB_ECOLI	Phosphopentomutase OS=Escherichia coli (
2::sp|P31979|NUOF_ECOLI	NADH-quinone oxidoreductase subunit F OS
2::sp|P18335|ARGD_ECOLI	Acetylornithine/succinyldiaminopimelate
2::sp|P0AG67|RS1_ECOLI	30S ribosomal protein S1 OS=Escherichia
2::sp|P07004|PROA_ECOLI	Gamma-glutamyl phosphate reductase OS=Es
2::sp|P0A825|GLYA_ECOLI	Serine hydroxymethyltransferase OS=Esche
2::sp|P0A6P9|ENO_ECOLI	Enolase OS=Escherichia coli (strain K12)
2::sp|P0A6B7|ISCS_ECOLI	Cysteine desulfurase IscS OS=Escherichia
2::sp|P37095|PEPB_ECOLI	Peptidase B OS=Escherichia coli (strain
2::sp|P08622|DNAJ_ECOLI	Chaperone protein DnaJ OS=Escherichia co
2::sp|P00509|AAT_ECOLI	Aspartate aminotransferase OS=Escherichi
2::sp|P0A6F1|CARA_ECOLI	Carbamoyl-phosphate synthase small chain
2::sp|P0A7A9|IPYR_ECOLI	Inorganic pyrophosphatase OS=Escherichia
2::sp|P60422|RL2_ECOLI	50S ribosomal protein L2 OS=Escherichia
2::sp|P33232|LLDD_ECOLI	L-lactate dehydrogenase OS=Escherichia c
2::sp|P0A7L0|RL1_ECOLI	50S ribosomal protein L1 OS=Escherichia
2::sp|P27248|GCST_ECOLI	Aminomethyltransferase OS=Escherichia co
2::sp|P0A858|TPIS_ECOLI	Triosephosphate isomerase OS=Escherichia
2::sp|P0ABU2|YCHF_ECOLI	Ribosome-binding ATPase YchF OS=Escheric
2::sp|P0ABZ6|SURA_ECOLI	Chaperone SurA OS=Escherichia coli (stra
2::sp|P69924|RIR2_ECOLI	Ribonucleoside-diphosphate reductase 1 s
2::sp|P67910|HLDD_ECOLI	ADP-L-glycero-D-manno-heptose-6-epimeras
2::sp|P0AEK4|FABI_ECOLI	Enoyl-[acyl-carrier-protein] reductase [
2::sp|P31224|ACRB_ECOLI	Multidrug efflux pump subunit AcrB OS=Es
2::sp|P23908|ARGE_ECOLI	Acetylornithine deacetylase OS=Escherich
2::sp|P62620|ISPG_ECOLI	4-hydroxy-3-methylbut-2-en-1-yl diphosph
2::sp|P0A9D8|DAPD_ECOLI	2,3,4,5-tetrahydropyridine-2,6-dicarboxy
2::sp|P0A6M8|EFG_ECOLI	Elongation factor G OS=Escherichia coli
2::sp|P0AEB2|DACA_ECOLI	D-alanyl-D-alanine carboxypeptidase DacA
2::sp|P0A717|KPRS_ECOLI	Ribose-phosphate pyrophosphokinase OS=Es
2::sp|P0A749|MURA_ECOLI	UDP-N-acetylglucosamine 1-carboxyvinyltr
2::sp|P0AB77|KBL_ECOLI	2-amino-3-ketobutyrate coenzyme A ligase
2::sp|P75876|RLMI_ECOLI	Ribosomal RNA large subunit methyltransf
2::sp|P0A9J6|RBSK_ECOLI	Ribokinase OS=Escherichia coli (strain K
2::sp|P00490|PHSM_ECOLI	Maltodextrin phosphorylase OS=Escherichi
2::sp|P77774|BAMB_ECOLI	Outer membrane protein assembly factor B
2::sp|P0A7V0|RS2_ECOLI	30S ribosomal protein S2 OS=Escherichia
2::sp|P0A6H1|CLPX_ECOLI	ATP-dependent Clp protease ATP-binding s
2::sp|P00448|SODM_ECOLI	Superoxide dismutase [Mn] OS=Escherichia
2::sp|P00954|SYW_ECOLI	Tryptophan--tRNA ligase OS=Escherichia c
2::sp|P60723|RL4_ECOLI	50S ribosomal protein L4 OS=Escherichia
2::sp|P0A862|TPX_ECOLI	Thiol peroxidase OS=Escherichia coli (st
2::sp|P0A7V8|RS4_ECOLI	30S ribosomal protein S4 OS=Escherichia
2::sp|P62707|GPMA_ECOLI	2,3-bisphosphoglycerate-dependent phosph
2::sp|P03023|LACI_ECOLI	Lactose operon repressor OS=Escherichia

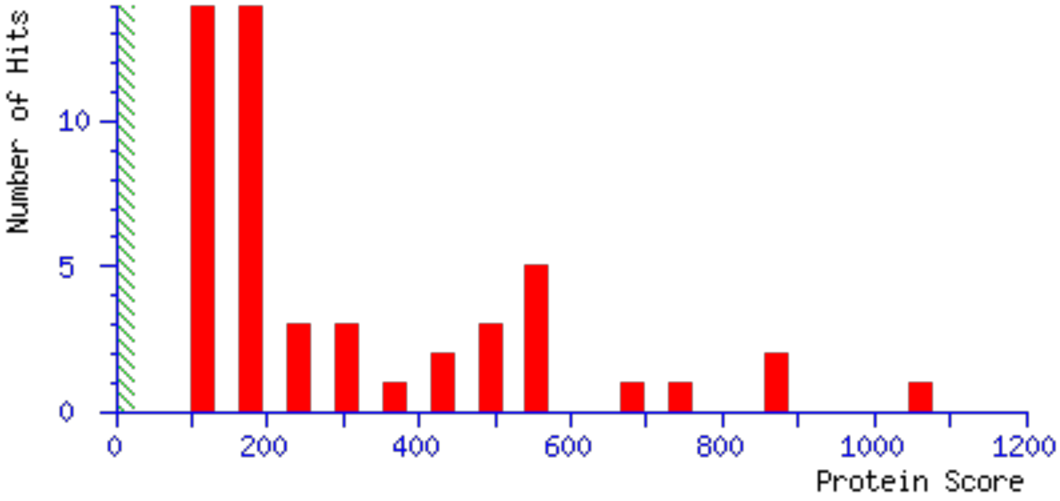
2::sp|P0A7J3|RL10_ECOLI	50S ribosomal protein L10 OS=Escherichia
2::sp|P09053|AVTA_ECOLI	Valine--pyruvate aminotransferase OS=Esc
2::sp|P0A9K3|PHOL_ECOLI	PhoH-like protein OS=Escherichia coli (s
2::sp|P07913|TDH_ECOLI	L-threonine 3-dehydrogenase OS=Escherich
2::sp|P0A7W7|RS8_ECOLI	30S ribosomal protein S8 OS=Escherichia
2::sp|P0A7V3|RS3_ECOLI	30S ribosomal protein S3 OS=Escherichia
2::sp|P0A6Y8|DNAK_ECOLI	Chaperone protein DnaK OS=Escherichia co
2::sp|P00960|SYGA_ECOLI	Glycine--tRNA ligase alpha subunit OS=Es
2::sp|P0A6N4|EFP_ECOLI	Elongation factor P OS=Escherichia coli
2::sp|P37759|RMLB1_ECOLI	dTDP-glucose 4,6-dehydratase 1 OS=Escher
2::sp|P0A6Y5|HSLO_ECOLI	33 kDa chaperonin OS=Escherichia coli (s
2::sp|P0ADG4|SUHB_ECOLI	Inositol-1-monophosphatase OS=Escherichi
2::sp|P77690|ARNB_ECOLI	UDP-4-amino-4-deoxy-L-arabinose--oxoglut
2::sp|P37652|BCSB_ECOLI	Cyclic di-GMP-binding protein OS=Escheri
2::sp|P69441|KAD_ECOLI	Adenylate kinase OS=Escherichia coli (st
2::sp|P0AG48|RL21_ECOLI	50S ribosomal protein L21 OS=Escherichia
2::sp|P0ABD8|BCCP_ECOLI	Biotin carboxyl carrier protein of acety
2::sp|P69783|PTGA_ECOLI	PTS system glucose-specific EIIA compone
2::sp|P60906|SYH_ECOLI	Histidine--tRNA ligase OS=Escherichia co
2::sp|P25745|MNMA_ECOLI	tRNA-specific 2-thiouridylase MnmA OS=Es
2::sp|P0A7S9|RS13_ECOLI	30S ribosomal protein S13 OS=Escherichia
2::sp|P0A9T0|SERA_ECOLI	D-3-phosphoglycerate dehydrogenase OS=Es
2::sp|P36979|RLMN_ECOLI	Dual-specificity RNA methyltransferase R
2::sp|P0A6F5|CH60_ECOLI	60 kDa chaperonin OS=Escherichia coli (s
2::sp|P0AG55|RL6_ECOLI	50S ribosomal protein L6 OS=Escherichia
2::sp|P0AEZ3|MIND_ECOLI	Septum site-determining protein MinD OS=
1::sp|cRAP087|P02769|ALBU_BOVIN	Serum albumin OS=Bos taurus GN=ALB PE=1
2::sp|P0ADY7|RL16_ECOLI	50S ribosomal protein L16 OS=Escherichia
2::sp|P68187|MALK_ECOLI	Maltose/maltodextrin import ATP-binding
2::sp|P0C018|RL18_ECOLI	50S ribosomal protein L18 OS=Escherichia
2::sp|P77395|YBBN_ECOLI	Uncharacterized protein YbbN OS=Escheric
2::sp|P45523|FKBA_ECOLI	FKBP-type peptidyl-prolyl cis-trans isom
1::sp|cRAP112|P00761|TRYP_PIG	Trypsin OS=Sus scrofa PE=1 SV=1
2::sp|P0A9K9|SLYD_ECOLI	FKBP-type peptidyl-prolyl cis-trans isom
2::sp|P75796|GSIA_ECOLI	Glutathione import ATP-binding protein G
2::sp|P07012|RF2_ECOLI	Peptide chain release factor RF2 OS=Esch
2::sp|P08390|USG_ECOLI	USG-1 protein OS=Escherichia coli (strai
2::sp|P0A9Q5|ACCD_ECOLI	Acetyl-coenzyme A carboxylase carboxyl t
2::sp|P42601|ALX_ECOLI	Putative membrane-bound redox modulator
2::sp|P15006|MCRC_ECOLI	Protein McrC OS=Escherichia coli (strain
2::sp|P0A7W1|RS5_ECOLI	30S ribosomal protein S5 OS=Escherichia
2::sp|P0A847|TGT_ECOLI	Queuine tRNA-ribosyltransferase OS=Esche
2::sp|P46853|YHHX_ECOLI	Uncharacterized oxidoreductase YhhX OS=E
2::sp|P62399|RL5_ECOLI	50S ribosomal protein L5 OS=Escherichia
2::sp|P77433|YKGG_ECOLI	Uncharacterized protein YkgG OS=Escheric
2::sp|P02943|LAMB_ECOLI	Maltoporin OS=Escherichia coli (strain K
2::sp|P36683|ACNB_ECOLI	Aconitate hydratase B OS=Escherichia col
2::sp|P46474|YHDP_ECOLI	Uncharacterized protein YhdP OS=Escheric

2::sp|P09424|MTLD_ECOLI	Mannitol-1-phosphate 5-dehydrogenase OS=
2::sp|P0A6L4|NANA_ECOLI	N-acetylneuraminate lyase OS=Escherichia
2::sp|P30176|RIBX_ECOLI	N-glycosidase YbiA OS=Escherichia coli (
2::sp|P04335|FRSA_ECOLI	Esterase FrsA OS=Escherichia coli (strai
2::sp|P0A988-2|DPO3B_ECOLI	Isoform Beta* of Beta sliding clamp OS=E
2::sp|P0A903|BAMC_ECOLI	Outer membrane protein assembly factor B
2::sp|P00393|DHNA_ECOLI	NADH dehydrogenase OS=Escherichia coli (
2::sp|P0ABD5|ACCA_ECOLI	Acetyl-coenzyme A carboxylase carboxyl t
2::sp|P0AG30|RHO_ECOLI	Transcription termination factor Rho OS=
2::sp|P0AFK9|POTD_ECOLI	Spermidine/putrescine-binding periplasmi
2::sp|P0ABP8|DEOD_ECOLI	Purine nucleoside phosphorylase DeoD-typ
2::sp|P77398|ARNA_ECOLI	Bifunctional polymyxin resistance protei
2::sp|P0AGD3|SODF_ECOLI	Superoxide dismutase [Fe] OS=Escherichia
2::sp|P23482|HYFB_ECOLI	Hydrogenase-4 component B OS=Escherichia
2::sp|P0AAX8|YBIS_ECOLI	Probable L,D-transpeptidase YbiS OS=Esch
2::sp|P0A7J7|RL11_ECOLI	50S ribosomal protein L11 OS=Escherichia
2::sp|P0ABJ1|CYOA_ECOLI	Cytochrome bo(3) ubiquinol oxidase subun
2::sp|P0A927|TSX_ECOLI	Nucleoside-specific channel-forming prot
2::sp|P0A7G6|RECA_ECOLI	Protein RecA OS=Escherichia coli (strain
2::sp|P32717|YJCS_ECOLI	Putative alkyl/aryl-sulfatase YjcS OS=Es
2::sp|P77454|GLSA1_ECOLI	Glutaminase 1 OS=Escherichia coli (strai
2::sp|P23869|PPIB_ECOLI	Peptidyl-prolyl cis-trans isomerase B OS
2::sp|P77561|YDEP_ECOLI	Protein YdeP OS=Escherichia coli (strain
2::sp|P0A7B5|PROB_ECOLI	Glutamate 5-kinase OS=Escherichia coli (
2::sp|P52643|LDHD_ECOLI	D-lactate dehydrogenase OS=Escherichia c
2::sp|P0A7K2|RL7_ECOLI	50S ribosomal protein L7/L12 OS=Escheric
2::sp|P0AE48|YTFP_ECOLI	Gamma-glutamylcyclotransferase family pr
2::sp|P0C0V0|DEGP_ECOLI	Periplasmic serine endoprotease DegP OS=
2::sp|P25553|ALDA_ECOLI	Lactaldehyde dehydrogenase OS=Escherichi
2::sp|Q2EES3|YOEF_ECOLI	Putative uncharacterized protein YoeF OS
2::sp|P37047|CDAR_ECOLI	Carbohydrate diacid regulator OS=Escheri
2::sp|P45955|CPOB_ECOLI	Cell division coordinator CpoB OS=Escher
2::sp|P0AFH2|OPPB_ECOLI	Oligopeptide transport system permease p
2::sp|P37663|YHJY_ECOLI	Uncharacterized protein YhjY OS=Escheric
2::sp|P19926|AGP_ECOLI	Glucose-1-phosphatase OS=Escherichia col
2::sp|P0ACE0|MBHM_ECOLI	Hydrogenase-2 large chain OS=Escherichia
2::sp|P76299|FLHB_ECOLI	Flagellar biosynthetic protein FlhB OS=E
2::sp|P0ABK5|CYSK_ECOLI	Cysteine synthase A OS=Escherichia coli
2::sp|P0A912|PAL_ECOLI	Peptidoglycan-associated lipoprotein OS=
2::sp|P33352|YEHP_ECOLI	Uncharacterized protein YehP OS=Escheric
2::sp|P33349|YEHM_ECOLI	Uncharacterized protein YehM OS=Escheric
2::sp|P38134|ETK_ECOLI	Tyrosine-protein kinase etk OS=Escherich
2::sp|P76322|YEDM_ECOLI	Uncharacterized protein YedM OS=Escheric
2::sp|P31548|THIQ_ECOLI	Thiamine import ATP-binding protein ThiQ
2::sp|P0A6D3|AROA_ECOLI	3-phosphoshikimate 1-carboxyvinyltransfe
2::sp|P0DP63|YBEH_ECOLI	Putative protein YbeH OS=Escherichia col
2::sp|P76042|YCJN_ECOLI	Putative ABC transporter periplasmic-bin
2::sp|P0A877|TRPA_ECOLI	Tryptophan synthase alpha chain OS=Esche

2::sp|P39382|YJIK_ECOLI	Uncharacterized protein YjiK OS=Escheric
1::sp|cRAP054|P04264|K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo
2::sp|Q46839|GLCA_ECOLI	Glycolate permease GlcA OS=Escherichia c
2::sp|P0A6R0|FABH_ECOLI	3-oxoacyl-[acyl-carrier-protein] synthas
2::sp|P77223|RSXB_ECOLI	Ion-translocating oxidoreductase complex
2::sp|P08142|ILVB_ECOLI	Acetolactate synthase isozyme 1 large su
2::sp|P0A9S5|GLDA_ECOLI	Glycerol dehydrogenase OS=Escherichia co
2::sp|P42630|TDCG_ECOLI	L-serine dehydratase TdcG OS=Escherichia
2::sp|P0AEN4|FTSL_ECOLI	Cell division protein FtsL OS=Escherichi

Mascot Score Histogram

Ions score is -10*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 meningiti
Species information unavailable

Error tolerant

1. 2::sp|P0CE47|EFTU1_ECOLI **Mass:** 43427 **Score:** 1062 **Matches:** 93(80) **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	Peptid
177	395.2390	788.4634	788.4644	-1.22	0	(34)	0.0032	1	U	L.TAAI
179	395.2394	788.4641	788.4644	-0.28	0	42	0.00052	1	U	L.TAAI
796	438.2402	874.4659	874.4661	-0.23	0	21	0.11	1	U	L.GRQV
1258	473.2687	944.5229	944.5219	1.04	1	(41)	0.0012	1	U	F.LLPI
1259	473.2687	944.5229	944.5219	1.11	1	52	8.1e-05	1	U	F.LLPI
1941	509.7452	1017.4758	1017.4767	-0.88	1	(33)	0.0066	1	U	L.KALE
1943	509.7456	1017.4767	1017.4767	-0.03	1	(23)	0.069	1	U	L.KALE
1944	509.7458	1017.4770	1017.4767	0.32	1	(31)	0.012	1	U	L.KALE
1945	509.7459	1017.4771	1017.4767	0.44	1	36	0.004	1	U	L.KALE
2388	541.2707	1080.5268	1080.5274	-0.51	0	62	1.2e-05	1	U	L.IHPI
2389	541.2709	1080.5272	1080.5274	-0.17	0	(58)	2.7e-05	1	U	L.IHPI
2542	549.2682	1096.5219	1096.5223	-0.31	0	(43)	0.00068	1	U	L.IHPI
2543	549.2686	1096.5227	1096.5223	0.36	0	(33)	0.0065	1	U	L.IHPI
2544	549.2687	1096.5228	1096.5223	0.47	0	(30)	0.014	1	U	L.IHPI
2545	549.2688	1096.5230	1096.5223	0.69	0	(27)	0.029	1	U	L.IHPI
2546	549.2688	1096.5230	1096.5223	0.69	0	(29)	0.019	1	U	L.IHPI
2547	549.2692	1096.5239	1096.5223	1.47	0	(43)	0.00074	1	U	L.IHPI
2548	549.2699	1096.5252	1096.5223	2.69	0	(31)	0.012	1	U	L.IHPI
3660	608.3033	1214.5921	1214.5891	2.47	0	(32)	0.011	1	U	L.DEGR
3663	608.3048	1214.5951	1214.5891	4.89	0	46	0.00034	1	U	L.DEGR
3836	621.2541	1240.4937	1240.4931	0.49	0	(23)	0.027	1	U	Y.AHVD
3838	621.2552	1240.4958	1240.4931	2.17	0	39	0.00077	1	U	Y.AHVD
3839	621.2553	1240.4961	1240.4931	2.37	0	(28)	0.0081	1	U	Y.AHVD
3881	623.8212	1245.6279	1245.6275	0.36	1	(54)	8.4e-05	1	U	L.ELVE
3882	623.8216	1245.6286	1245.6275	0.94	1	61	1.7e-05	1	U	L.ELVE
4023	631.8172	1261.6198	1261.6224	-2.00	1	(29)	0.027	1	U	L.ELVE
4024	631.8173	1261.6200	1261.6224	-1.91	1	(41)	0.0016	1	U	L.ELVE
4530	664.8433	1327.6721	1327.6732	-0.83	1	(36)	0.0042	1	U	L.LDEG
4531	664.8434	1327.6722	1327.6732	-0.74	1	(46)	0.00039	1	U	L.DEGR
4532	664.8442	1327.6739	1327.6732	0.56	1	53	8.6e-05	1	U	L.LDEG
4533	664.8453	1327.6761	1327.6732	2.22	1	61	1.1e-05	1	U	L.DEGR
4541	665.3480	1328.6815	1328.6572	18.3	1	(22)	0.12	1	U	L.DEGR
4803	688.3621	1374.7096	1374.7064	2.28	2	53	0.00011	1	U	L.ELVE
4804	688.3625	1374.7104	1374.7064	2.90	2	(48)	0.00031	2	U	L.ELVE
4821	692.8556	1383.6967	1383.6969	-0.11	1	45	0.00048	1	U	L.IHPI
4822	462.2396	1383.6970	1383.6969	0.10	1	(45)	0.0005	1	U	L.IHPI
4823	692.8558	1383.6971	1383.6969	0.15	1	(23)	0.081	1	U	L.IHPI
4824	462.2398	1383.6977	1383.6969	0.57	1	(41)	0.0014	1	U	L.IHPI
4893	700.8528	1399.6911	1399.6918	-0.49	1	(43)	0.00096	1	U	L.IHPI
4894	467.5710	1399.6912	1399.6918	-0.44	1	(44)	0.00075	1	U	L.IHPI
4895	467.5715	1399.6928	1399.6918	0.67	1	(41)	0.0013	1	U	L.IHPI
4896	700.8539	1399.6933	1399.6918	1.08	1	(36)	0.0051	1	U	L.IHPI
4938	706.3849	1410.7552	1410.7507	3.22	0	36	0.0028	1	U	Y.IPEP

4939	706.3853	1410.7561	1410.7507	3.81	0	(25)	0.039	1	U	Y.IPEP
5151	721.3862	1440.7578	1440.7572	0.37	2	49	0.00019	1	U	L.LDEG
5153	721.3878	1440.7611	1440.7572	2.67	2	(47)	0.00027	1	U	L.LDEG
5218	728.8810	1455.7475	1455.7470	0.35	1	(35)	0.005	1	U	Y.ILSK
5220	486.2566	1455.7479	1455.7470	0.63	1	(23)	0.082	1	U	Y.ILSK
5225	728.8825	1455.7505	1455.7470	2.37	1	46	0.00044	1	U	Y.ILSK
5226	728.8832	1455.7519	1455.7470	3.37	1	(28)	0.026	1	U	Y.ILSK
5227	728.8834	1455.7523	1455.7470	3.62	1	(25)	0.057	1	U	Y.ILSK
5375	740.8180	1479.6214	1479.6221	-0.48	1	42	0.0005	1	U	L.NKCD
5482	748.8156	1495.6165	1495.6171	-0.34	1	(31)	0.0051	1	U	L.NKCD
5483	748.8188	1495.6231	1495.6171	4.08	1	(25)	0.023	1	U	L.NKCD
5789	520.5944	1558.7614	1558.7628	-0.85	0	(21)	0.18	1	U	Y.DFPG
5790	780.3886	1558.7625	1558.7628	-0.13	0	(39)	0.0026	1	U	Y.DFPG
5791	780.3892	1558.7638	1558.7628	0.65	0	(53)	0.0001	1	U	Y.DFPG
5793	780.3893	1558.7641	1558.7628	0.88	0	(62)	1.3e-05	1	U	Y.DFPG
5795	780.3896	1558.7646	1558.7628	1.20	0	(60)	2e-05	1	U	Y.DFPG
5796	780.3899	1558.7652	1558.7628	1.59	0	(26)	0.054	1	U	Y.DFPG
5797	780.3903	1558.7660	1558.7628	2.06	0	63	1.2e-05	1	U	Y.DFPG
5798	520.5960	1558.7660	1558.7628	2.10	0	(24)	0.084	1	U	Y.DFPG
5941	797.3614	1592.7083	1592.7062	1.35	2	(31)	0.012	1	U	F.LNKC
5942	797.3615	1592.7085	1592.7062	1.43	2	(47)	0.00029	1	U	F.LNKC
5943	797.3626	1592.7105	1592.7062	2.73	2	64	5.9e-06	1	U	F.LNKC
5944	797.3626	1592.7107	1592.7062	2.81	2	(31)	0.011	1	U	F.LNKC
6027	805.3574	1608.7003	1608.7011	-0.51	2	(35)	0.0039	1	U	F.LNKC
6028	805.3574	1608.7003	1608.7011	-0.51	2	(40)	0.0012	1	U	F.LNKC
6029	805.3583	1608.7020	1608.7011	0.56	2	(25)	0.039	1	U	F.LNKC
6030	805.3584	1608.7022	1608.7011	0.71	2	(51)	0.0001	1	U	F.LNKC
6031	805.3587	1608.7028	1608.7011	1.08	2	(30)	0.012	1	U	F.LNKC
6032	805.3600	1608.7054	1608.7011	2.68	2	(31)	0.01	1	U	F.LNKC
6033	805.3605	1608.7065	1608.7011	3.35	2	(49)	0.00014	1	U	F.LNKC
6034	805.3611	1608.7076	1608.7011	4.04	2	(29)	0.018	1	U	F.LNKC
6219	824.9236	1647.8326	1647.8324	0.13	0	43	0.0012	1	U	Y.VKNM
6220	824.9249	1647.8352	1647.8324	1.69	0	(43)	0.0012	1	U	Y.VKNM
6314	832.9200	1663.8255	1663.8273	-1.07	0	(20)	0.23	1	U	Y.VKNM
6315	832.9202	1663.8258	1663.8273	-0.92	0	(38)	0.0037	1	U	Y.VKNM
6317	832.9203	1663.8260	1663.8273	-0.77	0	(29)	0.029	1	U	Y.VKNM
6319	832.9210	1663.8274	1663.8273	0.03	0	(36)	0.0061	1	U	Y.VKNM
6320	832.9212	1663.8278	1663.8273	0.32	0	(27)	0.052	1	U	Y.VKNM
6321	832.9216	1663.8286	1663.8273	0.76	0	(24)	0.095	1	U	Y.VKNM
6322	832.9237	1663.8329	1663.8273	3.34	0	(41)	0.0019	1	U	Y.VKNM
6328	833.4171	1664.8197	1664.8113	5.01	0	(32)	0.015	1	U	Y.VKNM
6573	863.4837	1724.9528	1724.9533	-0.27	2	(34)	0.0037	1	U	F.RKLL
6577	863.4849	1724.9553	1724.9533	1.15	2	37	0.0021	1	U	F.RKLL
6757	888.9445	1775.8744	1775.8730	0.78	1	38	0.0035	1	U	L.DSYI
6760	888.9468	1775.8790	1775.8730	3.39	1	(37)	0.0043	1	U	L.DSYI
7152	945.4872	1888.9599	1888.9570	1.53	2	27	0.048	1	U	F.LDSY
7154	630.6615	1888.9627	1888.9570	2.98	2	(23)	0.1	1	U	F.LDSY
7155	945.4893	1888.9641	1888.9570	3.73	2	(24)	0.096	1	U	F.LDSY
7967	1098.5510	3292.6313	3292.6241	2.18	0	(38)	0.0025	1	U	F.RTTD
7968	1098.5542	3292.6408	3292.6241	5.06	0	58	2.3e-05	1	U	F.RTTD

Proteins matching the same set of peptides:

2::sp|P0CE48|EFTU2_ECOLI **Mass:** 43457 **Score:** 1062 **Matches:** 93(80) **Sequences:**

Elongation factor Tu 2 OS=Escherichia coli (strain K12) OX=83333 GN=tufB PE=1 SV=1

---

2. 2::sp|P02931|OMPF_ECOLI **Mass:** 39309 **Score:** 891 **Matches:** 60(51) **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
445	409.2111	816.4076	816.4090	-1.71	0	(20)	0.14	1	U	Y.GAADR
446	409.2119	816.4091	816.4090	0.22	0	55	4.2e-05	1	U	Y.GAADR
447	409.2120	816.4095	816.4090	0.69	0	(38)	0.0022	1	U	Y.GAADR
556	417.7212	833.4278	833.4283	-0.67	2	(40)	0.0013	1		F.GLVDG
557	417.7213	833.4281	833.4283	-0.24	2	43	0.00065	1		F.GLVDG
810	438.7507	875.4868	875.4865	0.42	1	26	0.021	1	U	F.GLRPS
811	438.7507	875.4868	875.4865	0.42	1	(24)	0.033	1	U	F.GLRPS
870	443.7189	885.4233	885.4232	0.08	1	(49)	0.0001	1	U	L.KYADV
871	443.7191	885.4236	885.4232	0.45	1	67	1.8e-06	1	U	L.KYADV
1578	489.7718	977.5290	977.5294	-0.43	0	(29)	0.014	1	U	F.VGRVG
1579	489.7718	977.5291	977.5294	-0.37	0	34	0.005	1	U	F.VGRVG
1787	500.7402	999.4658	999.4661	-0.28	1	29	0.013	1		L.KYDAN
1790	500.7407	999.4668	999.4661	0.70	1	(29)	0.014	1		L.KYDAN
1807	501.2850	1000.5554	1000.5553	0.15	1	(42)	0.00077	1	U	F.ANKTQ
1808	501.2851	1000.5557	1000.5553	0.41	1	44	0.00055	1	U	F.ANKTQ
1817	502.7282	1003.4419	1003.4433	-1.43	1	(28)	0.016	1		Y.FNKNM
1818	502.7283	1003.4421	1003.4433	-1.19	1	31	0.0085	1		Y.FNKNM
1924	509.2597	1016.5048	1016.5039	0.91	0	21	0.16	1	U	L.GNGKK
2374	540.2725	1078.5304	1078.5295	0.84	0	34	0.0079	1	U	L.VAGTA
2375	540.2736	1078.5327	1078.5295	2.99	0	(25)	0.07	1	U	L.VAGTA
2589	551.7427	1101.4709	1101.4727	-1.60	1	(33)	0.0037	1	U	Y.FSKGN
2590	551.7435	1101.4725	1101.4727	-0.16	1	46	0.0002	1	U	Y.FSKGN
2597	552.2348	1102.4550	1102.4567	-1.49	1	(44)	0.00027	1	U	Y.FSKGN
2598	552.2355	1102.4564	1102.4567	-0.28	1	(43)	0.00029	1	U	Y.FSKGN
2609	552.7804	1103.5462	1103.5459	0.36	0	33	0.0087	1	U	F.KGETQ
2610	552.7807	1103.5468	1103.5459	0.90	0	(24)	0.075	1	U	F.KGETQ
3205	583.2969	1164.5793	1164.5775	1.58	1	(25)	0.058	1	U	Y.NKDGN
3206	583.2972	1164.5799	1164.5775	2.10	1	33	0.011	1	U	Y.NKDGN
3375	592.2589	1182.5031	1182.5015	1.36	2	27	0.02	1		Y.YFNKN
4112	636.8439	1271.6732	1271.6721	0.85	0	(48)	0.00029	1	U	Y.IINQI
4113	636.8440	1271.6734	1271.6721	1.04	0	(44)	0.00068	1	U	Y.IINQI
4114	636.8443	1271.6740	1271.6721	1.53	0	(33)	0.0086	1	U	Y.IINQI
4115	636.8448	1271.6751	1271.6721	2.39	0	52	9.4e-05	1	U	Y.IINQI
4130	637.3336	1272.6527	1272.6561	-2.69	0	(51)	0.00015	1	U	Y.IINQI
4960	708.8030	1415.5914	1415.5915	-0.07	1	(38)	0.0012	1	U	Y.TDMLP
4961	708.8036	1415.5927	1415.5915	0.88	1	(50)	7.5e-05	1	U	Y.TDMLP
5030	713.3453	1424.6760	1424.6783	-1.63	1	(30)	0.021	1	U	F.KGETQ
5031	713.3466	1424.6786	1424.6783	0.17	1	(45)	0.00069	1	U	F.KGETQ
5032	713.3475	1424.6804	1424.6783	1.45	1	(53)	0.00011	1	U	F.KGETQ
5033	713.3484	1424.6823	1424.6783	2.82	1	(52)	0.00013	1	U	F.KGETQ
5038	713.8381	1425.6616	1425.6623	-0.53	1	(49)	0.00022	1	U	F.KGETQ
5039	713.8384	1425.6623	1425.6623	-0.01	1	(44)	0.00075	1	U	F.KGETQ
5040	713.8388	1425.6631	1425.6623	0.51	1	(53)	8.8e-05	1	U	F.KGETQ
5041	713.8403	1425.6660	1425.6623	2.56	1	54	7.2e-05	1	U	F.KGETQ
5079	716.8009	1431.5872	1431.5864	0.57	1	(57)	1.4e-05	1	U	Y.TDMLP
5080	716.8016	1431.5886	1431.5864	1.51	1	61	6.6e-06	1	U	Y.TDMLP
5394	495.2549	1482.7428	1482.7426	0.11	1	(21)	0.15	1	U	Y.GAADR
5395	742.3792	1482.7439	1482.7426	0.82	1	(34)	0.0061	1	U	Y.GAADR

5396	742.3795	1482.7444	1482.7426	1.16	1	37	0.0033	1	U	Y.GAADR
5397	742.3812	1482.7479	1482.7426	3.55	1	(24)	0.065	1	U	Y.GAADR
5402	742.8753	1483.7361	1483.7267	6.34	1	(36)	0.0038	1	U	Y.GAADR
6129	815.3913	1628.7680	1628.7682	-0.10	2	(61)	1.7e-05	1	U	L.GFKGE
6130	815.3920	1628.7694	1628.7682	0.72	2	72	1.4e-06	1	U	L.GFKGE
7044	620.9647	1859.8723	1859.8722	0.09	0	39	0.0026	1	U	F.QGNNS
7045	930.9442	1859.8737	1859.8722	0.85	0	(22)	0.12	1	U	F.QGNNS
7047	620.9659	1859.8760	1859.8722	2.06	0	(38)	0.0035	1	U	F.QGNNS
7517	708.0026	2120.9860	2120.9835	1.19	1	(21)	0.18	1	U	Y.NFQGN
7518	708.0039	2120.9897	2120.9835	2.93	1	31	0.021	1	U	Y.NFQGN
7795	869.1187	2604.3343	2604.3283	2.31	1	(20)	0.16	1	U	Y.IINQI
7796	869.1198	2604.3376	2604.3283	3.57	1	27	0.033	1	U	Y.IINQI

Proteins matching a subset of these peptides:

2::sp|P21420|NMPC_ECOLI **Mass:** 40277 **Score:** 73 **Matches:** 4(4) **Sequences:** 2

Putative outer membrane porin protein NmpC OS=Escherichia coli (strain K12) OX=83333

2::sp|P02932|PHOE_ECOLI **Mass:** 38898 **Score:** 29 **Matches:** 2(2) **Sequences:** 1

Outer membrane pore protein E OS=Escherichia coli (strain K12) OX=83333 GN=phoE PE=1

---

3. 2::sp|P0AE06|ACRA_ECOLI **Mass:** 42228 **Score:** 854 **Matches:** 61(54) **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
69	384.1995	766.3845	766.3861	-2.02	0	(27)	0.021	1	U	Y.ISKQ
71	384.2001	766.3856	766.3861	-0.66	0	30	0.011	1	U	Y.ISKQ
333	404.1981	806.3816	806.3810	0.75	0	20	0.14	1		Y.QIDP
930	451.2400	900.4655	900.4665	-1.11	0	(24)	0.049	1	U	L.VQNG
942	451.7316	901.4486	901.4505	-2.05	0	25	0.046	1	U	L.VQNG
943	451.7319	901.4493	901.4505	-1.32	0	(22)	0.08	1	U	L.VQNG
1509	487.2689	972.5232	972.5240	-0.78	1	(48)	0.00023	1	U	L.KQEL
1510	487.2694	972.5243	972.5240	0.35	1	(51)	0.00012	1	U	L.KQEL
1521	487.7613	973.5081	973.5080	0.09	1	59	2.2e-05	1	U	L.KQEL
1522	487.7617	973.5089	973.5080	0.92	1	(56)	5.3e-05	1	U	L.KQEL
2671	556.2490	1110.4835	1110.4830	0.48	0	34	0.0056	1		Y.VDVT
2714	557.8319	1113.6491	1113.6506	-1.31	0	(29)	0.012	1	U	L.KAGD
2715	557.8321	1113.6497	1113.6506	-0.77	0	(22)	0.054	1	U	L.KAGD
2716	557.8325	1113.6505	1113.6506	-0.10	0	(28)	0.014	1	U	L.KAGD
2717	557.8336	1113.6526	1113.6506	1.76	0	30	0.0095	1	U	L.KAGD
3466	597.8032	1193.5919	1193.5928	-0.75	1	28	0.034	1	U	Y.ISKQ
3546	401.5626	1201.6659	1201.6666	-0.63	0	26	0.032	1	U	L.KQEN
3547	401.5627	1201.6662	1201.6666	-0.33	0	(21)	0.092	1	U	L.KQEN
3565	602.8062	1203.5977	1203.5983	-0.44	0	44	0.00089	1	U	F.KEGS
3567	602.8077	1203.6009	1203.5983	2.20	0	(29)	0.026	1	U	F.KEGS
3852	621.8635	1241.7124	1241.7092	2.59	2	(32)	0.0056	1	U	L.RLKQ
3853	621.8637	1241.7129	1241.7092	2.99	2	32	0.0056	1	U	L.RLKQ
3858	622.3552	1242.6958	1242.6932	2.10	2	(31)	0.009	1	U	L.RLKQ
3859	622.3555	1242.6965	1242.6932	2.69	2	(29)	0.013	1	U	L.RLKQ
4751	684.3382	1366.6618	1366.6616	0.18	1	(45)	0.00073	1	U	F.KEGS
4753	684.3389	1366.6633	1366.6616	1.25	1	52	0.00012	1	U	F.KEGS
4755	684.3395	1366.6645	1366.6616	2.14	1	(40)	0.0018	1	U	F.KEGS
4756	684.3397	1366.6648	1366.6616	2.31	1	(42)	0.0015	1	U	F.KEGS
4757	684.3398	1366.6651	1366.6616	2.58	1	(29)	0.028	1	U	F.KEGS

4758	684.3399	1366.6652	1366.6616	2.66	1	(45)	0.00073	1	U	F.KEGS
5116	718.8739	1435.7332	1435.7307	1.78	0	43	0.0012	1	U	L.QITT
5459	746.3879	1490.7613	1490.7617	-0.24	0	(57)	5.5e-05	1	U	L.ITSD
5460	746.3882	1490.7618	1490.7617	0.08	0	(56)	7e-05	1	U	L.ITSD
5461	746.3889	1490.7633	1490.7617	1.07	0	(63)	1.4e-05	1	U	L.ITSD
5462	746.3905	1490.7664	1490.7617	3.19	0	(28)	0.035	1	U	L.ITSD
5463	746.3906	1490.7666	1490.7617	3.27	0	69	2.7e-06	1	U	L.ITSD
5760	517.6506	1549.9299	1549.9304	-0.33	0	(25)	0.0043	1	U	Y.RIAE
5761	775.9730	1549.9315	1549.9304	0.71	0	(27)	0.0023	1	U	Y.RIAE
5763	775.9750	1549.9354	1549.9304	3.24	0	(34)	0.00048	1	U	Y.RIAE
5767	776.4658	1550.9170	1550.9144	1.66	0	35	0.00061	1	U	Y.RIAE
5975	800.3625	1598.7104	1598.7101	0.24	1	(31)	0.012	1		L.DPIY
5976	800.3637	1598.7129	1598.7101	1.76	1	32	0.0096	1		L.DPIY
6733	884.4436	1766.8726	1766.8727	-0.03	1	(55)	6.7e-05	1	U	L.ITSD
6734	884.4442	1766.8737	1766.8727	0.60	1	63	1.3e-05	1	U	L.ITSD
6987	921.4721	1840.9297	1840.9294	0.13	1	42	0.0012	1	U	L.RAIF
6989	921.4738	1840.9331	1840.9294	1.99	1	(41)	0.0014	1	U	L.RAIF
7030	928.4974	1854.9803	1854.9799	0.24	1	60	1.4e-05	1	U	Y.DSAK
7031	928.5004	1854.9862	1854.9799	3.40	1	(54)	5e-05	1	U	Y.DSAK
7599	1120.5408	2239.0670	2239.0645	1.12	2	(58)	4.3e-05	1		L.ATVQ
7600	747.3635	2239.0688	2239.0645	1.91	2	(55)	8.4e-05	1		L.ATVQ
7601	747.3645	2239.0717	2239.0645	3.21	2	(61)	2.1e-05	1		L.ATVQ
7602	1120.5443	2239.0741	2239.0645	4.28	2	92	1.5e-08	1		L.ATVQ
7717	1227.6505	2453.2865	2453.2914	-2.03	0	46	0.00034	1	U	L.VVGA
7718	614.3300	2453.2907	2453.2914	-0.29	0	(21)	0.11	1	U	L.VVGA
7720	818.7712	2453.2919	2453.2914	0.18	0	(39)	0.0015	1	U	L.VVGA
7721	1227.6549	2453.2953	2453.2914	1.56	0	(37)	0.0026	1	U	L.VVGA
7722	818.7734	2453.2985	2453.2914	2.87	0	(45)	0.00035	1	U	L.VVGA
7723	614.5766	2454.2773	2454.2755	0.75	0	(22)	0.094	1	U	L.VVGA
7724	819.0998	2454.2775	2454.2755	0.85	0	(45)	0.00051	1	U	L.VVGA
7725	614.5767	2454.2778	2454.2755	0.95	0	(24)	0.062	1	U	L.VVGA
7726	819.1006	2454.2801	2454.2755	1.90	0	(40)	0.0013	1	U	L.VVGA

---

4. 2::sp|P0A799|PGK_ECOLI **Mass:** 41264 **Score:** 725 **Matches:** 32(30) **Sequences:** 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
703	433.7344	865.4543	865.4545	-0.28	0	49	0.00013	1	U	F.GIADK
704	433.7345	865.4544	865.4545	-0.08	0	(29)	0.013	1	U	F.GIADK
774	437.2103	872.4060	872.4062	-0.18	0	71	7.3e-07	1	U	F.ADVAC
775	437.2108	872.4069	872.4062	0.85	0	(53)	5.6e-05	1	U	F.ADVAC
961	452.7602	903.5059	903.5066	-0.68	1	41	0.001	1	U	F.SLLPV
962	452.7606	903.5066	903.5066	0.07	1	(37)	0.0027	1	U	F.SLLPV
971	453.2637	904.5129	904.5130	-0.15	1	(25)	0.024	1	U	L.DLAGK
972	453.2638	904.5131	904.5130	0.11	1	29	0.0095	1	U	L.DLAGK
1278	474.7608	947.5070	947.5076	-0.69	0	(31)	0.011	1	U	L.IVGGG
1279	474.7614	947.5083	947.5076	0.66	0	34	0.0051	1	U	L.IVGGG
2484	545.2924	1088.5703	1088.5713	-0.96	1	58	2.7e-05	1	U	L.DSLSK
2485	545.2931	1088.5717	1088.5713	0.38	1	(44)	0.00064	1	U	L.DSLSK
3989	629.8356	1257.6567	1257.6564	0.21	1	(25)	0.057	1	U	Y.EADLV
3990	420.2266	1257.6579	1257.6564	1.19	1	(23)	0.085	1	U	Y.EADLV
3992	629.8368	1257.6590	1257.6564	2.05	1	32	0.0097	1	U	Y.EADLV
4702	453.5729	1357.6968	1357.6990	-1.62	1	(32)	0.011	1	U	F.IAAQG

4703	453.5731	1357.6976	1357.6990	-1.02	1	(30)	0.02	1	U	F.IAAQG
4704	679.8571	1357.6996	1357.6990	0.41	1	52	0.0001	1	U	F.IAAQG
4705	679.8580	1357.7015	1357.6990	1.84	1	(41)	0.0013	1	U	F.IAAQG
4785	686.3775	1370.7404	1370.7405	-0.04	2	53	7.4e-05	1	U	Y.EADLV
4786	686.3777	1370.7409	1370.7405	0.32	2	(50)	0.00013	1	U	Y.EADLV
5042	714.3091	1426.6037	1426.6001	2.57	1	(41)	0.00061	1	U	L.GRPTE
5043	714.3095	1426.6045	1426.6001	3.08	1	44	0.00034	1	U	L.GRPTE
5238	729.8939	1457.7732	1457.7726	0.42	0	(39)	0.0023	1	U	L.KSVND
5239	729.8940	1457.7735	1457.7726	0.67	0	60	1.9e-05	1	U	L.KSVND
5574	759.9148	1517.8150	1517.8163	-0.87	1	(46)	0.00039	1	U	L.EFVEG
5575	759.9155	1517.8165	1517.8163	0.11	1	54	6.9e-05	1	U	L.EFVEG
6081	811.4009	1620.7872	1620.7883	-0.66	2	49	0.00035	1	U	L.VKDYL
6082	811.4017	1620.7888	1620.7883	0.31	2	(39)	0.0029	1	U	L.VKDYL
7200	953.4720	1904.9295	1904.9302	-0.36	0	37	0.0049	1	U	L.TTCNI
7731	820.0824	2457.2254	2457.2234	0.78	1	71	1.6e-06	1	U	L.KSVND
7732	820.0828	2457.2265	2457.2234	1.22	1	(62)	1.3e-05	1	U	L.KSVND

---

5. 1::sp|cRAP022|P00766|CTRA_BOVIN **Mass:** 26220 **Score:** 675 **Matches:** 47(40) **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
490	412.7290	823.4434	823.4440	-0.61	1	(47)	0.00012	1	U	L.KLST
491	412.7291	823.4436	823.4440	-0.47	1	(39)	0.00091	1	U	L.KLST
492	412.7292	823.4438	823.4440	-0.15	1	(40)	0.0006	1	U	L.KLST
493	412.7292	823.4439	823.4440	-0.01	1	54	2.6e-05	1	U	L.KLST
617	422.7352	843.4558	843.4450	12.8	1	20	0.11	1	U	W.VQQT
793	437.7552	873.4959	873.4960	-0.08	1	(32)	0.0096	1	U	W.TLVG
794	437.7558	873.4970	873.4960	1.11	1	41	0.00093	1	U	W.TLVG
951	452.2425	902.4705	902.4709	-0.46	0	(24)	0.075	1	U	L.TINN
952	452.2428	902.4710	902.4709	0.16	0	39	0.002	2	U	L.TINN
1666	494.7577	987.5008	987.5025	-1.80	1	25	0.048	1	U	L.VNWV
1802	501.2543	1000.4941	1000.4938	0.35	0	(27)	0.024	1	U	Y.TNAN
1803	501.2547	1000.4949	1000.4938	1.15	0	(24)	0.054	1	U	Y.TNAN
1811	501.7453	1001.4760	1001.4778	-1.72	0	(26)	0.03	1	U	Y.TNAN
1812	501.7459	1001.4771	1001.4778	-0.62	0	31	0.01	1	U	Y.TNAN
1913	508.7844	1015.5543	1015.5550	-0.66	1	50	0.00015	1	U	L.TINN
1914	508.7848	1015.5550	1015.5550	0.06	1	(44)	0.00067	1	U	L.TINN
1915	508.7849	1015.5551	1015.5550	0.18	1	(42)	0.00098	1	U	L.TINN
1919	508.7856	1015.5567	1015.5550	1.74	1	(34)	0.006	1	U	L.TINN
2051	515.2960	1028.5775	1028.5767	0.76	1	(24)	0.037	1	U	Y.ARVT
2052	515.2965	1028.5783	1028.5767	1.60	1	26	0.024	1	U	Y.ARVT
2773	561.7933	1121.5721	1121.5717	0.36	1	(45)	0.00065	1	U	W.QVSL
2774	561.7935	1121.5724	1121.5717	0.59	1	47	0.00039	1	U	W.QVSL
2775	561.7938	1121.5731	1121.5717	1.24	1	(36)	0.0048	1	U	W.QVSL
2776	561.7941	1121.5736	1121.5717	1.68	1	(45)	0.00064	1	U	W.QVSL
2777	561.7943	1121.5741	1121.5717	2.11	1	(45)	0.00068	1	U	W.QVSL
2778	561.7944	1121.5743	1121.5717	2.32	1	(39)	0.0024	1	U	W.QVSL
3037	575.2536	1148.4926	1148.4921	0.52	1	(30)	0.0097	1	U	F.CGGS
3038	575.2539	1148.4933	1148.4921	1.06	1	34	0.0038	1	U	F.CGGS
4457	660.3433	1318.6720	1318.6728	-0.66	0	57	4.5e-05	1	U	F.DQGS
4458	660.3433	1318.6721	1318.6728	-0.57	0	(26)	0.05	1	U	F.DQGS
4461	660.3444	1318.6742	1318.6728	1.01	0	(34)	0.0084	1	U	F.DQGS
4462	660.3449	1318.6753	1318.6728	1.84	0	(39)	0.0023	1	U	F.DQGS

4470	660.8347	1319.6548	1319.6568	-1.57	0	(22)	0.14	1	U	F.DQGS
4546	665.8665	1329.7185	1329.7140	3.39	2	21	0.11	1	U	Y.NSLT
5970	799.9575	1597.9004	1597.8940	3.97	2	30	0.0079	1	U	Y.ARVT
6431	842.3801	1682.7457	1682.7458	-0.05	0	(21)	0.11	1	U	F.SQTV
6432	842.3818	1682.7490	1682.7458	1.90	0	38	0.0025	1	U	F.SQTV
6623	869.9577	1737.9008	1737.9009	-0.05	1	47	0.00031	1	U	Y.TNAN
6625	869.9580	1737.9015	1737.9009	0.30	1	(39)	0.0021	1	U	Y.TNAN
6630	870.4537	1738.8928	1738.8849	4.51	1	(39)	0.0019	1	U	Y.TNAN
6631	870.4543	1738.8940	1738.8849	5.21	1	(35)	0.0054	1	U	Y.TNAN
6782	892.4423	1782.8700	1782.8689	0.58	0	(21)	0.19	1	U	L.SRIV
6783	892.4427	1782.8708	1782.8689	1.07	0	47	0.00039	1	U	L.SRIV
7015	926.5005	1850.9865	1850.9850	0.84	2	(27)	0.023	1	U	Y.TNAN
7016	926.5009	1850.9873	1850.9850	1.24	2	37	0.0023	1	U	Y.TNAN
7419	1009.9979	2017.9812	2017.9780	1.59	0	(28)	0.037	1	U	W.VVTA
7420	1009.9986	2017.9826	2017.9780	2.33	0	29	0.028	1	U	W.VVTA

Proteins matching a subset of these peptides:

1::sp|cRAP023|P00767|CTRB_BOVIN **Mass:** 26309 **Score:** 29 **Matches:** 2(2) **Seque**

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

---

6. 2::sp|P0A817|METK_ECOLI **Mass:** 42153 **Score:** 581 **Matches:** 28(25) **Sequences:**

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
606	422.2555	842.4964	842.4974	-1.20	2	(34)	0.0032	1	U	L.LRDAA
607	422.2555	842.4964	842.4974	-1.20	2	39	0.0011	1	U	L.LRDAA
736	435.7391	869.4636	869.4647	-1.27	2	(22)	0.031	1	U	L.DLLHP
738	435.7398	869.4651	869.4647	0.43	2	22	0.034	1	U	L.DLLHP
1340	478.3001	954.5857	954.5862	-0.49	0	(47)	5.6e-05	1	U	Y.VAKNI
1341	478.3005	954.5863	954.5862	0.16	0	51	2.1e-05	1	U	Y.VAKNI
1961	510.7539	1019.4933	1019.4924	0.87	0	33	0.0095	1	U	L.VGGEI
2452	544.2847	1086.5548	1086.5557	-0.83	0	41	0.0013	1	U	F.GTEKV
2454	544.2850	1086.5554	1086.5557	-0.28	0	(31)	0.013	1	U	F.GTEKV
2492	546.2460	1090.4775	1090.4787	-1.13	0	38	0.0019	1	U	F.VIGGP
3829	620.7858	1239.5570	1239.5554	1.30	0	26	0.045	1	U	L.ADRCE
3830	620.7867	1239.5588	1239.5554	2.77	0	(23)	0.083	1	U	L.ADRCE
4015	421.2347	1260.6823	1260.6826	-0.26	1	(27)	0.031	1	U	W.LRPDA
4017	631.3501	1260.6856	1260.6826	2.39	1	(25)	0.049	1	U	W.LRPDA
4018	631.3502	1260.6859	1260.6826	2.58	1	28	0.023	1	U	W.LRPDA
4409	657.3678	1312.7210	1312.7238	-2.13	0	31	0.0087	1	U	Y.DDGKI
4410	657.3680	1312.7214	1312.7238	-1.86	0	(29)	0.013	1	U	Y.DDGKI
5505	751.3633	1500.7121	1500.7056	4.35	0	39	0.0028	1	U	L.STQHS
5506	751.3638	1500.7131	1500.7056	5.00	0	(25)	0.061	1	U	L.STQHS
5881	790.8978	1579.7810	1579.7804	0.39	0	39	0.0028	1	U	Y.AIGVA
5882	790.8992	1579.7838	1579.7804	2.17	0	(26)	0.058	1	U	Y.AIGVA
6009	802.9315	1603.8485	1603.8457	1.71	1	41	0.0014	1	U	F.QYDDG
6236	826.3983	1650.7821	1650.7811	0.61	1	29	0.032	1	U	Y.ATNET
6237	826.3993	1650.7840	1650.7811	1.78	1	(22)	0.17	1	U	Y.ATNET
7093	936.4421	1870.8696	1870.8659	2.00	2	25	0.062	1	U	F.GYATN
7492	694.3582	2080.0526	2080.0549	-1.09	0	33	0.0096	1	U	L.SAIGK
7943	979.4833	2935.4282	2935.4272	0.35	1	74	8.5e-07	1	U	L.SAIGK
7944	979.4867	2935.4382	2935.4272	3.78	1	(68)	2.9e-06	1	U	L.SAIGK

---

7. 2::sp|P0A910|OMPA_ECOLI **Mass:** 37292 **Score:** 581 **Matches:** 28(24) **Sequences:**
Outer membrane protein A OS=Escherichia coli (strain K12) OX=83333 GN=ompA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1103	461.7660	921.5174	921.5171	0.25	2	38	0.0012	1	U	F.TLKSD
1104	461.7660	921.5174	921.5171	0.32	2	(21)	0.07	1	U	F.TLKSD
1323	477.7013	953.3880	953.3879	0.05	1	47	0.00013	1	U	W.SQYHD
1324	477.7016	953.3886	953.3879	0.76	1	(39)	0.00075	1	U	W.SQYHD
1753	499.2332	996.4519	996.4512	0.66	0	(41)	0.00099	1	U	Y.TDRIG
1754	499.2335	996.4524	996.4512	1.14	0	47	0.0003	1	U	Y.TDRIG
2177	527.2445	1052.4743	1052.4749	-0.57	2	24	0.06	1	U	Y.DWLGR
2178	527.2446	1052.4747	1052.4749	-0.23	2	(21)	0.12	1	U	Y.DWLGR
2181	527.2695	1052.5245	1052.5251	-0.52	0	(27)	0.031	1	U	W.RADTK
2182	527.2700	1052.5254	1052.5251	0.30	0	29	0.022	1	U	W.RADTK
2414	542.8215	1083.6284	1083.6288	-0.37	0	41	0.00051	1	U	Y.AITPE
2415	542.8217	1083.6289	1083.6288	0.10	0	(33)	0.0035	1	U	Y.AITPE
3675	609.2770	1216.5395	1216.5360	2.88	1	49	0.00013	1	U	L.GYTDR
3978	629.3157	1256.6168	1256.6150	1.44	0	(21)	0.12	1	U	Y.GKNHD
3979	629.3170	1256.6194	1256.6150	3.50	0	27	0.029	1	U	Y.GKNHD
4200	642.8045	1283.5944	1283.5921	1.79	1	23	0.079	1	U	L.GYPIT
4552	666.8433	1331.6721	1331.6721	-0.01	2	45	0.00071	1	U	L.KPEGQ
4553	666.8448	1331.6751	1331.6721	2.29	2	(32)	0.014	1	U	L.KPEGQ
4589	670.8803	1339.7459	1339.7459	0.02	1	70	6.9e-07	1	U	F.NKATL
4590	670.8810	1339.7474	1339.7459	1.11	1	(56)	1.7e-05	1	U	F.NKATL
4596	671.8657	1341.7169	1341.7140	2.15	1	(45)	0.0004	1	U	L.SNLDP
4597	671.8661	1341.7176	1341.7140	2.70	1	53	6.9e-05	1	U	L.SNLDP
6346	835.9524	1669.8902	1669.8887	0.93	2	(34)	0.0058	1	U	Y.SQLSN
6347	835.9537	1669.8928	1669.8887	2.46	2	40	0.0014	1	U	Y.SQLSN
6678	877.4166	1752.8186	1752.8179	0.35	1	(53)	0.00011	1	U	F.INNNG
6681	877.4191	1752.8236	1752.8179	3.22	1	(37)	0.0049	1	U	F.INNNG
6686	877.9113	1753.8081	1753.8020	3.50	1	(52)	0.00014	1	U	F.INNNG
6687	877.9122	1753.8098	1753.8020	4.47	1	55	7.4e-05	1	U	F.INNNG

---

8. 2::sp|P08200|IDH_ECOLI **Mass:** 46070 **Score:** 541 **Matches:** 25(21) **Sequences:** 1
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
348	404.7134	807.4123	807.4126	-0.39	1	20	0.12	1	U	L.DLIRE
682	427.2852	852.5558	852.5545	1.48	0	33	0.0006	1	U	Y.RVAIK
874	446.7299	891.4452	891.4450	0.25	1	28	0.025	1	U	Y.QLARE
1165	468.7430	935.4715	935.4712	0.33	2	22	0.11	1	U	L.RQELD
1316	477.2217	952.4289	952.4290	-0.19	1	(30)	0.013	1	U	F.TEGAF
1317	477.2219	952.4293	952.4290	0.32	1	40	0.0013	1	U	F.TEGAF
1868	506.7509	1011.4873	1011.4873	0.06	0	28	0.021	1	U	Y.TGEKS
1869	506.7509	1011.4873	1011.4873	0.06	0	(25)	0.05	1	U	Y.TGEKS
3084	578.3059	1154.5973	1154.5972	0.10	0	(22)	0.064	1	U	L.NVPEN
3085	578.3061	1154.5976	1154.5972	0.41	0	33	0.0051	1	U	L.NVPEN
3297	587.8064	1173.5982	1173.5990	-0.60	0	(28)	0.033	1	U	Y.AIAND
3298	587.8080	1173.6015	1173.5990	2.19	0	33	0.01	1	U	Y.AIAND
3456	398.2231	1191.6476	1191.6499	-1.95	0	(34)	0.0055	1	U	L.KVVDA

3457	398.2238	1191.6495	1191.6499	-0.32	0	(32)	0.0088	1	U	L.KVVDA
3458	596.8332	1191.6518	1191.6499	1.60	0	(56)	3e-05	1	U	L.KVVDA
3459	596.8336	1191.6526	1191.6499	2.22	0	65	3.7e-06	1	U	L.KVVDA
4392	656.3666	1310.7187	1310.7194	-0.52	0	(43)	0.00045	1	U	Y.AGQDK
4393	656.3671	1310.7196	1310.7194	0.14	0	47	0.00019	1	U	Y.AGQDK
5000	474.5932	1420.7579	1420.7562	1.19	0	(34)	0.0053	1	U	W.KADSA
5001	711.3875	1420.7605	1420.7562	3.03	0	51	0.00012	1	U	W.KADSA
5507	751.8769	1501.7392	1501.7334	3.86	0	42	0.0015	1	U	Y.IEGDG
6143	816.8892	1631.7639	1631.7580	3.62	2	(48)	0.00034	1	U	L.AREEF
6144	816.8898	1631.7651	1631.7580	4.37	2	67	4.1e-06	1	U	L.AREEF
6483	848.4572	1694.8999	1694.8991	0.43	1	34	0.0054	1	U	L.QNGKL
6485	848.4579	1694.9013	1694.8991	1.30	1	(22)	0.083	1	U	L.QNGKL

---

9. 2::sp|P0AAI5|FABF_ECOLI **Mass:** 43247 **Score:** 533 **Matches:** 27(24) **Sequences:**

3-oxoacyl-[acyl-carrier-protein] synthase 2 OS=Escherichia coli (strain K12) OX=8333

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
654	424.7121	847.4097	847.4110	-1.48	1	40	0.0019	1	U	F.VLGD
655	424.7126	847.4106	847.4110	-0.40	1	(22)	0.11	1	U	F.VLGD
1166	469.2335	936.4525	936.4552	-2.88	0	(21)	0.15	1	U	L.GAAG
1167	469.2345	936.4544	936.4552	-0.92	0	34	0.0068	1	U	L.GAAG
2683	556.7826	1111.5506	1111.5509	-0.28	1	43	0.0007	1	U	L.GLIE
2684	556.7830	1111.5515	1111.5509	0.50	1	(38)	0.002	1	U	L.GLIE
3862	622.8152	1243.6158	1243.6197	-3.12	1	(31)	0.012	1	U	L.AGQS
3863	622.8162	1243.6179	1243.6197	-1.46	1	49	0.00021	1	U	L.AGQS
4165	640.3154	1278.6163	1278.6204	-3.21	0	(48)	0.00035	1	U	L.RDAG
4166	640.3157	1278.6168	1278.6204	-2.83	0	(42)	0.0016	1	U	L.RDAG
4167	640.3185	1278.6225	1278.6204	1.66	0	49	0.00026	1	U	L.RDAG
4648	676.8177	1351.6208	1351.6190	1.33	0	(38)	0.0029	1	U	Y.HMTS
4649	676.8184	1351.6222	1351.6190	2.32	0	(51)	0.00017	1	U	Y.HMTS
4687	679.3588	1356.7030	1356.7038	-0.59	2	(84)	6.8e-08	1	U	L.LAGQ
4688	679.3608	1356.7070	1356.7038	2.39	2	92	1.1e-08	1	U	L.LAGQ
4766	684.8146	1367.6146	1367.6140	0.48	0	(52)	0.00011	1	U	Y.HMTS
4767	684.8150	1367.6154	1367.6140	1.09	0	(42)	0.0012	1	U	Y.HMTS
4768	684.8153	1367.6161	1367.6140	1.55	0	(57)	3.5e-05	1	U	Y.HMTS
4769	684.8163	1367.6180	1367.6140	2.97	0	63	8.7e-06	1	U	Y.HMTS
5355	739.3528	1476.6911	1476.6919	-0.52	1	58	3.2e-05	1	U	L.GMLS
5356	739.3534	1476.6923	1476.6919	0.31	1	(55)	6.2e-05	1	U	L.GMLS
5977	533.9253	1598.7542	1598.7549	-0.45	0	33	0.01	1	U	L.STRN
5978	533.9255	1598.7548	1598.7549	-0.10	0	(22)	0.13	1	U	L.STRN
6499	852.9094	1703.8042	1703.8036	0.32	0	38	0.0038	1	U	Y.GDAD
6500	852.9098	1703.8050	1703.8036	0.83	0	(37)	0.0048	1	U	Y.GDAD
7703	808.3881	2422.1424	2422.1434	-0.45	2	(30)	0.024	1	U	L.ALRD
7704	1212.0791	2422.1436	2422.1434	0.08	2	39	0.0025	1	U	L.ALRD

---

10. 2::sp|P0AEX9|MALE_ECOLI **Mass:** 43360 **Score:** 531 **Matches:** 24(22) **Sequences:**

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
37	382.1849	762.3552	762.3548	0.54	1	22	0.084	1	U	F.NLQEP

939	451.7156	901.4167	901.4181	-1.53	1	(21)	0.057	1	U	F.KYENG
940	451.7157	901.4168	901.4181	-1.46	1	27	0.017	1	U	F.KYENG
1876	507.2506	1012.4866	1012.4865	0.08	2	46	0.00034	1	U	L.AKEFL
1877	507.2509	1012.4872	1012.4865	0.69	2	(23)	0.061	1	U	L.AKEFL
2259	530.3093	1058.6040	1058.6012	2.67	0	27	0.022	1	U	L.IAYPI
2283	531.8006	1061.5866	1061.5869	-0.26	1	33	0.0053	1	U	Y.NGLAE
2284	531.8007	1061.5868	1061.5869	-0.15	1	(30)	0.01	1	U	Y.NGLAE
2613	552.7998	1103.5850	1103.5863	-1.10	1	46	0.00041	1	U	L.LAEIT
2614	552.8000	1103.5854	1103.5863	-0.75	1	(41)	0.0014	1	U	L.LAEIT
2950	570.7790	1139.5434	1139.5459	-2.13	0	59	2.1e-05	1	U	W.SNIDT
2951	570.7796	1139.5446	1139.5459	-1.06	0	(46)	0.00039	1	U	W.SNIDT
3097	578.8099	1155.6052	1155.6023	2.53	1	36	0.0035	1	U	W.EEIPA
4095	636.3336	1270.6526	1270.6517	0.69	0	40	0.0016	1	U	L.SAGIN
4097	636.3350	1270.6555	1270.6517	2.99	0	(39)	0.0017	1	U	L.SAGIN
5012	711.8907	1421.7668	1421.7667	0.11	1	(27)	0.022	1	U	Y.NKDLL
5013	711.8921	1421.7696	1421.7667	2.07	1	44	0.00041	1	U	Y.NKDLL
5092	717.8377	1433.6609	1433.6609	-0.03	0	(55)	6.9e-05	1	U	F.NKGET
5093	717.8391	1433.6637	1433.6609	1.93	0	59	2.7e-05	1	U	F.NKGET
5709	514.9424	1541.8053	1541.8049	0.25	0	(34)	0.0064	1	U	Y.DIKDV
5710	514.9427	1541.8062	1541.8049	0.85	0	(31)	0.014	1	U	Y.DIKDV
5711	771.9108	1541.8070	1541.8049	1.33	0	70	1.7e-06	1	U	Y.DIKDV
5712	771.9125	1541.8104	1541.8049	3.55	0	(60)	1.6e-05	1	U	Y.DIKDV
6819	597.6479	1789.9218	1789.9210	0.45	1	27	0.046	1	U	Y.DIKDV

---

11. 2::sp|P0C8J8|GATZ_ECOLI **Mass:** 47535 **Score:** 514 **Matches:** 27(21) **Sequences:**

D-tagatose-1,6-bisphosphate aldolase subunit GatZ 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
52	383.2172	764.4198	764.4181	2.21	0	22	0.037	1	U	L.SAIPH
143	391.7094	781.4043	781.4044	-0.15	0	(22)	0.063	1	U	L.IMDKI
144	391.7098	781.4051	781.4044	0.87	0	(20)	0.089	1	U	L.IMDKI
255	399.7064	797.3983	797.3993	-1.28	0	(20)	0.087	1	U	L.IMDKI
256	399.7066	797.3987	797.3993	-0.75	0	25	0.033	1	U	L.IMDKI
469	410.2398	818.4649	818.4650	-0.08	1	28	0.015	1	U	F.ALREA
470	410.2399	818.4652	818.4650	0.29	1	(27)	0.019	1	U	F.ALREA
547	416.7498	831.4850	831.4854	-0.50	1	46	0.00012	1		L.KVGPA
548	416.7498	831.4851	831.4854	-0.35	1	(44)	0.00019	1		L.KVGPA
1054	458.2375	914.4605	914.4610	-0.51	1	(20)	0.11	1	U	W.ELVRD
1055	458.2378	914.4610	914.4610	0.02	1	27	0.021	1	U	W.ELVRD
1142	466.2456	930.4766	930.4770	-0.48	0	25	0.048	1	U	F.ERIQS
1143	466.2456	930.4767	930.4770	-0.33	0	(24)	0.06	1	U	F.ERIQS
1765	499.7384	997.4622	997.4617	0.52	0	22	0.1	1	U	F.DHSNI
1894	507.7768	1013.5390	1013.5393	-0.26	1	(53)	5.1e-05	1	U	F.ALAQI
1895	507.7776	1013.5407	1013.5393	1.44	1	62	6.7e-06	1	U	F.ALAQI
1978	511.7669	1021.5193	1021.5193	0.07	2	33	0.011	1	U	Y.RTGFN
1979	511.7673	1021.5200	1021.5193	0.77	2	(21)	0.15	1	U	Y.RTGFN
3724	613.8419	1225.6692	1225.6666	2.07	0	59	1e-05	1	U	L.APETV
3725	613.8419	1225.6693	1225.6666	2.17	0	(48)	0.00014	1	U	L.APETV
3919	625.8045	1249.5944	1249.5939	0.46	0	(50)	0.0002	1	U	L.IEATS
3920	625.8064	1249.5982	1249.5939	3.50	0	68	3.4e-06	1	U	L.IEATS
5871	789.3639	1576.7132	1576.7151	-1.20	0	(35)	0.005	1	U	F.AAESV
5872	789.3658	1576.7170	1576.7151	1.20	0	49	0.00023	1	U	F.AAESV
6302	831.8854	1661.7563	1661.7566	-0.18	0	50	0.00015	1	U	W.QQENA

6380	839.8856	1677.7566	1677.7515	3.00	0	(42)	0.0011	1	U	W.QQENA
6381	839.8873	1677.7600	1677.7515	5.03	0	(47)	0.00041	1	U	W.QQENA

---

12. 2::sp|P0ABH7|CISY_ECOLI **Mass:** 48383 **Score:** 486 **Matches:** 34(29) **Sequences:**

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
2078	516.7637	1031.5129	1031.5135	-0.58	1	(40)	0.0018	1	U	L.TLNGD
2079	516.7646	1031.5147	1031.5135	1.21	1	(38)	0.0027	1	U	L.TLNGD
2081	517.2560	1032.4974	1032.4975	-0.10	1	(33)	0.0088	1	U	L.TLNGD
2082	517.2562	1032.4979	1032.4975	0.38	1	42	0.001	1	U	L.TLNGD
2144	524.7502	1047.4858	1047.4873	-1.39	1	40	0.0017	1	U	L.ENIAL
2145	524.7505	1047.4864	1047.4873	-0.79	1	(38)	0.0028	1	U	L.ENIAL
2305	532.7594	1063.5042	1063.5047	-0.38	0	25	0.057	1	U	W.GPAHG
2306	532.7595	1063.5045	1063.5047	-0.16	0	(22)	0.12	3	U	W.GPAHG
2397	541.7905	1081.5664	1081.5669	-0.45	0	28	0.02	1	U	L.HRGFP
2398	541.7909	1081.5672	1081.5669	0.32	0	(23)	0.066	1	U	L.HRGFP
2404	542.7613	1083.5081	1083.5093	-1.04	0	33	0.0072	1	U	L.KAMGI
2405	542.7623	1083.5101	1083.5093	0.77	0	(28)	0.025	1	U	L.KAMGI
2566	550.7590	1099.5034	1099.5042	-0.73	0	(20)	0.13	1	U	L.KAMGI
2870	566.3165	1130.6185	1130.6183	0.20	2	(28)	0.021	1	U	L.KELGT
2871	566.3171	1130.6196	1130.6183	1.17	2	32	0.0089	1	U	L.KELGT
3461	597.2745	1192.5345	1192.5360	-1.24	0	(34)	0.0065	1	U	L.NGEKP
3462	597.2761	1192.5377	1192.5360	1.41	0	40	0.0017	1	U	L.NGEKP
3464	597.7665	1193.5184	1193.5200	-1.35	0	(29)	0.016	1	U	L.NGEKP
3465	597.7682	1193.5219	1193.5200	1.62	0	(25)	0.042	1	U	L.NGEKP
4547	666.3107	1330.6068	1330.6075	-0.52	0	26	0.035	1	U	F.TSTAS
4548	666.3108	1330.6071	1330.6075	-0.25	0	(25)	0.042	1	U	F.TSTAS
4578	669.7640	1337.5135	1337.5124	0.85	0	28	0.0033	1	U	L.SKMPT
5184	725.3606	1448.7066	1448.7068	-0.14	2	60	3e-05	1	U	L.GTKDD
5185	725.3627	1448.7109	1448.7068	2.80	2	(41)	0.0022	1	U	L.GTKDD
5633	510.2945	1527.8616	1527.8621	-0.27	1	(36)	0.0023	1	U	L.KGTLG
5634	510.2955	1527.8648	1527.8621	1.77	1	40	0.00087	1	U	L.KGTLG
5652	766.9026	1531.7907	1531.7882	1.67	2	(33)	0.011	1	U	Y.ILLNG
5655	767.3942	1532.7738	1532.7722	1.03	2	48	0.00034	1	U	Y.ILLNG
5656	767.3943	1532.7740	1532.7722	1.19	2	(48)	0.00038	1	U	Y.ILLNG
5900	792.8434	1583.6722	1583.6740	-1.11	1	(39)	0.0013	1	U	L.NGEKP
5903	792.8455	1583.6764	1583.6740	1.52	1	(37)	0.0024	1	U	L.NGEKP
5904	792.8466	1583.6786	1583.6740	2.91	1	(22)	0.081	1	U	L.NGEKP
5908	793.3372	1584.6599	1584.6580	1.21	1	(38)	0.0014	1	U	L.NGEKP
5909	793.3386	1584.6626	1584.6580	2.90	1	45	0.00032	1	U	L.NGEKP

---

13. 2::sp|P0A836|SUCC_ECOLI **Mass:** 41652 **Score:** 466 **Matches:** 21(17) **Sequences:**

Succinate--CoA ligase [ADP-forming] subunit beta OS=Escherichia coli (strain K12) OX

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2524	547.7831	1093.5516	1093.5511	0.42	0	24	0.075	2	U	L.AMGTM
2665	555.7798	1109.5450	1109.5461	-0.94	0	(21)	0.16	1	U	L.AMGTM
2748	559.8136	1117.6126	1117.6132	-0.46	2	(29)	0.016	1	U	L.GLEGK
2749	559.8148	1117.6151	1117.6132	1.73	2	32	0.0088	1	U	L.GLEGK

3132	580.3136	1158.6126	1158.6132	-0.47	0	51	0.00014	1	U	L.VEAAT
3133	580.3149	1158.6153	1158.6132	1.85	0	(43)	0.00087	1	U	L.VEAAT
3322	589.2961	1176.5777	1176.5775	0.19	2	(39)	0.0031	1	U	L.DGKLG
3324	589.2970	1176.5794	1176.5775	1.66	2	44	0.00086	1	U	L.DGKLG
4001	630.3565	1258.6985	1258.6955	2.35	1	29	0.015	1	U	L.VITKQ
4476	661.8457	1321.6768	1321.6765	0.25	1	79	2.2e-07	1	U	L.VEAAT
4477	661.8472	1321.6799	1321.6765	2.57	1	(62)	1.1e-05	1	U	L.VEAAT
4835	693.8649	1385.7152	1385.7151	0.09	0	98	2.7e-09	1	U	L.TDAAQ
4836	693.8669	1385.7192	1385.7151	3.00	0	(96)	5.2e-09	1	U	L.TDAAQ
5155	481.3042	1440.8908	1440.8915	-0.53	1	(21)	0.011	1	U	F.KIILS
5156	481.3047	1440.8922	1440.8915	0.42	1	24	0.005	1	U	F.KIILS
5677	768.8864	1535.7583	1535.7580	0.18	0	45	0.00094	1	U	L.DVGGG
5678	768.8874	1535.7602	1535.7580	1.45	0	(38)	0.0044	1	U	L.DVGGG
6223	825.4269	1648.8393	1648.8421	-1.65	1	42	0.0016	1	U	F.LDVGG
6224	550.6212	1648.8418	1648.8421	-0.14	1	(22)	0.14	1	U	F.LDVGG
6225	550.6224	1648.8455	1648.8421	2.08	1	(21)	0.18	1	U	F.LDVGG
6226	825.4305	1648.8464	1648.8421	2.64	1	(28)	0.036	1	U	F.LDVGG

---

14. 2::sp|P0A6P1|EFTS_ECOLI **Mass:** 30518 **Score:** 449 **Matches:** 25(25) **Sequences:**

Elongation factor Ts OS=Escherichia coli (strain K12) OX=83333 GN=tsf PE=1 SV=2

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2860	566.2755	1130.5365	1130.5356	0.74	0	38	0.0025	1	U	L.KEHNA
2861	566.2764	1130.5383	1130.5356	2.37	0	(38)	0.0025	1	U	L.KEHNA
2894	568.2846	1134.5547	1134.5557	-0.93	1	41	0.0017	1	U	F.TGEVS
2895	568.2862	1134.5578	1134.5557	1.85	1	(32)	0.014	1	U	F.TGEVS
3405	594.8188	1187.6231	1187.6220	0.96	0	(26)	0.044	1	U	F.VMEPS
3571	602.8169	1203.6192	1203.6169	1.91	0	35	0.0065	1	U	F.VMEPS
3572	602.8170	1203.6194	1203.6169	2.03	0	(28)	0.034	1	U	F.VMEPS
4312	651.3616	1300.7087	1300.7061	2.03	1	(33)	0.0084	1	U	F.VMEPS
4313	651.3618	1300.7091	1300.7061	2.32	1	33	0.0078	1	U	F.VMEPS
4464	440.5702	1318.6887	1318.6881	0.43	1	(42)	0.0012	1	U	L.KAQFE
4465	440.5702	1318.6887	1318.6881	0.50	1	(40)	0.0019	1	U	L.KAQFE
4466	660.3518	1318.6891	1318.6881	0.75	1	(43)	0.00088	1	U	L.KAQFE
4467	660.3528	1318.6911	1318.6881	2.31	1	49	0.0002	1	U	L.KAQFE
4897	700.8856	1399.7567	1399.7559	0.59	0	73	6.3e-07	1	U	L.DAAVA
4898	700.8861	1399.7577	1399.7559	1.29	0	(55)	3.7e-05	1	U	L.DAAVA
5191	726.3503	1450.6860	1450.6828	2.24	0	67	5e-06	1	U	F.EVGEG
5192	726.3505	1450.6864	1450.6828	2.49	0	(59)	3e-05	1	U	F.EVGEG
5193	726.3511	1450.6876	1450.6828	3.33	0	(57)	5.3e-05	1	U	F.EVGEG
7078	934.4756	1866.9367	1866.9363	0.22	1	(41)	0.0019	1	U	F.IRFEV
7079	623.3201	1866.9384	1866.9363	1.09	1	47	0.00049	1	U	F.IRFEV
7080	623.3226	1866.9461	1866.9363	5.21	1	(44)	0.00085	1	U	F.IRFEV
7241	643.0293	1926.0661	1926.0674	-0.66	1	(30)	0.0076	1	U	F.ADKVL
7242	964.0422	1926.0698	1926.0674	1.28	1	(50)	8e-05	1	U	F.ADKVL
7243	964.0431	1926.0717	1926.0674	2.28	1	67	1.6e-06	1	U	F.ADKVL
7244	643.0314	1926.0723	1926.0674	2.56	1	(32)	0.0044	1	U	F.ADKVL

---

15. 2::sp|P0A6A3|ACKA_ECOLI **Mass:** 43605 **Score:** 449 **Matches:** 25(22) **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
161	393.7575	785.5004	785.5011	-0.86	2	35	0.00085	1	U	L.SLGKL
162	393.7575	785.5004	785.5011	-0.86	2	(27)	0.0054	1	U	L.SLGKL
859	442.2163	882.4179	882.4195	-1.79	0	(27)	0.033	1	U	L.GAGAA
860	442.2166	882.4186	882.4195	-1.04	0	32	0.0084	1	U	L.GAGAA
886	448.7124	895.4103	895.4109	-0.72	2	(21)	0.1	1	U	Y.LSGLA
887	448.7125	895.4105	895.4109	-0.52	2	21	0.098	1	U	Y.LSGLA
1829	503.7653	1005.5160	1005.5165	-0.49	0	34	0.0067	1	U	Y.VTQEA
1830	503.7655	1005.5165	1005.5165	0.04	0	(29)	0.021	1	U	Y.VTQEA
2410	542.8032	1083.5918	1083.5924	-0.58	1	35	0.0026	1	U	L.AQKPE
2411	542.8045	1083.5944	1083.5924	1.90	1	(35)	0.0025	1	U	L.AQKPE
2762	561.2328	1120.4511	1120.4495	1.46	0	(20)	0.033	1	U	F.HQTMP
2904	569.2291	1136.4437	1136.4444	-0.63	0	38	0.00041	1	U	F.HQTMP
2905	569.2302	1136.4458	1136.4444	1.18	0	(20)	0.034	1	U	F.HQTMP
3236	585.2979	1168.5813	1168.5798	1.27	1	(24)	0.059	1	U	F.YVTQE
3237	585.2980	1168.5815	1168.5798	1.47	1	27	0.025	1	U	F.YVTQE
3652	608.2922	1214.5698	1214.5680	1.49	1	41	0.001	1	U	L.GFEVD
4298	650.7956	1299.5766	1299.5765	0.08	1	51	9.8e-05	1	U	L.GLTEV
4299	650.7961	1299.5777	1299.5765	0.93	1	(49)	0.00016	1	U	L.GLTEV
5018	712.3658	1422.7170	1422.7177	-0.49	2	(32)	0.012	1	U	Y.TALMD
5019	712.3660	1422.7174	1422.7177	-0.23	2	50	0.00019	1	U	Y.TALMD
5087	717.3560	1432.6974	1432.6980	-0.45	0	39	0.0035	1	U	F.TGGIG
7343	660.6982	1979.0729	1979.0687	2.11	0	47	0.00024	1	U	F.INKEG
7344	660.6987	1979.0742	1979.0687	2.76	0	(33)	0.0051	1	U	F.INKEG
7345	990.5453	1979.0761	1979.0687	3.75	0	(46)	0.00027	1	U	F.INKEG
7346	990.5457	1979.0767	1979.0687	4.05	0	(37)	0.002	1	U	F.INKEG

---

16. 2::sp|P0A953|FABB_ECOLI **Mass:** 42928 **Score:** 342 **Matches:** 20(16) **Sequences:**
3-oxoacyl-[acyl-carrier-protein] synthase 1 OS=Escherichia coli (strain K12) OX=8333
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
312	403.2319	804.4492	804.4494	-0.23	0	(39)	0.0011	1	U	L.AAIRE
313	403.2323	804.4500	804.4494	0.84	0	41	0.0007	1	U	L.AAIRE
566	419.2085	836.4024	836.4028	-0.48	1	28	0.026	1	U	F.GFGGT
567	419.2088	836.4030	836.4028	0.17	1	(26)	0.044	1	U	F.GFGGT
4184	641.3070	1280.5995	1280.5997	-0.16	0	(22)	0.13	1	U	Y.NDTPE
4185	641.3079	1280.6012	1280.5997	1.17	0	31	0.016	1	U	Y.NDTPE
4230	645.8246	1289.6346	1289.6463	-9.07	0	(39)	0.0036	1	U	L.NIVTE
4231	645.8250	1289.6355	1289.6463	-8.40	0	(35)	0.0075	1	U	L.NIVTE
4232	645.8306	1289.6466	1289.6463	0.22	0	46	0.00057	1	U	L.NIVTE
4233	645.8327	1289.6508	1289.6463	3.53	0	(45)	0.00074	1	U	L.NIVTE
5232	729.3843	1456.7540	1456.7522	1.26	0	57	3.5e-05	1	U	L.GIVSS
5233	729.3846	1456.7547	1456.7522	1.76	0	(51)	0.00016	1	U	L.GIVSS
6242	826.8772	1651.7398	1651.7399	-0.04	1	23	0.099	1	U	L.SMEQA
6251	827.4265	1652.8383	1652.8370	0.83	1	70	1.9e-06	1	U	Y.LNSHG
6252	551.9539	1652.8398	1652.8370	1.68	1	(25)	0.056	1	U	Y.LNSHG
6253	551.9540	1652.8401	1652.8370	1.90	1	(42)	0.0013	1	U	Y.LNSHG
6254	827.4280	1652.8414	1652.8370	2.68	1	(53)	0.00011	1	U	Y.LNSHG
6330	834.8750	1667.7354	1667.7348	0.37	1	(22)	0.094	1	U	L.SMEQA
6780	891.9622	1781.9098	1781.9047	2.86	1	(24)	0.075	1	U	F.IAPSI
6781	891.9633	1781.9121	1781.9047	4.17	1	45	0.00061	1	U	F.IAPSI

17. 2::sp|P0A9B2|G3P1_ECOLI **Mass:** 35681 **Score:** 296 **Matches:** 16(15) **Sequences:**
Glyceraldehyde-3-phosphate dehydrogenase A OS=Escherichia coli (strain K12) OX=83333
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
172	**394.7287**	**787.4428**	**787.4440**	**-1.48**	**1**	**22**	**0.077**	**1**	**U**	**Y.SNKVL**
879	**447.7664**	**893.5183**	**893.5011**	**19.3**	**2**	**36**	**0.0011**	**1**	**U**	**F.VKLVS**
880	**447.7677**	**893.5208**	**893.5011**	**22.1**	**2**	**(26)**	**0.008**	**1**	**U**	**F.VKLVS**
895	**448.7635**	**895.5124**	**895.5127**	**-0.30**	**1**	**24**	**0.011**	**1**	**U**	**L.DLIAH**
1094	**460.7456**	**919.4766**	**919.4763**	**0.29**	**0**	**(51)**	**0.00014**	**1**	**U**	**L.AKVIN**
1095	**460.7457**	**919.4768**	**919.4763**	**0.51**	**0**	**52**	**0.00011**	**1**	**U**	**L.AKVIN**
1280	**474.7790**	**947.5435**	**947.5440**	**-0.56**	**0**	**(34)**	**0.0025**	**1**	**U**	**M.TIKVG**
1281	**474.7794**	**947.5443**	**947.5440**	**0.28**	**0**	**34**	**0.0025**	**1**	**U**	**M.TIKVG**
1294	**475.2702**	**948.5258**	**948.5280**	**-2.30**	**0**	**(34)**	**0.0044**	**1**	**U**	**M.TIKVG**
1295	**475.2706**	**948.5266**	**948.5280**	**-1.52**	**0**	**(31)**	**0.0077**	**1**	**U**	**M.TIKVG**
1296	**475.2711**	**948.5277**	**948.5280**	**-0.36**	**0**	**(31)**	**0.0066**	**1**	**U**	**M.TIKVG**
3052	**384.5520**	**1150.6342**	**1150.6346**	**-0.37**	**1**	**25**	**0.028**	**1**	**U**	**L.TVRLE**
3908	**624.8157**	**1247.6169**	**1247.6146**	**1.85**	**1**	**(52)**	**0.00016**	**1**	**U**	**F.DAKAG**
3909	**624.8159**	**1247.6173**	**1247.6146**	**2.16**	**1**	**56**	**5.9e-05**	**1**	**U**	**F.DAKAG**
4265	**648.3690**	**1294.7234**	**1294.7245**	**-0.89**	**0**	**48**	**0.00011**	**1**	**U**	**F.RVPTP**
4266	**648.3697**	**1294.7248**	**1294.7245**	**0.24**	**0**	**(44)**	**0.00024**	**1**	**U**	**F.RVPTP**

---

18. 2::sp|P02925|RBSB_ECOLI **Mass:** 30931 **Score:** 284 **Matches:** 15(13) **Sequences:**
Ribose import binding protein RbsB OS=Escherichia coli (strain K12) OX=83333 GN=rbsE
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
141	**390.6978**	**779.3811**	**779.3814**	**-0.38**	**0**	**60**	**1.6e-05**	**1**	**U**	**L.GGKIA**
142	**390.6981**	**779.3817**	**779.3814**	**0.42**	**0**	**(47)**	**0.00038**	**1**	**U**	**L.GGKIA**
2406	**542.7739**	**1083.5333**	**1083.5349**	**-1.49**	**0**	**(31)**	**0.0092**	**1**	**U**	**L.TAHPD**
2407	**542.7744**	**1083.5341**	**1083.5349**	**-0.72**	**0**	**31**	**0.0085**	**1**	**U**	**L.TAHPD**
2718	558.2696	1114.5246	1114.5254	-0.72	0	(21)	0.12	2	U	L.DSQNN
2719	558.2703	1114.5260	1114.5254	0.48	0	25	0.04	2	U	L.DSQNN
4662	**677.8384**	**1353.6623**	**1353.6599**	**1.81**	**0**	**(29)**	**0.029**	**1**	**U**	**L.QTAGK**
4663	**677.8391**	**1353.6635**	**1353.6599**	**2.71**	**0**	**33**	**0.011**	**1**	**U**	**L.QTAGK**
5560	**505.9145**	**1514.7216**	**1514.7213**	**0.19**	**0**	**(23)**	**0.099**	**1**	**U**	**F.DGTPD**
5562	**758.3687**	**1514.7229**	**1514.7213**	**1.06**	**0**	**31**	**0.017**	**1**	**U**	**F.DGTPD**
5563	**758.3710**	**1514.7275**	**1514.7213**	**4.12**	**0**	**(28)**	**0.028**	**1**	**U**	**F.DGTPD**
6255	**827.4436**	**1652.8726**	**1652.8733**	**-0.41**	**2**	**75**	**4.6e-07**	**1**	**U**	**Y.NLVVL**
6256	**827.4448**	**1652.8750**	**1652.8733**	**1.00**	**2**	**(55)**	**4e-05**	**1**	**U**	**Y.NLVVL**
7642	**770.4291**	**2308.2654**	**2308.2638**	**0.69**	**0**	**31**	**0.0053**	**1**	**U**	**L.AATIA**
7643	**770.4293**	**2308.2661**	**2308.2638**	**1.01**	**0**	**(30)**	**0.0066**	**1**	**U**	**L.AATIA**

---

19. 2::sp|P0AB71|ALF_ECOLI **Mass:** 39351 **Score:** 272 **Matches:** 19(16) **Sequences:**
Fructose-bisphosphate aldolase class 2 OS=Escherichia coli (strain K12) OX=83333 GN=
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4412	**438.8945**	**1313.6617**	**1313.6616**	**0.09**	**2**	**(24)**	**0.058**	**1**	**U**	**W.IDGLL**
4413	**438.8945**	**1313.6618**	**1313.6616**	**0.15**	**2**	**29**	**0.021**	**1**	**U**	**W.IDGLL**

5339	492.2470	1473.7192	1473.7212	-1.34	0	31	0.02	1	U	L.GNPKG
5340	492.2475	1473.7207	1473.7212	-0.34	0	(29)	0.029	1	U	L.GNPKG
5589	761.8644	1521.7143	1521.7134	0.63	0	37	0.0043	1	U	Y.GVVKM
5590	761.8648	1521.7151	1521.7134	1.12	0	(33)	0.011	1	U	Y.GVVKM
6094	812.4747	1622.9349	1622.9355	-0.39	0	38	0.00058	1	U	F.IAGKG
6095	541.9856	1622.9350	1622.9355	-0.35	0	(30)	0.004	1	U	F.IAGKG
6097	812.4776	1622.9406	1622.9355	3.14	0	(29)	0.0049	1	U	F.IAGKG
6559	574.9355	1721.7846	1721.7857	-0.59	0	(24)	0.075	1	U	F.HGGSG
6560	574.9360	1721.7863	1721.7857	0.37	0	(26)	0.045	1	U	F.HGGSG
6561	861.9008	1721.7870	1721.7857	0.76	0	(58)	3.2e-05	1	U	F.HGGSG
6562	861.9026	1721.7907	1721.7857	2.96	0	65	7.5e-06	1	U	F.HGGSG
7071	932.4962	1862.9779	1862.9779	0.02	1	39	0.002	1	U	F.DFVKP
7072	622.0001	1862.9785	1862.9779	0.36	1	(29)	0.02	1	U	F.DFVKP
7073	932.4975	1862.9804	1862.9779	1.39	1	(36)	0.0041	1	U	F.DFVKP
7074	622.0012	1862.9818	1862.9779	2.13	1	(31)	0.013	1	U	F.DFVKP
7411	672.0170	2013.0291	2013.0279	0.58	2	34	0.0077	1	U	Y.LQGQL
7412	672.0177	2013.0313	2013.0279	1.66	2	(22)	0.11	1	U	Y.LQGQL

---

20. 2::sp|P0A9A6|FTSZ_ECOLI **Mass:** 40299 **Score:** 270 **Matches:** 9(6) **Sequences:** 6

Cell division protein FtsZ OS=Escherichia coli (strain K12) OX=83333 GN=ftsZ 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	Peptid
986	454.2294	906.4442	906.4447	-0.55	2	20	0.16	1	U	F.DLRL
987	454.2299	906.4452	906.4447	0.60	2	(20)	0.17	1	U	F.DLRL
1399	481.2895	960.5644	960.5644	-0.07	0	44	0.00023	1	U	L.TVAV
1400	481.2898	960.5650	960.5644	0.55	0	(41)	0.00039	1	U	L.TVAV
1636	493.2879	984.5612	984.5604	0.82	0	26	0.021	1	U	L.KGAV
3478	598.2931	1194.5717	1194.5703	1.21	1	39	0.0027	1	U	L.RAAL
3479	598.2932	1194.5719	1194.5703	1.32	1	(20)	0.18	1	U	L.RAAL
4696	679.3692	1356.7238	1356.7249	-0.76	2	50	0.00014	1	U	L.LEDI
7524	1065.0496	2128.0846	2128.0834	0.53	0	91	1.5e-08	1	U	F.IAAG

---

21. 2::sp|P23893|GSA_ECOLI **Mass:** 45907 **Score:** 245 **Matches:** 11(10) **Sequences:** 7

Glutamate-1-semialdehyde 2,1-aminomutase OS=Escherichia coli (strain K12) OX=83333 G

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1378	480.2421	958.4696	958.4695	0.16	0	31	0.0082	1	U	L.VVNHV
1379	480.2422	958.4699	958.4695	0.41	0	(31)	0.0094	1	U	L.VVNHV
1874	507.2501	1012.4856	1012.4865	-0.90	1	29	0.017	1	U	L.FIEKA
1875	507.2504	1012.4863	1012.4865	-0.23	1	(24)	0.049	1	U	L.FIEKA
2110	522.2551	1042.4956	1042.4971	-1.47	2	28	0.018	1	U	Y.LYDVD
4825	693.2946	1384.5746	1384.5751	-0.42	0	36	0.002	1	U	Y.QDVMA
5111	718.8411	1435.6676	1435.6687	-0.78	0	(22)	0.14	1	U	F.GAPTE
5112	718.8438	1435.6731	1435.6687	3.05	0	34	0.008	1	U	F.GAPTE
6234	825.9037	1649.7928	1649.7897	1.91	1	53	0.00011	1	U	L.NEVAQ
6235	825.9050	1649.7955	1649.7897	3.54	1	(39)	0.003	1	U	L.NEVAQ
7357	997.9770	1993.9394	1993.9415	-1.04	2	32	0.015	1	U	F.ACLNE

---

22. 2::sp|P61889|MDH_ECOLI **Mass:** 32488 **Score:** 231 **Matches:** 12(11) **Sequences:** 6

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1325	477.7269	953.4392	953.4389	0.38	0	(30)	0.016	1	U	L.SMGQA
1326	477.7270	953.4395	953.4389	0.63	0	37	0.003	1	U	L.SMGQA
1426	483.2563	964.4980	964.4978	0.25	0	24	0.053	1	U	L.DIIRS
1428	483.2565	964.4984	964.4978	0.69	0	(21)	0.13	1	U	L.DIIRS
2251	530.2867	1058.5588	1058.5608	-1.86	0	(38)	0.0026	1	U	L.KTQLP
2253	530.2882	1058.5619	1058.5608	1.03	0	41	0.0014	1	U	L.KTQLP
3039	575.3110	1148.6074	1148.6077	-0.28	1	(32)	0.01	1	U	L.KKDIA
3040	575.3119	1148.6092	1148.6077	1.32	1	47	0.0003	1	U	L.KKDIA
3275	586.8292	1171.6439	1171.6448	-0.81	1	(40)	0.0012	1	U	L.LKTQL
3276	586.8302	1171.6458	1171.6448	0.86	1	40	0.0011	1	U	L.LKTQL
5717	772.3787	1542.7429	1542.7413	1.01	1	(26)	0.05	1	U	F.SGEDA
5718	772.3802	1542.7458	1542.7413	2.91	1	44	0.00076	1	U	F.SGEDA

---

23. 2::sp|P02930|TOLC_ECOLI **Mass:** 53708 **Score:** 208 **Matches:** 10(9) **Sequences:** 5
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
2173	526.2748	1050.5350	1050.5345	0.44	0	33	0.0092	1	U	Y.TQAQK
2174	526.2752	1050.5357	1050.5345	1.14	0	(33)	0.0086	1	U	Y.TQAQK
3619	605.8424	1209.6701	1209.6717	-1.30	0	37	0.0015	1	U	F.KTDKP
5450	745.8645	1489.7144	1489.7121	1.60	0	67	4.8e-06	1	U	Y.RDANG
5451	745.8654	1489.7162	1489.7121	2.75	0	(59)	3.1e-05	1	U	Y.RDANG
5456	746.3570	1490.6994	1490.6961	2.25	0	(47)	0.00042	1	U	Y.RDANG
5457	746.3591	1490.7037	1490.6961	5.12	0	(52)	0.00013	1	U	Y.RDANG
5679	768.8994	1535.7843	1535.7831	0.74	1	(48)	0.00036	1	U	L.TLQEK
5680	768.9012	1535.7878	1535.7831	3.05	1	52	0.00014	1	U	L.TLQEK
6026	804.9248	1607.8350	1607.8307	2.69	2	22	0.12	1	U	L.RQITG

---

24. 2::sp|P76373|UDG_ECOLI **Mass:** 43744 **Score:** 206 **Matches:** 10(10) **Sequences:** 6
UDP-glucose 6-dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=ugd 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
1170	469.2529	936.4912	936.4916	-0.42	0	(38)	0.002	1	U	L.KDVAD
1171	469.2530	936.4914	936.4916	-0.29	0	41	0.0011	1	U	L.KDVAD
1652	494.2669	986.5193	986.5185	0.81	1	29	0.02	1	U	F.LQSDK
2520	547.3046	1092.5947	1092.5927	1.80	0	27	0.021	1	U	L.IAQNH
2914	569.7740	1137.5334	1137.5302	2.85	1	39	0.0027	1	U	F.NATLD
2916	569.7744	1137.5341	1137.5302	3.49	1	(32)	0.013	1	U	F.NATLD
4493	662.8347	1323.6548	1323.6558	-0.77	1	(44)	0.0009	1	U	F.TDSTE
4495	662.8362	1323.6579	1323.6558	1.61	1	44	0.00082	1	U	F.TDSTE
6851	601.3186	1800.9340	1800.9370	-1.68	0	29	0.029	1	U	L.NDRIS
6852	601.3195	1800.9366	1800.9370	-0.25	0	(27)	0.04	1	U	L.NDRIS

---

25. 2::sp|P0AE08|AHPC_ECOLI **Mass:** 20862 **Score:** 205 **Matches:** 12(11) **Sequences:**

Alkyl hydroperoxide reductase C OS=Escherichia coli (strain K12) OX=83333 GN=ahpC 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	Peptid
1870	506.7938	1011.5731	1011.5964	-23.08	2	(43)	0.00028	1	U	L.APSL
1871	506.7960	1011.5774	1011.5964	-18.79	2	(39)	0.00069	1	U	L.APSL
1872	506.8059	1011.5971	1011.5964	0.70	2	(47)	8.2e-05	1	U	L.APSL
1873	506.8080	1011.6015	1011.5964	4.97	2	57	8.1e-06	1	U	L.APSL
5348	738.3270	1474.6394	1474.6399	-0.32	1	24	0.041	1	U	F.VCPT
6695	585.9251	1754.7535	1754.7530	0.31	1	42	0.00089	1	U	F.DNMR
6697	585.9262	1754.7566	1754.7530	2.09	1	(27)	0.026	1	U	F.DNMR
6698	585.9265	1754.7575	1754.7530	2.60	1	(39)	0.0017	1	U	F.DNMR
7003	923.9125	1845.8105	1845.8091	0.78	2	45	0.00037	1	U	F.VCPT
7004	923.9155	1845.8165	1845.8091	4.02	2	(41)	0.001	1	U	F.VCPT
7451	684.6719	2050.9938	2050.9960	-1.05	1	37	0.0057	1	U	F.KNGE
7452	684.6723	2050.9951	2050.9960	-0.43	1	(25)	0.08	1	U	F.KNGE

---

26. 2::sp|P0A855|TOLB_ECOLI **Mass:** 45927 **Score:** 197 **Matches:** 9(8) **Sequences:** 5
Tol-Pal system protein TolB OS=Escherichia coli (strain K12) OX=83333 GN=tolB 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
3599	605.2977	1208.5808	1208.5826	-1.51	0	(32)	0.012	1	U	Y.VVQTN
3600	605.2983	1208.5820	1208.5826	-0.50	0	33	0.012	1	U	Y.VVQTN
3696	611.2971	1220.5796	1220.5786	0.82	0	49	0.00028	1	U	F.TSDQA
3697	611.2977	1220.5808	1220.5786	1.82	0	(32)	0.013	1	U	F.TSDQA
6429	842.3612	1682.7079	1682.7020	3.49	0	60	9.3e-06	1	U	W.EGSQN
6430	842.3618	1682.7090	1682.7020	4.14	0	(54)	4.1e-05	1	U	W.EGSQN
6806	894.4454	1786.8763	1786.8738	1.42	0	(31)	0.018	1	U	L.GIDAV
6807	894.4469	1786.8792	1786.8738	3.06	0	35	0.007	1	U	L.GIDAV
7578	735.7119	2204.1137	2204.1086	2.30	0	20	0.21	1	U	L.DRARL

---

27. 2::sp|P0A7Z4|RPOA_ECOLI **Mass:** 36717 **Score:** 187 **Matches:** 9(8) **Sequences:** 5
DNA-directed RNA polymerase subunit alpha OS=Escherichia coli (strain K12) OX=83333
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
540	416.2212	830.4278	830.4286	-1.02	0	26	0.038	1	U	L.KAEAI
1154	467.7533	933.4920	933.4920	0.03	0	(36)	0.0039	1	U	Y.SPVER
1155	467.7535	933.4924	933.4920	0.48	0	36	0.0037	1	U	Y.SPVER
4518	663.8915	1325.7685	1325.7667	1.38	0	(41)	0.00036	1	U	L.AVRVQ
4519	663.8917	1325.7688	1325.7667	1.57	0	42	0.00027	1	U	L.AVRVQ
5403	742.9206	1483.8266	1483.8246	1.37	2	(45)	0.00027	1	U	Y.IGDLV
5404	742.9216	1483.8287	1483.8246	2.77	2	59	1.3e-05	1	U	Y.IGDLV
7034	619.6661	1855.9764	1855.9752	0.68	1	(21)	0.11	1	U	Y.NVEAA
7035	619.6668	1855.9786	1855.9752	1.86	1	24	0.057	1	U	Y.NVEAA

---

28. 2::sp|P0A870|TALB_ECOLI **Mass:** 35368 **Score:** 178 **Matches:** 8(7) **Sequences:** 5
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
2221	528.8053	1055.5960	1055.5975	-1.35	1	(24)	0.032	1	U	F.RNIGE
2223	528.8058	1055.5971	1055.5975	-0.31	1	30	0.0085	1	U	F.RNIGE
3389	593.8328	1185.6510	1185.6506	0.32	1	28	0.021	1	U	Y.RKLID
3394	594.3044	1186.5943	1186.5942	0.11	0	54	6.5e-05	1	U	Y.NDAGI
3395	594.3051	1186.5957	1186.5942	1.24	0	(38)	0.0027	1	U	Y.NDAGI
4886	467.2320	1398.6741	1398.6878	-9.78	1	21	0.17	3	U	Y.QPQDA
5650	766.8785	1531.7424	1531.7406	1.18	0	45	0.00074	1	U	Y.APAED
5651	766.8789	1531.7433	1531.7406	1.74	0	(44)	0.001	1	U	Y.APAED

---

29. 2::sp|P0AGJ9|SYY_ECOLI **Mass:** 47896 **Score:** 170 **Matches:** 7(5) **Sequences:** 4(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
956	452.7297	903.4449	903.4450	-0.19	0	22	0.11	1	U	F.GKTEG
1589	490.7739	979.5333	979.5338	-0.55	0	32	0.0048	1	U	L.ITKAD
1590	490.7749	979.5353	979.5338	1.49	0	(24)	0.032	1	U	L.ITKAD
2316	533.2515	1064.4884	1064.4887	-0.29	0	(25)	0.06	1	U	L.NREDQ
2317	533.2522	1064.4898	1064.4887	1.10	0	28	0.028	1	U	L.NREDQ
5723	772.4039	1542.7933	1542.7889	2.84	1	88	3.3e-08	1	U	L.VAQVT
5724	772.4039	1542.7933	1542.7889	2.84	1	(85)	5.9e-08	1	U	L.VAQVT

---

30. 2::sp|P0AGE9|SUCD_ECOLI **Mass:** 30044 **Score:** 169 **Matches:** 7(6) **Sequences:** 4

Succinate--CoA ligase [ADP-forming] subunit alpha 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
1138	465.2690	928.5233	928.5229	0.46	0	(24)	0.045	1	U	L.EAIDA
1139	465.2690	928.5235	928.5229	0.66	0	33	0.0062	1	U	L.EAIDA
2190	527.7555	1053.4964	1053.4978	-1.35	0	(41)	0.0011	1	U	Y.EAVKQ
2191	527.7560	1053.4974	1053.4978	-0.42	0	52	8.6e-05	1	U	Y.EAVKQ
5643	765.4309	1528.8473	1528.8422	3.30	1	20	0.13	1	U	L.IITIT
6833	897.4759	1792.9372	1792.9319	2.96	0	63	8.2e-06	1	U	F.NTVRE
6834	897.4767	1792.9388	1792.9319	3.84	0	(36)	0.0045	1	U	F.NTVRE

---

31. 2::sp|P23721|SERC_ECOLI **Mass:** 39986 **Score:** 168 **Matches:** 6(6) **Sequences:** 4

Phosphoserine aminotransferase OS=Escherichia coli (strain K12) OX=83333 GN=serC 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
1077	459.2500	916.4854	916.4866	-1.23	0	36	0.0048	1	U	F.DAKVT
3254	585.8585	1169.7024	1169.7020	0.34	1	29	0.0057	1	U	L.TIVIV
3255	585.8596	1169.7047	1169.7020	2.33	1	(27)	0.0091	1	U	L.TIVIV
3606	605.8005	1209.5864	1209.5877	-1.09	1	59	2.2e-05	1	U	L.NILGD
3607	605.8016	1209.5887	1209.5877	0.83	1	(54)	8.1e-05	1	U	L.NILGD
6304	831.9210	1661.8275	1661.8260	0.87	1	46	0.00066	1	U	F.IQVAE

---

32. 2::sp|P0A6K6|DEOB_ECOLI **Mass:** 44684 **Score:** 158 **Matches:** 9(9) **Sequences:** 4
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
479	411.2110	820.4074	820.4079	-0.57	0	(28)	0.019	1	U	F.IGDKA
480	411.2111	820.4077	820.4079	-0.27	0	31	0.01	1	U	F.IGDKA
3199	583.2776	1164.5407	1164.5411	-0.31	0	47	0.00041	1	U	F.GIGAT
3200	583.2789	1164.5433	1164.5411	1.89	0	(44)	0.00075	1	U	F.GIGAT
4009	631.3076	1260.6007	1260.6020	-1.01	1	(30)	0.021	1	U	Y.ELCEI
4010	631.3080	1260.6015	1260.6020	-0.34	1	40	0.0021	1	U	Y.ELCEI
4011	631.3093	1260.6040	1260.6020	1.61	1	(32)	0.013	1	U	Y.ELCEI
7172	947.4453	1892.8761	1892.8752	0.45	1	(38)	0.0033	1	U	F.GIGAT
7173	947.4462	1892.8778	1892.8752	1.36	1	43	0.0012	1	U	F.GIGAT

---

33. 2::sp|P31979|NUOF_ECOLI **Mass:** 49774 **Score:** 152 **Matches:** 8(5) **Sequences:** 4
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
2183	527.2712	1052.5278	1052.5291	-1.21	2	(22)	0.11	1	U	L.VRNLE
2184	527.2725	1052.5304	1052.5291	1.22	2	28	0.027	1	U	L.VRNLE
4611	674.3674	1346.7203	1346.7194	0.69	2	23	0.074	1	U	F.LRGEY
4612	674.3683	1346.7221	1346.7194	2.06	2	(23)	0.081	1	U	F.LRGEY
4891	700.8373	1399.6600	1399.6579	1.49	0	41	0.0014	1	U	L.ERGEG
4892	700.8381	1399.6617	1399.6579	2.70	0	(34)	0.007	1	U	L.ERGEG
6741	885.9292	1769.8438	1769.8432	0.39	1	(34)	0.01	1	U	L.ERGEG
6742	885.9293	1769.8441	1769.8432	0.53	1	62	1.4e-05	1	U	L.ERGEG

---

34. 2::sp|P18335|ARGD_ECOLI **Mass:** 44081 **Score:** 148 **Matches:** 3(3) **Sequences:** 2
Acetylornithine/succinyldiaminopimelate aminotransferase OS=Escherichia coli (strai
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
1882	507.2790	1012.5434	1012.5441	-0.63	0	(24)	0.032	1	U	F.DIIN
1885	507.2796	1012.5446	1012.5441	0.51	0	32	0.0047	1	U	F.DIIN
7382	1004.4743	2006.9340	2006.9255	4.25	1	116	5.6e-11	1	U	F.APSL

---

35. 2::sp|P0AG67|RS1_ECOLI **Mass:** 61235 **Score:** 147 **Matches:** 6(4) **Sequences:** 4(2
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
1137	465.2563	928.4981	928.4866	12.4	1	20	0.11	1	U	F.IGLDG
3583	603.8034	1205.5923	1205.5928	-0.43	0	21	0.16	1	U	L.KSESA
3815	618.7970	1235.5794	1235.5782	1.01	0	36	0.0048	1	U	W.NVAGE
3816	618.7977	1235.5808	1235.5782	2.09	0	(35)	0.006	1	U	W.NVAGE
4244	646.8417	1291.6688	1291.6660	2.17	1	(58)	3e-05	1	U	L.VLSVG

4245	646.8426	1291.6706	1291.6660	3.59	1	69	2.5e-06	1	U	L.VLSVG

---

36. 2::sp|P07004|PROA_ECOLI **Mass:** 45001 **Score:** 147 **Matches:** 5(5) **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
218	397.7111	793.4077	793.4082	-0.63	0	24	0.043	1	U	Y.VNAST
4776	685.8683	1369.7221	1369.7201	1.47	0	(52)	7.4e-05	1	U	Y.EARPN
4777	685.8691	1369.7237	1369.7201	2.62	0	61	1.1e-05	1	U	Y.EARPN
6492	850.9523	1699.8901	1699.8879	1.28	1	(34)	0.007	1	U	L.EKIAD
6494	850.9541	1699.8936	1699.8879	3.36	1	62	1.1e-05	1	U	L.EKIAD

---

37. 2::sp|P0A825|GLYA_ECOLI **Mass:** 45459 **Score:** 144 **Matches:** 7(5) **Sequences:** 4(

Serine hydroxymethyltransferase OS=Escherichia coli (strain K12) OX=83333 GN=glyA 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
2042	514.8027	1027.5908	1027.5914	-0.55	2	(35)	0.0032	1	U	F.LVDLV
2044	514.8031	1027.5916	1027.5914	0.29	2	47	0.00019	1	U	F.LVDLV
2268	531.2492	1060.4839	1060.4825	1.25	0	47	0.00025	1	U	Y.GIDAT
2269	531.2496	1060.4847	1060.4825	2.04	0	(46)	0.00032	1	U	Y.GIDAT
2832	564.8105	1127.6064	1127.6074	-0.87	2	25	0.033	1	U	Y.TALLE
4122	637.3304	1272.6462	1272.6463	-0.05	1	(24)	0.081	1	U	Y.KVVSG
4126	637.3330	1272.6515	1272.6463	4.08	1	25	0.059	1	U	Y.KVVSG

---

38. 2::sp|P0A6P9|ENO_ECOLI **Mass:** 45683 **Score:** 144 **Matches:** 5(3) **Sequences:** 4(2

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
3173	581.8285	1161.6425	1161.6393	2.76	0	(61)	8.7e-06	1	U	L.AVIAE
3174	581.8290	1161.6435	1161.6393	3.60	0	69	1.4e-06	1	U	L.AVIAE
4463	660.3457	1318.6768	1318.6769	-0.04	2	31	0.015	1	U	L.GDKIQ
5438	496.9403	1487.7992	1487.7983	0.57	1	21	0.16	1	U	L.IRIEE
6994	615.3360	1842.9862	1842.9839	1.23	2	24	0.065	1	U	Y.NQLIR

---

39. 2::sp|P0A6B7|ISCS_ECOLI **Mass:** 45232 **Score:** 143 **Matches:** 7(7) **Sequences:** 4(

Cysteine desulfurase IscS OS=Escherichia coli (strain K12) OX=83333 GN=iscS 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
189	396.2231	790.4317	790.4337	-2.52	0	(38)	0.0017	1	U	L.AIKGA
190	396.2232	790.4318	790.4337	-2.41	0	40	0.0011	1	U	L.AIKGA
2001	512.7888	1023.5631	1023.5641	-0.95	2	28	0.012	1	U	M.KLPIY
3259	586.3056	1170.5966	1170.5995	-2.40	2	(34)	0.0048	1	U	-.MKLPI
3260	586.3067	1170.5988	1170.5995	-0.52	2	43	0.00061	1	U	-.MKLPI
4217	644.8301	1287.6457	1287.6459	-0.14	1	35	0.0066	1	U	Y.KQGVD

4218	**644.8306**	**1287.6467**	**1287.6459**	**0.62**	**1**	**(34)**	**0.0074**	**1**	**U**	**Y.KQGVD**

---

40. 2::sp\|P37095\|PEPB_ECOLI **Mass:** 46436 **Score:** 141 **Matches:** 6(6) **Sequences:** 3(

Peptidase B OS=Escherichia coli (strain K12) OX=83333 GN=pepB PE=1 SV=2

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5820	**522.2740**	**1563.8003**	**1563.8005**	**-0.11**	**1**	**(36)**	**0.0052**	**1**	**U**	**Y.RITKG**
5821	**522.2743**	**1563.8010**	**1563.8005**	**0.35**	**1**	**38**	**0.0031**	**1**	**U**	**Y.RITKG**
6243	**826.8952**	**1651.7758**	**1651.7729**	**1.76**	**2**	**48**	**0.00034**	**1**	**U**	**L.ALDYN**
6244	**826.8962**	**1651.7778**	**1651.7729**	**2.94**	**2**	**(46)**	**0.00056**	**1**	**U**	**L.ALDYN**
6876	**905.4707**	**1808.9268**	**1808.9268**	**0.02**	**1**	**(46)**	**0.00053**	**1**	**U**	**W.VRDTI**
6877	**905.4733**	**1808.9321**	**1808.9268**	**2.92**	**1**	**58**	**3.5e-05**	**1**	**U**	**W.VRDTI**

---

41. 2::sp\|P08622\|DNAJ_ECOLI **Mass:** 41645 **Score:** 137 **Matches:** 9(5) **Sequences:** 5(

Chaperone protein DnaJ OS=Escherichia coli (strain K12) OX=83333 GN=dnaJ 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
59	**383.6899**	**765.3653**	**765.3657**	**-0.59**	**2**	**29**	**0.019**	**1**	**U**	**F.FDDLTR**
60	**383.6900**	**765.3654**	**765.3657**	**-0.36**	**2**	**(22)**	**0.11**	**1**	**U**	**F.FDDLTR**
837	**440.7421**	**879.4697**	**879.4701**	**-0.49**	**0**	**(22)**	**0.067**	**1**	**U**	**F.KEIKEA**
838	**440.7422**	**879.4698**	**879.4701**	**-0.42**	**0**	**26**	**0.031**	**1**	**U**	**F.KEIKEA**
1713	**497.2480**	**992.4815**	**992.4815**	**0.09**	**2**	**(24)**	**0.065**	**1**	**U**	**L.LQELQE**
1714	**497.2483**	**992.4820**	**992.4815**	**0.57**	**2**	**30**	**0.02**	**1**	**U**	**L.LQELQE**
4648	676.8177	1351.6208	1351.6152	4.17	1	22	0.13	2	U	Y.CEVPIN
6488	**424.9978**	**1695.9621**	**1695.9632**	**-0.63**	**0**	**31**	**0.0037**	**1**	**U**	**L.SVKIPA**
6489	**424.9978**	**1695.9622**	**1695.9632**	**-0.56**	**0**	**(27)**	**0.0096**	**1**	**U**	**L.SVKIPA**

---

42. 2::sp\|P00509\|AAT_ECOLI **Mass:** 43831 **Score:** 136 **Matches:** 5(5) **Sequences:** 3(3

Aspartate aminotransferase OS=Escherichia coli (strain K12) OX=83333 GN=aspC 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
2038	**514.7924**	**1027.5703**	**1027.5702**	**0.07**	**1**	**24**	**0.04**	**1**	**U**	**L.SVEKG**
3709	**612.8088**	**1223.6031**	**1223.6033**	**-0.18**	**2**	**46**	**0.00048**	**1**	**U**	**Y.LLENE**
3710	**612.8101**	**1223.6057**	**1223.6033**	**1.91**	**2**	**(36)**	**0.0053**	**1**	**U**	**Y.LLENE**
4176	**640.8096**	**1279.6046**	**1279.6044**	**0.11**	**0**	**(65)**	**6.6e-06**	**1**	**U**	**L.VAADS**
4177	**640.8118**	**1279.6091**	**1279.6044**	**3.64**	**0**	**68**	**3e-06**	**1**	**U**	**L.VAADS**

---

43. 2::sp\|P0A6F1\|CARA_ECOLI **Mass:** 41633 **Score:** 136 **Matches:** 7(6) **Sequences:** 5(

Carbamoyl-phosphate synthase small chain OS=Escherichia coli (strain K12) OX=83333 G

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
506	**413.2636**	**824.5126**	**824.5120**	**0.76**	**0**	**(24)**	**0.0061**	**1**	**U**	**L.VIRDLP**
507	**413.2636**	**824.5127**	**824.5120**	**0.91**	**0**	**31**	**0.0013**	**1**	**U**	**L.VIRDLP**
2319	**533.2596**	**1064.5046**	**1064.5026**	**1.89**	**1**	**24**	**0.078**	**1**	**U**	**Y.QEILTD**

2395	541.7721	1081.5296	1081.5291	0.46	0	(28)	0.022	1	U	L.AKEVTT
2396	541.7726	1081.5307	1081.5291	1.48	0	30	0.018	1	U	L.AKEVTT
4605	672.3564	1342.6983	1342.6980	0.25	0	27	0.038	1	U	L.TIVPAQ
6135	544.2814	1629.8223	1629.8250	-1.66	0	27	0.041	1	U	L.TGGLPE

---

44. 2::sp|P0A7A9|IPYR_ECOLI **Mass:** 19805 **Score:** 130 **Matches:** 6(3) **Sequences:** 3(

Inorganic pyrophosphatase OS=Escherichia coli (strain K12) OX=83333 GN=ppa PE=1 SV=2

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2642	554.7797	1107.5448	1107.5448	-0.02	1	34	0.0071	1	U	Y.EIDKE
2643	554.7814	1107.5482	1107.5448	3.07	1	(22)	0.14	1	U	Y.EIDKE
5069	715.8615	1429.7085	1429.7089	-0.30	0	(20)	0.21	1	U	L.NVPAG
5070	715.8643	1429.7140	1429.7089	3.55	0	21	0.16	1	U	L.NVPAG
5707	771.4323	1540.8501	1540.8501	0.00	0	(69)	1.2e-06	1	U	Y.VVIEI
5708	771.4329	1540.8513	1540.8501	0.79	0	74	3.5e-07	1	U	Y.VVIEI

---

45. 2::sp|P60422|RL2_ECOLI **Mass:** 29956 **Score:** 128 **Matches:** 5(5) **Sequences:** 3(3

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
1097	461.2500	920.4854	920.4868	-1.52	0	26	0.033	1	U	F.GKHPV
2499	546.2963	1090.5780	1090.5771	0.79	0	(50)	0.00014	1	U	Y.VQIVA
2500	546.2967	1090.5789	1090.5771	1.69	0	61	1.3e-05	1	U	Y.VQIVA
4736	681.8362	1361.6578	1361.6575	0.23	1	41	0.0018	1	U	L.EYDPN
4737	681.8365	1361.6585	1361.6575	0.77	1	(35)	0.0083	1	U	L.EYDPN

---

46. 2::sp|P33232|LLDD_ECOLI **Mass:** 42872 **Score:** 127 **Matches:** 6(6) **Sequences:** 4(

L-lactate dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=lldD 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
2376	540.2973	1078.5800	1078.5560	22.3	1	28	0.017	1	U	Y.LQAVTH
2505	546.7831	1091.5516	1091.5499	1.58	2	33	0.011	1	U	Y.LGKPTG
2506	546.7831	1091.5516	1091.5499	1.58	2	(28)	0.033	1	U	Y.LGKPTG
3704	612.2894	1222.5643	1222.5652	-0.75	0	(26)	0.054	1	U	F.TVDMPT
3705	612.2915	1222.5684	1222.5652	2.63	0	39	0.0025	1	U	F.TVDMPT
4569	668.8441	1335.6737	1335.6724	0.96	2	32	0.013	1	U	Y.LQAVTH

---

47. 2::sp|P0A7L0|RL1_ECOLI **Mass:** 24714 **Score:** 123 **Matches:** 4(3) **Sequences:** 2(2

50S ribosomal protein L1 OS=Escherichia coli (strain K12) OX=83333 GN=rplA 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
2115	522.7817	1043.5489	1043.5499	-0.93	0	(23)	0.067	1	U	F.VESVD
2116	522.7827	1043.5509	1043.5499	0.93	0	30	0.012	1	U	F.VESVD
5328	736.8732	1471.7318	1471.7266	3.50	0	(83)	9.4e-08	1	U	F.TQGAN

5329	736.8737	1471.7329	1471.7266	4.25	0	93	1.1e-08	1	U	F.TQGAN

---

48. 2::sp|P27248|GCST_ECOLI **Mass:** 40235 **Score:** 118 **Matches:** 5(4) **Sequences:** 4(
Aminomethyltransferase OS=Escherichia coli (strain K12) OX=83333 GN=gcvT PE=1 SV=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1359	478.7924	955.5703	955.5702	0.09	2	(29)	0.0055	1	U	Y.LLANDV
1360	478.7927	955.5708	955.5702	0.59	2	35	0.0017	1	U	Y.LLANDV
2065	515.7932	1029.5719	1029.5719	-0.07	0	23	0.066	1	U	L.RNELPV
5924	397.9757	1587.8737	1587.8403	21.1	1	23	0.057	1	U	F.RLVVNS
6744	888.4136	1774.8126	1774.8122	0.20	0	37	0.0039	1	U	F.TDAQGN

---

49. 2::sp|P0A858|TPIS_ECOLI **Mass:** 27126 **Score:** 116 **Matches:** 5(3) **Sequences:** 3(
Triosephosphate isomerase OS=Escherichia coli (strain K12) OX=83333 GN=tpiA 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
199	397.2126	792.4107	792.4130	-2.91	0	(21)	0.094	1	U	L.KTQGA
202	397.2131	792.4116	792.4130	-1.70	0	30	0.012	1	U	L.KTQGA
4081	635.3778	1268.7411	1268.7452	-3.25	0	(41)	0.00038	1	U	F.AVIVK
4084	635.3800	1268.7454	1268.7452	0.20	0	61	3.5e-06	1	U	F.AVIVK
4349	653.3256	1304.6366	1304.6361	0.38	2	25	0.072	1	U	L.GAQNV

---

50. 2::sp|P0ABU2|YCHF_ECOLI **Mass:** 39984 **Score:** 113 **Matches:** 5(3) **Sequences:** 3(
Ribosome-binding ATPase YchF OS=Escherichia coli (strain K12) OX=83333 GN=ychF 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
4040	633.3293	1264.6440	1264.6452	-0.92	0	32	0.014	1	U	L.TKAGI
4041	633.3301	1264.6456	1264.6452	0.34	0	(21)	0.16	1	U	L.TKAGI
5573	759.8684	1517.7223	1517.7218	0.33	1	24	0.081	1	U	L.EKCLP
5955	798.3529	1594.6913	1594.6899	0.83	1	58	2.1e-05	1	U	Y.IANVN
5956	798.3531	1594.6916	1594.6899	1.06	1	(54)	5.3e-05	1	U	Y.IANVN

---

51. 2::sp|P0ABZ6|SURA_ECOLI **Mass:** 47254 **Score:** 112 **Matches:** 4(3) **Sequences:** 3(
Chaperone SurA OS=Escherichia coli (strain K12) OX=83333 GN=surA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2849	565.3218	1128.6291	1128.6291	-0.01	0	22	0.083	1	U	W.GRIQE
5337	737.8434	1473.6722	1473.6696	1.80	0	68	2.9e-06	1	U	L.AQQVG
5338	737.8434	1473.6723	1473.6696	1.88	0	(50)	0.00019	1	U	L.AQQVG
6817	597.0035	1787.9886	1787.9894	-0.44	0	23	0.049	1	U	L.STAKK

---

52. 2::sp|P69924|RIR2_ECOLI **Mass:** 43775 **Score:** 112 **Matches:** 4(3) **Sequences:** 3(

Ribonucleoside-diphosphate reductase 1 subunit beta 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
1814	502.2695	1002.5244	1002.5247	-0.22	0	32	0.011	1	U	F.GQPVN
5764	776.3580	1550.7015	1550.7001	0.90	1	(56)	4.5e-05	1	U	F.VQAAQ
5765	776.3595	1550.7044	1550.7001	2.79	1	62	9.3e-06	1	U	F.VQAAQ
6592	576.9478	1727.8214	1727.8189	1.48	2	20	0.21	1	U	F.SQTKN

---

53. 2::sp|P67910|HLDD_ECOLI **Mass:** 34985 **Score:** 107 **Matches:** 5(5) **Sequences:** 3(
ADP-L-glycero-D-manno-heptose-6-epimerase OS=Escherichia coli (strain K12) OX=83333
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2449	544.2750	1086.5354	1086.5346	0.71	1	27	0.031	1	U	Y.VGDVAD
2534	548.7797	1095.5449	1095.5448	0.08	0	40	0.0014	1	U	F.KTVAEG
6350	835.9648	1669.9151	1669.9151	-0.01	0	(40)	0.0012	1	U	Y.VRQILP
6351	835.9669	1669.9192	1669.9151	2.41	0	(31)	0.0081	1	U	Y.VRQILP
6352	835.9675	1669.9205	1669.9151	3.21	0	40	0.001	1	U	Y.VRQILP

---

54. 2::sp|P0AEK4|FABI_ECOLI **Mass:** 28074 **Score:** 105 **Matches:** 3(3) **Sequences:** 2(
Enoyl-[acyl-carrier-protein] reductase [NADH] FabI OS=Escherichia coli (strain K12)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1707	496.7612	991.5078	991.5087	-0.92	0	32	0.009	1	U	Y.VNAVT
5066	715.8498	1429.6850	1429.6838	0.86	0	(63)	1.1e-05	1	U	L.SAGIS
5067	715.8510	1429.6875	1429.6838	2.57	0	73	1e-06	1	U	L.SAGIS

---

55. 2::sp|P31224|ACRB_ECOLI **Mass:** 113615 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(
Multidrug efflux pump subunit AcrB OS=Escherichia coli (strain K12) OX=83333 GN=acrB
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
1710	496.7745	991.5345	991.5338	0.63	0	32	0.0071	1	U	L.ASKL
5869	788.9202	1575.8259	1575.8256	0.17	2	28	0.033	1	U	L.LRDV
7469	1032.5210	2063.0274	2063.0171	5.01	0	47	0.00047	1	U	L.LPQE

---

56. 2::sp|P23908|ARGE_ECOLI **Mass:** 42777 **Score:** 104 **Matches:** 2(2) **Sequences:** 1(
Acetylornithine deacetylase OS=Escherichia coli (strain K12) OX=83333 GN=argE 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
6541	857.9022	1713.7898	1713.7879	1.07	1	104	7.9e-10	1	U	Y.ILATA
6542	857.9026	1713.7906	1713.7879	1.57	1	(76)	4.9e-07	1	U	Y.ILATA

---

57. 2::sp|P62620|ISPG_ECOLI **Mass:** 40943 **Score:** 104 **Matches:** 3(3) **Sequences:** 2(
4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin) OS=Escherichia col
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1029	456.7607	911.5069	911.5076	-0.75	0	36	0.0012	1	U	L.AKQID
4131	637.8345	1273.6544	1273.6554	-0.80	0	(58)	3.1e-05	1	U	L.AADPV
4132	637.8354	1273.6562	1273.6554	0.64	0	68	3.6e-06	1	U	L.AADPV

---

58. 2::sp|P0A9D8|DAPD_ECOLI **Mass:** 30044 **Score:** 102 **Matches:** 5(4) **Sequences:** 3(
2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase OS=Escherichia co
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1640	493.7139	985.4133	985.4141	-0.81	1	(30)	0.0068	1	U	F.ADYDEA
1641	493.7143	985.4141	985.4141	-0.02	1	37	0.0014	1	U	F.ADYDEA
3532	601.3189	1200.6233	1200.6251	-1.53	0	40	0.0015	1	U	L.RVAEKI
3534	601.3195	1200.6244	1200.6251	-0.62	0	(32)	0.011	1	U	L.RVAEKI
6718	882.4383	1762.8620	1762.8598	1.27	0	25	0.076	1	U	F.RINDNQ

---

59. 2::sp|P0A6M8|EFG_ECOLI **Mass:** 77704 **Score:** 99 **Matches:** 2(2) **Sequences:** 2(2
Elongation factor G OS=Escherichia coli (strain K12) OX=83333 GN=fusA PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2706	557.7812	1113.5479	1113.5455	2.24	1	43	0.00066	1	U	L.QLAIG
5641	765.4077	1528.8009	1528.7984	1.60	2	56	4.2e-05	1	U	Y.LGGEE

---

60. 2::sp|P0AEB2|DACA_ECOLI **Mass:** 44530 **Score:** 98 **Matches:** 4(3) **Sequences:** 3(
D-alanyl-D-alanine carboxypeptidase DacA OS=Escherichia coli (strain K12) OX=83333 G
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3891	624.3401	1246.6657	1246.6670	-1.00	0	22	0.12	1	U	L.QKNQV
5253	731.3638	1460.7130	1460.7147	-1.19	1	(49)	0.00029	1	U	F.KETDL
5254	731.3667	1460.7188	1460.7147	2.82	1	52	0.00015	1	U	F.KETDL
5706	514.5943	1540.7611	1540.7594	1.12	0	27	0.041	1	U	L.AEQNA

---

61. 2::sp|P0A717|KPRS_ECOLI **Mass:** 34425 **Score:** 96 **Matches:** 5(4) **Sequences:** 3(
Ribose-phosphate pyrophosphokinase OS=Escherichia coli (strain K12) OX=83333 GN=prs
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
846	441.2219	880.4292	880.4187	12.0	1	21	0.13	1	U	-.MPDMKL
1146	466.2643	930.5141	930.5135	0.72	0	41	0.0011	1	U	L.SSVGVD
1147	466.2644	930.5142	930.5135	0.85	0	(37)	0.0031	1	U	L.SSVGVD
2517	547.2862	1092.5578	1092.5564	1.32	1	34	0.0078	1	U	Y.TSLGDA

2518	547.2862	1092.5579	1092.5564	1.43	1	(29)	0.024	1	U	Y.TSLGDA

---

62. 2::sp|P0A749|MURA_ECOLI **Mass:** 45132 **Score:** 96 **Matches:** 3(2) **Sequences:** 3(
UDP-N-acetylglucosamine 1-carboxyvinyltransferase OS=Escherichia coli (strain K12) O
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4905	702.3844	1402.7542	1402.7569	-1.87	0	28	0.025	1	U	Y.RVLPD
6960	918.9808	1835.9470	1835.9451	1.00	1	44	0.00083	1	U	L.VLAGC
7659	787.7239	2360.1498	2360.1496	0.11	0	26	0.063	1	U	L.AEGTT

---

63. 2::sp|P0AB77|KBL_ECOLI **Mass:** 43432 **Score:** 95 **Matches:** 4(4) **Sequences:** 2(2
2-amino-3-ketobutyrate coenzyme A ligase OS=Escherichia coli (strain K12) OX=83333 G
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3472	597.8333	1193.6521	1193.6517	0.34	0	38	0.0013	1	U	L.NHASI
3473	597.8335	1193.6524	1193.6517	0.66	0	(35)	0.0027	1	U	L.NHASI
5114	718.8543	1435.6941	1435.6943	-0.17	2	(56)	5.5e-05	1	U	L.TNDLE
5115	718.8548	1435.6950	1435.6943	0.52	2	57	4.7e-05	1	U	L.TNDLE

---

64. 2::sp|P75876|RLMI_ECOLI **Mass:** 44671 **Score:** 94 **Matches:** 2(2) **Sequences:** 1(
Ribosomal RNA large subunit methyltransferase I OS=Escherichia coli (strain K12) OX=
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6284	830.9315	1659.8484	1659.8468	0.94	0	(83)	1.1e-07	1	U	L.IAGES
6285	830.9316	1659.8487	1659.8468	1.16	0	94	9e-09	1	U	L.IAGES

---

65. 2::sp|P0A9J6|RBSK_ECOLI **Mass:** 32328 **Score:** 94 **Matches:** 5(3) **Sequences:** 3(
Ribokinase OS=Escherichia coli (strain K12) OX=83333 GN=rbsK PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5262	732.3767	1462.7387	1462.7416	-1.97	0	30	0.022	1	U	F.RVQAV
5266	732.3789	1462.7433	1462.7416	1.12	0	(25)	0.079	1	U	F.RVQAV
6699	878.4730	1754.9314	1754.9302	0.69	1	(42)	0.00074	1	U	L.ALVDI
6700	878.4730	1754.9314	1754.9302	0.69	1	42	0.00063	1	U	L.ALVDI
7189	633.9981	1898.9723	1898.9697	1.36	0	21	0.14	1	U	L.TGIRV

---

66. 2::sp|P00490|PHSM_ECOLI **Mass:** 90865 **Score:** 94 **Matches:** 4(1) **Sequences:** 4(
Maltodextrin phosphorylase OS=Escherichia coli (strain K12) OX=83333 GN=malP 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

1941	509.7452	1017.4758	1017.4879	-11.91	1	22	0.083	2	U	F.QEALS
2062	515.7799	1029.5453	1029.5706	-24.62	2	20	0.16	1	U	L.ALNGA
4238	646.3483	1290.6821	1290.6820	0.11	1	29	0.021	1	U	Y.VEAQK
4693	679.3641	1356.7137	1356.6997	10.3	0	22	0.098	2	U	L.RAEQQ

---

67. 2::sp|P77774|BAMB_ECOLI **Mass:** 41918 **Score:** 93 **Matches:** 3(3) **Sequences:** 3(

Outer membrane protein assembly factor BamB OS=Escherichia coli (strain K12) OX=8333

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1291	475.2588	948.5030	948.5029	0.10	0	26	0.028	1	U	F.IVDGNR
2966	571.3322	1140.6499	1140.6503	-0.36	1	31	0.0058	1	U	L.SRPVVS
4307	651.3264	1300.6381	1300.6411	-2.30	1	36	0.004	1	U	L.QALNEA

---

68. 2::sp|P0A7V0|RS2_ECOLI **Mass:** 26784 **Score:** 92 **Matches:** 3(3) **Sequences:** 2(2

30S ribosomal protein S2 OS=Escherichia coli (strain K12) OX=83333 GN=rpsB PE=1 SV=2

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4770	684.8185	1367.6225	1367.6205	1.48	1	43	0.00092	1	U	L.KDLET
5273	732.8288	1463.6430	1463.6416	0.96	0	51	9.5e-05	1	U	F.AIVDT
5274	732.8303	1463.6460	1463.6416	2.95	0	(41)	0.001	1	U	F.AIVDT

---

69. 2::sp|P0A6H1|CLPX_ECOLI **Mass:** 46726 **Score:** 85 **Matches:** 4(3) **Sequences:** 3(

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
1498	486.2979	970.5813	970.5811	0.17	1	20	0.04	1	U	L.RSIVEA
1914	508.7848	1015.5550	1015.5437	11.2	1	23	0.074	4	U	L.SEEALI
4219	644.8446	1287.6746	1287.6711	2.79	1	41	0.0015	1	U	L.AQVEPE
4220	644.8446	1287.6746	1287.6711	2.79	1	(37)	0.0044	1	U	L.AQVEPE

---

70. 2::sp|P00448|SODM_ECOLI **Mass:** 23083 **Score:** 85 **Matches:** 4(4) **Sequences:** 2(

Superoxide dismutase [Mn] OS=Escherichia coli (strain K12) OX=83333 GN=sodA 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
4740	454.9050	1361.6932	1361.6939	-0.54	1	31	0.018	1	U	L.QGDLK
4741	454.9052	1361.6938	1361.6939	-0.08	1	(29)	0.031	1	U	L.QGDLK
4851	696.3385	1390.6624	1390.6629	-0.36	1	(50)	0.00024	1	U	W.NVVNW
4852	696.3398	1390.6650	1390.6629	1.48	1	54	9.4e-05	1	U	W.NVVNW

---

71. 2::sp|P00954|SYW_ECOLI **Mass:** 37642 **Score:** 84 **Matches:** 3(2) **Sequences:** 2(1

Tryptophan--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=trpS PE=1 SV=3

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5971	533.6424	1597.9054	1597.8675	23.7	2	21	0.055	1	U	Y.DVQNK
6145	817.4253	1632.8360	1632.8359	0.08	1	(49)	0.0003	1	U	L.SAVTG
6146	817.4275	1632.8405	1632.8359	2.85	1	65	6.2e-06	1	U	L.SAVTG

---

72. 2::sp|P60723|RL4 ECOLI **Mass:** 22073 **Score:** 83 **Matches:** 6(4) **Sequences:** 3(3

50S ribosomal protein L4 OS=Escherichia coli (strain K12) OX=83333 GN=rplD 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
176	395.2388	788.4630	788.4643	-1.64	1	(20)	0.084	1	U	L.KSILSE
178	395.2392	788.4639	788.4643	-0.55	1	22	0.051	1	U	L.KSILSE
1237	472.7739	943.5332	943.5338	-0.70	1	(30)	0.012	1	U	L.VLKDAQ
1238	472.7740	943.5335	943.5338	-0.36	1	32	0.0068	1	U	L.VLKDAQ
4027	632.3277	1262.6408	1262.6394	1.13	2	29	0.029	1	U	L.IITGEL
4028	632.3283	1262.6421	1262.6394	2.10	2	(23)	0.12	1	U	L.IITGEL

---

73. 2::sp|P0A862|TPX ECOLI **Mass:** 17995 **Score:** 83 **Matches:** 3(2) **Sequences:** 2(1

Thiol peroxidase OS=Escherichia coli (strain K12) OX=83333 GN=tpx PE=1 SV=2

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4134	637.8641	1273.7137	1273.7129	0.62	2	(56)	2.6e-05	1	U	F.TLVAK
4135	637.8646	1273.7146	1273.7129	1.28	2	63	4.7e-06	1	U	F.TLVAK
5058	715.3805	1428.7464	1428.7460	0.29	1	20	0.18	1	U	F.NQLAT

---

74. 2::sp|P0A7V8|RS4 ECOLI **Mass:** 23512 **Score:** 83 **Matches:** 6(4) **Sequences:** 3(3

30S ribosomal protein S4 OS=Escherichia coli (strain K12) OX=83333 GN=rpsD PE=1 SV=2

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
656	424.7346	847.4547	847.4552	-0.60	1	26	0.026	1	U	Y.GVLERQ
657	424.7349	847.4552	847.4552	0.03	1	(20)	0.091	1	U	Y.GVLERQ
1251	473.2538	944.4929	944.4927	0.27	1	(23)	0.088	7	U	L.KGNTGE
1253	473.2539	944.4933	944.4927	0.61	1	25	0.047	2	U	L.KGNTGE
5564	758.3884	1514.7623	1514.7616	0.44	2	(29)	0.023	1	U	L.SADINE
5565	758.3898	1514.7651	1514.7616	2.29	2	32	0.013	1	U	L.SADINE

---

75. 2::sp|P62707|GPMA ECOLI **Mass:** 28539 **Score:** 81 **Matches:** 4(4) **Sequences:** 2

2,3-bisphosphoglycerate-dependent phosphoglycerate mutase OS=Escherichia coli (strai

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2915	569.7744	1137.5341	1137.5342	-0.07	2	(34)	0.0077	1	U	Y.EFDENF
2917	569.7755	1137.5365	1137.5342	1.97	2	35	0.0076	1	U	Y.EFDENF

3875	623.3317	1244.6489	1244.6500	-0.85	1	(37)	0.0037	1	U	L.SEKELP
3876	623.3323	1244.6500	1244.6500	0.04	1	47	0.0004	1	U	L.SEKELP

---

76. 2::sp|P03023|LACI_ECOLI **Mass:** 38737 **Score:** 81 **Matches:** 5(4) **Sequences:** 3(

Lactose operon repressor OS=Escherichia coli (strain K12) OX=83333 GN=lacI 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
346	404.7133	807.4120	807.4201	-9.95	1	25	0.042	1	U	M.KPVTLY
347	404.7133	807.4121	807.4201	-9.80	1	(21)	0.093	1	U	M.KPVTLY
1669	494.7744	987.5341	987.5349	-0.77	1	28	0.023	1	U	L.GQTSVD
4120	636.8633	1271.7120	1271.7125	-0.42	1	31	0.0093	1	U	Y.IPPLTT
4121	636.8633	1271.7121	1271.7125	-0.32	1	(30)	0.01	1	U	Y.IPPLTT

---

77. 2::sp|P0A7J3|RL10_ECOLI **Mass:** 17757 **Score:** 80 **Matches:** 3(2) **Sequences:** 2(

50S ribosomal protein L10 OS=Escherichia coli (strain K12) OX=83333 GN=rplJ PE=1 SV=

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5136	720.8880	1439.7614	1439.7620	-0.37	1	22	0.084	1	U	F.EGELI
5175	724.3933	1446.7721	1446.7718	0.18	1	(55)	5.4e-05	1	U	L.ATLPT
5176	724.3934	1446.7722	1446.7718	0.26	1	58	2.8e-05	1	U	L.ATLPT

---

78. 2::sp|P09053|AVTA_ECOLI **Mass:** 47080 **Score:** 78 **Matches:** 3(3) **Sequences:** 2(

Valine--pyruvate aminotransferase OS=Escherichia coli (strain K12) OX=83333 GN=avtA

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
5288	734.3915	1466.7684	1466.8021	-22.94	2	(27)	0.032	1	U	W.FKDL
5289	734.3926	1466.7707	1466.8021	-21.36	2	34	0.0053	1	U	W.FKDL
6338	835.4492	1668.8839	1668.8835	0.23	1	44	0.00061	1	U	F.VSAR

---

79. 2::sp|P0A9K3|PHOL_ECOLI **Mass:** 39129 **Score:** 77 **Matches:** 3(3) **Sequences:** 2(

PhoH-like protein OS=Escherichia coli (strain K12) OX=83333 GN=ybeZ PE=1 SV=2

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3250	585.8278	1169.6410	1169.6404	0.48	0	41	0.00079	1	U	L.TRPAV
3935	626.8669	1251.7192	1251.7187	0.44	0	(24)	0.016	1	U	L.IERNV
3936	626.8671	1251.7196	1251.7187	0.74	0	36	0.0011	1	U	L.IERNV

---

80. 2::sp|P07913|TDH_ECOLI **Mass:** 37557 **Score:** 74 **Matches:** 2(2) **Sequences:** 1(1

L-threonine 3-dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=tdh 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

4974	709.3882	1416.7618	1416.7613	0.35	0	74	6.5e-07	1	U	Y.VGEVV
4975	709.3883	1416.7621	1416.7613	0.54	0	(52)	0.0001	1	U	Y.VGEVV

---

81. 2::sp|P0A7W7|RS8_ECOLI **Mass:** 14175 **Score:** 73 **Matches:** 4(3) **Sequences:** 2(2

30S ribosomal protein S8 OS=Escherichia coli (strain K12) OX=83333 GN=rpsH 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
2696	557.2583	1112.5020	1112.5026	-0.49	1	(28)	0.02	1	U	L.KEEGF
2697	557.2585	1112.5025	1112.5026	-0.06	1	43	0.00072	1	U	L.KEEGF
4691	679.3630	1356.7114	1356.7136	-1.64	1	(22)	0.095	1	U	F.KVEGD
4693	679.3641	1356.7137	1356.7136	0.07	1	30	0.015	1	U	F.KVEGD

---

82. 2::sp|P0A7V3|RS3_ECOLI **Mass:** 25967 **Score:** 73 **Matches:** 3(2) **Sequences:** 2(1

30S ribosomal protein S3 OS=Escherichia coli (strain K12) OX=83333 GN=rpsC 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
1148	467.2482	932.4819	932.4815	0.46	0	50	0.00018	1	U	L.VADSI
1149	467.2485	932.4824	932.4815	0.98	0	(48)	0.00026	1	U	L.VADSI
5912	793.8522	1585.6899	1585.6896	0.18	2	23	0.065	1	U	F.ANTKE

---

83. 2::sp|P0A6Y8|DNAK_ECOLI **Mass:** 69130 **Score:** 72 **Matches:** 3(3) **Sequences:** 2

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
3282	587.2996	1172.5847	1172.5826	1.81	0	30	0.014	1	U	F.KIIAAD
6157	818.8927	1635.7708	1635.7740	-1.93	0	(28)	0.032	1	U	L.ENAEGD
6158	818.8928	1635.7711	1635.7740	-1.78	0	42	0.0015	1	U	L.ENAEGD

---

84. 2::sp|P00960|SYGA_ECOLI **Mass:** 35037 **Score:** 71 **Matches:** 4(4) **Sequences:** 2

Glycine--tRNA ligase alpha subunit OS=Escherichia coli (strain K12) OX=83333 GN=gly

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3804	617.7710	1233.5274	1233.5262	1.02	0	30	0.0067	1	U	F.HQNEVE
3805	617.7715	1233.5284	1233.5262	1.80	0	(25)	0.026	1	U	F.HQNEVE
6639	871.9705	1741.9265	1741.9250	0.83	1	43	0.0007	1	U	F.QVVIKP
6640	871.9723	1741.9300	1741.9250	2.87	1	(34)	0.0054	1	U	F.QVVIKP

---

85. 2::sp|P0A6N4|EFP_ECOLI **Mass:** 20635 **Score:** 69 **Matches:** 4(4) **Sequences:** 2(2

Elongation factor P OS=Escherichia coli (strain K12) OX=83333 GN=efp PE=1 SV=2

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide

1493	485.8003	969.5860	969.5859	0.08	0	(23)	0.019	1	U	L.STGAVV
1494	485.8004	969.5863	969.5859	0.41	0	31	0.0028	1	U	L.STGAVV
7584	738.3841	2212.1304	2212.1223	3.67	1	(36)	0.0045	1	U	L.EIVDTD
7585	738.3847	2212.1323	2212.1223	4.49	1	38	0.0027	1	U	L.EIVDTD

---

86. 2::sp|P37759|RMLB1_ECOLI **Mass:** 40704 **Score:** 69 **Matches:** 2(2) **Sequences:** 1
dTDP-glucose 4,6-dehydratase 1 OS=Escherichia coli (strain K12) OX=83333 GN=rfbB 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
3946	627.8159	1253.6173	1253.6140	2.66	0	69	2.1e-06	1	U	Y.TVVTE
3947	627.8161	1253.6176	1253.6140	2.95	0	(50)	0.00017	1	U	Y.TVVTE

---

87. 2::sp|P0A6Y5|HSLO_ECOLI **Mass:** 32856 **Score:** 68 **Matches:** 3(3) **Sequences:** 2
33 kDa chaperonin OS=Escherichia coli (strain K12) OX=83333 GN=hslO 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
4792	687.3843	1372.7541	1372.7562	-1.51	1	36	0.003	1	U	F.AVRGEL
5268	732.3920	1462.7695	1462.7668	1.88	0	(28)	0.029	1	U	Y.VVITIT
5269	732.3923	1462.7700	1462.7668	2.21	0	32	0.012	1	U	Y.VVITIT

---

88. 2::sp|P0ADG4|SUHB_ECOLI **Mass:** 29211 **Score:** 68 **Matches:** 3(2) **Sequences:** 2
Inositol-1-monophosphatase OS=Escherichia coli (strain K12) OX=83333 GN=suhB 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
3433	596.2960	1190.5774	1190.5819	-3.84	1	(39)	0.0027	1	U	W.VIDPL
3434	596.2967	1190.5788	1190.5819	-2.61	1	47	0.00038	1	U	W.VIDPL
7924	723.3570	2889.3989	2889.4212	-7.72	2	21	0.17	1	U	L.TGNIV

---

89. 2::sp|P77690|ARNB_ECOLI **Mass:** 42439 **Score:** 67 **Matches:** 4(3) **Sequences:** 2
UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase OS=Escherichia coli
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5417	743.8801	1485.7457	1485.7464	-0.43	0	(21)	0.13	1	U	Y.GIAVIE
5418	743.8828	1485.7511	1485.7464	3.17	0	30	0.019	1	U	Y.GIAVIE
5515	752.8687	1503.7229	1503.7239	-0.71	0	(32)	0.013	1	U	L.GATPVM
5516	752.8701	1503.7257	1503.7239	1.16	0	37	0.0048	1	U	L.GATPVM

---

90. 2::sp|P37652|BCSB_ECOLI **Mass:** 86140 **Score:** 66 **Matches:** 5(0) **Sequences:** 3
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

1144	466.2584	930.5022	930.4923	10.6	0	22	0.087	2	U	W.RGQNFP
1145	466.2584	930.5023	930.4923	10.7	0	(20)	0.14	3	U	W.RGQNFP
3537	601.3417	1200.6689	1200.6503	15.5	0	(21)	0.12	1	U	F.IGAQTG
3538	601.3435	1200.6725	1200.6503	18.5	0	22	0.079	3	U	F.IGAQTG
6046	807.9265	1613.8383	1613.8335	3.03	2	22	0.12	1	U	L.QGLLDG

---

91. 2::sp|P69441|KAD_ECOLI **Mass:** 23628 **Score:** 64 **Matches:** 3(3) **Sequences:** 2(2

Adenylate kinase OS=Escherichia coli (strain K12) OX=83333 GN=adk PE=1 SV=1

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3417	595.3017	1188.5888	1188.5887	0.09	0	36	0.0049	1	U	L.GAPGAG
3418	595.3023	1188.5901	1188.5887	1.11	0	(36)	0.005	1	U	L.GAPGAG
4327	651.8447	1301.6748	1301.6728	1.52	1	28	0.031	1	U	L.LGAPGA

---

92. 2::sp|P0AG48|RL21_ECOLI **Mass:** 11557 **Score:** 64 **Matches:** 3(3) **Sequences:** 2(

50S ribosomal protein L21 OS=Escherichia coli (strain K12) OX=83333 GN=rplU PE=1 SV=

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3050	576.3187	1150.6229	1150.6234	-0.43	1	38	0.0015	1	U	W.FTDVKI
3051	576.3200	1150.6255	1150.6234	1.80	1	(30)	0.011	1	U	W.FTDVKI
5512	752.3989	1502.7833	1502.7803	2.01	0	25	0.056	1	U	L.MIANGE

---

93. 2::sp|P0ABD8|BCCP_ECOLI **Mass:** 16733 **Score:** 63 **Matches:** 2(2) **Sequences:** 1(

Biotin carboxyl carrier protein of acetyl-CoA carboxylase OS=Escherichia coli (strai

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4780	686.3763	1370.7381	1370.7406	-1.77	0	63	7.7e-06	1	U	F.IEVGQ
4781	686.3767	1370.7387	1370.7406	-1.32	0	(48)	0.00026	1	U	F.IEVGQ

---

94. 2::sp|P69783|PTGA_ECOLI **Mass:** 18240 **Score:** 61 **Matches:** 1(1) **Sequences:** 1(

PTS system glucose-specific EIIA 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
5995	802.4180	1602.8215	1602.8175	2.53	0	61	1.7e-05	1	U	L.TPVVI

---

95. 2::sp|P60906|SYH_ECOLI **Mass:** 47285 **Score:** 60 **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
5468	747.9317	1493.8488	1493.8453	2.36	0	60	5.2e-06	1	U	Y.SEIRL

5469	747.9324	1493.8502	1493.8453	3.26	0	(56)	1.2e-05	1	U	Y.SEIRL

---

96. 2::sp|P25745|MNMA_ECOLI **Mass:** 41333 **Score:** 60 **Matches:** 3(2) **Sequences:** 2

tRNA-specific 2-thiouridylase MnmA OS=Escherichia coli (strain K12) OX=83333 GN=mnm

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4188	641.8037	1281.5929	1281.5949	-1.61	1	22	0.12	1	U	L.RGLDSN
4987	710.8697	1419.7248	1419.7245	0.20	1	38	0.0031	1	U	W.YVVDKD
4988	710.8703	1419.7260	1419.7245	1.06	1	(37)	0.0039	1	U	W.YVVDKD

---

97. 2::sp|P0A7S9|RS13_ECOLI **Mass:** 13148 **Score:** 59 **Matches:** 2(2) **Sequences:** 1

30S ribosomal protein S13 OS=Escherichia coli (strain K12) OX=83333 GN=rpsM PE=1 SV=

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4837	693.8776	1385.7407	1385.7402	0.37	0	59	2.3e-05	1	U	L.AAAGI
4838	693.8793	1385.7440	1385.7402	2.75	0	(55)	5.4e-05	1	U	L.AAAGI

---

98. 2::sp|P0A9T0|SERA_ECOLI **Mass:** 44376 **Score:** 59 **Matches:** 2(2) **Sequences:** 1

D-3-phosphoglycerate dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=ser

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6594	864.9493	1727.8841	1727.8829	0.72	0	61	1.6e-05	1	U	Y.VVIDI
6595	864.9515	1727.8884	1727.8829	3.19	0	(55)	6.3e-05	1	U	Y.VVIDI

---

99. 2::sp|P36979|RLMN_ECOLI **Mass:** 43514 **Score:** 58 **Matches:** 2(2) **Sequences:** 1

Dual-specificity RNA methyltransferase RlmN OS=Escherichia coli (strain K12) OX=8333

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4990	710.8747	1419.7348	1419.7358	-0.68	0	(54)	7.2e-05	1	U	W.AIAVG
4991	710.8755	1419.7365	1419.7358	0.53	0	58	2.6e-05	1	U	W.AIAVG

---

100. 2::sp|P0A6F5|CH60_ECOLI **Mass:** 57464 **Score:** 57 **Matches:** 3(3) **Sequences:** 2

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
605	422.2553	842.4961	842.4974	-1.55	0	21	0.06	1	U	L.QERVAK
6768	889.4535	1776.8924	1776.8934	-0.55	2	36	0.0066	1	U	Y.FINKPE
6769	889.4535	1776.8925	1776.8934	-0.48	2	(34)	0.0095	1	U	Y.FINKPE

---

101. 2::sp|P0AG55|RL6_ECOLI **Mass:** 18949 **Score:** 57 **Matches:** 3(2) **Sequences:** 2(2
50S ribosomal protein L6 OS=Escherichia coli (strain K12) OX=83333 GN=rplF PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2515	547.2388	1092.4631	1092.4625	0.58	1	25	0.024	1	U	F.GPRDGY
5034	713.3539	1424.6932	1424.6896	2.56	0	31	0.015	1	U	L.NDAVEV
5035	713.3558	1424.6971	1424.6896	5.30	0	(24)	0.086	1	U	L.NDAVEV

---

102. 2::sp|P0AEZ3|MIND_ECOLI **Mass:** 29710 **Score:** 56 **Matches:** 2(2) **Sequences:** 1
Septum site-determining protein MinD OS=Escherichia coli (strain K12) OX=83333 GN=mi
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4236	646.3297	1290.6447	1290.6456	-0.66	1	(34)	0.0096	1	U	Y.DFVNV
4237	646.3311	1290.6475	1290.6456	1.51	1	56	6.1e-05	1	U	Y.DFVNV

---

103. 1::sp|cRAP087|P02769|ALBU_BOVIN **Mass:** 71244 **Score:** 55 **Matches:** 2(2) **Seque**
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
3356	590.8280	1179.6414	1179.6400	1.20	2	(55)	2.9e-05	1	U	Y.GFQNA
3357	590.8291	1179.6436	1179.6400	3.07	2	55	2.6e-05	1	U	Y.GFQNA

---

104. 2::sp|P0ADY7|RL16_ECOLI **Mass:** 15271 **Score:** 55 **Matches:** 4(4) **Sequences:** 2
50S ribosomal protein L16 OS=Escherichia coli (strain K12) OX=83333 GN=rplP 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
3161	387.5722	1159.6947	1159.6965	-1.54	0	26	0.0066	1	U	L.AAAKLP
6245	413.9986	1651.9652	1651.9661	-0.57	0	(29)	0.0045	1	U	W.IRVFPD
6246	551.6626	1651.9660	1651.9661	-0.08	0	30	0.0035	1	U	W.IRVFPD
6247	551.6639	1651.9698	1651.9661	2.24	0	(30)	0.0032	1	U	W.IRVFPD

---

105. 2::sp|P68187|MALK_ECOLI **Mass:** 41136 **Score:** 55 **Matches:** 2(2) **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
5865	788.9023	1575.7901	1575.7893	0.53	1	55	7.4e-05	1	U	Y.RQNDV
5866	788.9026	1575.7906	1575.7893	0.85	1	(38)	0.0044	1	U	Y.RQNDV

---

106. 2::sp|P0C018|RL18_ECOLI **Mass:** 12762 **Score:** 52 **Matches:** 4(3) **Sequences:** 1
50S ribosomal protein L18 OS=Escherichia coli (strain K12) OX=83333 GN=rplR PE=1 SV=

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5062	477.2670	1428.7793	1428.7824	-2.18	0	(25)	0.044	1	U	L.VAAST
5063	477.2680	1428.7821	1428.7824	-0.21	0	(20)	0.12	1	U	L.VAAST
5064	715.3998	1428.7850	1428.7824	1.84	0	(45)	0.00042	1	U	L.VAAST
5065	715.4004	1428.7862	1428.7824	2.69	0	52	8.2e-05	1	U	L.VAAST

---

107. 2::sp|P77395|YBBN_ECOLI **Mass:** 31885 **Score:** 51 **Matches:** 2(2) **Sequences:** 1
Uncharacterized protein YbbN OS=Escherichia coli (strain K12) OX=83333 GN=ybbN PE=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4593	671.3544	1340.6942	1340.6936	0.46	0	(48)	0.00022	1	U	L.KQAAD
4594	671.3544	1340.6942	1340.6936	0.46	0	51	9.6e-05	1	U	L.KQAAD

---

108. 2::sp|P45523|FKBA_ECOLI **Mass:** 28864 **Score:** 50 **Matches:** 2(1) **Sequences:** 2
FKBP-type peptidyl-prolyl cis-trans isomerase FkpA 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
2638	554.3080	1106.6014	1106.5972	3.83	1	21	0.079	1	U	Y.KGTLID
6513	853.4379	1704.8612	1704.8417	11.4	1	29	0.03	1	U	F.ADKSKL

---

109. 1::sp|cRAP112|P00761|TRYP_PIG **Mass:** 25078 **Score:** 49 **Matches:** 2(1) **Sequenc**
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
2355	538.2630	1074.5114	1074.5094	1.88	1	28	0.024	1	U	Y.QVSLNS
3980	629.3333	1256.6521	1256.6513	0.59	1	21	0.11	1	U	Y.VNWIQQ

---

110. 2::sp|P0A9K9|SLYD_ECOLI **Mass:** 21182 **Score:** 49 **Matches:** 2(2) **Sequences:** 1
FKBP-type peptidyl-prolyl cis-trans isomerase SlyD OS=Escherichia coli (strain K12)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
7401	1006.0234	2010.0323	2010.0270	2.67	1	49	0.00021	1	U	Y.QVRT
7402	1006.0236	2010.0327	2010.0270	2.85	1	(38)	0.0027	1	U	Y.QVRT

---

111. 2::sp|P75796|GSIA_ECOLI **Mass:** 69299 **Score:** 49 **Matches:** 2(1) **Sequences:** 2
Glutathione import ATP-binding protein GsiA OS=Escherichia coli (strain K12) OX=8333
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide

1807	501.2850	1000.5554	1000.5441	11.4	0	25	0.04	3	U	L.DVTIQA
2369	539.7809	1077.5473	1077.5342	12.1	0	24	0.075	1	U	L.VESQGG

---

112. 2::sp|P07012|RF2_ECOLI **Mass:** 41339 **Score:** 47 **Matches:** 2(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
5742	774.3536	1546.6926	1546.6900	1.70	1	47	0.00026	1	U	Y.LDIQA
5743	774.3553	1546.6960	1546.6900	3.92	1	(21)	0.12	1	U	Y.LDIQA

---

113. 2::sp|P08390|USG_ECOLI **Mass:** 36456 **Score:** 47 **Matches:** 3(1) **Sequences:** 2(1

USG-1 protein OS=Escherichia coli (strain K12) OX=83333 GN=usg 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
1581	490.2267	978.4388	978.4406	-1.88	0	24	0.044	1	U	L.AAEEAR
1582	490.2269	978.4392	978.4406	-1.43	0	(22)	0.077	1	U	L.AAEEAR
3987	629.8240	1257.6334	1257.6313	1.67	1	23	0.1	3	U	Y.ALARNE

---

114. 2::sp|P0A9Q5|ACCD_ECOLI **Mass:** 33642 **Score:** 47 **Matches:** 1(1) **Sequences:** 1

Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta OS=Escherichia coli

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6044	807.4038	1612.7931	1612.7879	3.21	1	47	0.00046	1	U	F.VRAVE

---

115. 2::sp|P42601|ALX_ECOLI **Mass:** 35885 **Score:** 46 **Matches:** 2(1) **Sequences:** 2(1

Putative membrane-bound redox modulator Alx OS=Escherichia coli (strain K12) OX=8333

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
427	408.2602	814.5058	814.4986	8.75	0	24	0.02	1	U	F.AVVVAIML
1251	473.2538	944.4929	944.5001	-7.58	1	22	0.096	8	U	-.MNTVGTPL

---

116. 2::sp|P15006|MCRC_ECOLI **Mass:** 40792 **Score:** 46 **Matches:** 3(0) **Sequences:** 2

Protein McrC OS=Escherichia coli (strain K12) OX=83333 GN=mcrC 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
2229	529.3042	1056.5938	1056.5815	11.7	1	22	0.072	1	U	Y.LQEIK
5023	712.8489	1423.6832	1423.7055	-15.67	1	(22)	0.13	1	U	L.NSTIR
5025	712.8507	1423.6869	1423.7055	-13.10	1	24	0.089	2	U	L.NSTIR

117. 2::sp|P0A7W1|RS5_ECOLI **Mass:** 17592 **Score:** 46 **Matches:** 3(2) **Sequences:** 1(1
30S ribosomal protein S5 OS=Escherichia coli (strain K12) OX=83333 GN=rpsE 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
3325	589.3016	1176.5886	1176.5888	-0.16	0	(24)	0.086	1	U	L.TVVGD
3326	589.3021	1176.5896	1176.5888	0.67	0	(30)	0.022	1	U	L.TVVGD
3330	589.7935	1177.5724	1177.5728	-0.35	0	46	0.00062	1	U	L.TVVGD

---

118. 2::sp|P0A847|TGT_ECOLI **Mass:** 43022 **Score:** 45 **Matches:** 2(2) **Sequences:** 1(1
Queuine tRNA-ribosyltransferase OS=Escherichia coli (strain K12) OX=83333 GN=tgt 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
2497	546.2897	1090.5649	1090.5659	-0.90	1	(31)	0.013	1	U	W.KGPIL
2498	546.2899	1090.5653	1090.5659	-0.55	1	45	0.00056	1	U	W.KGPIL

---

119. 2::sp|P46853|YHHX_ECOLI **Mass:** 38912 **Score:** 45 **Matches:** 2(2) **Sequences:** 1
Uncharacterized oxidoreductase YhhX OS=Escherichia coli (strain K12) OX=83333 GN=yhh
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3441	596.3209	1190.6273	1190.6295	-1.87	2	45	0.00057	1	U	L.TNLEI
3442	596.3232	1190.6318	1190.6295	1.92	2	(30)	0.015	1	U	L.TNLEI

---

120. 2::sp|P62399|RL5_ECOLI **Mass:** 20346 **Score:** 44 **Matches:** 2(2) **Sequences:** 1(1
50S ribosomal protein L5 OS=Escherichia coli (strain K12) OX=83333 GN=rplE PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
864	442.7636	883.5127	883.5127	0.04	0	44	0.00023	1	U	L.AAISGQK
865	442.7637	883.5128	883.5127	0.17	0	(36)	0.0013	1	U	L.AAISGQK

---

121. 2::sp|P77433|YKGG_ECOLI **Mass:** 25539 **Score:** 43 **Matches:** 2(0) **Sequences:** 2
Uncharacterized protein YkgG OS=Escherichia coli (strain K12) OX=83333 GN=ykgG 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
1145	466.2584	930.5023	930.5022	0.06	1	21	0.11	1	U	Y.GLTES
4056	423.5615	1267.6627	1267.6772	-11.39	2	22	0.076	1	U	F.LNNVA

---

122. 2::sp|P02943|LAMB_ECOLI **Mass:** 49995 **Score:** 43 **Matches:** 3(1) **Sequences:** 2
Maltoporin OS=Escherichia coli (strain K12) OX=83333 GN=lamB PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1632	493.2512	984.4879	984.4876	0.27	0	23	0.05	2	U	F.TAEHTQSV
1659	494.2839	986.5533	986.5549	-1.59	1	23	0.067	1	U	Y.KITLAQQW
1660	494.2844	986.5543	986.5549	-0.56	1	(22)	0.07	1	U	Y.KITLAQQW

---

123. 2::sp|P36683|ACNB_ECOLI **Mass:** 94009 **Score:** 42 **Matches:** 1(1) **Sequences:** 1

Aconitate hydratase B OS=Escherichia coli (strain K12) OX=83333 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
4374	655.3353	1308.6560	1308.6562	-0.13	0	42	0.0011	1	U	Y.VAQVDK

---

124. 2::sp|P46474|YHDP_ECOLI **Mass:** 139081 **Score:** 42 **Matches:** 2(2) **Sequences:** 1

Uncharacterized protein YhdP OS=Escherichia coli (strain K12) OX=83333 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
2108	522.2510	1042.4875	1042.4819	5.44	0	42	0.00075	1	U	L.DDPQI
2109	522.2510	1042.4875	1042.4819	5.44	0	(33)	0.0061	1	U	L.DDPQI

---

125. 2::sp|P09424|MTLD_ECOLI **Mass:** 41171 **Score:** 41 **Matches:** 2(0) **Sequences:** 2

Mannitol-1-phosphate 5-dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=mt

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2521	547.7507	1093.4869	1093.4829	3.70	1	20	0.13	1	U	Y.GFDADK
4208	644.2927	1286.5708	1286.5739	-2.40	0	21	0.089	1	U	F.RSEDDP

---

126. 2::sp|P0A6L4|NANA_ECOLI **Mass:** 32801 **Score:** 41 **Matches:** 2(0) **Sequences:** 2

N-acetylneuraminate lyase OS=Escherichia coli (strain K12) OX=83333 GN=nanA 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
5847	524.6273	1570.8601	1570.8606	-0.31	2	21	0.094	1	U	F.GPVDEK
6153	818.4210	1634.8275	1634.8338	-3.85	0	22	0.13	1	U	Y.RAIIDS

---

127. 2::sp|P30176|RIBX_ECOLI **Mass:** 18658 **Score:** 40 **Matches:** 2(2) **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
1089	459.7481	917.4817	917.4640	19.2	1	40	0.0018	1	U	L.MELREQL.
1090	459.7482	917.4819	917.4640	19.5	1	(26)	0.04	1	U	L.MELREQL.

---

128. 2::sp|P04335|FRSA_ECOLI **Mass:** 47321 **Score:** 39 **Matches:** 2(2) **Sequences:** 1(
Esterase FrsA OS=Escherichia coli (strain K12) OX=83333 GN=frsA 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
3563	602.7969	1203.5793	1203.5772	1.80	1	39	0.0022	1	U	F.DKGLQE
3564	602.7971	1203.5796	1203.5772	2.00	1	(37)	0.0042	1	U	F.DKGLQE

---

129. 2::sp|P0A988-2|DPO3B_ECOLI **Mass:** 26122 **Score:** 39 **Matches:** 2(2) **Sequences:**
Isoform Beta* of Beta sliding clamp OS=Escherichia coli (strain K12) OX=83333 GN=dna
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
7640	1153.5584	2305.1021	2305.0961	2.62	1	39	0.0026	1	U	L.KITAN
7641	1153.5588	2305.1031	2305.0961	3.05	1	(33)	0.01	1	U	L.KITAN

Proteins matching the same set of peptides:
2::sp|P0A988|DPO3B_ECOLI **Mass:** 40789 **Score:** 39 **Matches:** 2(2) **Sequences:** 1
Beta sliding clamp OS=Escherichia coli (strain K12) OX=83333 GN=dnaN PE=1 SV=1

---

130. 2::sp|P0A903|BAMC_ECOLI **Mass:** 36877 **Score:** 38 **Matches:** 2(2) **Sequences:** 1(
Outer membrane protein assembly factor BamC OS=Escherichia coli (strain K12) OX=8333
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4450	659.8348	1317.6551	1317.6525	2.02	0	(40)	0.002	1	U	Y.TITQRD
4451	659.8353	1317.6560	1317.6525	2.67	0	41	0.0018	1	U	Y.TITQRD

---

131. 2::sp|P00393|DHNA_ECOLI **Mass:** 47557 **Score:** 38 **Matches:** 1(1) **Sequences:** 1(
NADH dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=ndh 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
3232	584.8731	1167.7317	1167.7339	-1.95	0	38	0.00027	1	U	L.KKIVI

---

132. 2::sp|P0ABD5|ACCA_ECOLI **Mass:** 35333 **Score:** 38 **Matches:** 2(2) **Sequences:** 1(
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha OS=Escherichia coli
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4287	433.5857	1297.7353	1297.7354	-0.04	0	(37)	0.0015	1	U	Y.ADDKAI
4288	433.5858	1297.7356	1297.7354	0.19	0	38	0.0012	1	U	Y.ADDKAI

---

133. 2::sp|P0AG30|RHO_ECOLI **Mass:** 47032 **Score:** 37 **Matches:** 2(2) **Sequences:** 1(1

Transcription termination factor Rho OS=Escherichia coli (strain K12) OX=83333 GN=rh
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2412	542.8205	1083.6264	1083.6288	-2.18	0	37	0.0015	1	U	Y.NTVVPA
2413	542.8207	1083.6268	1083.6288	-1.85	0	(35)	0.0024	1	U	Y.NTVVPA

---

134. 2::sp|P0AFK9|POTD_ECOLI **Mass:** 38842 **Score:** 36 **Matches:** 2(2) **Sequences:** 1
Spermidine/putrescine-binding periplasmic protein 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
1783	500.2789	998.5433	998.5437	-0.38	2	36	0.0024	1	U	Y.VPPGLLEQ
1784	500.2807	998.5469	998.5437	3.23	2	(30)	0.0075	1	U	Y.VPPGLLEQ

---

135. 2::sp|P0ABP8|DEOD_ECOLI **Mass:** 26161 **Score:** 35 **Matches:** 2(2) **Sequences:** 1
Purine nucleoside phosphorylase DeoD-type 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
1445	483.7605	965.5064	965.5070	-0.53	1	35	0.004	1	U	Y.TKELITDF
1446	483.7608	965.5070	965.5070	0.03	1	(31)	0.011	1	U	Y.TKELITDF

---

136. 2::sp|P77398|ARNA_ECOLI **Mass:** 74869 **Score:** 35 **Matches:** 1(1) **Sequences:** 1
Bifunctional polymyxin resistance protein ArnA OS=Escherichia coli (strain K12) OX=8
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3921	625.8240	1249.6334	1249.6303	2.50	1	35	0.0056	1	U	Y.GLDIGS

---

137. 2::sp|P0AGD3|SODF_ECOLI **Mass:** 21310 **Score:** 35 **Matches:** 2(2) **Sequences:** 1
Superoxide dismutase [Fe] OS=Escherichia coli (strain K12) OX=83333 GN=sodB 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
834	440.2312	878.4479	878.4498	-2.12	0	(32)	0.011	1	U	F.TDAAIKNF
835	440.2318	878.4491	878.4498	-0.73	0	35	0.0054	1	U	F.TDAAIKNF

---

138. 2::sp|P23482|HYFB_ECOLI **Mass:** 73048 **Score:** 33 **Matches:** 2(2) **Sequences:** 1
Hydrogenase-4 component B OS=Escherichia coli (strain K12) OX=83333 GN=hyfB 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
1785	500.2848	998.5550	998.5437	11.4	2	33	0.0033	1	U	L.LAQTGLPL
1786	500.2849	998.5552	998.5437	11.6	2	(25)	0.025	1	U	L.LAQTGLPL

---

139. 2::sp|P0AAX8|YBIS_ECOLI **Mass:** 33418 **Score:** 33 **Matches:** 3(1) **Sequences:** 1(
Probable L,D-transpeptidase YbiS OS=Escherichia coli (strain K12) OX=83333 GN=ybiS P
Check to include this hit in error tolerant search or archive report

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**ppm**	**Miss**	**Score**	**Expect**	**Rank**	**Unique**	**Peptide**
6765	**593.2925**	**1776.8556**	**1776.8530**	**1.47**	**0**	**33**	**0.012**	**1**	**U**	**F.IDEPVK**
6766	**593.2929**	**1776.8567**	**1776.8530**	**2.10**	**0**	**(22)**	**0.15**	**1**	**U**	**F.IDEPVK**
6767	**889.4368**	**1776.8590**	**1776.8530**	**3.37**	**0**	**(23)**	**0.12**	**1**	**U**	**F.IDEPVK**

---

140. 2::sp|P0A7J7|RL11_ECOLI **Mass:** 14923 **Score:** 33 **Matches:** 1(1) **Sequences:** 1(
50S ribosomal protein L11 OS=Escherichia coli (strain K12) OX=83333 GN=rplK 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**
1750	**498.8078**	**995.6010**	**995.6015**	**-0.49**	**0**	**33**	**0.0013**	**1**	**U**	**F.VTKTPPAA**

---

141. 2::sp|P0ABJ1|CYOA_ECOLI **Mass:** 34946 **Score:** 32 **Matches:** 2(2) **Sequences:** 1(
Cytochrome bo(3) ubiquinol oxidase subunit 2 OS=Escherichia coli (strain K12) OX=833
Check to include this hit in error tolerant search or archive report

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**ppm**	**Miss**	**Score**	**Expect**	**Rank**	**Unique**	**Peptide**
320	**403.7235**	**805.4325**	**805.4334**	**-1.15**	**0**	**(29)**	**0.014**	**1**	**U**	**F.ADVINKF.**
322	**403.7239**	**805.4332**	**805.4334**	**-0.23**	**0**	**32**	**0.0058**	**1**	**U**	**F.ADVINKF.**

---

142. 2::sp|P0A927|TSX_ECOLI **Mass:** 33568 **Score:** 32 **Matches:** 1(1) **Sequences:** 1(1
Nucleoside-specific channel-forming protein Tsx OS=Escherichia coli (strain K12) OX=
Check to include this hit in error tolerant search or archive report

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**ppm**	**Miss**	**Score**	**Expect**	**Rank**	**Unique**	**Peptide**
2296	**532.2622**	**1062.5097**	**1062.5094**	**0.31**	**0**	**32**	**0.013**	**1**	**U**	**F.GPQIRN**

---

143. 2::sp|P0A7G6|RECA_ECOLI **Mass:** 38121 **Score:** 32 **Matches:** 2(1) **Sequences:** 1(
Protein RecA OS=Escherichia coli (strain K12) OX=83333 GN=recA PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**ppm**	**Miss**	**Score**	**Expect**	**Rank**	**Unique**	**Peptide**
1556	**488.7503**	**975.4861**	**975.4873**	**-1.25**	**0**	**32**	**0.012**	**1**	**U**	**Y.GPESSGKT**
1557	**488.7509**	**975.4872**	**975.4873**	**-0.06**	**0**	**(24)**	**0.077**	**1**	**U**	**Y.GPESSGKT**

---

144. 2::sp|P32717|YJCS_ECOLI **Mass:** 73219 **Score:** 32 **Matches:** 1(1) **Sequences:** 1(
Putative alkyl/aryl-sulfatase YjcS OS=Escherichia coli (strain K12) OX=83333 GN=yjcS
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6336	835.4445	1668.8745	1668.8570	10.5	0	32	0.01	1	U	L.KQVIAA

---

145. 2::sp|P77454|GLSA1_ECOLI **Mass:** 33168 **Score:** 32 **Matches:** 1(1) **Sequences:** 1
Glutaminase 1 OS=Escherichia coli (strain K12) OX=83333 GN=glsA1 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
2100	521.2707	1040.5268	1040.5502	-22.48	1	32	0.0082	1	U	L.GATLA

---

146. 2::sp|P23869|PPIB_ECOLI **Mass:** 18256 **Score:** 32 **Matches:** 1(1) **Sequences:** 1
Peptidyl-prolyl cis-trans isomerase B OS=Escherichia coli (strain K12) OX=83333 GN=
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2147	524.7705	1047.5265	1047.5237	2.66	1	32	0.012	1	U	F.INVVDN

---

147. 2::sp|P77561|YDEP_ECOLI **Mass:** 84240 **Score:** 31 **Matches:** 2(1) **Sequences:** 1
Protein YdeP OS=Escherichia coli (strain K12) OX=83333 GN=ydeP PE=2 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
6692	585.6559	1753.9460	1753.9322	7.85	2	(20)	0.1	1	U	L.LIERDD
6693	877.9806	1753.9466	1753.9322	8.21	2	35	0.0033	1	U	L.LIERDD

---

148. 2::sp|P0A7B5|PROB_ECOLI **Mass:** 39204 **Score:** 31 **Matches:** 2(2) **Sequences:** 1
Glutamate 5-kinase OS=Escherichia coli (strain K12) OX=83333 GN=proB PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1063	458.2968	914.5791	914.5801	-1.10	1	31	0.0012	1	U	L.VVKLGTSV
1064	458.2976	914.5806	914.5801	0.58	1	(31)	0.0013	1	U	L.VVKLGTSV

---

149. 2::sp|P52643|LDHD_ECOLI **Mass:** 36854 **Score:** 31 **Matches:** 1(1) **Sequences:** 1
D-lactate dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=ldhA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6343	835.8821	1669.7497	1669.7472	1.54	1	33	0.0087	1	U	F.FEDKSN

---

150. 2::sp|P0A7K2|RL7_ECOLI **Mass:** 12288 **Score:** 31 **Matches:** 2(2) **Sequences:** 1(1
50S ribosomal protein L7/L12 OS=Escherichia coli (strain K12) OX=83333 GN=rplL PE=1

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4013	631.3169	1260.6192	1260.6197	-0.40	0	31	0.019	1	U	L.KEGVSK
4014	631.3170	1260.6195	1260.6197	-0.20	0	(30)	0.024	1	U	L.KEGVSK

---

151. 2::sp|P0AE48|YTFP_ECOLI **Mass:** 12858 **Score:** 30 **Matches:** 2(2) **Sequences:** 1(
Gamma-glutamylcyclotransferase family protein YtfP 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
291	401.7183	801.4220	801.4344	-15.57	0	(30)	0.017	1	U	Y.RIDNATL
292	401.7183	801.4221	801.4344	-15.42	0	30	0.016	1	U	Y.RIDNATL

---

152. 2::sp|P0C0V0|DEGP_ECOLI **Mass:** 49438 **Score:** 30 **Matches:** 1(1) **Sequences:** 1(
Periplasmic serine endoprotease DegP OS=Escherichia coli (strain K12) OX=83333 GN=de
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5615	763.3845	1524.7544	1524.7494	3.26	1	30	0.019	1	U	F.MALGSG

---

153. 2::sp|P25553|ALDA_ECOLI **Mass:** 52411 **Score:** 30 **Matches:** 1(1) **Sequences:** 1(
Lactaldehyde dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=aldA 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
4320	651.8190	1301.6235	1301.6537	-23.19	0	30	0.019	1	U	L.IVEEG

---

154. 2::sp|Q2EES3|YOEF_ECOLI **Mass:** 13189 **Score:** 29 **Matches:** 1(1) **Sequences:** 1(
Putative uncharacterized protein YoeF OS=Escherichia coli (strain K12) OX=83333 GN=y
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2764	561.2709	1120.5273	1120.5553	-24.96	2	29	0.025	1	U	L.FWQQA

---

155. 2::sp|P37047|CDAR_ECOLI **Mass:** 43774 **Score:** 29 **Matches:** 1(1) **Sequences:** 1(
Carbohydrate diacid regulator OS=Escherichia coli (strain K12) OX=83333 GN=cdaR 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
2237	529.7952	1057.5758	1057.5729	2.71	2	29	0.017	1	U	Y.QDLMLP

---

156. 2::sp|P45955|CPOB_ECOLI **Mass:** 28214 **Score:** 29 **Matches:** 1(1) **Sequences:** 1(

Cell division coordinator CpoB OS=Escherichia coli (strain K12) OX=83333 GN=cpoB 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
2893	568.2787	1134.5429	1134.5418	1.04	0	31	0.015	1	U	L.RGQIQE

---

157. 2::sp|P0AFH2|OPPB_ECOLI **Mass:** 33478 **Score:** 29 **Matches:** 1(1) **Sequences:** 1
Oligopeptide transport system permease protein OppB 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
211	397.6894	793.3642	793.3793	-19.02	1	29	0.018	1	U	W.NGGALKF

---

158. 2::sp|P37663|YHJY_ECOLI **Mass:** 25935 **Score:** 28 **Matches:** 2(2) **Sequences:** 1
Uncharacterized protein YhjY OS=Escherichia coli (strain K12) OX=83333 GN=yhjY PE=4
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5687	770.8494	1539.6842	1539.6994	-9.86	2	28	0.023	1	U	L.RPWAQI
5688	770.8519	1539.6892	1539.6994	-6.61	2	(27)	0.031	1	U	L.RPWAQI

---

159. 2::sp|P19926|AGP_ECOLI **Mass:** 45996 **Score:** 28 **Matches:** 2(2) **Sequences:** 1(1
Glucose-1-phosphatase OS=Escherichia coli (strain K12) OX=83333 GN=agp 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
2163	525.2857	1048.5569	1048.5553	1.48	1	(27)	0.033	1	U	L.KVGNSL
2164	525.2858	1048.5571	1048.5553	1.71	1	28	0.022	1	U	L.KVGNSL

---

160. 2::sp|P0ACE0|MBHM_ECOLI **Mass:** 62908 **Score:** 28 **Matches:** 1(1) **Sequences:** 1
Hydrogenase-2 large chain OS=Escherichia coli (strain K12) OX=83333 GN=hybC PE=1 SV=
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1975	511.7313	1021.4481	1021.4716	-23.04	1	28	0.019	1	U	L.QDILQ

---

161. 2::sp|P76299|FLHB_ECOLI **Mass:** 42268 **Score:** 28 **Matches:** 1(1) **Sequences:** 1
Flagellar biosynthetic protein FlhB OS=Escherichia coli (strain K12) OX=83333 GN=flh
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
627	423.2400	844.4655	844.4840	-21.95	1	28	0.02	1	U	L.LIREAML

---

162. 2::sp|P0ABK5|CYSK_ECOLI **Mass:** 34525 **Score:** 28 **Matches:** 2(2) **Sequences:** 1
Cysteine synthase A OS=Escherichia coli (strain K12) OX=83333 GN=cysK PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6778	891.4871	1780.9597	1780.9571	1.47	1	28	0.017	1	U	L.KPGVEL
6779	891.4893	1780.9640	1780.9571	3.87	1	(26)	0.024	1	U	L.KPGVEL

---

163. 2::sp|P0A912|PAL_ECOLI **Mass:** 18869 **Score:** 28 **Matches:** 1(1) **Sequences:** 1(1
Peptidoglycan-associated lipoprotein OS=Escherichia coli (strain K12) OX=83333 GN=pa
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6323	832.9497	1663.8847	1663.8781	4.00	1	28	0.023	1	U	Y.LQGKGV

---

164. 2::sp|P33352|YEHP_ECOLI **Mass:** 42378 **Score:** 27 **Matches:** 1(1) **Sequences:** 1
Uncharacterized protein YehP OS=Escherichia coli (strain K12) OX=83333 GN=yehP 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
3621	605.8611	1209.7077	1209.7332	-21.08	0	27	0.008	1	U	L.IEQPA

---

165. 2::sp|P33349|YEHM_ECOLI **Mass:** 84193 **Score:** 26 **Matches:** 2(1) **Sequences:** 1
Uncharacterized protein YehM OS=Escherichia coli (strain K12) OX=83333 GN=yehM 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
3987	629.8240	1257.6334	1257.6353	-1.54	2	26	0.043	1	U	W.QWGLQK
3988	629.8264	1257.6383	1257.6353	2.35	2	(21)	0.13	1	U	W.QWGLQK

---

166. 2::sp|P38134|ETK_ECOLI **Mass:** 81191 **Score:** 26 **Matches:** 1(1) **Sequences:** 1(1
Tyrosine-protein kinase etk OS=Escherichia coli (strain K12) OX=83333 GN=etk 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
4427	658.3643	1314.7141	1314.7442	-22.87	2	26	0.039	1	U	Y.RALLE

---

167. 2::sp|P76322|YEDM_ECOLI **Mass:** 13445 **Score:** 25 **Matches:** 1(1) **Sequences:** 1
Uncharacterized protein YedM OS=Escherichia coli (strain K12) OX=83333 GN=yedM 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
1890	507.3089	1012.6032	1012.5917	11.4	1	25	0.016	1	U	L.SLKTQP

168. 2::sp|P31548|THIQ_ECOLI **Mass:** 25097 **Score:** 25 **Matches:** 1(1) **Sequences:** 1(
Thiamine import ATP-binding protein ThiQ OS=Escherichia coli (strain K12) OX=83333 G
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1645	493.7851	985.5557	985.5444	11.5	1	25	0.027	1	U	L.TVAQNIGL

169. 2::sp|P0A6D3|AROA_ECOLI **Mass:** 46409 **Score:** 25 **Matches:** 2(2) **Sequences:** 1(
3-phosphoshikimate 1-carboxyvinyltransferase OS=Escherichia coli (strain K12) OX=833
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2458	544.7534	1087.4923	1087.4934	-1.04	0	25	0.029	1	U	F.GVEIEN
2459	544.7549	1087.4953	1087.4934	1.75	0	(24)	0.039	1	U	F.GVEIEN

170. 2::sp|P0DP63|YBEH_ECOLI **Mass:** 8021 **Score:** 25 **Matches:** 1(1) **Sequences:** 1(
Putative protein YbeH OS=Escherichia coli (strain K12) OX=83333 GN=ybeH PE=5 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
7272	486.4748	1941.8699	1941.9102	-20.73	2	28	0.027	1	U	L.LARDD

171. 2::sp|P76042|YCJN_ECOLI **Mass:** 46893 **Score:** 25 **Matches:** 1(1) **Sequences:** 1(
Putative ABC transporter periplasmic-binding protein YcjN OS=Escherichia coli (strai
Check 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	393.7452	785.4758	785.4647	14.2	1	25	0.019	1	U	L.LDVAQKL.

172. 2::sp|P0A877|TRPA_ECOLI **Mass:** 28877 **Score:** 25 **Matches:** 2(2) **Sequences:** 1(
Tryptophan synthase alpha chain OS=Escherichia coli (strain K12) OX=83333 GN=trpA 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
2583	551.2664	1100.5182	1100.5350	-15.26	0	25	0.04	1	U	L.ADGPT
2584	551.2665	1100.5185	1100.5350	-14.93	0	(25)	0.043	1	U	L.ADGPT

173. 2::sp|P39382|YJIK_ECOLI **Mass:** 32107 **Score:** 25 **Matches:** 2(1) **Sequences:** 1(
Uncharacterized protein YjiK OS=Escherichia coli (strain K12) OX=83333 GN=yjiK 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
2651	555.2946	1108.5747	1108.5652	8.57	1	(22)	0.1	1	U	F.VKDLET
2652	555.2950	1108.5755	1108.5652	9.33	1	25	0.049	1	U	F.VKDLET

---

174. 1::sp|cRAP054|P04264|K2C1_HUMAN **Mass:** 66170 **Score:** 25 **Matches:** 1(1) **Seque**
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
5557	757.8012	1513.5877	1513.5819	3.89	1	25	0.0092	1	U	Y.GSGGGS

---

175. 2::sp|Q46839|GLCA_ECOLI **Mass:** 58996 **Score:** 25 **Matches:** 1(1) **Sequences:** 1
Glycolate permease GlcA OS=Escherichia coli (strain K12) OX=83333 GN=glcA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3644	607.8190	1213.6234	1213.6455	-18.23	1	25	0.048	1	U	F.QIPHL

---

176. 2::sp|P0A6R0|FABH_ECOLI **Mass:** 33779 **Score:** 25 **Matches:** 1(1) **Sequences:** 1
3-oxoacyl-[acyl-carrier-protein] synthase 3 OS=Escherichia coli (strain K12) OX=8333
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
17	380.2335	758.4525	758.4538	-1.65	0	25	0.032	1	U	F.KVAVTEL.

---

177. 2::sp|P77223|RSXB_ECOLI **Mass:** 21328 **Score:** 25 **Matches:** 1(0) **Sequences:** 1
Ion-translocating oxidoreductase complex subunit B 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
5322	736.4036	1470.7926	1470.8268	-23.29	2	25	0.056	1	U	-.MNAIW

---

178. 2::sp|P08142|ILVB_ECOLI **Mass:** 60915 **Score:** 25 **Matches:** 1(0) **Sequences:** 1
Acetolactate synthase isozyme 1 large subunit OS=Escherichia coli (strain K12) OX=83
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6318	555.6161	1663.8264	1663.8174	5.42	2	25	0.088	1	U	L.GMLGMH

---

179. 2::sp|P0A9S5|GLDA_ECOLI **Mass:** 39087 **Score:** 24 **Matches:** 1(0) **Sequences:** 1
Glycerol dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=gldA 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
4716	680.3686	1358.7226	1358.6976	18.4	0	24	0.07	1	U	L.RGIAET

180. 2::sp|P42630|TDCG_ECOLI **Mass:** 48947 **Score:** 24 **Matches:** 1(0) **Sequences:** 1
L-serine dehydratase TdcG OS=Escherichia coli (strain K12) OX=83333 GN=tdcG 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
2592	551.7961	1101.5777	1101.6030	-22.91	2	24	0.068	1	U	F.IDRLE

---

181. 2::sp|P0AEN4|FTSL_ECOLI **Mass:** 13732 **Score:** 24 **Matches:** 1(1) **Sequences:** 1
Cell division protein FtsL OS=Escherichia coli (strain K12) OX=83333 GN=ftsL 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
284	401.2216	800.4286	800.4279	0.77	1	24	0.044	1	U	L.ILEENAL.

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 : 7977