Cambridge Centre for Proteomics
Mascot Search Results

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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_band5.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 11:11:37 GMT

Protein hits    : 2::sp|P02931|OMPF_ECOLI          Outer membrane protein F OS=Escherichia
                  2::sp|P02930|TOLC_ECOLI          Outer membrane protein TolC OS=Escherich
                  2::sp|P0ABB4|ATPB_ECOLI          ATP synthase subunit beta OS=Escherichia
                  2::sp|P0A9P0|DLDH_ECOLI          Dihydrolipoyl dehydrogenase OS=Escherich
                  2::sp|P0CE47|EFTU1_ECOLI         Elongation factor Tu 1 OS=Escherichia co
                  2::sp|P0AE06|ACRA_ECOLI          Multidrug efflux pump subunit AcrA OS=Es
                  2::sp|P00350|6PGD_ECOLI          6-phosphogluconate dehydrogenase, decarb
                  2::sp|P0A850|TIG_ECOLI           Trigger factor OS=Escherichia coli (stra
                  2::sp|P0A6P9|ENO_ECOLI           Enolase OS=Escherichia coli (strain K12)
                  2::sp|P0AFG6|ODO2_ECOLI          Dihydrolipoyllysine-residue succinyltran
                  2::sp|P0A799|PGK_ECOLI           Phosphoglycerate kinase OS=Escherichia c
                  2::sp|P0A9B2|G3P1_ECOLI          Glyceraldehyde-3-phosphate dehydrogenase
                  1::sp|cRAP022|P00766|CTRA_BOVIN  Chymotrypsinogen A OS=Bos taurus PE=1 SV
                  2::sp|P0A910|OMPA_ECOLI          Outer membrane protein A OS=Escherichia
                  2::sp|P0AEX9|MALE_ECOLI          Maltose-binding periplasmic protein OS=E
                  2::sp|P0A836|SUCC_ECOLI          Succinate--CoA ligase [ADP-forming] subu
                  2::sp|P0A8L1|SYS_ECOLI           Serine--tRNA ligase OS=Escherichia coli
                  2::sp|P0A7D4|PURA_ECOLI          Adenylosuccinate synthetase OS=Escherich
                  2::sp|P08200|IDH_ECOLI           Isocitrate dehydrogenase [NADP] OS=Esche
                  2::sp|P0A8M0|SYN_ECOLI           Asparagine--tRNA ligase OS=Escherichia c
                  2::sp|P0A7Z4|RPOA_ECOLI          DNA-directed RNA polymerase subunit alph
                  2::sp|P0A6E4|ASSY_ECOLI          Argininosuccinate synthase OS=Escherichi
                  2::sp|P0A6P1|EFTS_ECOLI          Elongation factor Ts OS=Escherichia coli
                  2::sp|P27306|STHA_ECOLI          Soluble pyridine nucleotide transhydroge
                  2::sp|P0C8J8|GATZ_ECOLI          D-tagatose-1,6-bisphosphate aldolase sub
                  2::sp|P0A6H5|HSLU_ECOLI          ATP-dependent protease ATPase subunit Hs
                  2::sp|P0AAI5|FABF_ECOLI          3-oxoacyl-[acyl-carrier-protein] synthas
                  2::sp|P0C0V0|DEGP_ECOLI          Periplasmic serine endoprotease DegP OS=
```

2::sp|P21165|PEPQ_ECOLI	Xaa-Pro dipeptidase OS=Escherichia coli
2::sp|P0AB71|ALF_ECOLI	Fructose-bisphosphate aldolase class 2 O
2::sp|P0ABH7|CISY_ECOLI	Citrate synthase OS=Escherichia coli (st
2::sp|P0AG30|RHO_ECOLI	Transcription termination factor Rho OS=
2::sp|P31224|ACRB_ECOLI	Multidrug efflux pump subunit AcrB OS=Es
2::sp|P0A825|GLYA_ECOLI	Serine hydroxymethyltransferase OS=Esche
2::sp|P0A817|METK_ECOLI	S-adenosylmethionine synthase OS=Escheri
2::sp|P0A6F3|GLPK_ECOLI	Glycerol kinase OS=Escherichia coli (str
2::sp|P0A6M8|EFG_ECOLI	Elongation factor G OS=Escherichia coli
2::sp|P0A6A3|ACKA_ECOLI	Acetate kinase OS=Escherichia coli (stra
2::sp|P06715|GSHR_ECOLI	Glutathione reductase OS=Escherichia col
2::sp|P02925|RBSB_ECOLI	Ribose import binding protein RbsB OS=Es
2::sp|P04805|SYE_ECOLI	Glutamate--tRNA ligase OS=Escherichia co
2::sp|P0AGD7|SRP54_ECOLI	Signal recognition particle protein OS=E
2::sp|P31979|NUOF_ECOLI	NADH-quinone oxidoreductase subunit F OS
2::sp|P0A870|TALB_ECOLI	Transaldolase B OS=Escherichia coli (str
2::sp|P0A6H1|CLPX_ECOLI	ATP-dependent Clp protease ATP-binding s
2::sp|P0A953|FABB_ECOLI	3-oxoacyl-[acyl-carrier-protein] synthas
2::sp|P11447|ARLY_ECOLI	Argininosuccinate lyase OS=Escherichia c
2::sp|P0AB89|PUR8_ECOLI	Adenylosuccinate lyase OS=Escherichia co
2::sp|P61889|MDH_ECOLI	Malate dehydrogenase OS=Escherichia coli
2::sp|P0ABC7|HFLK_ECOLI	Modulator of FtsH protease HflK OS=Esche
2::sp|P60906|SYH_ECOLI	Histidine--tRNA ligase OS=Escherichia co
2::sp|P0A855|TOLB_ECOLI	Tol-Pal system protein TolB OS=Escherich
2::sp|P0AEK4|FABI_ECOLI	Enoyl-[acyl-carrier-protein] reductase [
2::sp|P0ABB0|ATPA_ECOLI	ATP synthase subunit alpha OS=Escherichi
2::sp|P08390|USG_ECOLI	USG-1 protein OS=Escherichia coli (strai
2::sp|P07913|TDH_ECOLI	L-threonine 3-dehydrogenase OS=Escherich
2::sp|P02943|LAMB_ECOLI	Maltoporin OS=Escherichia coli (strain K
2::sp|P24182|ACCC_ECOLI	Biotin carboxylase OS=Escherichia coli (
2::sp|P00509|AAT_ECOLI	Aspartate aminotransferase OS=Escherichi
2::sp|P27248|GCST_ECOLI	Aminomethyltransferase OS=Escherichia co
2::sp|P00960|SYGA_ECOLI	Glycine--tRNA ligase alpha subunit OS=Es
2::sp|P00926|SDHD_ECOLI	D-serine dehydratase OS=Escherichia coli
2::sp|P0AGE9|SUCD_ECOLI	Succinate--CoA ligase [ADP-forming] subu
2::sp|P33232|LLDD_ECOLI	L-lactate dehydrogenase OS=Escherichia c
2::sp|P0AE08|AHPC_ECOLI	Alkyl hydroperoxide reductase C OS=Esche
2::sp|P27434|RODZ_ECOLI	Cytoskeleton protein RodZ OS=Escherichia
2::sp|P77774|BAMB_ECOLI	Outer membrane protein assembly factor B
2::sp|P37095|PEPB_ECOLI	Peptidase B OS=Escherichia coli (strain
2::sp|P52643|LDHD_ECOLI	D-lactate dehydrogenase OS=Escherichia c
2::sp|P15034|AMPP_ECOLI	Xaa-Pro aminopeptidase OS=Escherichia co
2::sp|P0AGJ9|SYY_ECOLI	Tyrosine--tRNA ligase OS=Escherichia col
2::sp|P24180|ACRE_ECOLI	Multidrug export protein AcrE OS=Escheri
2::sp|P00954|SYW_ECOLI	Tryptophan--tRNA ligase OS=Escherichia c
2::sp|P23721|SERC_ECOLI	Phosphoserine aminotransferase OS=Escher
2::sp|P0A7V3|RS3_ECOLI	30S ribosomal protein S3 OS=Escherichia
2::sp|P0A7A9|IPYR_ECOLI	Inorganic pyrophosphatase OS=Escherichia

2::sp|P0A8J8|RHLB_ECOLI	ATP-dependent RNA helicase RhlB OS=Esche
2::sp|P0A6F5|CH60_ECOLI	60 kDa chaperonin OS=Escherichia coli (s
2::sp|P0ABK5|CYSK_ECOLI	Cysteine synthase A OS=Escherichia coli
2::sp|P0AG67|RS1_ECOLI	30S ribosomal protein S1 OS=Escherichia
2::sp|P0A9K9|SLYD_ECOLI	FKBP-type peptidyl-prolyl cis-trans isom
2::sp|P67910|HLDD_ECOLI	ADP-L-glycero-D-manno-heptose-6-epimeras
2::sp|P0ABU2|YCHF_ECOLI	Ribosome-binding ATPase YchF OS=Escheric
2::sp|P03841|MALM_ECOLI	Maltose operon periplasmic protein OS=Es
2::sp|P0AB77|KBL_ECOLI	2-amino-3-ketobutyrate coenzyme A ligase
2::sp|P0A717|KPRS_ECOLI	Ribose-phosphate pyrophosphokinase OS=Es
2::sp|P21507|SRMB_ECOLI	ATP-dependent RNA helicase SrmB OS=Esche
2::sp|P60422|RL2_ECOLI	50S ribosomal protein L2 OS=Escherichia
2::sp|P0AGJ5|YFIF_ECOLI	Uncharacterized tRNA/rRNA methyltransfer
2::sp|P39099|DEGQ_ECOLI	Periplasmic pH-dependent serine endoprot
2::sp|P03023|LACI_ECOLI	Lactose operon repressor OS=Escherichia
2::sp|P0A9S3|GATD_ECOLI	Galactitol 1-phosphate 5-dehydrogenase O
2::sp|P0A7V0|RS2_ECOLI	30S ribosomal protein S2 OS=Escherichia
2::sp|P0A9K3|PHOL_ECOLI	PhoH-like protein OS=Escherichia coli (s
2::sp|P0A9A6|FTSZ_ECOLI	Cell division protein FtsZ OS=Escherichi
2::sp|P0AGG8|TLDD_ECOLI	Metalloprotease TldD OS=Escherichia coli
2::sp|P36672|PTTBC_ECOLI	PTS system trehalose-specific EIIBC comp
2::sp|P30845|EPTA_ECOLI	Phosphoethanolamine transferase EptA OS=
2::sp|P25553|ALDA_ECOLI	Lactaldehyde dehydrogenase OS=Escherichi
2::sp|P37773|MPL_ECOLI	UDP-N-acetylmuramate--L-alanyl-gamma-D-g
2::sp|P21599|KPYK2_ECOLI	Pyruvate kinase II OS=Escherichia coli (
2::sp|P0A858|TPIS_ECOLI	Triosephosphate isomerase OS=Escherichia
2::sp|P07012|RF2_ECOLI	Peptide chain release factor RF2 OS=Esch
2::sp|P21888|SYC_ECOLI	Cysteine--tRNA ligase OS=Escherichia col
2::sp|P0AC38|ASPA_ECOLI	Aspartate ammonia-lyase OS=Escherichia c
2::sp|P0A9J6|RBSK_ECOLI	Ribokinase OS=Escherichia coli (strain K
2::sp|P62707|GPMA_ECOLI	2,3-bisphosphoglycerate-dependent phosph
2::sp|P00448|SODM_ECOLI	Superoxide dismutase [Mn] OS=Escherichia
2::sp|P0A9D8|DAPD_ECOLI	2,3,4,5-tetrahydropyridine-2,6-dicarboxy
2::sp|P0A6Y8|DNAK_ECOLI	Chaperone protein DnaK OS=Escherichia co
2::sp|P31120|GLMM_ECOLI	Phosphoglucosamine mutase OS=Escherichia
2::sp|P0A7L0|RL1_ECOLI	50S ribosomal protein L1 OS=Escherichia
2::sp|P0AFK9|POTD_ECOLI	Spermidine/putrescine-binding periplasmi
2::sp|P0ABJ1|CYOA_ECOLI	Cytochrome bo(3) ubiquinol oxidase subun
2::sp|P16095|SDHL_ECOLI	L-serine dehydratase 1 OS=Escherichia co
2::sp|P0ADR8|PPNN_ECOLI	Pyrimidine/purine nucleotide 5'-monophos
2::sp|P0A7S9|RS13_ECOLI	30S ribosomal protein S13 OS=Escherichia
2::sp|P39336|YJGL_ECOLI	Uncharacterized protein YjgL OS=Escheric
2::sp|P08660|AK3_ECOLI	Lysine-sensitive aspartokinase 3 OS=Esch
2::sp|P05459|PDXB_ECOLI	Erythronate-4-phosphate dehydrogenase OS
2::sp|P37349|DHAM_ECOLI	Protein-lysine deacetylase OS=Escherichi
2::sp|P0A6B7|ISCS_ECOLI	Cysteine desulfurase IscS OS=Escherichia
2::sp|P60723|RL4_ECOLI	50S ribosomal protein L4 OS=Escherichia
2::sp|P24181|ACRF_ECOLI	Multidrug export protein AcrF OS=Escheri

2::sp|P0A6N4|EFP_ECOLI	Elongation factor P OS=Escherichia coli
2::sp|P0C018|RL18_ECOLI	50S ribosomal protein L18 OS=Escherichia
2::sp|P77300|YAGI_ECOLI	Uncharacterized HTH-type transcriptional
2::sp|P07004|PROA_ECOLI	Gamma-glutamyl phosphate reductase OS=Es
2::sp|P0A7V8|RS4_ECOLI	30S ribosomal protein S4 OS=Escherichia
2::sp|P76373|UDG_ECOLI	UDP-glucose 6-dehydrogenase OS=Escherich
2::sp|P0A6Y5|HSLO_ECOLI	33 kDa chaperonin OS=Escherichia coli (s
2::sp|P0ACB2|HEM2_ECOLI	Delta-aminolevulinic acid dehydratase OS
2::sp|P05042|FUMC_ECOLI	Fumarate hydratase class II OS=Escherich
2::sp|P39371|NANM_ECOLI	N-acetylneuraminate epimerase OS=Escheri
2::sp|P0A7G6|RECA_ECOLI	Protein RecA OS=Escherichia coli (strain
2::sp|P39406|RSMC_ECOLI	Ribosomal RNA small subunit methyltransf
2::sp|P37759|RMLB1_ECOLI	dTDP-glucose 4,6-dehydratase 1 OS=Escher
2::sp|P0A6J5|DADA_ECOLI	D-amino acid dehydrogenase OS=Escherichi
2::sp|P0AG48|RL21_ECOLI	50S ribosomal protein L21 OS=Escherichia
2::sp|P0AFK0|PMBA_ECOLI	Metalloprotease PmbA OS=Escherichia coli
2::sp|P0ADA3|NLPD_ECOLI	Murein hydrolase activator NlpD OS=Esche
2::sp|P39173|YEAD_ECOLI	Putative glucose-6-phosphate 1-epimerase
2::sp|P0A6F1|CARA_ECOLI	Carbamoyl-phosphate synthase small chain
2::sp|P0AEZ3|MIND_ECOLI	Septum site-determining protein MinD OS=
2::sp|P27837|YIFK_ECOLI	Probable transport protein YifK OS=Esche
2::sp|P0A908|MIPA_ECOLI	MltA-interacting protein OS=Escherichia
2::sp|P0AC41|SDHA_ECOLI	Succinate dehydrogenase flavoprotein sub
2::sp|P08312|SYFA_ECOLI	Phenylalanine--tRNA ligase alpha subunit
2::sp|P25522|MNME_ECOLI	tRNA modification GTPase MnmE OS=Escheri
2::sp|P75876|RLMI_ECOLI	Ribosomal RNA large subunit methyltransf
2::sp|P23908|ARGE_ECOLI	Acetylornithine deacetylase OS=Escherich
2::sp|P39382|YJIK_ECOLI	Uncharacterized protein YjiK OS=Escheric
1::sp|cRAP087|P02769|ALBU_BOVIN	Serum albumin OS=Bos taurus GN=ALB PE=1
2::sp|P0A903|BAMC_ECOLI	Outer membrane protein assembly factor B
2::sp|P36683|ACNB_ECOLI	Aconitate hydratase B OS=Escherichia col
2::sp|P0A7W7|RS8_ECOLI	30S ribosomal protein S8 OS=Escherichia
2::sp|P25744|MDTG_ECOLI	Multidrug resistance protein MdtG OS=Esc
2::sp|P62623|ISPH_ECOLI	4-hydroxy-3-methylbut-2-enyl diphosphate
2::sp|P37653|BCSA_ECOLI	Cellulose synthase catalytic subunit [UD
2::sp|P0ADK0|YIAF_ECOLI	Uncharacterized protein YiaF OS=Escheric
2::sp|P09832|GLTD_ECOLI	Glutamate synthase [NADPH] small chain O
1::sp|cRAP008|P00722|BGAL_ECOLI	Beta-galactosidase OS=Escherichia coli (
2::sp|P33353|YEHQ_ECOLI	Putative uncharacterized protein YehQ OS
2::sp|P69924|RIR2_ECOLI	Ribonucleoside-diphosphate reductase 1 s
2::sp|P0ADN0|VIAA_ECOLI	Protein ViaA OS=Escherichia coli (strain
2::sp|P76083|PAAH_ECOLI	3-hydroxyadipyl-CoA dehydrogenase OS=Esc
2::sp|P0ABH0|FTSA_ECOLI	Cell division protein FtsA OS=Escherichi
2::sp|P28904|TREC_ECOLI	Trehalose-6-phosphate hydrolase OS=Esche
2::sp|P0AFG3|ODO1_ECOLI	2-oxoglutarate dehydrogenase E1 componen
2::sp|P76269|YEBQ_ECOLI	Uncharacterized transporter YebQ OS=Esch
2::sp|P76658|HLDE_ECOLI	Bifunctional protein HldE OS=Escherichia
2::sp|P0A862|TPX_ECOLI	Thiol peroxidase OS=Escherichia coli (st

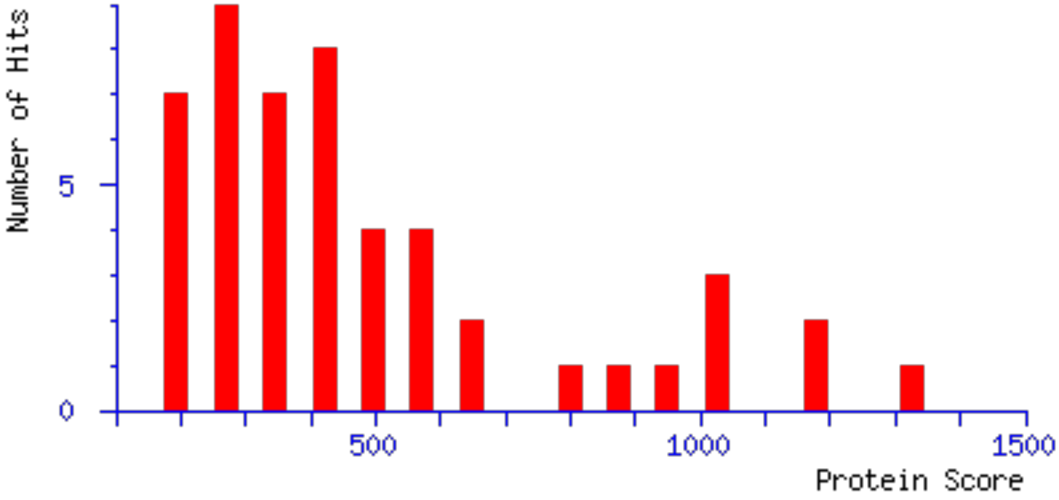
2::sp|P0AEW6|INGK_ECOLI	Inosine-guanosine kinase OS=Escherichia
2::sp|P0A6L4|NANA_ECOLI	N-acetylneuraminate lyase OS=Escherichia
2::sp|P0AAX8|YBIS_ECOLI	Probable L,D-transpeptidase YbiS OS=Esch
2::sp|P0AF08|APBC_ECOLI	Iron-sulfur cluster carrier protein OS=E
2::sp|P76464|YFAS_ECOLI	Putative UPF0192 protein YfaS OS=Escheri
2::sp|P0ACC7|GLMU_ECOLI	Bifunctional protein GlmU OS=Escherichia
2::sp|P0ABD5|ACCA_ECOLI	Acetyl-coenzyme A carboxylase carboxyl t
2::sp|P0A6K6|DEOB_ECOLI	Phosphopentomutase OS=Escherichia coli (
2::sp|P60438|RL3_ECOLI	50S ribosomal protein L3 OS=Escherichia
2::sp|P0A9W3|ETTA_ECOLI	Energy-dependent translational throttle
2::sp|P37344|PSPF_ECOLI	Psp operon transcriptional activator OS=
2::sp|P62399|RL5_ECOLI	50S ribosomal protein L5 OS=Escherichia
2::sp|P11880|MURF_ECOLI	UDP-N-acetylmuramoyl-tripeptide--D-alany
2::sp|P75882|GFCD_ECOLI	Uncharacterized lipoprotein GfcD OS=Esch
2::sp|P23482|HYFB_ECOLI	Hydrogenase-4 component B OS=Escherichia
2::sp|P77455|PAAZ_ECOLI	Bifunctional protein PaaZ OS=Escherichia
2::sp|P0AEG4|DSBA_ECOLI	Thiol:disulfide interchange protein DsbA
2::sp|P0A7B5|PROB_ECOLI	Glutamate 5-kinase OS=Escherichia coli (
2::sp|P0A7J3|RL10_ECOLI	50S ribosomal protein L10 OS=Escherichia
2::sp|P0AEP3|GALU_ECOLI	UTP--glucose-1-phosphate uridylyltransfe
2::sp|P46474|YHDP_ECOLI	Uncharacterized protein YhdP OS=Escheric
2::sp|P0ABP8|DEOD_ECOLI	Purine nucleoside phosphorylase DeoD-typ
2::sp|P06616|ERA_ECOLI	GTPase Era OS=Escherichia coli (strain K
2::sp|P76372|WZZB_ECOLI	Chain length determinant protein OS=Esch
2::sp|P77690|ARNB_ECOLI	UDP-4-amino-4-deoxy-L-arabinose--oxoglut
2::sp|P62620|ISPG_ECOLI	4-hydroxy-3-methylbut-2-en-1-yl diphosph
2::sp|P06720|AGAL_ECOLI	Alpha-galactosidase OS=Escherichia coli
2::sp|P0A9L5|PPIC_ECOLI	Peptidyl-prolyl cis-trans isomerase C OS
2::sp|P75697|YAIX_ECOLI	Putative uncharacterized acetyltransfera
2::sp|P0ABD8|BCCP_ECOLI	Biotin carboxyl carrier protein of acety
2::sp|P63284-2|CLPB_ECOLI	Isoform ClpB-3 of Chaperone protein ClpB
2::sp|P31446|YIDI_ECOLI	Inner membrane protein YidI OS=Escherich
2::sp|P69797|PTNAB_ECOLI	PTS system mannose-specific EIIAB compon
2::sp|P60716|LIPA_ECOLI	Lipoyl synthase OS=Escherichia coli (str
2::sp|P27243|RFAL_ECOLI	O-antigen ligase OS=Escherichia coli (st
2::sp|P0A7W1|RS5_ECOLI	30S ribosomal protein S5 OS=Escherichia
2::sp|P09151|LEU1_ECOLI	2-isopropylmalate synthase OS=Escherichi
2::sp|P31068|FLIH_ECOLI	Flagellar assembly protein FliH OS=Esche
2::sp|P46855|YHHZ_ECOLI	Uncharacterized protein YhhZ OS=Escheric
2::sp|Q46851|GPR_ECOLI	L-glyceraldehyde 3-phosphate reductase O
2::sp|O52982|YFJS_ECOLI	Lipoprotein YfjS OS=Escherichia coli (st
2::sp|P69441|KAD_ECOLI	Adenylate kinase OS=Escherichia coli (st
2::sp|P24183|FDNG_ECOLI	Formate dehydrogenase, nitrate-inducible
2::sp|P04128|FIMA1_ECOLI	Type-1 fimbrial protein, A chain OS=Esch
2::sp|P0A6V1|GLGC_ECOLI	Glucose-1-phosphate adenylyltransferase
2::sp|P15639|PUR9_ECOLI	Bifunctional purine biosynthesis protein
2::sp|P0AFB8|NTRC_ECOLI	DNA-binding transcriptional regulator Nt
2::sp|P25552|GPPA_ECOLI	Guanosine-5'-triphosphate,3'-diphosphate

2::sp|P09053|AVTA_ECOLI	Valine--pyruvate aminotransferase OS=Esc
2::sp|P0AAB6|GALF_ECOLI	UTP--glucose-1-phosphate uridylyltransfe
2::sp|P0A6R0|FABH_ECOLI	3-oxoacyl-[acyl-carrier-protein] synthas
2::sp|P0AE48|YTFP_ECOLI	Gamma-glutamylcyclotransferase family pr
2::sp|P77454|GLSA1_ECOLI	Glutaminase 1 OS=Escherichia coli (strai
2::sp|P0AC33|FUMA_ECOLI	Fumarate hydratase class I, aerobic OS=E
2::sp|P77171|YDCI_ECOLI	Uncharacterized HTH-type transcriptional
2::sp|P0A7K2|RL7_ECOLI	50S ribosomal protein L7/L12 OS=Escheric
2::sp|P0ADE8|YGFZ_ECOLI	tRNA-modifying protein YgfZ OS=Escherich
2::sp|P0AG55|RL6_ECOLI	50S ribosomal protein L6 OS=Escherichia
2::sp|P77173|ZIPA_ECOLI	Cell division protein ZipA OS=Escherichi
2::sp|P52612|FLII_ECOLI	Flagellum-specific ATP synthase OS=Esche
2::sp|P37640|YHJB_ECOLI	Putative HTH-type transcriptional regula
2::sp|P23841|XAPR_ECOLI	HTH-type transcriptional regulator XapR
2::sp|P77260|YDFI_ECOLI	Uncharacterized oxidoreductase YdfI OS=E
2::sp|P37663|YHJY_ECOLI	Uncharacterized protein YhjY OS=Escheric
2::sp|P30176|RIBX_ECOLI	N-glycosidase YbiA OS=Escherichia coli (
2::sp|P52143|YPJA_ECOLI	Uncharacterized outer membrane protein Y
2::sp|P69801|PTNC_ECOLI	PTS system mannose-specific EIIC compone
2::sp|P15723|DGTP_ECOLI	Deoxyguanosinetriphosphate triphosphohyd
2::sp|P76224|YNJC_ECOLI	Inner membrane ABC transporter permease
2::sp|P76403|YEGQ_ECOLI	Uncharacterized protease YegQ OS=Escheri
2::sp|P06983|HEM3_ECOLI	Porphobilinogen deaminase OS=Escherichia
2::sp|P0ABC3|HFLC_ECOLI	Modulator of FtsH protease HflC OS=Esche
2::sp|P64481|YDJM_ECOLI	Inner membrane protein YdjM OS=Escherich
2::sp|P0ABF6|CDD_ECOLI	Cytidine deaminase OS=Escherichia coli (
2::sp|P0AA25|THIO_ECOLI	Thioredoxin 1 OS=Escherichia coli (strai
2::sp|P37649|PDEK_ECOLI	Probable cyclic di-GMP phosphodiesterase
2::sp|P75682|YAGE_ECOLI	Putative 2-dehydro-3-deoxy-D-gluconate a
2::sp|P63020|NFUA_ECOLI	Fe/S biogenesis protein NfuA OS=Escheric
2::sp|P0A8H3|ZUPT_ECOLI	Zinc transporter ZupT OS=Escherichia col
2::sp|Q46836|PPPA_ECOLI	Leader peptidase PppA OS=Escherichia col
2::sp|P00861|DCDA_ECOLI	Diaminopimelate decarboxylase OS=Escheri
2::sp|P76425|RCNA_ECOLI	Nickel/cobalt efflux system RcnA OS=Esch
2::sp|P76204|YDIV_ECOLI	Putative anti-FlhC(2)FlhD(4) factor YdiV
2::sp|P36999|RLMA_ECOLI	23S rRNA (guanine(745)-N(1))-methyltrans
2::sp|P0A9C5|GLN1B_ECOLI	Glutamine synthetase OS=Escherichia coli
2::sp|P08839|PT1_ECOLI	Phosphoenolpyruvate-protein phosphotrans
2::sp|P0AB24|EFEO_ECOLI	Iron uptake system component EfeO OS=Esc
2::sp|P42620|YQJG_ECOLI	Glutathionyl-hydroquinone reductase YqjG
2::sp|P39321|TAMB_ECOLI	Translocation and assembly module subuni
2::sp|P66948|BEPA_ECOLI	Beta-barrel assembly-enhancing protease
2::sp|P77674|ABDH_ECOLI	Gamma-aminobutyraldehyde dehydrogenase O
2::sp|P15006|MCRC_ECOLI	Protein McrC OS=Escherichia coli (strain
2::sp|P00490|PHSM_ECOLI	Maltodextrin phosphorylase OS=Escherichi
2::sp|P33011|YEEA_ECOLI	Inner membrane protein YeeA OS=Escherich
2::sp|P17115|GUTQ_ECOLI	Arabinose 5-phosphate isomerase GutQ OS=
2::sp|P08202|ARAA_ECOLI	L-arabinose isomerase OS=Escherichia col

2::sp|P08722|PTV3B_ECOLI	PTS system beta-glucoside-specific EIIBC
2::sp|P16525|TUS_ECOLI	DNA replication terminus site-binding pr
2::sp|P75916|YCDZ_ECOLI	Inner membrane protein YcdZ OS=Escherich

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|P02931|OMPF_ECOLI **Mass:** 39309 **Score:** 1327 **Matches:** 83(72) **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	Pepti
477	409.2107	816.4069	816.4090	-2.55	0	25	0.056	1	U	Y.GAA
478	409.2108	816.4069	816.4090	-2.47	0	(22)	0.083	1	U	Y.GAA
628	417.7209	833.4273	833.4283	-1.25	2	(36)	0.0034	1		F.GLV
629	417.7210	833.4273	833.4283	-1.18	2	(40)	0.0015	1		F.GLV
630	417.7214	833.4282	833.4283	-0.17	2	(46)	0.0003	1		F.GLV
631	417.7214	833.4283	833.4283	-0.00	2	52	7.7e-05	1		F.GLV
959	438.7505	875.4865	875.4865	0.08	1	(25)	0.03	1	U	F.GLR
960	438.7506	875.4866	875.4865	0.15	1	(23)	0.043	1	U	F.GLR
963	438.7510	875.4875	875.4865	1.20	1	26	0.023	1	U	F.GLR
1027	443.7189	885.4232	885.4232	-0.05	1	(45)	0.00026	1	U	L.KYA
1028	443.7191	885.4237	885.4232	0.51	1	67	1.7e-06	1	U	L.KYA
1031	444.7430	887.4715	887.4712	0.26	0	41	0.0016	1	U	F.ANK
1032	444.7430	887.4715	887.4712	0.26	0	(34)	0.0078	1	U	F.ANK
1872	489.7717	977.5289	977.5294	-0.55	0	(26)	0.029	1	U	F.VGR
1873	489.7718	977.5290	977.5294	-0.49	0	36	0.0031	1	U	F.VGR
2109	500.7402	999.4659	999.4661	-0.22	1	38	0.0018	1		L.KYD
2132	501.2850	1000.5554	1000.5553	0.09	1	44	0.00048	1	U	F.ANK
2134	501.2856	1000.5566	1000.5553	1.31	1	(44)	0.00056	1	U	F.ANK
2141	501.7759	1001.5372	1001.5393	-2.10	1	(29)	0.023	1	U	F.ANK
2149	502.7282	1003.4417	1003.4433	-1.54	1	35	0.003	1		Y.FNK
2150	502.7288	1003.4430	1003.4433	-0.33	1	(31)	0.0079	1		Y.FNK
2312	509.2593	1016.5041	1016.5039	0.14	0	21	0.13	1	U	L.GNG
2313	509.2598	1016.5051	1016.5039	1.17	0	(21)	0.14	1	U	L.GNG
2875	540.2708	1078.5271	1078.5295	-2.22	0	(27)	0.047	1	U	L.VAG
2876	540.2735	1078.5324	1078.5295	2.77	0	42	0.0014	1	U	L.VAG
3097	551.7434	1101.4723	1101.4727	-0.38	1	(40)	0.00079	1	U	Y.FSK
3098	551.7444	1101.4742	1101.4727	1.38	1	63	3.8e-06	1	U	Y.FSK
3108	552.2336	1102.4527	1102.4567	-3.60	1	(46)	0.00014	1	U	Y.FSK
3109	552.2354	1102.4561	1102.4567	-0.50	1	(40)	0.0006	1	U	Y.FSK
3117	552.7802	1103.5459	1103.5459	0.01	0	43	0.00083	1	U	F.KGE
3118	552.7805	1103.5464	1103.5459	0.47	0	(40)	0.0018	1	U	F.KGE
3127	553.2654	1104.5163	1104.5299	-12.25	0	(23)	0.084	2	U	F.KGE
3335	563.3060	1124.5974	1124.5979	-0.43	1	(26)	0.021	1	U	F.FVG
3336	563.3063	1124.5980	1124.5979	0.10	1	28	0.016	1	U	F.FVG
3845	583.2956	1164.5766	1164.5775	-0.74	1	(36)	0.0055	1	U	Y.NKD
3847	583.2960	1164.5774	1164.5775	-0.10	1	40	0.0023	1	U	Y.NKD
4041	592.2583	1182.5020	1182.5015	0.43	2	37	0.002	1		Y.YFN
4042	592.2592	1182.5038	1182.5015	1.88	2	(33)	0.0053	1		Y.YFN
4936	636.8435	1271.6725	1271.6721	0.29	0	(63)	7.8e-06	1	U	Y.IIN
4937	636.8436	1271.6726	1271.6721	0.38	0	(53)	7.4e-05	1	U	Y.IIN
4938	636.8440	1271.6734	1271.6721	1.04	0	(58)	2.6e-05	1	U	Y.IIN
4939	636.8453	1271.6761	1271.6721	3.16	0	(53)	7.6e-05	1	U	Y.IIN
4957	637.3354	1272.6562	1272.6561	0.09	0	(47)	0.00039	1	U	Y.IIN
4960	637.3374	1272.6602	1272.6561	3.25	0	65	6.9e-06	1	U	Y.IIN
5617	676.3428	1350.6710	1350.6667	3.14	0	23	0.12	1	U	L.GVG
6052	708.8047	1415.5948	1415.5915	2.35	1	(35)	0.0029	1	U	Y.TDM
6126	713.3464	1424.6782	1424.6783	-0.10	1	(33)	0.0094	1	U	F.KGE
6127	713.3473	1424.6800	1424.6783	1.19	1	(25)	0.06	1	U	F.KGE
6128	713.3474	1424.6801	1424.6783	1.28	1	(57)	4e-05	1	U	F.KGE
6129	713.3475	1424.6805	1424.6783	1.53	1	(49)	0.00026	1	U	F.KGE
6130	713.3478	1424.6811	1424.6783	1.96	1	(54)	7.7e-05	1	U	F.KGE

6131	713.3487	1424.6828	1424.6783	3.16	1	82	1.4e-07	1	U	F.KGE
6135	713.8384	1425.6623	1425.6623	-0.01	1	(49)	0.00023	1	U	F.KGE
6136	713.8389	1425.6632	1425.6623	0.60	1	(65)	6e-06	1	U	F.KGE
6137	713.8391	1425.6637	1425.6623	0.93	1	(62)	1.2e-05	1	U	F.KGE
6138	713.8397	1425.6648	1425.6623	1.70	1	(54)	7.5e-05	1	U	F.KGE
6171	716.8009	1431.5872	1431.5864	0.57	1	66	2.2e-06	1	U	Y.TDM
6173	716.8013	1431.5881	1431.5864	1.17	1	(61)	6e-06	1	U	Y.TDM
6174	716.8025	1431.5904	1431.5864	2.80	1	(34)	0.0036	1	U	Y.TDM
6571	742.3797	1482.7448	1482.7426	1.49	1	(32)	0.01	1	U	Y.GAA
6572	742.3800	1482.7454	1482.7426	1.89	1	(24)	0.075	1	U	Y.GAA
6573	742.3810	1482.7474	1482.7426	3.21	1	(30)	0.017	1	U	Y.GAA
6574	742.3811	1482.7476	1482.7426	3.37	1	(40)	0.0014	1	U	Y.GAA
6577	742.8752	1483.7359	1483.7267	6.25	1	45	0.0005	1	U	Y.GAA
7154	795.3848	1588.7551	1588.7522	1.82	2	38	0.0033	1	U	Y.SDD
7335	815.3919	1628.7693	1628.7682	0.64	2	(65)	6.9e-06	1	U	L.GFK
7336	815.3923	1628.7700	1628.7682	1.09	2	69	2.5e-06	1	U	L.GFK
7341	815.8854	1629.7563	1629.7522	2.52	2	(36)	0.0049	1	U	L.GFK
7896	876.3421	1750.6696	1750.6740	-2.51	1	(27)	0.0045	1	U	F.SKG
7951	884.3425	1766.6704	1766.6690	0.81	1	65	6.7e-07	1	U	F.SKG
7952	884.3438	1766.6731	1766.6690	2.32	1	(55)	6.6e-06	1	U	F.SKG
8297	620.9660	1859.8762	1859.8722	2.16	0	(40)	0.002	1	U	F.QGN
8298	620.9662	1859.8767	1859.8722	2.46	0	43	0.001	1	U	F.QGN
8742	1026.0385	2050.0623	2050.0582	2.00	1	(48)	0.00031	1	U	Y.TKS
8743	1026.0404	2050.0663	2050.0582	3.91	1	59	2.3e-05	1	U	Y.TKS
8846	708.0041	2120.9904	2120.9835	3.27	1	43	0.0013	1	U	Y.NFQ
8847	708.0044	2120.9913	2120.9835	3.69	1	(31)	0.018	1	U	Y.NFQ
8905	733.3826	2197.1259	2197.1267	-0.36	2	24	0.071	1	U	Y.TKS
9164	869.1164	2604.3273	2604.3283	-0.37	1	(21)	0.14	1	U	Y.IIN
9165	1303.1710	2604.3275	2604.3283	-0.31	1	74	7.7e-07	1	U	Y.IIN
9166	869.1172	2604.3297	2604.3283	0.56	1	(21)	0.13	1	U	Y.IIN
9168	869.1180	2604.3323	2604.3283	1.54	1	(41)	0.0014	1	U	Y.IIN
9171	1303.1775	2604.3404	2604.3283	4.66	1	(46)	0.00038	1	U	Y.IIN

Proteins matching a subset of these peptides:

2::sp|P21420|NMPC_ECOLI **Mass:** 40277 **Score:** 90 **Matches:** 5(5) **Sequences:** 2

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

2::sp|P02932|PHOE_ECOLI **Mass:** 38898 **Score:** 38 **Matches:** 1(1) **Sequences:** 1

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

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2. 2::sp|P02930|TOLC_ECOLI **Mass:** 53708 **Score:** 1210 **Matches:** 72(68) **Sequences:**

Outer membrane protein TolC OS=Escherichia coli (strain K12) OX=83333 GN=tolC PE=1 S

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
813	426.2218	850.4290	850.4297	-0.77	0	(27)	0.031	1	U	L.RQITG
814	426.2219	850.4292	850.4297	-0.56	0	27	0.028	1	U	L.RQITG
1263	458.7769	915.5392	915.5389	0.28	1	41	0.00064	1	U	L.NIKSA
1264	458.7769	915.5393	915.5389	0.48	1	(34)	0.0031	1	U	L.NIKSA
1528	474.7357	947.4568	947.4560	0.85	1	29	0.025	1	U	F.SSLSQ
1696	482.7403	963.4660	963.4662	-0.20	1	43	0.0008	1	U	Y.NFVGA
1697	482.7408	963.4670	963.4662	0.88	1	(42)	0.00096	1	U	Y.NFVGA

2139	501.7585	1001.5024	1001.5029	-0.52	2	25	0.05	1	U	L.GTLNE
2568	523.7789	1045.5433	1045.5444	-1.05	2	42	0.0012	1	U	L.LPQLG
2569	523.7792	1045.5438	1045.5444	-0.59	2	(35)	0.0055	1	U	L.LPQLG
2614	526.2744	1050.5341	1050.5345	-0.38	0	(22)	0.14	1	U	Y.TQAQK
2615	526.2747	1050.5348	1050.5345	0.21	0	44	0.0009	1	U	Y.TQAQK
2617	526.2752	1050.5359	1050.5345	1.26	0	(40)	0.0018	1	U	Y.TQAQK
3264	559.3136	1116.6126	1116.6139	-1.10	0	53	6.8e-05	1	U	Y.KQAVV
3265	559.3140	1116.6135	1116.6139	-0.33	0	(46)	0.00032	1	U	Y.KQAVV
3719	578.8201	1155.6257	1155.6247	0.84	0	43	0.00056	1	U	F.EKINE
3720	578.8204	1155.6263	1155.6247	1.36	0	(39)	0.0015	1	U	F.EKINE
3764	580.3377	1158.6607	1158.6609	-0.09	0	35	0.0031	1	U	Y.SVGTR
3765	580.3390	1158.6634	1158.6609	2.22	0	(35)	0.0027	1	U	Y.SVGTR
4340	605.8436	1209.6727	1209.6717	0.82	0	(37)	0.0013	1	U	F.KTDKP
4341	605.8444	1209.6742	1209.6717	2.02	0	37	0.0012	1	U	F.KTDKP
4991	639.2933	1276.5720	1276.5718	0.18	0	38	0.0025	1	U	Y.DDSNM
4992	639.2941	1276.5737	1276.5718	1.52	0	(34)	0.0066	1	U	Y.DDSNM
5033	642.3217	1282.6288	1282.6266	1.71	0	(26)	0.043	1	U	Y.SGSKT
5035	642.3220	1282.6295	1282.6266	2.27	0	26	0.041	1	U	Y.SGSKT
5108	647.2921	1292.5697	1292.5667	2.31	0	(34)	0.0054	1	U	Y.DDSNM
5109	647.2926	1292.5706	1292.5667	3.07	0	(35)	0.004	1	U	Y.DDSNM
5110	647.2932	1292.5719	1292.5667	4.01	0	(22)	0.089	1	U	Y.DDSNM
5182	651.3228	1300.6311	1300.6299	0.90	1	(38)	0.0027	1	U	L.SYTQA
5183	651.3245	1300.6345	1300.6299	3.53	1	43	0.00094	1	U	L.SYTQA
5408	661.8328	1321.6511	1321.6514	-0.22	0	53	0.00013	1	U	L.QEKAA
5409	661.8333	1321.6521	1321.6514	0.52	0	(45)	0.00087	1	U	L.QEKAA
5429	662.3853	1322.7559	1322.7558	0.12	1	42	0.00025	1	U	F.KTDKP
5431	441.9264	1322.7573	1322.7558	1.11	1	(24)	0.013	1	U	F.KTDKP
5432	662.3859	1322.7573	1322.7558	1.15	1	(37)	0.00057	1	U	F.KTDKP
5482	665.8037	1329.5929	1329.5936	-0.56	1	40	0.0012	1	U	L.DLTAS
5483	665.8046	1329.5947	1329.5936	0.82	1	(33)	0.0063	1	U	L.DLTAS
5845	690.8407	1379.6668	1379.6681	-0.88	0	(63)	1.2e-05	1	U	F.NNINA
5846	690.8409	1379.6672	1379.6681	-0.62	0	63	1.1e-05	1	U	F.NNINA
5847	691.3337	1380.6529	1380.6521	0.62	0	(31)	0.014	1	U	F.NNINA
5848	691.3339	1380.6533	1380.6521	0.88	0	(38)	0.0033	1	U	F.NNINA
6305	724.8788	1447.7430	1447.7419	0.75	0	(36)	0.0054	1	U	L.VAITD
6306	724.8788	1447.7430	1447.7419	0.75	0	(21)	0.19	1	U	L.VAITD
6317	725.3701	1448.7256	1448.7259	-0.25	0	(52)	0.00015	1	U	L.VAITD
6318	725.3711	1448.7277	1448.7259	1.25	0	54	0.0001	1	U	L.VAITD
6319	725.3726	1448.7307	1448.7259	3.28	0	(52)	0.00016	1	U	L.VAITD
6620	745.8635	1489.7125	1489.7121	0.30	0	82	1.4e-07	1	U	Y.RDANG
6621	745.8645	1489.7144	1489.7121	1.60	0	(74)	9.6e-07	1	U	Y.RDANG
6624	746.3563	1490.6980	1490.6961	1.27	0	(74)	9e-07	1	U	Y.RDANG
6625	746.3572	1490.6998	1490.6961	2.50	0	(69)	2.9e-06	1	U	Y.RDANG
6876	768.9000	1535.7854	1535.7831	1.46	1	(37)	0.0047	1	U	L.TLQEK
6877	768.9000	1535.7854	1535.7831	1.46	1	(27)	0.043	1	U	L.TLQEK
6878	768.9003	1535.7860	1535.7831	1.86	1	(59)	2.7e-05	1	U	L.TLQEK
6879	768.9016	1535.7887	1535.7831	3.61	1	(26)	0.048	1	U	L.TLQEK
6880	768.9019	1535.7892	1535.7831	3.93	1	65	6e-06	1	U	L.TLQEK
6884	769.3943	1536.7740	1536.7671	4.48	1	(51)	0.00016	1	U	L.TLQEK
6974	777.3754	1552.7362	1552.7304	3.73	0	25	0.083	1	U	Y.QGGMV
7248	804.9232	1607.8318	1607.8307	0.65	2	(43)	0.001	1	U	L.RQITG
7249	804.9251	1607.8355	1607.8307	3.00	2	65	5.1e-06	1	U	L.RQITG
7252	805.4169	1608.8193	1608.8147	2.85	2	(30)	0.018	1	U	L.RQITG
7253	805.4204	1608.8263	1608.8147	7.17	2	(32)	0.013	1	U	L.RQITG
8267	927.9515	1853.8884	1853.8829	2.97	1	(67)	5.1e-06	1	U	Y.KQAVV
8327	935.9462	1869.8779	1869.8778	0.05	1	76	5.4e-07	1	U	Y.KQAVV
8328	935.9483	1869.8820	1869.8778	2.26	1	(70)	1.9e-06	1	U	Y.KQAVV

8329	935.9662	1869.9179	1869.9180	-0.04	1	(57)	3.9e-05	1	U	L.ANEVT
8330	935.9672	1869.9199	1869.9180	0.99	1	(68)	3.6e-06	1	U	L.ANEVT
8333	936.4609	1870.9073	1870.9020	2.83	1	(48)	0.00035	1	U	L.ANEVT
8334	936.4612	1870.9078	1870.9020	3.08	1	70	2.2e-06	1	U	L.ANEVT
8448	956.9371	1911.8596	1911.8558	1.97	1	(51)	0.00015	1	U	Y.SNGYR
8449	956.9394	1911.8643	1911.8558	4.46	1	(65)	6.6e-06	1	U	Y.SNGYR
8453	957.4310	1912.8474	1912.8398	3.95	1	(28)	0.023	1	U	Y.SNGYR
8454	957.4329	1912.8512	1912.8398	5.93	1	66	4.1e-06	1	U	Y.SNGYR

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3. 2::sp|P0ABB4|ATPB_ECOLI **Mass:** 50351 **Score:** 1189 **Matches:** 79(67) **Sequences:**
ATP synthase subunit beta OS=Escherichia coli (strain K12) OX=83333 GN=atpD PE=1 SV=
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
136	387.7267	773.4388	773.4395	-0.93	0	29	0.012	1	U	L.SRQIA
137	387.7274	773.4402	773.4395	0.83	0	(27)	0.02	1	U	L.SRQIA
172	393.2602	784.5059	784.5058	0.09	0	27	0.0063	1	U	L.KDIIA
965	438.7685	875.5224	875.5229	-0.59	1	(21)	0.033	1	U	F.AKGGK
966	438.7686	875.5227	875.5229	-0.16	1	25	0.013	1	U	F.AKGGK
1015	442.2314	882.4483	882.4487	-0.51	2	20	0.1	1	U	L.LFVDN
1324	463.7180	925.4215	925.4215	-0.01	0	(29)	0.018	1	U	F.KGIME
1325	463.7184	925.4222	925.4215	0.77	0	(28)	0.024	1	U	F.KGIME
1407	469.2318	936.4491	936.4487	0.43	0	(27)	0.034	1	U	L.GRMPS
1408	469.2319	936.4492	936.4487	0.49	0	(25)	0.057	1	U	L.GRMPS
1442	471.7157	941.4169	941.4164	0.53	0	31	0.0089	1	U	F.KGIME
1443	471.7158	941.4170	941.4164	0.65	0	(22)	0.066	1	U	F.KGIME
1581	477.2294	952.4442	952.4436	0.63	0	(24)	0.05	1	U	L.GRMPS
1582	477.2298	952.4451	952.4436	1.53	0	33	0.007	1	U	L.GRMPS
1609	478.7268	955.4390	955.4399	-0.98	0	23	0.054	1	U	Y.DHLPE
1610	478.7269	955.4392	955.4399	-0.79	0	(22)	0.072	1	U	Y.DHLPE
1621	478.7741	955.5336	955.5338	-0.25	1	45	0.00023	1	U	L.VLEVQ
1622	478.7745	955.5344	955.5338	0.59	1	(30)	0.0058	1	U	L.VLEVQ
1654	480.2482	958.4819	958.4832	-1.35	0	(25)	0.037	1	U	F.RDEGR
1655	480.2485	958.4825	958.4832	-0.70	0	25	0.034	1	U	F.RDEGR
1679	481.2637	960.5128	960.5128	0.02	1	35	0.0051	1	U	Y.TLAGT
1680	481.2638	960.5130	960.5128	0.27	1	(27)	0.036	1	U	Y.TLAGT
2243	507.2518	1012.4891	1012.4899	-0.81	1	39	0.0017	1	U	L.TGLTM
2244	507.2519	1012.4892	1012.4899	-0.69	1	(32)	0.009	1	U	L.TGLTM
2720	530.2940	1058.5735	1058.5720	1.37	0	21	0.12	1	U	Y.DTARG
2789	533.7713	1065.5280	1065.5277	0.32	1	23	0.092	1	U	L.LGRMP
2839	537.8055	1073.5964	1073.5968	-0.39	2	53	7.2e-05	1	U	Y.TLAGT
2840	537.8062	1073.5977	1073.5968	0.85	2	(38)	0.0024	1	U	Y.TLAGT
3083	550.8309	1099.6472	1099.6489	-1.53	1	56	1.6e-05	1	U	L.LETGI
3084	550.8320	1099.6495	1099.6489	0.58	1	(56)	1.7e-05	1	U	L.LETGI
3279	560.2585	1118.5025	1118.5033	-0.66	1	(29)	0.014	1	U	Y.DHLPE
3280	560.2598	1118.5051	1118.5033	1.65	1	30	0.013	1	U	Y.DHLPE
3452	568.3278	1134.6411	1134.6397	1.22	1	35	0.0022	1	U	Y.VSLKD
3453	568.3280	1134.6414	1134.6397	1.53	1	(33)	0.004	1	U	Y.VSLKD
3700	578.3542	1154.6939	1154.6910	2.52	1	35	0.0016	1	U	Y.QELKD
3701	578.3543	1154.6941	1154.6910	2.62	1	(21)	0.034	5	U	Y.QELKD
3702	578.7859	1155.5572	1155.5560	1.02	1	43	0.00068	1	U	L.DPLVV
3703	578.7868	1155.5590	1155.5560	2.60	1	(43)	0.00069	1	U	L.DPLVV
4357	606.7936	1211.5726	1211.5717	0.76	0	(22)	0.11	1	U	Y.GQMNE
4359	606.7940	1211.5735	1211.5717	1.47	0	(32)	0.01	1	U	Y.GQMNE

4518	614.7907	1227.5667	1227.5666	0.12	0	(27)	0.026	1	U	Y.GQMNE
4519	614.7912	1227.5678	1227.5666	1.01	0	(30)	0.013	1	U	Y.GQMNE
4520	614.7913	1227.5680	1227.5666	1.11	0	36	0.0036	1	U	Y.GQMNE
4521	614.7929	1227.5713	1227.5666	3.80	0	(33)	0.0077	1	U	Y.GQMNE
4842	633.2822	1264.5498	1264.5493	0.41	1	58	1.7e-05	1	U	L.GMDEL
4843	633.2823	1264.5500	1264.5493	0.60	1	(45)	0.00033	1	U	L.GMDEL
4932	424.8946	1271.6619	1271.6622	-0.27	0	(28)	0.024	1	U	L.IRNIA
4934	636.8387	1271.6628	1271.6622	0.48	0	36	0.0042	1	U	L.IRNIA
4935	636.8402	1271.6659	1271.6622	2.88	0	(33)	0.0096	1	U	L.IRNIA
5676	679.3391	1356.6637	1356.6633	0.25	1	48	0.00027	1	U	Y.DALEV
5678	679.3406	1356.6667	1356.6633	2.50	1	(45)	0.00046	1	U	Y.DALEV
5685	679.8308	1357.6471	1357.6473	-0.20	1	(44)	0.00069	1	U	Y.DALEV
5686	679.8315	1357.6484	1357.6473	0.79	1	(37)	0.0037	1	U	Y.DALEV
5915	698.3341	1394.6537	1394.6534	0.19	0	(51)	0.0002	1	U	F.GGAGV
5916	698.3356	1394.6567	1394.6534	2.37	0	60	2e-05	1	U	F.GGAGV
6885	769.8838	1537.7530	1537.7520	0.64	1	29	0.034	1	U	L.ETGIK
6935	773.8678	1545.7210	1545.7199	0.75	1	31	0.013	1	U	Y.VPADD
6936	773.8697	1545.7249	1545.7199	3.27	1	(29)	0.024	1	U	Y.VPADD
7047	785.4152	1568.8158	1568.8158	-0.03	2	52	8.7e-05	1	U	Y.DALEV
7048	785.4169	1568.8193	1568.8158	2.23	2	(43)	0.00066	1	U	Y.DALEV
7059	785.9081	1569.8016	1569.7998	1.14	2	(49)	0.00021	1	U	Y.DALEV
7060	785.9090	1569.8034	1569.7998	2.31	2	(48)	0.00029	1	U	Y.DALEV
7136	529.9279	1586.7618	1586.7610	0.46	0	(28)	0.03	1	U	Y.HEMTD
7137	794.3889	1586.7633	1586.7610	1.43	0	39	0.0026	1	U	Y.HEMTD
7138	529.9285	1586.7636	1586.7610	1.62	0	(20)	0.19	1	U	Y.HEMTD
7139	794.3898	1586.7651	1586.7610	2.58	0	(30)	0.02	1	U	Y.HEMTD
7218	535.2590	1602.7553	1602.7559	-0.42	0	(27)	0.039	1	U	Y.HEMTD
7219	802.3867	1602.7588	1602.7559	1.77	0	(37)	0.0046	1	U	Y.HEMTD
7352	408.7310	1630.8949	1630.8963	-0.91	0	(31)	0.0087	1	U	Y.MVGSI
7353	408.7311	1630.8953	1630.8963	-0.62	0	33	0.0063	1	U	Y.MVGSI
7426	549.9719	1646.8939	1646.8913	1.62	0	(21)	0.11	1	U	Y.MVGSI
7851	866.4503	1730.8861	1730.8839	1.26	1	54	8.4e-05	1	U	L.GIYPA
7852	866.4520	1730.8895	1730.8839	3.23	1	(51)	0.00018	1	U	L.GIYPA
8319	622.6363	1864.8870	1864.8877	-0.34	1	25	0.088	1	U	Y.HEMTD
8320	622.6378	1864.8915	1864.8877	2.02	1	(22)	0.16	1	U	Y.HEMTD
8560	654.0292	1959.0659	1959.0677	-0.92	1	65	4.1e-06	1	U	L.DVKDL
8561	980.5405	1959.0664	1959.0677	-0.66	1	(56)	2.8e-05	1	U	L.DVKDL
8562	980.5409	1959.0673	1959.0677	-0.17	1	(44)	0.0005	1	U	L.DVKDL
8563	654.0299	1959.0679	1959.0677	0.11	1	(63)	6.3e-06	1	U	L.DVKDL

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4. 2::sp|P0A9P0|DLDH_ECOLI **Mass:** 50942 **Score:** 1045 **Matches:** 55(47) **Sequences:**
Dihydrolipoyl dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=lpdA PE=1 S
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
622	417.2127	832.4109	832.4113	-0.45	1	22	0.11	1	U	Y.NTLGG
623	417.2129	832.4113	832.4113	-0.02	1	(21)	0.12	1	U	Y.NTLGG
811	426.2002	850.3859	850.3861	-0.25	0	38	0.0017	1	U	Y.ETATF
812	426.2005	850.3864	850.3861	0.38	0	(29)	0.018	1	U	Y.ETATF
886	435.7557	869.4967	869.4970	-0.34	0	(22)	0.023	2	U	L.KEVPE
887	435.7559	869.4973	869.4970	0.35	0	24	0.016	1	U	L.KEVPE
902	436.2717	870.5289	870.5287	0.25	0	21	0.04	4	U	F.IRVDK
1803	486.2977	970.5808	970.5811	-0.32	0	21	0.039	2	U	W.KEKVI
1919	492.2980	982.5814	982.5811	0.35	1	24	0.013	1	U	L.KEVPE

2689	529.7867	1057.5588	1057.5590	-0.19	0	37	0.0028	1	U	L.NVGCI
2690	529.7876	1057.5606	1057.5590	1.55	0	(24)	0.055	1	U	L.NVGCI
3799	388.2044	1161.5915	1161.5931	-1.37	0	(22)	0.15	1	U	F.IPHED
3801	388.2049	1161.5928	1161.5931	-0.28	0	28	0.035	1	U	F.IPHED
3803	581.8048	1161.5951	1161.5931	1.71	0	(21)	0.16	1	U	F.IPHED
3927	586.3283	1170.6421	1170.6431	-0.85	1	39	0.0014	1	U	L.NVGCI
4004	589.8241	1177.6336	1177.6343	-0.53	1	52	7.4e-05	1	U	L.GLETV
4005	589.8242	1177.6339	1177.6343	-0.33	1	(39)	0.0017	1	U	L.GLETV
4423	608.8609	1215.7072	1215.7075	-0.17	0	(34)	0.0027	1	U	M.STEIK
4424	608.8611	1215.7076	1215.7075	0.12	0	43	0.00032	1	U	M.STEIK
4618	619.3712	1236.7279	1236.7302	-1.90	0	42	0.00015	1	U	L.VAIGR
4619	619.3730	1236.7314	1236.7302	0.96	0	(30)	0.0023	1	U	L.VAIGR
4627	619.8657	1237.7169	1237.7142	2.13	0	(36)	0.00085	1	U	L.VAIGR
4722	625.3445	1248.6744	1248.6754	-0.81	1	(28)	0.021	1	U	Y.FDPKV
4723	625.3470	1248.6794	1248.6754	3.20	1	32	0.0066	1	U	Y.FDPKV
5265	436.5939	1306.7600	1306.7608	-0.68	0	(27)	0.0056	1	U	L.HVAKV
5266	436.5942	1306.7609	1306.7608	0.03	0	28	0.0044	1	U	L.HVAKV
5995	704.3098	1406.6051	1406.6057	-0.48	0	38	0.0017	1	U	L.AIEMG
6086	474.2890	1419.8451	1419.8449	0.12	1	26	0.004	1	U	L.LHVAK
6195	479.2320	1434.6743	1434.6739	0.23	0	(25)	0.074	1	U	L.DAGKA
6196	479.2324	1434.6753	1434.6739	0.98	0	(30)	0.02	1	U	L.DAGKA
6197	718.3456	1434.6766	1434.6739	1.86	0	(58)	3.8e-05	1	U	L.DAGKA
6198	718.3456	1434.6767	1434.6739	1.95	0	68	3.7e-06	1	U	L.DAGKA
6199	718.3572	1434.6999	1434.6991	0.60	0	(45)	0.00077	1	U	L.EVEGE
6200	718.3588	1434.7030	1434.6991	2.72	0	(46)	0.0007	1	U	L.EVEGE
6205	718.8489	1435.6833	1435.6831	0.18	0	58	3.6e-05	1	U	L.EVEGE
6206	718.8492	1435.6838	1435.6831	0.51	0	(44)	0.001	1	U	L.EVEGE
6403	731.3558	1460.6970	1460.6970	0.01	1	66	5.9e-06	1	U	Y.HALGS
6404	731.3578	1460.7011	1460.6970	2.86	1	(59)	3e-05	1	U	Y.HALGS
6717	504.6038	1510.7895	1510.7892	0.21	1	23	0.076	1	U	L.TIHAH
7391	821.4161	1640.8177	1640.8154	1.43	2	24	0.081	1	U	L.LVMGG
7462	826.4493	1650.8841	1650.8828	0.80	1	(36)	0.0034	1	U	W.VGLTE
7463	551.3022	1650.8849	1650.8828	1.28	1	(27)	0.025	1	U	W.VGLTE
7464	551.3024	1650.8855	1650.8828	1.60	1	(43)	0.00058	1	U	W.VGLTE
7465	826.4527	1650.8908	1650.8828	4.87	1	61	7.7e-06	1	U	W.VGLTE
7505	553.3098	1656.9076	1656.9087	-0.65	0	(27)	0.024	1	U	F.DQVIP
7507	553.3115	1656.9126	1656.9087	2.34	0	(20)	0.11	1	U	F.DQVIP
7508	829.4642	1656.9138	1656.9087	3.09	0	(45)	0.00037	1	U	F.DQVIP
7509	829.4643	1656.9140	1656.9087	3.23	0	56	2.9e-05	1	U	F.DQVIP
7626	841.9680	1681.9214	1681.9151	3.71	0	57	1.7e-05	1	U	F.DNAII
7794	574.2947	1719.8624	1719.8614	0.59	0	53	0.00014	1	U	Y.VTMEG
7795	574.2952	1719.8637	1719.8614	1.34	0	(39)	0.0036	1	U	Y.VTMEG
8622	996.9985	1991.9824	1991.9800	1.20	1	(63)	1.3e-05	1	U	F.TGANT
8623	997.0014	1991.9882	1991.9800	4.14	1	(55)	7.2e-05	1	U	F.TGANT
8624	997.4909	1992.9673	1992.9640	1.64	1	(42)	0.0016	1	U	F.TGANT
8625	997.4914	1992.9682	1992.9640	2.12	1	69	3.5e-06	1	U	F.TGANT

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5. 2::sp|P0CE47|EFTU1_ECOLI **Mass:** 43427 **Score:** 1039 **Matches:** 65(59) **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
211	395.2391	788.4636	788.4644	-0.99	0	28	0.013	1	U	L.TAAI
950	438.2405	874.4663	874.4661	0.27	0	(22)	0.079	1	U	L.GRQV

951	438.2407	874.4668	874.4661	0.82	0	23	0.073	1	U	L.GRQV
1504	473.2685	944.5224	944.5219	0.52	1	52	8.1e-05	1	U	F.LLPI
1505	473.2688	944.5230	944.5219	1.24	1	(39)	0.0017	1	U	F.LLPI
2326	509.7457	1017.4769	1017.4767	0.20	1	(24)	0.066	1	U	L.KALE
2327	509.7460	1017.4774	1017.4767	0.74	1	(28)	0.021	1	U	L.KALE
2328	509.7462	1017.4779	1017.4767	1.23	1	38	0.0024	1	U	L.KALE
2901	541.2706	1080.5266	1080.5274	-0.73	0	(55)	5.3e-05	1	U	L.IHPI
2902	541.2711	1080.5277	1080.5274	0.29	0	57	3.8e-05	1	U	L.IHPI
3058	549.2683	1096.5221	1096.5223	-0.21	0	(25)	0.043	1	U	L.IHPI
3059	549.2684	1096.5222	1096.5223	-0.10	0	(51)	0.00012	1	U	L.IHPI
3060	549.2698	1096.5251	1096.5223	2.59	0	(46)	0.00031	1	U	L.IHPI
4401	608.3024	1214.5902	1214.5891	0.87	0	(25)	0.049	1	U	L.DEGR
4402	608.3032	1214.5918	1214.5891	2.17	0	38	0.0024	1	U	L.DEGR
4638	621.2541	1240.4936	1240.4931	0.40	0	30	0.0056	1	U	Y.AHVD
4639	621.2546	1240.4947	1240.4931	1.28	0	(24)	0.025	1	U	Y.AHVD
4692	623.8229	1245.6312	1245.6275	3.01	1	64	8.1e-06	1	U	L.ELVE
4693	623.8230	1245.6314	1245.6275	3.20	1	(60)	1.9e-05	1	U	L.ELVE
4825	631.8181	1261.6217	1261.6224	-0.54	1	(44)	0.00087	1	U	L.ELVE
4826	631.8201	1261.6257	1261.6224	2.64	1	(38)	0.0035	1	U	L.ELVE
5469	664.8400	1327.6654	1327.6732	-5.87	1	(38)	0.0026	1	U	L.LDEG
5470	664.8433	1327.6720	1327.6732	-0.92	1	69	1.9e-06	1	U	L.LDEG
5471	664.8438	1327.6731	1327.6732	-0.09	1	50	0.00016	1	U	L.DEGR
5472	664.8453	1327.6760	1327.6732	2.12	1	(45)	0.00046	1	U	L.DEGR
5821	688.3602	1374.7058	1374.7064	-0.47	2	(46)	0.00046	1	U	L.ELVE
5822	688.3607	1374.7068	1374.7064	0.24	2	47	0.00044	1	U	L.ELVE
5855	462.2394	1383.6965	1383.6969	-0.29	1	(44)	0.00067	1	U	L.IHPI
5856	462.2397	1383.6973	1383.6969	0.31	1	52	9.8e-05	1	U	L.IHPI
5857	692.8561	1383.6976	1383.6969	0.51	1	(27)	0.036	1	U	L.IHPI
5858	692.8578	1383.7010	1383.6969	2.98	1	(32)	0.011	1	U	L.IHPI
5956	700.8534	1399.6923	1399.6918	0.38	1	(24)	0.073	1	U	L.IHPI
5957	467.5714	1399.6924	1399.6918	0.42	1	(38)	0.0026	1	U	L.IHPI
5958	467.5717	1399.6933	1399.6918	1.08	1	(45)	0.00054	1	U	L.IHPI
6013	706.3830	1410.7514	1410.7507	0.54	0	27	0.026	1	U	Y.IPEP
6016	706.3849	1410.7552	1410.7507	3.22	0	(25)	0.043	1	U	Y.IPEP
6238	721.3860	1440.7575	1440.7572	0.21	2	(35)	0.0045	1	U	L.LDEG
6241	721.3881	1440.7616	1440.7572	3.00	2	45	0.0004	1	U	L.LDEG
6372	728.8810	1455.7474	1455.7470	0.26	1	(42)	0.001	1	U	Y.ILSK
6374	728.8815	1455.7484	1455.7470	0.94	1	44	0.00066	1	U	Y.ILSK
6543	740.8176	1479.6206	1479.6221	-1.04	1	(31)	0.0063	1	U	L.NKCD
6544	740.8190	1479.6234	1479.6221	0.85	1	38	0.0015	1	U	L.NKCD
6648	748.8164	1495.6181	1495.6171	0.73	1	(29)	0.009	1	U	L.NKCD
6649	748.8175	1495.6204	1495.6171	2.27	1	(25)	0.022	1	U	L.NKCD
7001	780.3886	1558.7625	1558.7628	-0.13	0	(54)	7.8e-05	1	U	Y.DFPG
7002	780.3893	1558.7640	1558.7628	0.80	0	(59)	2.5e-05	1	U	Y.DFPG
7003	780.3893	1558.7641	1558.7628	0.88	0	(60)	2e-05	1	U	Y.DFPG
7004	780.3909	1558.7673	1558.7628	2.92	0	74	8.7e-07	1	U	Y.DFPG
7173	797.3621	1592.7097	1592.7062	2.20	2	(55)	4.4e-05	1	U	F.LNKC
7174	797.3628	1592.7110	1592.7062	3.04	2	60	1.6e-05	1	U	F.LNKC
7250	805.3581	1608.7016	1608.7011	0.32	2	(56)	2.6e-05	1	U	F.LNKC
7251	805.3583	1608.7021	1608.7011	0.63	2	(51)	8.9e-05	1	U	F.LNKC
7432	824.9256	1647.8366	1647.8324	2.58	0	(43)	0.0012	1	U	Y.VKNM
7433	824.9266	1647.8387	1647.8324	3.84	0	55	7.9e-05	1	U	Y.VKNM
7544	832.9205	1663.8265	1663.8273	-0.49	0	(27)	0.049	1	U	Y.VKNM
7545	832.9211	1663.8277	1663.8273	0.25	0	(28)	0.04	1	U	Y.VKNM
7549	832.9236	1663.8326	1663.8273	3.18	0	(38)	0.0036	1	U	Y.VKNM
7815	863.4841	1724.9536	1724.9533	0.16	2	38	0.0014	1	U	F.RKLL
7982	592.9665	1775.8778	1775.8730	2.72	1	(23)	0.12	1	U	L.DSYI

7984	888.9467	1775.8789	1775.8730	3.32	1	35	0.0069	1	U	L.DSYI
7985	888.9467	1775.8789	1775.8730	3.32	1	(34)	0.0091	1	U	L.DSYI
8395	630.6595	1888.9568	1888.9570	-0.12	2	(28)	0.04	1	U	F.LDSY
8397	945.4860	1888.9575	1888.9570	0.23	2	31	0.017	1	U	F.LDSY
8399	945.4891	1888.9636	1888.9570	3.46	2	(22)	0.15	1	U	F.LDSY
9335	1098.5472	3292.6199	3292.6241	-1.28	0	55	4.6e-05	1	U	F.RTTD

Proteins matching the same set of peptides:

2::sp|P0CE48|EFTU2_ECOLI **Mass:** 43457 **Score:** 1039 **Matches:** 65(59) **Sequences:**

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

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6. 2::sp|P0AE06|ACRA_ECOLI **Mass:** 42228 **Score:** 988 **Matches:** 73(63) **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
73	384.2002	766.3859	766.3861	-0.24	0	(22)	0.066	1	U	Y.ISKQ
74	384.2008	766.3870	766.3861	1.19	0	32	0.006	1	U	Y.ISKQ
184	393.7452	785.4758	785.4759	-0.12	1	21	0.053	1	U	L.RLKQ
1093	451.2403	900.4660	900.4665	-0.49	0	(28)	0.019	1	U	L.VQNG
1094	451.2404	900.4662	900.4665	-0.29	0	39	0.0013	1	U	L.VQNG
1111	451.7321	901.4497	901.4505	-0.90	0	(28)	0.019	1	U	L.VQNG
1112	451.7323	901.4500	901.4505	-0.50	0	(29)	0.019	1	U	L.VQNG
1548	475.7686	949.5227	949.5233	-0.55	2	25	0.028	2	U	Y.QKLL
1821	487.2693	972.5240	972.5240	-0.02	1	(45)	0.00051	1	U	L.KQEL
1822	487.2696	972.5246	972.5240	0.60	1	(55)	5.5e-05	1	U	L.KQEL
1828	487.7612	973.5079	973.5080	-0.09	1	(38)	0.0033	1	U	L.KQEL
1829	487.7617	973.5088	973.5080	0.79	1	(51)	0.00014	1	U	L.KQEL
1830	487.7620	973.5094	973.5080	1.41	1	59	2.4e-05	1	U	L.KQEL
1831	487.7620	973.5094	973.5080	1.41	1	(33)	0.011	1	U	L.KQEL
3232	557.8327	1113.6508	1113.6506	0.22	0	42	0.00059	1	U	L.KAGD
3233	557.8328	1113.6511	1113.6506	0.43	0	(35)	0.0028	1	U	L.KAGD
3234	557.8335	1113.6524	1113.6506	1.66	0	(26)	0.021	1	U	L.KAGD
4150	597.8041	1193.5936	1193.5928	0.69	1	41	0.0016	1	U	Y.ISKQ
4152	597.8062	1193.5979	1193.5928	4.26	1	(24)	0.072	1	U	Y.ISKQ
4155	597.8072	1193.5998	1193.5928	5.90	1	(28)	0.032	1	U	Y.ISKQ
4246	601.3504	1200.6862	1200.6826	3.04	0	(27)	0.018	1	U	L.KQEN
4257	401.5612	1201.6618	1201.6666	-3.98	0	(23)	0.068	1	U	L.KQEN
4263	601.8415	1201.6684	1201.6666	1.51	0	(25)	0.033	1	U	L.KQEN
4264	601.8424	1201.6701	1201.6666	2.94	0	32	0.0072	1	U	L.KQEN
4283	602.8065	1203.5984	1203.5983	0.07	0	39	0.0027	1	U	F.KEGS
4284	602.8077	1203.6008	1203.5983	2.10	0	(26)	0.052	1	U	F.KEGS
4643	621.8625	1241.7104	1241.7092	1.03	2	(34)	0.0032	1	U	L.RLKQ
4644	621.8630	1241.7115	1241.7092	1.91	2	(30)	0.0075	1	U	L.RLKQ
4659	622.3558	1242.6970	1242.6932	3.08	2	(36)	0.0026	1	U	L.RLKQ
4660	622.3558	1242.6970	1242.6932	3.08	2	41	0.00088	1	U	L.RLKQ
5750	684.3379	1366.6613	1366.6616	-0.19	1	52	0.00014	1	U	F.KEGS
5751	684.3382	1366.6618	1366.6616	0.18	1	(24)	0.084	1	U	F.KEGS
5752	684.3386	1366.6626	1366.6616	0.70	1	(49)	0.00026	1	U	F.KEGS
5753	684.3387	1366.6628	1366.6616	0.88	1	(37)	0.004	1	U	F.KEGS
5755	684.3392	1366.6639	1366.6616	1.68	1	(44)	0.00077	1	U	F.KEGS
5758	684.3400	1366.6655	1366.6616	2.86	1	(44)	0.00081	1	U	F.KEGS
5760	684.3408	1366.6670	1366.6616	3.92	1	(24)	0.091	1	U	F.KEGS
6209	718.8732	1435.7318	1435.7307	0.76	0	(45)	0.00066	1	U	L.QITT

6210	718.8744	1435.7342	1435.7307	2.46	0	54	8.8e-05	1	U	L.QITT
6627	746.3881	1490.7617	1490.7617	0.00	0	(65)	7.9e-06	1	U	L.ITSD
6628	746.3887	1490.7628	1490.7617	0.74	0	(62)	1.7e-05	1	U	L.ITSD
6629	746.3890	1490.7634	1490.7617	1.15	0	(66)	6.6e-06	1	U	L.ITSD
6630	746.3913	1490.7680	1490.7617	4.27	0	69	2.9e-06	1	U	L.ITSD
6631	746.8827	1491.7509	1491.7457	3.52	0	(65)	8.2e-06	1	U	L.ITSD
6964	775.9743	1549.9340	1549.9304	2.36	0	36	0.00025	1	U	Y.RIAE
6965	775.9747	1549.9348	1549.9304	2.84	0	(25)	0.003	1	U	Y.RIAE
7955	884.4424	1766.8702	1766.8727	-1.41	1	77	4.7e-07	1	U	L.ITSD
7956	884.4433	1766.8720	1766.8727	-0.37	1	(55)	7.5e-05	1	U	L.ITSD
8234	614.6514	1840.9323	1840.9294	1.55	1	(21)	0.17	1	U	L.RAIF
8236	921.4739	1840.9333	1840.9294	2.12	1	(49)	0.00025	1	U	L.RAIF
8238	921.4764	1840.9382	1840.9294	4.77	1	49	0.00024	1	U	L.RAIF
8277	619.3338	1854.9796	1854.9799	-0.17	1	(20)	0.13	1	U	Y.DSAK
8279	928.5007	1854.9868	1854.9799	3.72	1	(55)	4.1e-05	1	U	Y.DSAK
8280	928.5012	1854.9879	1854.9799	4.31	1	56	3.2e-05	1	U	Y.DSAK
8950	747.3643	2239.0710	2239.0645	2.89	2	(58)	3.5e-05	1		L.ATVQ
8951	1120.5433	2239.0721	2239.0645	3.40	2	(35)	0.0084	1		L.ATVQ
8952	747.3647	2239.0724	2239.0645	3.55	2	(55)	7.9e-05	1		L.ATVQ
8953	1120.5436	2239.0726	2239.0645	3.63	2	(50)	0.00025	1		L.ATVQ
8954	1120.5441	2239.0736	2239.0645	4.07	2	86	5.9e-08	1		L.ATVQ
9085	818.7736	2453.2990	2453.2914	3.09	0	52	7.1e-05	1	U	L.VVGA
9087	818.7741	2453.3005	2453.2914	3.69	0	(46)	0.0003	1	U	L.VVGA
9088	614.5764	2454.2766	2454.2755	0.46	0	(22)	0.098	1	U	L.VVGA
9089	819.1000	2454.2783	2454.2755	1.16	0	(46)	0.00035	1	U	L.VVGA
9090	614.5784	2454.2844	2454.2755	3.64	0	(21)	0.11	1	U	L.VVGA
9091	819.1022	2454.2849	2454.2755	3.83	0	(46)	0.00032	1	U	L.VVGA
9310	981.4863	2941.4370	2941.4274	3.26	0	47	0.00034	1	U	L.TGCD
9311	981.4866	2941.4381	2941.4274	3.63	0	(39)	0.0024	1	U	L.TGCD
9313	986.8146	2957.4219	2957.4223	-0.14	0	(41)	0.0014	1	U	L.TGCD
9314	986.8152	2957.4239	2957.4223	0.54	0	(40)	0.0018	1	U	L.TGCD
9327	1042.8567	3125.5482	3125.5486	-0.10	1	(43)	0.0009	1	U	L.ALTG
9328	1042.8619	3125.5640	3125.5486	4.93	1	(44)	0.00057	1	U	L.ALTG
9329	1048.1899	3141.5480	3141.5435	1.43	1	45	0.00059	1	U	L.ALTG
9330	1048.1924	3141.5553	3141.5435	3.76	1	(40)	0.0017	1	U	L.ALTG

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7. 2::sp|P00350|6PGD_ECOLI **Mass:** 51563 **Score:** 933 **Matches:** 46(43) **Sequences:**

6-phosphogluconate dehydrogenase, decarboxylating OS=Escherichia coli (strain K12) 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
149	390.2360	778.4574	778.4589	-1.94	1	(30)	0.0023	1	U	Y.LGKIV
150	390.2361	778.4577	778.4589	-1.55	1	31	0.002	1	U	Y.LGKIV
174	393.7053	785.3960	785.3959	0.02	1	26	0.018	1	U	Y.YTVKE
175	393.7054	785.3963	785.3959	0.40	1	(26)	0.019	1	U	Y.YTVKE
1045	448.2422	894.4698	894.4698	-0.09	1	25	0.037	1	U	L.SLITE
1320	462.7852	923.5558	923.5552	0.59	0	33	0.001	1	U	Y.RAAVL
1321	462.7852	923.5558	923.5552	0.66	0	(32)	0.0013	1	U	Y.RAAVL
1558	476.2603	950.5060	950.5073	-1.34	1	(27)	0.017	1	U	F.LQKIT
1559	476.2611	950.5077	950.5073	0.41	1	34	0.0033	1	U	F.LQKIT
1703	482.7721	963.5296	963.5277	1.94	0	29	0.015	1	U	L.IDITK
1770	485.2536	968.4927	968.4927	0.03	0	(34)	0.0042	1	U	Y.AENPQ
1771	485.2537	968.4928	968.4927	0.16	0	41	0.00069	1	U	Y.AENPQ
2097	500.2427	998.4708	998.4709	-0.09	1	(45)	0.0003	1	U	Y.FKQIA

2098	500.2432	998.4718	998.4709	0.93	1	61	8.9e-06	1	U	Y.FKQIA
2372	511.7666	1021.5186	1021.5192	-0.62	1	(39)	0.0026	1	U	L.ALNIE
2373	511.7667	1021.5188	1021.5192	-0.39	1	48	0.00033	1	U	L.ALNIE
2521	520.7617	1039.5088	1039.5087	0.08	1	40	0.0015	1	U	L.IQAQR
2522	520.7620	1039.5095	1039.5087	0.78	1	(40)	0.0015	1	U	L.IQAQR
2862	539.3141	1076.6136	1076.6118	1.74	1	(48)	0.00012	1	U	Y.LIDIT
2863	539.3142	1076.6139	1076.6118	1.96	1	50	7.1e-05	1	U	Y.LIDIT
2912	541.7953	1081.5761	1081.5767	-0.54	1	(41)	0.00076	1	U	Y.AENPQ
2913	541.7963	1081.5780	1081.5767	1.14	1	43	0.00044	1	U	Y.AENPQ
3554	571.8154	1141.6163	1141.6132	2.75	0	(23)	0.051	1	U	Y.AVQNG
3561	572.3054	1142.5963	1142.5972	-0.78	0	(26)	0.038	1	U	Y.AVQNG
3562	572.3066	1142.5986	1142.5972	1.25	0	43	0.00074	1	U	Y.AVQNG
4297	603.3030	1204.5915	1204.5910	0.41	0	22	0.13	1	U	Y.VKMVH
5037	642.3309	1282.6473	1282.6445	2.20	2	31	0.012	1	U	W.DLNYG
5101	646.8297	1291.6447	1291.6408	3.05	1	42	0.0015	1	U	F.KQIAD
5102	646.8297	1291.6449	1291.6408	3.14	1	(33)	0.01	1	U	F.KQIAD
5998	704.3392	1406.6638	1406.6678	-2.84	1	29	0.028	1	U	F.NFIGT
5999	704.3432	1406.6718	1406.6678	2.89	1	(29)	0.031	1	U	F.NFIGT
6406	488.2504	1461.7295	1461.7286	0.61	0	(24)	0.093	1	U	L.KGPSI
6522	739.3812	1476.7479	1476.7460	1.27	1	63	1e-05	1	U	Y.LDKGD
6523	739.3823	1476.7501	1476.7460	2.75	1	(60)	2.3e-05	1	U	Y.LDKGD
6524	739.3829	1476.7512	1476.7460	3.49	1	(55)	6.4e-05	1	U	Y.LDKGD
6529	493.5820	1477.7243	1477.7235	0.52	0	(26)	0.055	1	U	L.KGPSI
6531	493.5825	1477.7256	1477.7235	1.45	0	(26)	0.065	1	U	L.KGPSI
6532	739.8710	1477.7274	1477.7235	2.63	0	30	0.024	1	U	L.KGPSI
6534	739.8721	1477.7296	1477.7235	4.12	0	(26)	0.054	1	U	L.KGPSI
8180	914.9943	1827.9740	1827.9731	0.50	2	(66)	3.8e-06	1	U	Y.LVDVI
8181	914.9969	1827.9793	1827.9731	3.44	2	81	1.3e-07	1	U	Y.LVDVI
9152	864.1007	2589.2803	2589.2745	2.26	1	(47)	0.00045	1	U	F.IGTGV
9172	869.4300	2605.2681	2605.2694	-0.47	1	(73)	1.2e-06	1	U	F.IGTGV
9173	869.4316	2605.2729	2605.2694	1.36	1	83	1.1e-07	1	U	F.IGTGV
9289	956.4662	2866.3769	2866.3807	-1.33	2	(52)	0.00011	1	U	F.NFIGT
9290	956.4709	2866.3908	2866.3807	3.53	2	54	7.2e-05	1	U	F.NFIGT

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8. 2::sp|P0A850|TIG_ECOLI **Mass:** 48163 **Score:** 909 **Matches:** 42(38) **Sequences:** 1

Trigger factor OS=Escherichia coli (strain K12) OX=83333 GN=tig PE=1 SV=1

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
1672	481.2278	960.4411	960.4400	1.16	0	(44)	0.00046	1	U	F.GVED
1673	481.2280	960.4414	960.4400	1.49	0	55	3.5e-05	1	U	F.GVED
1692	482.2131	962.4116	962.4127	-1.18	1	(22)	0.071	1	U	F.NELM
1693	482.2131	962.4117	962.4127	-1.05	1	23	0.056	1	U	F.NELM
1810	486.7371	971.4596	971.4600	-0.39	2	40	0.001	1	U	Y.KLGE
3130	553.2744	1104.5341	1104.5339	0.23	0	(34)	0.008	1	U	Y.EDPK
3131	553.2744	1104.5341	1104.5339	0.23	0	35	0.0056	1	U	Y.EDPK
3564	572.3229	1142.6313	1142.6295	1.58	1	30	0.012	1	U	L.LGEV
4120	596.7979	1191.5813	1191.5806	0.60	0	71	1.8e-06	1	U	-.MQVS
4121	596.7982	1191.5818	1191.5806	1.02	0	(68)	3e-06	1	U	-.MQVS
4321	604.7948	1207.5750	1207.5755	-0.35	0	(27)	0.045	1	U	-.MQVS
4322	604.7958	1207.5770	1207.5755	1.27	0	(28)	0.034	1	U	-.MQVS
4368	607.2839	1212.5533	1212.5550	-1.41	0	(48)	0.00024	1	U	F.TIDV
4369	607.2861	1212.5576	1212.5550	2.10	0	53	7.4e-05	1	U	F.TIDV
4536	615.3278	1228.6411	1228.6412	-0.07	1	(32)	0.012	1	U	Y.GASV

4537	615.3285	1228.6425	1228.6412	1.12	1	33	0.0094	1	U	Y.GASV
4770	628.8637	1255.7129	1255.7136	-0.56	2	53	4.9e-05	1	U	L.LLGE
4771	628.8638	1255.7131	1255.7136	-0.37	2	(50)	8.5e-05	1	U	L.LLGE
4876	634.8049	1267.5953	1267.5972	-1.50	1	(41)	0.0015	1	U	Y.EDPK
4877	634.8049	1267.5953	1267.5972	-1.50	1	46	0.00045	1	U	Y.EDPK
4979	638.3288	1274.6430	1274.6394	2.85	1	(55)	6.6e-05	1	U	F.EVYP
4980	638.3289	1274.6432	1274.6394	2.94	1	56	5.4e-05	1	U	F.EVYP
5626	451.5851	1351.7334	1351.7347	-0.96	0	(24)	0.039	1	U	L.AKAK
5627	451.5854	1351.7343	1351.7347	-0.27	0	(22)	0.069	1	U	L.AKAK
5628	676.8769	1351.7393	1351.7347	3.43	0	63	4.8e-06	1	U	L.AKAK
5629	676.8773	1351.7400	1351.7347	3.89	0	(53)	5.4e-05	1	U	L.AKAK
7847	866.3721	1730.7297	1730.7272	1.47	1	(67)	2e-06	1	U	F.TGSV
7848	866.3724	1730.7303	1730.7272	1.83	1	97	1.6e-09	1	U	F.TGSV
8123	907.5084	1813.0023	1812.9985	2.09	0	50	9.5e-05	1	U	F.IDAI
8125	907.5099	1813.0052	1812.9985	3.71	0	(45)	0.00024	1	U	F.IDAI
8146	909.4872	1816.9599	1816.9570	1.59	1	44	0.00069	1	U	L.KKVE
8147	606.6607	1816.9603	1816.9570	1.80	1	(21)	0.15	1	U	L.KKVE
8148	909.4892	1816.9638	1816.9570	3.75	1	(25)	0.053	1	U	L.KKVE
8470	641.3210	1920.9413	1920.9429	-0.82	0	(33)	0.013	1	U	W.KEKD
8471	641.3226	1920.9459	1920.9429	1.57	0	(33)	0.014	1	U	W.KEKD
8472	641.3228	1920.9466	1920.9429	1.94	0	42	0.0017	1	U	W.KEKD
9013	787.0914	2358.2523	2358.2471	2.21	1	(30)	0.011	1	U	F.IDAI
9014	1180.1342	2358.2538	2358.2471	2.84	1	43	0.00055	1	U	F.IDAI
9184	1309.1436	2616.2725	2616.2728	-0.10	1	77	4.8e-07	1	U	L.EAIE
9185	1309.1440	2616.2735	2616.2728	0.28	1	(69)	2.6e-06	1	U	L.EAIE
9186	873.0993	2616.2761	2616.2728	1.25	1	(60)	2.5e-05	1	U	L.EAIE
9187	873.0993	2616.2761	2616.2728	1.25	1	(58)	3.4e-05	1	U	L.EAIE

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9. 2::sp|P0A6P9|ENO_ECOLI **Mass:** 45683 **Score:** 773 **Matches:** 40(37) **Sequences:** 1

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

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
200	394.7471	787.4796	787.4803	-0.89	0	(40)	0.00041	1	U	F.VTNT
201	394.7474	787.4803	787.4803	-0.02	0	40	0.00034	1	U	F.VTNT
1033	444.7556	887.4966	887.4964	0.25	1	37	0.003	1	U	Y.ELGK
1034	444.7557	887.4968	887.4964	0.48	1	(26)	0.035	1	U	Y.ELGK
2158	503.2716	1004.5287	1004.5291	-0.41	1	42	0.0009	1	U	Y.VLAG
2159	503.2719	1004.5293	1004.5291	0.18	1	(31)	0.014	1	U	Y.VLAG
2667	528.7700	1055.5254	1055.5247	0.63	1	(24)	0.047	1	U	Y.APNL
2668	528.7711	1055.5276	1055.5247	2.71	1	32	0.007	1	U	Y.APNL
2846	538.2847	1074.5549	1074.5557	-0.73	1	(53)	9.9e-05	1	U	F.NQIG
2847	538.2862	1074.5578	1074.5557	1.99	1	70	2.1e-06	1	U	F.NQIG
3078	550.8109	1099.6073	1099.6098	-2.28	0	(25)	0.038	1	U	Y.NGRK
3080	550.8136	1099.6126	1099.6098	2.62	0	31	0.0089	1	U	Y.NGRK
3095	551.3037	1100.5929	1100.5938	-0.83	0	(24)	0.054	1	U	Y.NGRK
3096	551.3038	1100.5930	1100.5938	-0.72	0	(21)	0.11	1	U	Y.NGRK
3683	385.5337	1153.5792	1153.5801	-0.83	0	23	0.076	1	U	L.AAIK
3684	385.5337	1153.5794	1153.5801	-0.60	0	(20)	0.15	1	U	L.AAIK
3806	581.8271	1161.6397	1161.6393	0.35	0	(88)	1.9e-08	1	U	L.AVIA
3807	581.8276	1161.6407	1161.6393	1.19	0	(30)	0.012	1	U	L.AVIA
3808	581.8283	1161.6419	1161.6393	2.24	0	88	1.7e-08	1	U	L.AVIA
5388	660.3456	1318.6766	1318.6769	-0.22	2	45	0.00065	1	U	L.GDKI
5390	660.3464	1318.6782	1318.6769	0.98	2	(44)	0.00076	1	U	L.GDKI

6603	496.9403	1487.7990	1487.7983	0.45	1	(29)	0.025	1	U	L.IRIE
6604	744.9068	1487.7990	1487.7983	0.48	1	44	0.00086	1	U	L.IRIE
6605	496.9407	1487.8004	1487.7983	1.36	1	(33)	0.01	1	U	L.IRIE
6727	505.2364	1512.6873	1512.6879	-0.34	0	(28)	0.027	1	U	L.KAKG
6728	505.2366	1512.6881	1512.6879	0.14	0	(27)	0.036	1	U	L.KAKG
6729	757.3525	1512.6904	1512.6879	1.69	0	(60)	1.7e-05	1	U	L.KAKG
6730	757.3539	1512.6933	1512.6879	3.62	0	66	4.4e-06	1	U	L.KAKG
7429	824.9030	1647.7913	1647.7886	1.66	0	46	0.00055	1	U	F.VGMA
7430	824.9030	1647.7915	1647.7886	1.74	0	(45)	0.00073	1	U	F.VGMA
8239	615.3354	1842.9843	1842.9839	0.24	2	(51)	0.00013	1	U	Y.NQLI
8240	922.4996	1842.9847	1842.9839	0.44	2	61	1.2e-05	1	U	Y.NQLI
8241	615.3370	1842.9891	1842.9839	2.83	2	(46)	0.00039	1	U	Y.NQLI
8242	922.5022	1842.9898	1842.9839	3.23	2	(51)	0.00011	1	U	Y.NQLI
8384	943.9300	1885.8454	1885.8438	0.89	2	47	0.00038	1	U	Y.ELGK
8529	648.6885	1943.0438	1943.0397	2.09	0	(25)	0.049	1	U	L.IGKD
8530	648.6897	1943.0473	1943.0397	3.88	0	(30)	0.014	1	U	L.IGKD
8559	654.0165	1959.0278	1959.0347	-3.50	0	33	0.0092	1	U	L.IGKD
8814	1048.0013	2093.9881	2093.9793	4.20	1	(48)	0.00042	1	U	L.TKQY
8815	1048.0015	2093.9884	2093.9793	4.32	1	68	3.9e-06	1	U	L.TKQY

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10. 2::sp|P0AFG6|ODO2_ECOLI **Mass:** 43984 **Score:** 635 **Matches:** 36(33) **Sequences:**

Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrog

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
457	408.2653	814.5160	814.5164	-0.52	1	27	0.0067	1	U	F.LVTIK
458	408.2656	814.5167	814.5164	0.39	1	(22)	0.02	1	U	F.LVTIK
577	414.7629	827.5112	827.5116	-0.52	0	66	1.3e-06	1	U	Y.VKAVV
578	414.7632	827.5118	827.5116	0.20	0	(48)	8.2e-05	1	U	Y.VKAVV
726	422.2323	842.4501	842.4498	0.40	1	(27)	0.018	1	U	L.LEDPT
727	422.2324	842.4503	842.4498	0.69	1	27	0.018	1	U	L.LEDPT
1883	490.7385	979.4624	979.4644	-2.03	0	22	0.13	1	U	L.EAKNS
2018	496.2942	990.5739	990.5750	-1.03	1	40	0.00081	1	U	F.YVKAV
2019	496.2949	990.5752	990.5750	0.20	1	(38)	0.00085	1	U	F.YVKAV
2621	526.7479	1051.4812	1051.4822	-1.00	1	72	1e-06	1	U	L.TVEDL
2622	526.7480	1051.4814	1051.4822	-0.76	1	(45)	0.00047	1	U	L.TVEDL
3019	547.2799	1092.5453	1092.5485	-2.94	1	36	0.0056	1	U	L.LEAKN
3020	547.2823	1092.5500	1092.5485	1.42	1	(28)	0.034	1	U	L.LEAKN
4514	614.3506	1226.6867	1226.6871	-0.26	1	(30)	0.0093	1	U	L.VTPVL
4515	614.3525	1226.6905	1226.6871	2.82	1	42	0.00056	1	U	L.VTPVL
5193	434.5774	1300.7103	1300.7099	0.33	0	(42)	0.00087	1	U	L.DASAI
5194	651.3625	1300.7104	1300.7099	0.39	0	59	1.8e-05	1	U	L.DASAI
5195	434.5776	1300.7109	1300.7099	0.77	0	(40)	0.0015	1	U	L.DASAI
5196	651.3640	1300.7135	1300.7099	2.73	0	(51)	9.4e-05	1	U	L.DASAI
5218	652.3227	1302.6308	1302.6312	-0.26	0	68	2.9e-06	1	U	F.NEVNM
5219	652.3246	1302.6346	1302.6312	2.64	0	(68)	3e-06	1	U	F.NEVNM
5235	652.8253	1303.6360	1303.6152	16.0	0	(45)	0.00062	1	U	F.NEVNM
5383	660.3201	1318.6257	1318.6261	-0.28	0	(52)	0.00012	1	U	F.NEVNM
5384	660.3207	1318.6269	1318.6261	0.64	0	(35)	0.0059	1	U	F.NEVNM
5513	668.3193	1334.6240	1334.6210	2.24	0	(37)	0.004	1	U	F.NEVNM
5514	668.3195	1334.6245	1334.6210	2.61	0	(38)	0.0029	1	U	F.NEVNM
5816	687.8862	1373.7579	1373.7588	-0.64	0	37	0.0025	1	U	L.GMADI
5817	458.9270	1373.7593	1373.7588	0.34	0	(21)	0.091	1	U	L.GMADI
6809	509.6317	1525.8734	1525.8715	1.22	2	(26)	0.014	1	U	L.VTIKE

6810	509.6319	1525.8740	1525.8715	1.59	2	39	0.00072	1	U	L.VTIKE
7916	877.9720	1753.9294	1753.9284	0.57	1	25	0.041	1	U	F.GSLMS
8508	970.4686	1938.9226	1938.9323	-5.02	0	(27)	0.044	1	U	L.KRYPE
8511	970.4775	1938.9405	1938.9323	4.24	0	39	0.0033	1	U	L.KRYPE
8606	495.5224	1978.0606	1978.0596	0.53	2	(29)	0.016	1	U	L.LAEHN
8607	495.5230	1978.0629	1978.0596	1.70	2	(22)	0.082	1	U	L.LAEHN
8608	660.3620	1978.0642	1978.0596	2.33	2	44	0.00052	1	U	L.LAEHN

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11. 2::sp|P0A799|PGK_ECOLI **Mass:** 41264 **Score:** 629 **Matches:** 27(24) **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
200	394.7471	787.4796	787.4803	-0.85	0	22	0.023	4	U	L.KNAKT
257	398.1885	794.3625	794.3633	-0.95	1	23	0.082	1	U	Y.AALCD
857	433.7345	865.4544	865.4545	-0.08	0	33	0.0051	1	U	F.GIADK
858	433.7345	865.4544	865.4545	-0.08	0	(21)	0.087	1	U	F.GIADK
1134	452.7606	903.5067	903.5066	0.14	1	39	0.0018	1	U	F.SLLPV
1135	452.7607	903.5068	903.5066	0.27	1	(37)	0.0027	1	U	F.SLLPV
1148	453.2639	904.5132	904.5130	0.20	1	25	0.025	1	U	L.DLAGK
1530	474.7613	947.5081	947.5076	0.53	0	21	0.1	1	U	L.IVGGG
2990	545.2930	1088.5715	1088.5713	0.16	1	45	0.00054	1	U	L.DSLSK
2992	545.2938	1088.5730	1088.5713	1.50	1	(32)	0.013	1	U	L.DSLSK
4797	629.8367	1257.6588	1257.6564	1.86	1	26	0.039	1	U	Y.EADLV
5692	453.5733	1357.6982	1357.6990	-0.62	1	(29)	0.022	1	U	F.IAAQG
5693	679.8580	1357.7014	1357.6990	1.76	1	43	0.00084	1	U	F.IAAQG
5694	679.8587	1357.7028	1357.6990	2.83	1	(38)	0.0032	1	U	F.IAAQG
5790	686.3776	1370.7406	1370.7405	0.04	2	(45)	0.00041	1	U	Y.EADLV
5792	686.3779	1370.7413	1370.7405	0.58	2	53	6.7e-05	1	U	Y.EADLV
6139	714.3075	1426.6004	1426.6001	0.27	1	42	0.00048	1	U	L.GRPTE
6140	714.3088	1426.6031	1426.6001	2.15	1	(36)	0.0022	1	U	L.GRPTE
6391	729.8946	1457.7747	1457.7726	1.51	0	(45)	0.00056	1	U	L.KSVND
6392	729.8951	1457.7757	1457.7726	2.18	0	53	8.7e-05	1	U	L.KSVND
6752	759.9179	1517.8213	1517.8163	3.24	1	36	0.0038	1	U	L.EFVEG
6753	759.9179	1517.8213	1517.8163	3.24	1	(35)	0.0049	1	U	L.EFVEG
7291	811.4038	1620.7931	1620.7883	2.95	2	45	0.00083	1	U	L.VKDYL
8436	953.4731	1904.9316	1904.9302	0.72	0	48	0.0004	1	U	L.TTCNI
8437	953.4765	1904.9384	1904.9302	4.31	0	(46)	0.00064	1	U	L.TTCNI
9094	820.0820	2457.2243	2457.2234	0.33	1	82	1.4e-07	1	U	L.KSVND
9095	820.0846	2457.2319	2457.2234	3.46	1	(66)	4.7e-06	1	U	L.KSVND

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12. 2::sp|P0A9B2|G3P1_ECOLI **Mass:** 35681 **Score:** 603 **Matches:** 37(36) **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
198	394.7289	787.4432	787.4440	-0.95	1	(29)	0.015	1	U	Y.SNKVL
199	394.7297	787.4449	787.4440	1.16	1	29	0.014	1	U	Y.SNKVL
790	425.2268	848.4390	848.4392	-0.24	1	36	0.004	1	U	L.NDNFV
791	425.2269	848.4393	848.4392	0.12	1	(35)	0.0041	1	U	L.NDNFV
1036	447.7555	893.4965	893.5011	-5.14	2	(27)	0.015	1	U	F.VKLVS
1037	447.7564	893.4983	893.5011	-3.15	2	33	0.0033	1	U	F.VKLVS

1042	447.7669	893.5193	893.5011	20.4	2	(23)	0.02	1	U	F.VKLVS
1056	448.7635	895.5124	895.5127	-0.37	1	35	0.0008	1	U	L.DLIAH
1057	448.7636	895.5125	895.5127	-0.16	1	(32)	0.0015	1	U	L.DLIAH
1292	460.7454	919.4762	919.4763	-0.10	0	(31)	0.015	1	U	L.AKVIN
1293	460.7456	919.4767	919.4763	0.45	0	37	0.003	1	U	L.AKVIN
1533	474.7792	947.5439	947.5440	-0.16	0	(32)	0.0041	1	U	M.TIKVG
1534	474.7793	947.5440	947.5440	0.03	0	(39)	0.00079	1	U	M.TIKVG
1543	475.2705	948.5265	948.5280	-1.58	0	40	0.0011	1	U	M.TIKVG
1545	475.2714	948.5282	948.5280	0.21	0	(39)	0.00098	1	U	M.TIKVG
1546	475.2722	948.5299	948.5280	2.02	0	(26)	0.023	1	U	M.TIKVG
3661	576.3245	1150.6345	1150.6346	-0.10	1	39	0.0009	1	U	L.TVRLE
3662	384.5522	1150.6348	1150.6346	0.20	1	(25)	0.023	1	U	L.TVRLE
3663	384.5523	1150.6352	1150.6346	0.52	1	(21)	0.054	1	U	L.TVRLE
3665	576.3261	1150.6375	1150.6346	2.56	1	(38)	0.0011	1	U	L.TVRLE
4575	617.2567	1232.4987	1232.4986	0.14	2	39	0.00048	1	U	L.VSWYD
4576	617.2582	1232.5019	1232.4986	2.72	2	(36)	0.00099	1	U	L.VSWYD
4701	624.8145	1247.6145	1247.6146	-0.10	1	(50)	0.00026	1	U	F.DAKAG
4702	624.8147	1247.6148	1247.6146	0.20	1	(27)	0.048	1	U	F.DAKAG
4703	624.8161	1247.6176	1247.6146	2.45	1	57	4.7e-05	1	U	F.DAKAG
4704	624.8171	1247.6197	1247.6146	4.12	1	(21)	0.19	1	U	F.DAKAG
5134	648.3684	1294.7223	1294.7245	-1.74	0	54	2.5e-05	1	U	F.RVPTP
5135	648.3691	1294.7237	1294.7245	-0.61	0	(41)	0.00052	1	U	F.RVPTP
5578	674.2848	1346.5550	1346.5514	2.67	1	(36)	0.002	1	U	L.GYTED
5579	674.2852	1346.5559	1346.5514	3.31	1	39	0.00093	1	U	L.GYTED
7672	844.4324	1686.8503	1686.8465	2.27	1	51	0.00016	1	U	L.KWDEV
8196	917.9658	1833.9171	1833.9149	1.19	2	(42)	0.0016	1	U	L.KWDEV
8197	917.9675	1833.9205	1833.9149	3.06	2	(46)	0.00064	1	U	L.KWDEV
8198	917.9677	1833.9207	1833.9149	3.19	2	(36)	0.0056	1	U	L.KWDEV
8199	917.9677	1833.9207	1833.9149	3.19	2	63	1.1e-05	1	U	L.KWDEV
8555	653.6904	1958.0493	1958.0506	-0.68	0	49	0.00017	1	U	Y.EQIKA
8557	653.6931	1958.0575	1958.0506	3.53	0	(35)	0.0038	1	U	Y.EQIKA

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13. 1::sp|cRAP022|P00766|CTRA_BOVIN **Mass:** 26220 **Score:** 597 **Matches:** 33(30) **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
530	412.7292	823.4439	823.4440	-0.08	1	(51)	4.9e-05	1	U	L.KLST
531	412.7292	823.4439	823.4440	-0.01	1	55	2.1e-05	1	U	L.KLST
941	437.7555	873.4965	873.4960	0.54	1	48	0.00019	1	U	W.TLVG
942	437.7556	873.4967	873.4960	0.77	1	(32)	0.0086	1	U	W.TLVG
2125	501.2552	1000.4959	1000.4938	2.19	0	(22)	0.075	1	U	Y.TNAN
2137	501.7453	1001.4761	1001.4778	-1.66	0	31	0.009	1	U	Y.TNAN
2138	501.7454	1001.4762	1001.4778	-1.60	0	(31)	0.0097	1	U	Y.TNAN
2304	508.7851	1015.5556	1015.5550	0.68	1	53	7.1e-05	1	U	L.TINN
2305	508.7854	1015.5562	1015.5550	1.21	1	(42)	0.00084	1	U	L.TINN
2306	508.7859	1015.5572	1015.5550	2.17	1	(49)	0.00017	1	U	L.TINN
2307	508.7860	1015.5574	1015.5550	2.41	1	(44)	0.00056	1	U	L.TINN
2455	515.2952	1028.5759	1028.5767	-0.78	1	(22)	0.074	1	U	Y.ARVT
2456	515.2965	1028.5785	1028.5767	1.71	1	28	0.015	1	U	Y.ARVT
3304	561.7929	1121.5713	1121.5717	-0.39	1	50	0.00021	1	U	W.QVSL
3305	561.7935	1121.5724	1121.5717	0.59	1	(41)	0.0016	1	U	W.QVSL
3307	561.7944	1121.5743	1121.5717	2.32	1	(27)	0.035	1	U	W.QVSL
3308	561.7946	1121.5746	1121.5717	2.56	1	(42)	0.0013	1	U	W.QVSL

3633	575.2534	1148.4923	1148.4921	0.21	1	33	0.0043	1	U	F.CGGS
3634	575.2553	1148.4961	1148.4921	3.50	1	(24)	0.038	1	U	F.CGGS
5387	660.3442	1318.6738	1318.6728	0.74	0	41	0.0016	1	U	F.DQGS
5389	660.3456	1318.6766	1318.6728	2.86	0	(36)	0.0046	1	U	F.DQGS
5486	665.8648	1329.7151	1329.7140	0.82	2	(33)	0.0072	1	U	Y.NSLT
5487	665.8663	1329.7181	1329.7140	3.11	2	49	0.00018	1	U	Y.NSLT
7200	799.9576	1597.9007	1597.8940	4.19	2	25	0.022	1	U	Y.ARVT
7649	842.3809	1682.7472	1682.7458	0.82	0	38	0.0022	1	U	F.SQTV
7650	842.3825	1682.7505	1682.7458	2.78	0	(23)	0.084	1	U	F.SQTV
7864	869.9589	1737.9033	1737.9009	1.35	1	68	2.3e-06	1	U	Y.TNAN
7865	869.9605	1737.9065	1737.9009	3.18	1	(46)	0.00038	1	U	Y.TNAN
7868	870.4548	1738.8950	1738.8849	5.77	1	(26)	0.048	1	U	Y.TNAN
7869	870.4564	1738.8982	1738.8849	7.60	1	(36)	0.0043	1	U	Y.TNAN
8011	892.4422	1782.8698	1782.8689	0.52	0	48	0.00032	1	U	L.SRIV
8012	892.4423	1782.8700	1782.8689	0.58	0	(29)	0.024	1	U	L.SRIV
8699	1010.0005	2017.9864	2017.9780	4.20	0	28	0.04	1	U	W.VVTA

Proteins matching a subset of these peptides:

1::sp|cRAP023|P00767|CTRB_BOVIN **Mass:** 26309 **Score:** 28 **Matches:** 1(1) **Seque**

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

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14. 2::sp|P0A910|OMPA_ECOLI **Mass:** 37292 **Score:** 567 **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
1300	461.7658	921.5171	921.5171	-0.01	2	(27)	0.017	1	U	F.TLKSD
1301	461.7660	921.5174	921.5171	0.32	2	30	0.0079	1	U	F.TLKSD
1393	468.2416	934.4687	934.4695	-0.87	1	20	0.15	1	U	Y.TRLGG
1589	477.7011	953.3876	953.3879	-0.33	1	(23)	0.029	1	U	W.SQYHD
1590	477.7020	953.3894	953.3879	1.60	1	27	0.015	1	U	W.SQYHD
2077	499.2334	996.4523	996.4512	1.08	0	35	0.0043	1	U	Y.TDRIG
2634	527.2440	1052.4734	1052.4749	-1.50	2	26	0.042	1	U	Y.DWLGR
2635	527.2440	1052.4735	1052.4749	-1.38	2	(22)	0.092	1	U	Y.DWLGR
2641	527.2701	1052.5257	1052.5251	0.64	0	33	0.01	1	U	W.RADTK
2642	527.2708	1052.5269	1052.5251	1.80	0	(31)	0.014	1	U	W.RADTK
2927	542.8215	1083.6285	1083.6288	-0.25	0	44	0.00029	1	U	Y.AITPE
2929	542.8228	1083.6309	1083.6288	2.00	0	(33)	0.0028	1	U	Y.AITPE
4425	609.2754	1216.5363	1216.5360	0.26	1	(55)	3.2e-05	1	U	L.GYTDR
4426	609.2771	1216.5396	1216.5360	2.98	1	59	1.2e-05	1	U	L.GYTDR
4782	629.3163	1256.6180	1256.6150	2.41	0	(31)	0.011	1	U	Y.GKNHD
4783	629.3166	1256.6187	1256.6150	3.00	0	35	0.0053	1	U	Y.GKNHD
5046	642.8029	1283.5912	1283.5921	-0.76	1	39	0.0024	1	U	L.GYPIT
5047	642.8030	1283.5915	1283.5921	-0.48	1	(24)	0.069	1	U	L.GYPIT
5497	666.8441	1331.6737	1331.6721	1.19	2	25	0.063	1	U	L.KPEGQ
5543	670.8820	1339.7494	1339.7459	2.57	1	36	0.0019	1	U	F.NKATL
5549	671.8633	1341.7121	1341.7140	-1.40	1	(50)	0.00014	1	U	L.SNLDP
5552	671.8658	1341.7171	1341.7140	2.33	1	52	9.2e-05	1	U	L.SNLDP
7572	835.9541	1669.8936	1669.8887	2.98	2	59	1.5e-05	1	U	Y.SQLSN
7573	835.9544	1669.8943	1669.8887	3.35	2	(49)	0.00015	1	U	Y.SQLSN
7906	877.4174	1752.8203	1752.8179	1.34	1	(41)	0.002	1	U	F.INNNG
7907	877.4175	1752.8204	1752.8179	1.40	1	(37)	0.0048	1	U	F.INNNG
7913	877.9099	1753.8053	1753.8020	1.89	1	(48)	0.00037	1	U	F.INNNG
7914	877.9113	1753.8081	1753.8020	3.50	1	56	5.4e-05	1	U	F.INNNG

15. 2::sp|P0AEX9|MALE_ECOLI **Mass:** 43360 **Score:** 554 **Matches:** 25(19) **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
1188	455.7373	909.4600	909.4596	0.42	1	20	0.14	1	U	F.QDKLY
2008	496.2585	990.5025	990.5022	0.27	0	(20)	0.17	1	U	L.AEITP
2009	496.2591	990.5036	990.5022	1.44	0	26	0.041	1	U	L.AEITP
2242	507.2513	1012.4880	1012.4865	1.46	2	29	0.017	1	U	L.AKEFL
3122	552.8003	1103.5860	1103.5863	-0.21	1	38	0.0023	1	U	L.LAEIT
3512	570.7801	1139.5456	1139.5459	-0.20	0	(56)	3.5e-05	1	U	W.SNIDT
3515	570.7810	1139.5475	1139.5459	1.42	0	56	3.3e-05	1	U	W.SNIDT
3715	578.8079	1155.6013	1155.6023	-0.86	1	36	0.003	1	U	W.EEIPA
4916	636.3346	1270.6546	1270.6517	2.31	0	(39)	0.0019	1	U	L.SAGIN
4917	636.3348	1270.6551	1270.6517	2.71	0	40	0.0013	1	U	L.SAGIN
6104	711.8909	1421.7673	1421.7667	0.44	1	(34)	0.0042	1	U	Y.NKDLL
6105	711.8910	1421.7675	1421.7667	0.61	1	36	0.0026	1	U	Y.NKDLL
6184	717.8379	1433.6613	1433.6609	0.31	0	(62)	1.1e-05	1	U	F.NKGET
6185	717.8397	1433.6649	1433.6609	2.78	0	66	5.1e-06	1	U	F.NKGET
6914	514.9419	1541.8038	1541.8049	-0.71	0	(39)	0.0019	1	U	Y.DIKDV
6915	514.9427	1541.8062	1541.8049	0.85	0	(42)	0.001	1	U	Y.DIKDV
6916	771.9107	1541.8069	1541.8049	1.26	0	83	7.6e-08	1	U	Y.DIKDV
6917	771.9124	1541.8103	1541.8049	3.46	0	(69)	2.2e-06	1	U	Y.DIKDV
7009	780.9168	1559.8191	1559.8195	-0.28	2	47	0.00043	1	U	Y.AQSGL
7010	780.9169	1559.8192	1559.8195	-0.20	2	(25)	0.061	1	U	Y.AQSGL
7891	582.9733	1745.8980	1745.8948	1.85	1	20	0.22	1	U	L.SAGIN
8043	597.6476	1789.9211	1789.9210	0.03	1	37	0.0046	1	U	Y.DIKDV
8044	597.6478	1789.9217	1789.9210	0.35	1	(34)	0.0079	1	U	Y.DIKDV
8369	628.3247	1881.9521	1881.9512	0.46	2	(21)	0.15	1	U	L.AEITP
8370	628.3247	1881.9523	1881.9512	0.56	2	23	0.1	1	U	L.AEITP

16. 2::sp|P0A836|SUCC_ECOLI **Mass:** 41652 **Score:** 511 **Matches:** 26(23) **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
3034	547.7837	1093.5528	1093.5511	1.54	0	(26)	0.049	1	U	L.AMGTM
3035	547.7845	1093.5545	1093.5511	3.11	0	31	0.013	1	U	L.AMGTM
3275	559.8135	1117.6124	1117.6132	-0.67	2	(30)	0.015	1	U	L.GLEGK
3276	559.8138	1117.6130	1117.6132	-0.14	2	32	0.009	1	U	L.GLEGK
3758	580.3149	1158.6152	1158.6132	1.74	0	65	6.2e-06	1	U	L.VEAAT
3759	580.3150	1158.6154	1158.6132	1.95	0	(60)	2e-05	1	U	L.VEAAT
3983	589.2949	1176.5752	1176.5775	-1.98	2	(22)	0.14	1	U	L.DGKLG
3984	589.2957	1176.5769	1176.5775	-0.52	2	31	0.019	1	U	L.DGKLG
3985	589.2962	1176.5778	1176.5775	0.30	2	(24)	0.09	1	U	L.DGKLG
3986	589.2974	1176.5803	1176.5775	2.37	2	(31)	0.019	1	U	L.DGKLG
4807	630.3552	1258.6958	1258.6955	0.20	1	31	0.011	1	U	L.VITKQ
4808	630.3572	1258.6998	1258.6955	3.41	1	(25)	0.038	1	U	L.VITKQ
5412	661.8471	1321.6797	1321.6765	2.39	1	59	2.5e-05	1	U	L.VEAAT
5874	693.8650	1385.7155	1385.7151	0.35	0	104	7.5e-10	1	U	L.TDAAQ
5875	693.8652	1385.7159	1385.7151	0.61	0	(101)	1.4e-09	1	U	L.TDAAQ

5878	694.3647	1386.7148	1386.6991	11.4	0	(41)	0.0018	1	U	L.TDAAQ
6242	481.3035	1440.8887	1440.8915	-1.99	1	25	0.0046	1	U	F.KIILS
6243	481.3043	1440.8910	1440.8915	-0.41	1	(21)	0.012	1	U	F.KIILS
6874	768.8884	1535.7622	1535.7580	2.73	0	40	0.0024	1	U	L.DVGGG
6875	768.8889	1535.7631	1535.7580	3.35	0	(38)	0.0047	1	U	L.DVGGG
7438	825.4279	1648.8412	1648.8421	-0.54	1	(37)	0.0046	1	U	F.LDVGG
7439	550.6214	1648.8424	1648.8421	0.19	1	(28)	0.038	1	U	F.LDVGG
7440	550.6225	1648.8457	1648.8421	2.19	1	(23)	0.12	1	U	F.LDVGG
7441	825.4313	1648.8480	1648.8421	3.60	1	50	0.00022	1	U	F.LDVGG
8828	701.3371	2100.9895	2100.9898	-0.17	0	(42)	0.0014	1	U	Y.ACTTP
8829	701.3387	2100.9942	2100.9898	2.09	0	45	0.00065	1	U	Y.ACTTP

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17. 2::sp|P0A8L1|SYS_ECOLI **Mass:** 48669 **Score:** 484 **Matches:** 25(23) **Sequences:** 1

Serine--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=serS PE=1 SV=1

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
592	415.7522	829.4898	829.4909	-1.35	1	30	0.0095	1	U	F.KLDVD
593	415.7522	829.4898	829.4909	-1.28	1	(26)	0.026	1	U	F.KLDVD
634	417.7396	833.4646	833.4647	-0.15	1	(46)	0.00022	1	U	L.DFAAA
635	417.7398	833.4651	833.4647	0.45	1	46	0.00021	1	U	L.DFAAA
1707	483.2509	964.4873	964.4866	0.76	2	27	0.037	1	U	Y.LVNQD
2386	512.3076	1022.6006	1022.6012	-0.60	1	(49)	3.9e-05	1	U	Y.ALIPT
2387	512.3088	1022.6031	1022.6012	1.90	1	50	2.5e-05	1	U	Y.ALIPT
2435	514.7908	1027.5670	1027.5662	0.79	0	26	0.026	2	U	L.QAEIR
4551	615.8092	1229.6038	1229.6041	-0.18	1	36	0.0039	1	U	F.DFEVR
4553	615.8110	1229.6074	1229.6041	2.70	1	(34)	0.0074	1	U	F.DFEVR
4611	619.2858	1236.5570	1236.5557	1.03	0	(20)	0.15	1	U	Y.REISS
4612	619.2861	1236.5577	1236.5557	1.62	0	30	0.015	1	U	Y.REISS
4640	621.3295	1240.6444	1240.6411	2.63	0	51	9.3e-05	1	U	L.RNEPD
4641	621.3295	1240.6445	1240.6411	2.72	0	(35)	0.0038	1	U	L.RNEPD
5458	664.3643	1326.7140	1326.7143	-0.25	1	(37)	0.0025	1	U	L.DALQA
5459	664.3643	1326.7141	1326.7143	-0.16	1	40	0.0013	1	U	L.DALQA
5553	448.5398	1342.5977	1342.5976	0.06	2	31	0.012	1	U	F.MLDLH
5554	448.5400	1342.5981	1342.5976	0.40	2	(24)	0.055	1	U	F.MLDLH
5599	675.8561	1349.6976	1349.6980	-0.27	2	28	0.027	1	U	Y.GTGQL
5601	675.8569	1349.6993	1349.6980	0.99	2	(25)	0.052	1	U	Y.GTGQL
5702	680.3057	1358.5969	1358.5925	3.25	2	(27)	0.021	1	U	F.MLDLH
6345	727.3859	1452.7572	1452.7572	-0.06	0	28	0.021	1	U	Y.QQADG
6346	727.3879	1452.7613	1452.7572	2.81	0	(21)	0.1	1	U	Y.QQADG
7524	831.3749	1660.7353	1660.7329	1.48	1	(56)	3.4e-05	1	U	F.HTRPL
7526	831.3765	1660.7385	1660.7329	3.40	1	59	1.6e-05	1	U	F.HTRPL

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18. 2::sp|P0A7D4|PURA_ECOLI **Mass:** 47543 **Score:** 470 **Matches:** 35(23) **Sequences:**

Adenylosuccinate synthetase OS=Escherichia coli (strain K12) OX=83333 GN=purA PE=1 S

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
1105	451.2713	900.5281	900.5280	0.10	1	(22)	0.049	1	U	L.DGLK
1106	451.2713	900.5281	900.5280	0.10	1	22	0.049	1	U	L.DGLK
1813	486.7900	971.5654	971.5651	0.28	0	32	0.0051	1	U	L.VING
1814	486.7904	971.5663	971.5651	1.16	0	(20)	0.086	1	U	L.VING

2057	498.2341	994.4536	994.4542	-0.56	1	22	0.083	1	U	F.LCKQ
2058	498.2343	994.4540	994.4542	-0.20	1	(22)	0.091	1	U	F.LCKQ
2887	540.7346	1079.4547	1079.4560	-1.21	0	22	0.063	1	U	L.DIDH
4529	410.2427	1227.7064	1227.7074	-0.86	2	(21)	0.065	1	U	L.DVLD
4531	410.2429	1227.7068	1227.7074	-0.49	2	(27)	0.017	1	U	L.DVLD
4533	614.8620	1227.7094	1227.7074	1.63	2	27	0.015	1	U	L.DVLD
4632	620.3194	1238.6242	1238.6216	2.12	1	(21)	0.13	1	U	F.AEKL
4633	620.3201	1238.6256	1238.6216	3.20	1	(24)	0.068	1	U	F.AEKL
4652	622.3480	1242.6814	1242.6820	-0.48	1	(22)	0.095	2	U	W.GDEG
4653	415.2345	1242.6816	1242.6820	-0.30	1	(21)	0.1	1	U	W.GDEG
4654	622.3482	1242.6819	1242.6820	-0.07	1	26	0.034	1	U	W.GDEG
4758	628.3162	1254.6178	1254.6165	0.97	1	31	0.014	1	U	F.AEKL
4759	628.3164	1254.6183	1254.6165	1.37	1	(31)	0.014	1	U	F.AEKL
5444	442.8943	1325.6611	1325.6616	-0.33	2	(22)	0.12	1	U	L.RVGD
5445	442.8947	1325.6624	1325.6616	0.62	2	24	0.066	1	U	L.RVGD
6466	735.9174	1469.8203	1469.8202	0.07	0	58	1.5e-05	1	U	L.RENV
6467	735.9177	1469.8208	1469.8202	0.39	0	(46)	0.00025	1	U	L.RENV
6473	736.4111	1470.8076	1470.8042	2.30	0	(48)	0.00018	1	U	L.RENV
6474	736.4113	1470.8081	1470.8042	2.64	0	(56)	3.2e-05	1	U	L.RENV
6541	740.3686	1478.7226	1478.7213	0.90	0	57	4.5e-05	1	U	Y.VTSS
6542	740.3687	1478.7229	1478.7213	1.06	0	(56)	6.3e-05	1	U	Y.VTSS
6690	753.8688	1505.7230	1505.7224	0.36	1	(23)	0.12	1	U	W.KGVE
6691	753.8713	1505.7280	1505.7224	3.70	1	(33)	0.013	1	U	W.KGVE
6775	761.8651	1521.7157	1521.7174	-1.11	1	50	0.00025	1	U	W.KGVE
6777	761.8680	1521.7215	1521.7174	2.74	1	(45)	0.00067	1	U	W.KGVE
6846	766.4063	1530.7981	1530.7963	1.13	1	(50)	0.00022	1	U	Y.QKVL
6847	766.4076	1530.8006	1530.7963	2.80	1	(49)	0.00023	1	U	Y.QKVL
6951	774.4047	1546.7949	1546.7913	2.35	1	54	7.8e-05	1	U	Y.QKVL
6952	774.4050	1546.7954	1546.7913	2.67	1	(50)	0.0002	1	U	Y.QKVL
8788	1037.4770	2072.9395	2072.9401	-0.27	2	(45)	0.00052	1	U	W.KGVE
8789	1037.4785	2072.9425	2072.9401	1.15	2	46	0.00041	1	U	W.KGVE

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19. 2::sp|P08200|IDH_ECOLI **Mass:** 46070 **Score:** 462 **Matches:** 24(20) **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	Peptid
1403	468.7430	935.4714	935.4712	0.20	2	22	0.12	1	U	L.RQEL
1577	477.2221	952.4297	952.4290	0.65	1	(32)	0.0084	1	U	F.TEGA
1578	477.2222	952.4299	952.4290	0.90	1	37	0.0027	1	U	F.TEGA
2230	506.7503	1011.4860	1011.4873	-1.29	0	(20)	0.14	1	U	Y.TGEK
2231	506.7505	1011.4865	1011.4873	-0.73	0	27	0.029	1	U	Y.TGEK
3694	578.3057	1154.5969	1154.5972	-0.21	0	(23)	0.054	1	U	L.NVPE
3695	578.3071	1154.5997	1154.5972	2.21	0	26	0.031	1	U	L.NVPE
3909	586.3057	1170.5968	1170.6244	-23.62	2	21	0.11	1	U	L.NVAL
3957	587.8063	1173.5980	1173.5990	-0.82	0	40	0.002	1	U	Y.AIAN
3958	587.8082	1173.6019	1173.5990	2.52	0	(30)	0.019	1	U	Y.AIAN
4131	596.8328	1191.6511	1191.6499	0.98	0	52	8.1e-05	1	U	L.KVVD
4132	596.8337	1191.6529	1191.6499	2.53	0	(42)	0.00086	1	U	L.KVVD
5306	656.3665	1310.7185	1310.7194	-0.70	0	(38)	0.0015	1	U	Y.AGQD
5307	656.3687	1310.7227	1310.7194	2.55	0	62	5.3e-06	1	U	Y.AGQD
6090	474.5930	1420.7571	1420.7562	0.62	0	(36)	0.0035	1	U	W.KADS
6092	474.5931	1420.7576	1420.7562	1.00	0	(36)	0.0041	1	U	W.KADS
6093	711.3872	1420.7597	1420.7562	2.52	0	(46)	0.00041	1	U	W.KADS

6094	711.3876	1420.7607	1420.7562	3.20	0	57	3.1e-05	1	U	W.KADS
6669	751.8743	1501.7341	1501.7334	0.45	0	31	0.019	1	U	Y.IEGD
6670	751.8757	1501.7369	1501.7334	2.32	0	(22)	0.15	1	U	Y.IEGD
7356	816.8863	1631.7581	1631.7580	0.10	2	55	5.9e-05	1	U	L.AREE
7357	816.8865	1631.7585	1631.7580	0.34	2	(53)	9.3e-05	1	U	L.AREE
7707	848.4574	1694.9002	1694.8991	0.65	1	35	0.004	1	U	L.QNGK
7709	848.4591	1694.9035	1694.8991	2.60	1	(30)	0.013	1	U	L.QNGK

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20. 2::sp|P0A8M0|SYN_ECOLI **Mass:** 52766 **Score:** 434 **Matches:** 22(18) **Sequences:** 1
Asparagine--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=asnS PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
1073	449.7658	897.5171	897.5172	-0.09	0	48	6.1e-05	1	U	M.SVVP
1074	449.7658	897.5171	897.5172	-0.03	0	(36)	0.001	1	U	M.SVVP
1391	468.2310	934.4474	934.4470	0.40	1	(29)	0.021	1	U	W.MLEP
1392	468.2312	934.4479	934.4470	0.98	1	33	0.0089	1	U	W.MLEP
2412	513.7481	1025.4815	1025.4818	-0.24	1	30	0.014	1	U	L.ERFI
2413	513.7491	1025.4836	1025.4818	1.77	1	(22)	0.091	1	U	L.ERFI
3876	584.7789	1167.5433	1167.5408	2.16	1	(29)	0.02	1	U	L.TVSG
3877	584.7798	1167.5450	1167.5408	3.63	1	38	0.0023	1	U	L.TVSG
3889	585.7703	1169.5260	1169.5241	1.63	1	26	0.033	1	U	F.IEAD
5090	646.3012	1290.5879	1290.5840	2.97	1	(55)	4.7e-05	1	U	W.GVDL
5091	646.3017	1290.5888	1290.5840	3.73	1	55	4.9e-05	1	U	W.GVDL
5356	658.8451	1315.6756	1315.6772	-1.19	0	68	3.5e-06	1	U	F.EIQA
5357	658.8456	1315.6767	1315.6772	-0.36	0	(62)	1.4e-05	1	U	F.EIQA
5364	659.3449	1316.6753	1316.6612	10.7	0	(22)	0.11	1	U	F.EIQA
5463	664.7875	1327.5604	1327.5602	0.16	0	(32)	0.0049	1	U	L.ITAS
5464	664.7892	1327.5638	1327.5602	2.72	0	(22)	0.051	1	U	L.ITAS
5563	672.7852	1343.5558	1343.5551	0.49	0	(46)	0.00017	1	U	L.ITAS
5564	672.7855	1343.5565	1343.5551	1.02	0	53	3.3e-05	1	U	L.ITAS
5697	453.5844	1357.7313	1357.7314	-0.03	0	23	0.073	2	U	F.AERV
5728	454.8810	1361.6211	1361.6497	-20.98	0	22	0.12	1	U	L.NEDG
6048	708.3637	1414.7127	1414.7126	0.13	2	(27)	0.035	1	U	F.ANLN
6049	708.3651	1414.7157	1414.7126	2.19	2	38	0.0028	1	U	F.ANLN

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21. 2::sp|P0A7Z4|RPOA_ECOLI **Mass:** 36717 **Score:** 426 **Matches:** 19(16) **Sequences:**
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	Peptid
157	391.7110	781.4074	781.4082	-1.03	1	(22)	0.046	1	U	F.GHTL
158	391.7111	781.4077	781.4082	-0.64	1	31	0.0062	1	U	F.GHTL
482	409.2368	816.4590	816.4593	-0.30	0	25	0.04	2	U	L.TEIK
484	409.2369	816.4593	816.4593	0.07	0	(22)	0.092	2	U	L.TEIK
1387	467.7534	933.4923	933.4920	0.35	0	44	0.00059	1	U	Y.SPVE
1388	467.7536	933.4926	933.4920	0.67	0	(43)	0.00071	1	U	Y.SPVE
4536	615.3278	1228.6411	1228.6452	-3.31	1	(25)	0.053	2	U	L.KAEA
4537	615.3285	1228.6425	1228.6452	-2.12	1	26	0.045	2	U	L.KAEA
5454	663.8915	1325.7684	1325.7667	1.29	0	53	2.3e-05	1	U	L.AVRV
5455	663.8922	1325.7697	1325.7667	2.30	0	(49)	6.3e-05	1	U	L.AVRV

5791	686.3776	1370.7407	1370.7405	0.11	1	34	0.0064	1	U	Y.IGDL
6578	742.9202	1483.8259	1483.8246	0.88	2	72	5.9e-07	1	U	Y.IGDL
6579	742.9218	1483.8291	1483.8246	3.01	2	(66)	2.3e-06	1	U	Y.IGDL
8286	619.6662	1855.9768	1855.9752	0.87	1	29	0.019	1	U	Y.NVEA
8289	928.9969	1855.9792	1855.9752	2.19	1	(23)	0.081	1	U	Y.NVEA
8898	1096.9948	2191.9749	2191.9766	-0.74	1	(71)	1.1e-06	1	U	L.SSMP
8900	1096.9952	2191.9759	2191.9766	-0.30	1	83	7.8e-08	1	U	L.SSMP
8925	1104.9899	2207.9652	2207.9715	-2.86	1	(81)	9.8e-08	1	U	L.SSMP
9077	813.1095	2436.3067	2436.3012	2.23	2	29	0.011	1	U	L.RDVR

22. 2::sp|P0A6E4|ASSY_ECOLI **Mass:** 50038 **Score:** 425 **Matches:** 18(18) **Sequences:**
Argininosuccinate synthase OS=Escherichia coli (strain K12) OX=83333 GN=argG PE=1 SV
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1870	489.7538	977.4930	977.4930	-0.02	0	41	0.0014	1	U	Y.KGNDI
1871	489.7546	977.4947	977.4930	1.68	0	(41)	0.0017	1	U	Y.KGNDI
2991	545.2934	1088.5722	1088.5713	0.84	1	(29)	0.022	1	U	Y.SILNT
2993	545.2941	1088.5736	1088.5713	2.07	1	54	6.5e-05	1	U	Y.SILNT
3262	559.3082	1116.6018	1116.6027	-0.78	0	48	0.00027	1	U	W.VASQI
3263	559.3089	1116.6032	1116.6027	0.53	0	(29)	0.022	1	U	W.VASQI
3530	571.2877	1140.5608	1140.5564	3.87	1	27	0.023	1	U	Y.KGNDI
4614	619.3243	1236.6340	1236.6350	-0.81	1	27	0.043	1	U	L.DITDT
5612	676.2880	1350.5614	1350.5575	2.83	1	30	0.0067	1	U	Y.TANLG
5613	676.2886	1350.5627	1350.5575	3.84	1	(28)	0.0097	1	U	Y.TANLG
6075	710.3237	1418.6329	1418.6314	1.08	0	38	0.0021	1	U	L.TGIHN
7785	573.6359	1717.8860	1717.8887	-1.57	0	33	0.0096	1	U	W.DESVK
7786	573.6382	1717.8929	1717.8887	2.47	0	(30)	0.022	1	U	W.DESVK
8423	951.4647	1900.9148	1900.9126	1.13	1	70	2e-06	1	U	L.SSSAA
8424	951.4665	1900.9184	1900.9126	3.05	1	(57)	4.2e-05	1	U	L.SSSAA
8433	635.6630	1903.9671	1903.9680	-0.48	1	(52)	0.00016	1	U	F.WDESV
8434	635.6634	1903.9683	1903.9680	0.19	1	57	4.4e-05	1	U	F.WDESV
8435	952.9920	1903.9694	1903.9680	0.78	1	(41)	0.0017	1	U	F.WDESV

23. 2::sp|P0A6P1|EFTS_ECOLI **Mass:** 30518 **Score:** 422 **Matches:** 22(20) **Sequences:**
Elongation factor Ts OS=Escherichia coli (strain K12) OX=83333 GN=tsf PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3445	568.2847	1134.5549	1134.5557	-0.72	1	(25)	0.071	1	U	F.TGEVS
3448	568.2861	1134.5577	1134.5557	1.75	1	56	5e-05	1	U	F.TGEVS
4083	594.8195	1187.6244	1187.6220	1.99	0	(25)	0.053	1	U	F.VMEPS
4087	594.8202	1187.6259	1187.6220	3.32	0	(22)	0.11	1	U	F.VMEPS
4288	602.8173	1203.6201	1203.6169	2.63	0	(29)	0.023	1	U	F.VMEPS
4289	602.8175	1203.6204	1203.6169	2.92	0	36	0.0056	1	U	F.VMEPS
5191	651.3609	1300.7072	1300.7061	0.91	1	45	0.00049	1	U	F.VMEPS
5192	651.3622	1300.7098	1300.7061	2.87	1	(27)	0.035	1	U	F.VMEPS
5391	440.5700	1318.6881	1318.6881	0.02	1	(36)	0.0042	1	U	L.KAQFE
5392	660.3514	1318.6882	1318.6881	0.10	1	(38)	0.0028	1	U	L.KAQFE
5393	440.5702	1318.6887	1318.6881	0.50	1	(29)	0.024	1	U	L.KAQFE
5394	660.3540	1318.6934	1318.6881	4.07	1	43	0.00084	1	U	L.KAQFE
5960	700.8851	1399.7557	1399.7559	-0.11	0	(42)	0.0009	1	U	L.DAAVA

5961	700.8865	1399.7584	1399.7559	1.81	0	55	3.7e-05	1	U	L.DAAVA
6329	726.3481	1450.6817	1450.6828	-0.71	0	72	1.5e-06	1	U	F.EVGEG
6330	726.3485	1450.6825	1450.6828	-0.20	0	(57)	4.9e-05	1	U	F.EVGEG
8322	623.3199	1866.9380	1866.9363	0.90	1	43	0.0013	1	U	F.IRFEV
8323	623.3207	1866.9402	1866.9363	2.07	1	(42)	0.0013	1	U	F.IRFEV
8482	964.0416	1926.0687	1926.0674	0.70	1	72	4.7e-07	1	U	F.ADKVL
8483	964.0416	1926.0687	1926.0674	0.70	1	(54)	3e-05	1	U	F.ADKVL
8484	643.0309	1926.0710	1926.0674	1.89	1	(22)	0.044	1	U	F.ADKVL
8485	643.0314	1926.0725	1926.0674	2.65	1	(30)	0.008	1	U	F.ADKVL

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24. 2::sp|P27306|STHA_ECOLI **Mass:** 51984 **Score:** 415 **Matches:** 19(19) **Sequences:**
Soluble pyridine nucleotide transhydrogenase 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
540	413.2128	824.4110	824.4102	0.94	0	34	0.0044	1	U	L.TAMKV
541	413.2128	824.4110	824.4102	0.94	0	(33)	0.006	1	U	L.TAMKV
2367	511.7582	1021.5019	1021.5015	0.42	0	36	0.0058	1	U	F.VIACG
2368	511.7600	1021.5054	1021.5015	3.83	0	(28)	0.032	1	U	F.VIACG
2539	521.7855	1041.5564	1041.5567	-0.31	0	26	0.025	1	U	Y.DQGRI
3127	553.2654	1104.5163	1104.5160	0.33	0	32	0.01	1	U	Y.ANGRT
3128	553.2658	1104.5169	1104.5160	0.89	0	(30)	0.016	1	U	Y.ANGRT
3236	558.2387	1114.4629	1114.4615	1.27	0	(29)	0.0099	1	U	Y.QNVGG
3237	558.2394	1114.4642	1114.4615	2.47	0	41	0.00061	1	U	Y.QNVGG
4753	628.2788	1254.5431	1254.5438	-0.59	2	78	1.9e-07	1	U	L.AFLDQ
4754	628.2801	1254.5456	1254.5438	1.45	2	(65)	4.2e-06	1	U	L.AFLDQ
4903	636.2763	1270.5379	1270.5387	-0.61	2	(57)	1.8e-05	1	U	L.AFLDQ
4904	636.2772	1270.5398	1270.5387	0.82	2	(53)	5.3e-05	1	U	L.AFLDQ
6162	715.8663	1429.7180	1429.7161	1.31	1	53	0.0001	1	U	L.QNIGL
6165	715.8664	1429.7182	1429.7161	1.48	1	(45)	0.00066	1	U	L.QNIGL
6979	777.3967	1552.7789	1552.7773	1.03	1	(43)	0.0011	1	U	Y.AVGDV
6980	777.3980	1552.7815	1552.7773	2.68	1	46	0.0005	1	U	Y.AVGDV
7337	815.4388	1628.8631	1628.8621	0.63	0	69	2.3e-06	1	U	Y.TIPEI
7338	815.4392	1628.8639	1628.8621	1.08	0	(57)	3e-05	1	U	Y.TIPEI

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25. 2::sp|P0C8J8|GATZ_ECOLI **Mass:** 47535 **Score:** 404 **Matches:** 21(17) **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
285	399.7069	797.3993	797.3993	0.03	0	25	0.028	1	U	L.IMDKI
286	399.7071	797.3996	797.3993	0.33	0	(20)	0.091	1	U	L.IMDKI
503	410.2396	818.4647	818.4650	-0.32	1	24	0.036	1	U	F.ALREA
504	410.2397	818.4649	818.4650	-0.15	1	(21)	0.064	1	U	F.ALREA
615	416.7497	831.4848	831.4854	-0.81	1	33	0.0027	1		L.KVGPA
616	416.7499	831.4852	831.4854	-0.28	1	(29)	0.0061	1		L.KVGPA
805	425.7370	849.4594	849.4596	-0.28	0	25	0.035	1	U	F.TIADK
806	425.7370	849.4594	849.4596	-0.21	0	(21)	0.086	1	U	F.TIADK
1242	458.2376	914.4607	914.4610	-0.38	1	29	0.015	1	U	W.ELVRD
1243	458.2376	914.4607	914.4610	-0.38	1	(25)	0.035	1	U	W.ELVRD
1364	466.2460	930.4774	930.4770	0.44	0	(24)	0.068	2	U	F.ERIQS
1365	466.2461	930.4776	930.4770	0.57	0	27	0.031	1	U	F.ERIQS

2267	507.7778	1013.5410	1013.5393	1.67	1	44	0.0004	1	U	F.ALAQI
4493	613.8407	1225.6668	1225.6666	0.18	0	49	0.00013	1	U	L.APETV
4494	613.8420	1225.6695	1225.6666	2.37	0	(46)	0.00023	1	U	L.APETV
4724	625.8050	1249.5954	1249.5939	1.25	0	56	5.7e-05	1	U	L.IEATS
4725	625.8077	1249.6009	1249.5939	5.65	0	(52)	0.00014	1	U	L.IEATS
7094	789.3654	1576.7163	1576.7151	0.74	0	48	0.00025	1	U	F.AAESV
7532	831.8865	1661.7584	1661.7566	1.06	0	47	0.00037	1	U	W.QQENA
7603	839.8863	1677.7581	1677.7515	3.94	0	(37)	0.0035	1	U	W.QQENA
7604	839.8864	1677.7583	1677.7515	4.01	0	(32)	0.014	1	U	W.QQENA

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26. 2::sp|P0A6H5|HSLU_ECOLI **Mass:** 49677 **Score:** 395 **Matches:** 20(17) **Sequences:**
ATP-dependent protease ATPase subunit HslU OS=Escherichia coli (strain K12) OX=83333
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
605	416.2398	830.4649	830.4650	-0.08	1	(42)	0.00071	1	U	L.AKLAN
606	416.2399	830.4653	830.4650	0.36	1	45	0.00041	1	U	L.AKLAN
1399	468.2814	934.5483	934.5488	-0.48	0	34	0.0012	1	U	F.IKVEA
1400	468.2818	934.5490	934.5488	0.25	0	(33)	0.0014	1	U	F.IKVEA
2297	508.2867	1014.5588	1014.5597	-0.86	1	65	4e-06	1	U	L.LIEEE
2298	508.2871	1014.5595	1014.5597	-0.13	1	(49)	0.00017	1	U	L.LIEEE
3170	555.7601	1109.5056	1109.5063	-0.64	0	32	0.009	1	U	L.MATEG
3171	555.7603	1109.5059	1109.5063	-0.32	0	(32)	0.0092	1	U	L.MATEG
3882	585.2792	1168.5438	1168.5434	0.35	1	(22)	0.081	1	U	L.ERLME
3883	585.2802	1168.5459	1168.5434	2.13	1	30	0.016	1	U	L.ERLME
4050	593.2770	1184.5395	1184.5383	1.04	1	(22)	0.083	1	U	L.ERLME
4051	593.2774	1184.5402	1184.5383	1.64	1	(21)	0.093	1	U	L.ERLME
4182	598.7758	1195.5371	1195.5357	1.17	0	25	0.049	1	U	L.SGQNI
4183	598.7770	1195.5394	1195.5357	3.11	0	(24)	0.059	1	U	L.SGQNI
5594	675.8303	1349.6460	1349.6463	-0.25	2	(32)	0.015	1	U	L.DALVA
5595	675.8305	1349.6465	1349.6463	0.12	2	39	0.0028	1	U	L.DALVA
7582	836.9226	1671.8305	1671.8315	-0.58	1	(42)	0.0013	1	U	L.REGQL
7583	836.9256	1671.8366	1671.8315	3.07	1	61	1.8e-05	1	U	L.REGQL
7713	849.3796	1696.7446	1696.7428	1.08	1	(44)	0.00051	1	U	Y.DASDL
7714	849.3815	1696.7485	1696.7428	3.37	1	64	5.7e-06	1	U	Y.DASDL

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27. 2::sp|P0AAI5|FABF_ECOLI **Mass:** 43247 **Score:** 393 **Matches:** 14(12) **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	Peptide
3190	556.7826	1111.5507	1111.5509	-0.17	1	35	0.0044	1	U	L.GLIEE
3191	556.7830	1111.5515	1111.5509	0.50	1	(33)	0.0069	1	U	L.GLIEE
4665	622.8153	1243.6161	1243.6197	-2.92	1	(40)	0.0015	1	U	L.AGQSG
4666	622.8169	1243.6192	1243.6197	-0.38	1	53	9e-05	1	U	L.AGQSG
5011	640.3179	1278.6213	1278.6204	0.70	0	46	0.00061	1	U	L.RDAGI
5012	640.3182	1278.6218	1278.6204	1.10	0	(40)	0.0021	1	U	L.RDAGI
5680	679.3580	1356.7015	1356.7038	-1.66	2	(73)	7.1e-07	1	U	L.LAGQS
5681	679.3587	1356.7028	1356.7038	-0.68	2	78	2.5e-07	1	U	L.LAGQS
5769	684.8152	1367.6159	1367.6140	1.46	0	62	1.2e-05	1	U	Y.HMTSP
5770	684.8165	1367.6185	1367.6140	3.33	0	(58)	2.8e-05	1	U	Y.HMTSP
6518	739.3539	1476.6933	1476.6919	0.97	1	(44)	0.0009	1	U	L.GMLSP

6519	739.3555	1476.6965	1476.6919	3.12	1	77	4.6e-07	1	U	L.GMLSP
7205	533.9257	1598.7553	1598.7549	0.24	0	23	0.098	1	U	L.STRND
7720	852.9091	1703.8036	1703.8036	-0.03	0	23	0.11	1	U	Y.GDADV

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28. 2::sp|P0C0V0|DEGP_ECOLI **Mass:** 49438 **Score:** 379 **Matches:** 21(18) **Sequences:**

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
788	425.2267	848.4389	848.4392	-0.38	0	(25)	0.042	1	U	L.NGKPI
789	425.2267	848.4389	848.4392	-0.38	0	35	0.0048	1	U	L.NGKPI
2798	534.3139	1066.6132	1066.6135	-0.20	0	34	0.0016	1	U	L.IQIQN
2799	534.3147	1066.6148	1066.6135	1.30	0	(28)	0.0056	1	U	L.IQIQN
3446	568.2852	1134.5559	1134.5591	-2.79	0	(26)	0.048	1	U	L.TAIKM
3447	568.2855	1134.5564	1134.5591	-2.37	0	48	0.00031	1	U	L.TAIKM
3654	576.2850	1150.5554	1150.5540	1.23	0	(25)	0.062	1	U	L.TAIKM
3655	576.2857	1150.5569	1150.5540	2.52	0	(25)	0.056	1	U	L.TAIKM
3862	583.7949	1165.5752	1165.5727	2.08	0	(20)	0.19	1	U	L.NIQRG
3863	583.7950	1165.5755	1165.5727	2.39	0	28	0.031	1	U	L.NIQRG
4067	594.2540	1186.4935	1186.4931	0.32	2	33	0.0036	1	U	F.QQFFG
4068	594.2553	1186.4959	1186.4931	2.37	2	(28)	0.011	1	U	F.QQFFG
5598	675.8544	1349.6942	1349.6939	0.21	1	44	0.00072	1	U	L.ALNIQ
5600	675.8563	1349.6980	1349.6939	3.01	1	(30)	0.018	1	U	L.ALNIQ
5709	680.3768	1358.7391	1358.7340	3.74	0	23	0.075	1	U	L.RAQVG
6710	755.3865	1508.7585	1508.7545	2.69	1	(95)	6.3e-09	1	U	F.MALGS
6711	755.3871	1508.7596	1508.7545	3.40	1	(91)	1.7e-08	1	U	F.MALGS
6793	763.3817	1524.7489	1524.7494	-0.34	1	96	4.9e-09	1	U	F.MALGS
6794	763.3823	1524.7500	1524.7494	0.38	1	(91)	1.4e-08	1	U	F.MALGS
8059	898.9182	1795.8219	1795.8224	-0.31	1	(28)	0.036	1	U	L.ELQQS
8060	898.9203	1795.8261	1795.8224	2.07	1	38	0.0037	1	U	L.ELQQS

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29. 2::sp|P21165|PEPQ_ECOLI **Mass:** 50315 **Score:** 361 **Matches:** 16(14) **Sequences:**

Xaa-Pro dipeptidase OS=Escherichia coli (strain K12) OX=83333 GN=pepQ PE=1 SV=2

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
271	398.7377	795.4609	795.4603	0.81	0	37	0.00035	1	U	Y.KNHIA
272	398.7378	795.4610	795.4603	0.96	0	(22)	0.011	1	U	Y.KNHIA
1377	467.2435	932.4724	932.4716	0.87	1	(40)	0.0014	1	U	Y.AADLT
1378	467.2438	932.4731	932.4716	1.67	1	50	0.00014	1	U	Y.AADLT
1567	476.2848	950.5550	950.5549	0.07	0	20	0.023	1	U	Y.IGPVP
2710	530.2698	1058.5251	1058.5244	0.69	0	39	0.0019	1	U	L.VKDVN
2711	530.2699	1058.5252	1058.5244	0.80	0	(24)	0.071	1	U	L.VKDVN
4649	622.3315	1242.6484	1242.6456	2.28	1	60	1.5e-05	1	U	L.VKDVN
5605	675.8728	1349.7310	1349.7303	0.56	1	(45)	0.00037	1	U	Y.SNIVA
5606	675.8735	1349.7325	1349.7303	1.66	1	45	0.00029	1	U	Y.SNIVA
5735	682.3190	1362.6235	1362.6245	-0.70	2	(34)	0.0083	1	U	F.NVFLD
5736	682.3193	1362.6240	1362.6245	-0.35	2	50	0.00021	1	U	F.NVFLD
7157	795.4131	1588.8117	1588.8097	1.31	0	41	0.002	1	U	L.GIEAS
7158	795.4133	1588.8120	1588.8097	1.46	0	(36)	0.0055	1	U	L.GIEAS
7159	795.4155	1588.8164	1588.8097	4.23	0	(30)	0.023	1	U	L.GIEAS
8187	915.9853	1829.9560	1829.9523	2.04	1	21	0.17	1	U	L.QLGIE

30. 2::sp|P0AB71|ALF_ECOLI **Mass:** 39351 **Score:** 340 **Matches:** 22(21) **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
5322	438.8947	1313.6623	1313.6616	0.56	2	(24)	0.059	1	U	W.IDGLL
5323	438.8948	1313.6627	1313.6616	0.86	2	42	0.00089	1	U	W.IDGLL
6499	492.2473	1473.7201	1473.7212	-0.73	0	(27)	0.045	1	U	L.GNPKG
6500	492.2479	1473.7219	1473.7212	0.51	0	32	0.014	1	U	L.GNPKG
6774	761.8645	1521.7144	1521.7134	0.71	0	33	0.01	1	U	Y.GVVKM
6776	761.8669	1521.7193	1521.7134	3.92	0	(29)	0.029	1	U	Y.GVVKM
7305	541.9857	1622.9353	1622.9355	-0.13	0	(25)	0.013	1	U	F.IAGKG
7306	812.4753	1622.9360	1622.9355	0.28	0	(40)	0.00037	1	U	F.IAGKG
7307	541.9864	1622.9373	1622.9355	1.11	0	(26)	0.01	1	U	F.IAGKG
7308	812.4778	1622.9410	1622.9355	3.36	0	46	8.7e-05	1	U	F.IAGKG
7797	574.9363	1721.7870	1721.7857	0.79	0	(26)	0.049	1	U	F.HGGSG
7798	861.9011	1721.7877	1721.7857	1.18	0	(63)	9.6e-06	1	U	F.HGGSG
7799	574.9365	1721.7877	1721.7857	1.20	0	(28)	0.036	1	U	F.HGGSG
7800	861.9027	1721.7909	1721.7857	3.02	0	73	1e-06	1	U	F.HGGSG
8313	932.4971	1862.9796	1862.9779	0.93	1	41	0.0012	1	U	F.DFVKP
8315	622.0017	1862.9833	1862.9779	2.92	1	(22)	0.09	1	U	F.DFVKP
8316	622.0019	1862.9838	1862.9779	3.21	1	(32)	0.0089	1	U	F.DFVKP
8317	932.4995	1862.9843	1862.9779	3.48	1	(39)	0.002	1	U	F.DFVKP
8574	656.9808	1967.9205	1967.9225	-1.03	1	(42)	0.0015	1	U	F.VFHGG
8575	656.9835	1967.9287	1967.9225	3.17	1	42	0.0013	1	U	F.VFHGG
8680	672.0167	2013.0283	2013.0279	0.20	2	(28)	0.031	1	U	Y.LQGQL
8683	672.0182	2013.0327	2013.0279	2.39	2	29	0.022	1	U	Y.LQGQL

31. 2::sp|P0ABH7|CISY_ECOLI **Mass:** 48383 **Score:** 339 **Matches:** 19(15) **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
2487	516.7649	1031.5153	1031.5135	1.79	1	(21)	0.16	1	U	L.TLNGD
2488	516.7655	1031.5164	1031.5135	2.85	1	29	0.021	1	U	L.TLNGD
2586	524.7505	1047.4864	1047.4873	-0.79	1	33	0.0089	1	U	L.ENIAL
2587	524.7510	1047.4874	1047.4873	0.14	1	(32)	0.01	1	U	L.ENIAL
2766	532.7606	1063.5067	1063.5047	1.91	0	25	0.06	1	U	W.GPAHG
2767	532.7611	1063.5077	1063.5047	2.83	0	(22)	0.13	1	U	W.GPAHG
2910	541.7907	1081.5669	1081.5669	-0.01	0	(27)	0.025	1	U	L.HRGFP
2911	541.7912	1081.5678	1081.5669	0.90	0	28	0.02	1	U	L.HRGFP
4139	597.2750	1192.5354	1192.5360	-0.54	0	(24)	0.07	1	U	L.NGEKP
4140	597.2765	1192.5384	1192.5360	2.03	0	30	0.016	1	U	L.NGEKP
4144	597.7691	1193.5236	1193.5200	3.04	0	(26)	0.036	1	U	L.NGEKP
6314	725.3596	1448.7046	1448.7068	-1.57	2	40	0.0026	1	U	L.GTKDD
6828	510.2947	1527.8622	1527.8621	0.10	1	35	0.0033	1	U	L.KGTLG
6829	510.2954	1527.8645	1527.8621	1.59	1	(32)	0.006	1	U	L.KGTLG
6855	767.3942	1532.7738	1532.7722	1.03	2	(36)	0.0064	1	U	Y.ILLNG
6856	767.3944	1532.7741	1532.7722	1.27	2	40	0.0026	1	U	Y.ILLNG
7125	792.8443	1583.6740	1583.6740	0.05	1	(39)	0.0015	1	U	L.NGEKP
7126	792.8467	1583.6788	1583.6740	3.06	1	58	1.8e-05	1	U	L.NGEKP

7654	562.3062	1683.8966	1683.8978	-0.67	1	21	0.11	1	U	Y.EVNPI

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32. 2::sp|P0AG30|RHO_ECOLI **Mass:** 47032 **Score:** 337 **Matches:** 23(23) **Sequences:**
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
486	409.2425	816.4704	816.4705	-0.17	1	31	0.0074	1	U	L.LDSIT
487	409.2433	816.4720	816.4705	1.87	1	(28)	0.014	1	U	L.LDSIT
1068	449.7165	897.4184	897.4192	-0.91	1	35	0.0035	1	U	F.LRSAD
1069	449.7168	897.4191	897.4192	-0.09	1	(32)	0.0076	1	U	F.LRSAD
2506	518.7871	1035.5595	1035.5601	-0.51	0	55	4.1e-05	1	U	L.VKGEV
2507	518.7879	1035.5612	1035.5601	1.13	0	(46)	0.00027	1	U	L.VKGEV
2926	542.8214	1083.6281	1083.6288	-0.62	0	(36)	0.0017	1	U	Y.NTVVP
2928	542.8221	1083.6297	1083.6288	0.84	0	40	0.00064	1	U	Y.NTVVP
2946	543.3141	1084.6136	1084.6128	0.74	0	(31)	0.0069	1	U	Y.NTVVP
4293	603.2607	1204.5069	1204.5070	-0.10	1	(23)	0.039	1	U	L.AMTKT
4294	603.2624	1204.5102	1204.5070	2.64	1	28	0.015	1	U	L.AMTKT
4393	607.8533	1213.6920	1213.6918	0.16	1	(25)	0.036	1	U	L.KNTPV
4394	607.8547	1213.6949	1213.6918	2.59	1	32	0.0069	1	U	L.KNTPV
5114	647.3120	1292.6093	1292.6071	1.76	1	39	0.0022	1	U	L.TTQEE
5115	647.3123	1292.6101	1292.6071	2.33	1	(32)	0.011	1	U	L.TTQEE
5220	652.3316	1302.6486	1302.6489	-0.21	2	40	0.0019	1	U	L.ITLGE
5223	652.3321	1302.6496	1302.6489	0.54	2	(37)	0.0046	1	U	L.ITLGE
5276	655.3088	1308.6031	1308.6020	0.87	1	(33)	0.0097	1	U	L.TTQEE
5277	655.3093	1308.6040	1308.6020	1.53	1	(28)	0.027	1	U	L.TTQEE
7967	888.4091	1774.8037	1774.7971	3.70	1	(37)	0.0037	1	U	L.IDTGS
7968	888.4093	1774.8040	1774.7971	3.90	1	(39)	0.0022	1	U	L.IDTGS
8049	896.4037	1790.7928	1790.7920	0.44	1	42	0.001	1	U	L.IDTGS
8050	896.4052	1790.7957	1790.7920	2.07	1	(34)	0.0056	1	U	L.IDTGS

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33. 2::sp|P31224|ACRB_ECOLI **Mass:** 113615 **Score:** 319 **Matches:** 13(12) **Sequences:**
Multidrug efflux pump subunit AcrB OS=Escherichia coli (strain K12) OX=83333 GN=acr
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2033	496.7742	991.5338	991.5338	0.00	0	44	0.00049	1	U	L.ASKLP
2034	496.7748	991.5350	991.5338	1.17	0	(43)	0.00055	1	U	L.ASKLP
2463	515.7795	1029.5444	1029.5454	-1.00	0	40	0.0016	1	U	L.DTAAA
2905	541.3043	1080.5940	1080.5928	1.11	0	(30)	0.0081	1	U	L.GGTPP
2906	541.3043	1080.5940	1080.5928	1.11	0	35	0.0025	1	U	L.GGTPP
3137	553.7688	1105.5230	1105.5226	0.41	1	(24)	0.067	1	U	W.MNPNE
3138	553.7695	1105.5245	1105.5226	1.73	1	28	0.027	1	U	W.MNPNE
3613	573.8033	1145.5920	1145.5928	-0.71	0	(43)	0.00093	1	U	L.GVSIN
3614	573.8049	1145.5953	1145.5928	2.17	0	46	0.00052	1	U	L.GVSIN
5796	686.3784	1370.7423	1370.7405	1.30	0	55	4.6e-05	1	U	F.KIDID
5797	686.3792	1370.7439	1370.7405	2.45	0	(46)	0.00036	1	U	F.KIDID
7006	780.8865	1559.7584	1559.7580	0.25	1	35	0.0061	1	U	L.TSVRP
7089	788.9135	1575.8124	1575.8256	-8.37	2	37	0.0048	1	U	L.LRDVA

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34. 2::sp|P0A825|GLYA_ECOLI **Mass:** 45459 **Score:** 316 **Matches:** 14(13) **Sequences:**

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
448	408.2288	814.4430	814.4436	-0.82	0	59	1.7e-05	1	U	Y.VDIVE
449	408.2292	814.4439	814.4436	0.31	0	(46)	0.00035	1	U	Y.VDIVE
2441	514.8030	1027.5915	1027.5914	0.17	2	45	0.00029	1	U	F.LVDLV
2442	514.8036	1027.5927	1027.5914	1.36	2	(43)	0.00039	1	U	F.LVDLV
2733	531.2490	1060.4835	1060.4825	0.89	0	51	8.8e-05	1	U	Y.GIDAT
2734	531.2495	1060.4843	1060.4825	1.70	0	(49)	0.00013	1	U	Y.GIDAT
3371	564.8118	1127.6091	1127.6074	1.51	2	(36)	0.0027	1	U	Y.TALLE
3372	564.8122	1127.6098	1127.6074	2.15	2	40	0.0012	1	U	Y.TALLE
4947	637.3301	1272.6457	1272.6463	-0.43	1	(40)	0.002	1	U	Y.KVVSG
4949	425.2228	1272.6466	1272.6463	0.26	1	(22)	0.11	1	U	Y.KVVSG
4950	637.3311	1272.6475	1272.6463	1.00	1	54	7.3e-05	1	U	Y.KVVSG
5656	678.8192	1355.6237	1355.6218	1.42	0	44	0.00068	1	U	Y.ANVQP
5657	678.8199	1355.6253	1355.6218	2.60	0	(42)	0.0012	1	U	Y.ANVQP
5882	463.5526	1387.6360	1387.6329	2.21	1	25	0.039	1	U	L.KEAME

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35. 2::sp|P0A817|METK_ECOLI **Mass:** 42153 **Score:** 294 **Matches:** 15(13) **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
732	422.2553	842.4960	842.4974	-1.62	2	(23)	0.039	1	U	L.LRDAA
733	422.2554	842.4962	842.4974	-1.41	2	25	0.024	1	U	L.LRDAA
884	435.7391	869.4637	869.4647	-1.18	2	20	0.045	1	U	L.DLLHP
1605	478.3000	954.5854	954.5862	-0.87	0	(35)	0.00093	1	U	Y.VAKNI
1606	478.3005	954.5865	954.5862	0.28	0	53	1.3e-05	1	U	Y.VAKNI
2967	544.2852	1086.5559	1086.5557	0.18	0	28	0.026	1	U	F.GTEKV
2969	544.2853	1086.5561	1086.5557	0.40	0	(26)	0.037	1	U	F.GTEKV
4634	620.7850	1239.5554	1239.5554	0.01	0	25	0.049	1	U	L.ADRCE
4635	620.7850	1239.5555	1239.5554	0.11	0	(23)	0.093	1	U	L.ADRCE
4820	631.3501	1260.6856	1260.6826	2.39	1	25	0.048	1	U	W.LRPDA
4821	631.3531	1260.6916	1260.6826	7.14	1	(21)	0.1	1	U	W.LRPDA
7230	802.9308	1603.8470	1603.8457	0.80	1	(47)	0.00039	1	U	F.QYDDG
7231	802.9308	1603.8471	1603.8457	0.87	1	54	8.3e-05	1	U	F.QYDDG
9308	979.4810	2935.4212	2935.4272	-2.02	1	68	3e-06	1	U	L.SAIGK
9309	979.4861	2935.4364	2935.4272	3.15	1	(57)	4e-05	1	U	L.SAIGK

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36. 2::sp|P0A6F3|GLPK_ECOLI **Mass:** 56480 **Score:** 281 **Matches:** 15(13) **Sequences:**
Glycerol kinase OS=Escherichia coli (strain K12) OX=83333 GN=glpK PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
21	380.7188	759.4231	759.4239	-1.00	0	(31)	0.0094	1	U	Y.IRSNT
23	380.7196	759.4247	759.4239	1.10	0	39	0.0015	1	U	Y.IRSNT
848	432.2078	862.4010	862.4007	0.37	0	22	0.11	1	U	F.MAGAS
2060	498.2440	994.4734	994.4720	1.42	1	28	0.031	1	U	L.KRDGL
4109	595.7965	1189.5785	1189.5761	1.99	0	21	0.18	1	U	L.EAMQA
4156	597.8093	1193.6040	1193.6040	-0.05	0	(30)	0.019	1	U	F.ATKVQ
4157	597.8093	1193.6041	1193.6040	0.05	0	(39)	0.0024	1	U	F.ATKVQ

4158	597.8104	1193.6062	1193.6040	1.77	0	41	0.0014	1	U	F.ATKVQ
4159	597.8104	1193.6062	1193.6040	1.77	0	(36)	0.0044	1	U	F.ATKVQ
5517	668.3359	1334.6572	1334.6579	-0.48	0	45	0.0008	1	U	F.RPGIE
5520	668.3372	1334.6599	1334.6579	1.53	0	(32)	0.016	1	U	F.RPGIE
5850	691.8171	1381.6197	1381.6184	0.97	0	56	4.1e-05	1	U	L.TTIAC
5851	691.8173	1381.6200	1381.6184	1.14	0	(56)	4.2e-05	1	U	L.TTIAC
8564	654.3369	1959.9889	1959.9901	-0.63	2	32	0.016	1	U	W.QNLDE
8565	654.3385	1959.9937	1959.9901	1.81	2	(29)	0.034	1	U	W.QNLDE

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37. 2::sp|P0A6M8|EFG_ECOLI **Mass:** 77704 **Score:** 263 **Matches:** 10(10) **Sequences:** 5

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
218	396.2182	790.4218	790.4225	-0.90	0	(36)	0.0036	1	U	F.KIATD
219	396.2189	790.4233	790.4225	1.02	0	36	0.0034	1	U	F.KIATD
3225	557.7802	1113.5457	1113.5455	0.26	1	(44)	0.00051	1	U	L.QLAIG
3226	557.7804	1113.5462	1113.5455	0.71	1	49	0.00016	1	U	L.QLAIG
5293	655.8683	1309.7221	1309.7242	-1.53	0	(34)	0.0034	1	U	Y.IPAVD
5294	655.8685	1309.7225	1309.7242	-1.26	0	39	0.00091	1	U	Y.IPAVD
6836	765.4073	1528.8000	1528.7984	1.05	2	92	1.1e-08	1	U	Y.LGGEE
6838	765.4084	1528.8022	1528.7984	2.49	2	(73)	8.1e-07	1	U	Y.LGGEE
8524	972.4873	1942.9600	1942.9558	2.20	1	46	0.00053	1	U	L.KDVTT
8525	972.4914	1942.9682	1942.9558	6.41	1	(33)	0.011	1	U	L.KDVTT

---

38. 2::sp|P0A6A3|ACKA_ECOLI **Mass:** 43605 **Score:** 260 **Matches:** 14(13) **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
186	393.7575	785.5004	785.5011	-0.86	2	33	0.0014	1	U	L.SLGKL
187	393.7579	785.5013	785.5011	0.29	2	(25)	0.0086	1	U	L.SLGKL
1013	442.2171	882.4197	882.4195	0.21	0	32	0.0078	1	U	L.GAGAA
1014	442.2172	882.4198	882.4195	0.34	0	(32)	0.0089	1	U	L.GAGAA
2173	503.7654	1005.5161	1005.5165	-0.31	0	(26)	0.038	1	U	Y.VTQEA
2174	503.7655	1005.5165	1005.5165	0.04	0	27	0.03	1	U	Y.VTQEA
2924	542.8036	1083.5927	1083.5924	0.33	1	35	0.0028	1	U	L.AQKPE
2925	542.8043	1083.5941	1083.5924	1.57	1	(32)	0.0057	1	U	L.AQKPE
3459	569.2294	1136.4443	1136.4444	-0.10	0	24	0.0096	1	U	F.HQTMP
5168	650.7963	1299.5780	1299.5765	1.11	1	56	2.8e-05	1	U	L.GLTEV
5169	650.7976	1299.5807	1299.5765	3.19	1	(50)	0.00012	1	U	L.GLTEV
6108	712.3685	1422.7225	1422.7177	3.37	2	24	0.077	1	U	Y.TALMD
8610	660.6984	1979.0735	1979.0687	2.39	0	(28)	0.016	1	U	F.INKEG
8611	990.5455	1979.0765	1979.0687	3.93	0	30	0.01	1	U	F.INKEG

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39. 2::sp|P06715|GSHR_ECOLI **Mass:** 49084 **Score:** 257 **Matches:** 11(10) **Sequences:**

Glutathione reductase OS=Escherichia coli (strain K12) OX=83333 GN=gor PE=1 SV=1

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

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

```
   4857  633.8199  1265.6253  1265.6252   0.15   0    37    0.004   1      U    L.EAAGV
   5922  698.8632  1395.7118  1395.7106   0.84   0   (34)  0.0074   1      U    W.AIGRE
   5923  698.8649  1395.7153  1395.7106   3.37   0    35   0.0055   1      U    W.AIGRE
   6011  706.3572  1410.6999  1410.6991   0.61   0    63  8.7e-06   1      U    L.EVNGE
   6012  706.3572  1410.6999  1410.6991   0.61   0   (57) 3.2e-05   1      U    L.EVNGE
   6021  706.8480  1411.6814  1411.6831  -1.21   0   (34)  0.0072   1      U    L.EVNGE
   6772  761.8392  1521.6638  1521.6617   1.37   1    45  0.00041   1      U    L.ELEDG
   6773  761.8405  1521.6663  1521.6617   3.06   1   (40)  0.0015   1      U    L.ELEDG
   7108  791.9520  1581.8895  1581.8879   1.04   0   (47) 0.00014   1      U    F.ALPAL
   7109  791.9530  1581.8914  1581.8879   2.27   0    55  2.1e-05   1      U    F.ALPAL
   7413  549.3019  1644.8838  1644.8835   0.18   1    22      0.1   1      U    Y.ENVLG
```

```
40.   2::sp|P02925|RBSB_ECOLI     Mass: 30931     Score: 253     Matches: 11(9)   Sequences: 7
      Ribose import binding protein RbsB OS=Escherichia coli (strain K12) OX=83333 GN=rbsB
      Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score   Expect Rank Unique   Peptide
       151  390.6979   779.3811   779.3814  -0.28   0    47  0.00034   1      U    L.GGKIA
       152  390.6981   779.3816   779.3814   0.34   0   (45) 0.00052   1      U    L.GGKIA
      2920  542.7740  1083.5335  1083.5349  -1.27   0    31   0.0087   1      U    L.TAHPD
      2921  542.7742  1083.5339  1083.5349  -0.94   0   (25)   0.036   2      U    L.TAHPD
      3241  558.2706  1114.5267  1114.5254   1.14   0    29    0.017   1      U    L.DSQNN
      3242  558.2707  1114.5268  1114.5254   1.25   0   (23)   0.065   1      U    L.DSQNN
      4254  401.5501  1201.6285  1201.6302  -1.44   0    23    0.089   1      U    L.KDGAQ
      5639  677.8367  1353.6588  1353.6599  -0.81   0    28    0.034   1      U    L.QTAGK
      6740  758.3704  1514.7262  1514.7213   3.23   0    26    0.049   1      U    F.DGTPD
      7477  827.4443  1652.8740  1652.8733   0.40   2    71  1.2e-06   1      U    Y.NLVVL
      7478  827.4464  1652.8783  1652.8733   2.99   2   (68) 2.4e-06   1      U    Y.NLVVL
```

```
41.   2::sp|P04805|SYE_ECOLI     Mass: 54181     Score: 252     Matches: 15(11)   Sequences: 6
      Glutamate--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=gltX PE=1 SV=1
      Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)     ppm  Miss Score   Expect Rank Unique   Peptid
      2575  524.2592  1046.5038  1046.5033    0.47   0    48  0.00026   1      U    F.ANPQ
      2576  524.2592  1046.5039  1046.5033    0.58   0   (40)  0.0019   1      U    F.ANPQ
      3037  548.2347  1094.4549  1094.4556   -0.65   2    38   0.0012   1      U    L.SLEW
      4098  595.2961  1188.5777  1188.5775    0.19   0    39   0.0022   1      U    F.DDQI
      4099  595.2976  1188.5805  1188.5775    2.57   0   (33)  0.0097   1      U    F.DDQI
      4708  625.2953  1248.5761  1248.5735    2.16   1    45  0.00061   1      U    L.DFIA
      4709  625.2959  1248.5772  1248.5735    3.04   1   (40)  0.0019   1      U    L.DFIA
      4711  625.2998  1248.5850  1248.5735    9.28   1   (23)     0.1   1      U    L.DFIA
      4815  631.3262  1260.6379  1260.6350    2.31   2   (23)     0.1   1      U    Y.RDDG
      4816  631.3265  1260.6384  1260.6350    2.71   2    23    0.093   1      U    Y.RDDG
      6971  777.3502  1552.6858  1552.7079  -14.20   1    60  1.9e-05   1      U    Y.NAVI
      6972  777.3608  1552.7071  1552.7079   -0.50   1   (24)   0.079   1      U    Y.NAVI
      6973  777.3637  1552.7129  1552.7079    3.20   1   (44) 0.00082   1      U    Y.NAVI
      7040  785.3599  1568.7052  1568.7028    1.50   1   (27)   0.032   1      U    Y.NAVI
      7041  785.3603  1568.7060  1568.7028    2.05   1   (55) 5.4e-05   1      U    Y.NAVI
```

```
42.   2::sp|P0AGD7|SRP54_ECOLI     Mass: 49812     Score: 249     Matches: 10(9)   Sequences:
```

Signal recognition particle protein OS=Escherichia coli (strain K12) OX=83333 GN=ffh
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3016	546.8241	1091.6336	1091.6339	-0.21	1	(31)	0.0034	1	U	L.NLAAQ
3017	546.8244	1091.6342	1091.6339	0.34	1	41	0.00034	1	U	L.NLAAQ
5566	672.8618	1343.7090	1343.7085	0.34	0	57	3.9e-05	1	U	L.EADVA
5567	672.8633	1343.7120	1343.7085	2.60	0	(53)	9.5e-05	1	U	L.EADVA
5895	695.3661	1388.7177	1388.7187	-0.71	2	38	0.0035	1	U	F.LGVGE
5896	695.3686	1388.7226	1388.7187	2.80	2	(26)	0.046	1	U	F.LGVGE
7808	863.4100	1724.8054	1724.8040	0.83	0	77	3.8e-07	1	U	F.VVDAM
7809	863.4116	1724.8086	1724.8040	2.67	0	(55)	6.4e-05	1	U	F.VVDAM
8729	682.0358	2043.0857	2043.0847	0.45	1	(22)	0.099	1	U	L.SLIED
8732	682.0372	2043.0899	2043.0847	2.50	1	41	0.0011	1	U	L.SLIED

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43. 2::sp|P31979|NUOF_ECOLI **Mass:** 49774 **Score:** 247 **Matches:** 11(7) **Sequences:** 7

NADH-quinone oxidoreductase subunit F OS=Escherichia coli (strain K12) OX=83333 GN=n
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
140	388.6904	775.3662	775.3647	1.96	0	37	0.0029	1	U	Y.AGGMR
2643	527.2709	1052.5273	1052.5291	-1.67	2	(33)	0.0087	1	U	L.VRNLE
2644	527.2726	1052.5307	1052.5291	1.56	2	33	0.0078	1	U	L.VRNLE
4866	634.3108	1266.6071	1266.6092	-1.60	1	(21)	0.17	1	U	F.GTTAR
4867	634.3114	1266.6082	1266.6092	-0.73	1	24	0.09	1	U	F.GTTAR
5491	666.3356	1330.6566	1330.6551	1.11	0	21	0.16	1	U	W.GKPTC
5581	674.3683	1346.7220	1346.7194	1.97	2	23	0.078	1	U	F.LRGEY
5954	700.8369	1399.6591	1399.6579	0.87	0	46	0.0005	1	U	L.ERGEG
5955	700.8389	1399.6632	1399.6579	3.76	0	(38)	0.0028	1	U	L.ERGEG
7962	885.9288	1769.8431	1769.8432	-0.03	1	(54)	9.5e-05	1	U	L.ERGEG
7963	885.9294	1769.8442	1769.8432	0.59	1	65	6.9e-06	1	U	L.ERGEG

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44. 2::sp|P0A870|TALB_ECOLI **Mass:** 35368 **Score:** 229 **Matches:** 11(11) **Sequences:**

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
496	409.7419	817.4693	817.4698	-0.62	1	(42)	0.00044	1	U	L.IKLAS
497	409.7423	817.4700	817.4698	0.29	1	43	0.00043	1	U	L.IKLAS
2675	528.8055	1055.5964	1055.5975	-1.01	1	(28)	0.016	1	U	F.RNIGE
2676	528.8057	1055.5968	1055.5975	-0.67	1	28	0.013	1	U	F.RNIGE
4064	593.8337	1185.6529	1185.6506	1.97	1	26	0.035	1	U	Y.RKLID
4073	594.3052	1186.5958	1186.5942	1.36	0	(41)	0.0012	1	U	Y.NDAGI
4074	594.3059	1186.5973	1186.5942	2.59	0	50	0.00016	1	U	Y.NDAGI
6850	766.8784	1531.7422	1531.7406	1.02	0	51	0.00018	1	U	Y.APAED
6851	766.8799	1531.7453	1531.7406	3.09	0	(44)	0.00087	1	U	Y.APAED
7068	524.9584	1571.8533	1571.8518	0.93	1	32	0.01	1	U	L.KELAE
7069	524.9584	1571.8535	1571.8518	1.06	1	(29)	0.018	1	U	L.KELAE

Proteins matching a subset of these peptides:

2::sp|P0A867|TALA_ECOLI **Mass:** 35865 **Score:** 43 **Matches:** 2(2) **Sequences:** 1(
Transaldolase A OS=Escherichia coli (strain K12) OX=83333 GN=talA PE=3 SV=1

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45. 2::sp|P0A6H1|CLPX_ECOLI **Mass:** 46726 **Score:** 217 **Matches:** 11(9) **Sequences:** 6
ATP-dependent Clp protease ATP-binding subunit ClpX OS=Escherichia coli (strain K12)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1357	465.7737	929.5329	929.5334	-0.62	2	22	0.07	1	U	L.ARLLD
1802	486.2976	970.5806	970.5811	-0.51	1	35	0.0013	1	U	L.RSIVE
1804	486.2979	970.5813	970.5811	0.17	1	(26)	0.012	1	U	L.RSIVE
2310	508.8029	1015.5912	1015.5914	-0.18	1	(22)	0.055	1	U	F.LQVDT
2311	508.8032	1015.5918	1015.5914	0.47	1	22	0.046	1	U	F.LQVDT
2549	522.3074	1042.6002	1042.6023	-1.99	1	(43)	0.00046	1	U	L.LIGPT
2550	522.3078	1042.6010	1042.6023	-1.17	1	47	0.0002	1	U	L.LIGPT
3823	582.3381	1162.6617	1162.6598	1.66	2	49	8e-05	1	U	F.LQVDT
3824	582.3387	1162.6628	1162.6598	2.61	2	(45)	0.00022	1	U	F.LQVDT
5072	644.8427	1287.6707	1287.6711	-0.24	1	(42)	0.0012	1	U	L.AQVEP
5073	644.8429	1287.6712	1287.6711	0.15	1	47	0.0004	1	U	L.AQVEP

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46. 2::sp|P0A953|FABB_ECOLI **Mass:** 42928 **Score:** 213 **Matches:** 10(9) **Sequences:** 5
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
342	403.2319	804.4492	804.4494	-0.23	0	(41)	0.00073	1	U	L.AAIRE
343	403.2325	804.4505	804.4494	1.44	0	41	0.00069	1	U	L.AAIRE
5083	645.8318	1289.6490	1289.6463	2.11	0	(40)	0.0023	1	U	L.NIVTE
5085	645.8323	1289.6500	1289.6463	2.87	0	42	0.0014	1	U	L.NIVTE
6383	729.3843	1456.7540	1456.7522	1.26	0	59	2.4e-05	1	U	L.GIVSS
6384	729.3853	1456.7559	1456.7522	2.60	0	(41)	0.0014	1	U	L.GIVSS
7466	826.8785	1651.7424	1651.7399	1.51	1	20	0.17	1	U	L.SMEQA
7474	551.9530	1652.8372	1652.8370	0.12	1	(26)	0.051	1	U	Y.LNSHG
7475	551.9540	1652.8403	1652.8370	2.01	1	(30)	0.019	1	U	Y.LNSHG
7476	827.4282	1652.8418	1652.8370	2.90	1	50	0.00021	1	U	Y.LNSHG

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47. 2::sp|P11447|ARLY_ECOLI **Mass:** 50686 **Score:** 213 **Matches:** 10(6) **Sequences:** 7
Argininosuccinate lyase OS=Escherichia coli (strain K12) OX=83333 GN=argH PE=1 SV=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1401	468.7301	935.4456	935.4461	-0.47	0	(31)	0.015	1	U	F.TQAAD
1402	468.7305	935.4464	935.4461	0.38	0	31	0.013	1	U	F.TQAAD
1959	493.8162	985.6179	985.6172	0.71	1	25	0.0086	1	U	W.SKALV
2198	504.7525	1007.4904	1007.4884	2.07	0	24	0.084	1	U	L.SDRVT
2199	504.7531	1007.4917	1007.4884	3.29	0	(23)	0.097	1	U	L.SDRVT
2505	518.7509	1035.4873	1035.4873	-0.00	1	24	0.079	1	U	F.NTGEA
2770	532.7682	1063.5218	1063.5220	-0.12	1	26	0.052	1	U	W.CKDTV
2892	540.7637	1079.5129	1079.5135	-0.52	2	24	0.079	1	U	Y.ANATE
6255	722.3836	1442.7527	1442.7518	0.62	1	62	9.8e-06	1	U	Y.RLAEQ
6256	722.3837	1442.7528	1442.7518	0.71	1	(55)	5.1e-05	1	U	Y.RLAEQ

48. 2::sp|P0AB89|PUR8_ECOLI **Mass:** 51625 **Score:** 211 **Matches:** 13(10) **Sequences:**
Adenylosuccinate lyase OS=Escherichia coli (strain K12) OX=83333 GN=purB PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
896	436.2194	870.4242	870.4236	0.71	1	23	0.049	1	U	L.RGIFSE
1531	474.7667	947.5189	947.5189	0.03	1	37	0.0024	1	U	L.RNLGVG
1532	474.7672	947.5197	947.5189	0.94	1	(33)	0.0055	1	U	L.RNLGVG
3110	552.2534	1102.4922	1102.4931	-0.85	0	(21)	0.086	2	U	Y.TTQIEP
3111	552.2536	1102.4926	1102.4931	-0.41	0	22	0.066	1	U	Y.TTQIEP
3201	556.8244	1111.6342	1111.6349	-0.62	1	23	0.029	1	U	Y.RQLNQV
3202	556.8245	1111.6344	1111.6349	-0.51	1	(23)	0.03	1	U	Y.RQLNQV
3619	574.3010	1146.5875	1146.5881	-0.49	1	(23)	0.11	1	U	W.QRDLTD
3620	574.3013	1146.5880	1146.5881	-0.08	1	34	0.0066	1	U	W.QRDLTD
5863	693.3274	1384.6403	1384.6411	-0.57	0	(35)	0.0052	1	U	Y.NAHIAA
5864	693.3299	1384.6452	1384.6411	2.96	0	38	0.0026	1	U	Y.NAHIAA
6981	518.6230	1552.8471	1552.8460	0.72	1	33	0.0057	1	U	F.IDGLAL
6982	518.6234	1552.8484	1552.8460	1.53	1	(24)	0.047	1	U	F.IDGLAL

49. 2::sp|P61889|MDH_ECOLI **Mass:** 32488 **Score:** 211 **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
1381	467.2557	932.4969	932.4968	0.13	1	28	0.023	1	U	L.LSQVPG
1382	467.2558	932.4970	932.4968	0.32	1	(26)	0.035	1	U	L.LSQVPG
1709	483.2563	964.4981	964.4978	0.37	0	(23)	0.07	1	U	L.DIIRSN
1711	483.2566	964.4987	964.4978	0.93	0	24	0.054	1	U	L.DIIRSN
2528	521.3052	1040.5959	1040.5978	-1.82	0	(37)	0.001	1	U	F.NVNAGI
2529	521.3063	1040.5981	1040.5978	0.29	0	39	0.0008	1	U	F.NVNAGI
2717	530.2874	1058.5603	1058.5608	-0.48	0	40	0.0016	1	U	L.KTQLPS
2719	530.2887	1058.5628	1058.5608	1.96	0	(34)	0.0062	1	U	L.KTQLPS
3935	586.8293	1171.6441	1171.6448	-0.59	1	40	0.0011	1	U	L.LKTQLP
3936	586.8302	1171.6458	1171.6448	0.86	1	(30)	0.012	1	U	L.LKTQLP
6920	772.3783	1542.7420	1542.7413	0.46	1	42	0.0012	1	U	F.SGEDAT
6921	772.3808	1542.7470	1542.7413	3.70	1	(40)	0.0018	1	U	F.SGEDAT

50. 2::sp|P0ABC7|HFLK_ECOLI **Mass:** 45517 **Score:** 194 **Matches:** 8(5) **Sequences:** 6(
Modulator of FtsH protease HflK OS=Escherichia coli (strain K12) OX=83333 GN=hflK PE
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1689	481.7657	961.5169	961.5154	1.55	0	21	0.11	1	U	Y.IETME
2167	503.7515	1005.4885	1005.4879	0.56	0	(36)	0.0045	1	U	L.EAQGE
2168	503.7521	1005.4897	1005.4879	1.77	0	40	0.002	1	U	L.EAQGE
2178	503.7698	1005.5251	1005.5243	0.80	0	20	0.15	1	U	Y.RVTNP
3657	576.2971	1150.5797	1150.5771	2.25	2	20	0.16	1	U	F.SHLVE
7940	881.9267	1761.8388	1761.8381	0.43	1	(56)	6.1e-05	1	U	Y.SVTSP
7941	881.9288	1761.8430	1761.8381	2.78	1	70	2.7e-06	1	U	Y.SVTSP

9304	973.1396	2916.3971	2916.4001	-1.04	1	26	0.046	1	U	F.QAARP

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51. 2::sp|P60906|SYH_ECOLI **Mass:** 47285 **Score:** 193 **Matches:** 7(6) **Sequences:** 5(4

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	Peptid
153	390.7159	779.4173	779.4177	-0.61	1	27	0.023	1	U	L.KNVL
1817	487.2461	972.4776	972.4777	-0.14	1	21	0.087	1	U	Y.NQEQ
4371	607.3252	1212.6358	1212.6350	0.70	1	40	0.0014	1	U	L.DSKN
6635	747.9296	1493.8447	1493.8453	-0.41	0	72	3.3e-07	1	U	Y.SEIR
6636	747.9303	1493.8460	1493.8453	0.49	0	(51)	4.4e-05	1	U	Y.SEIR
8690	1009.0386	2016.0627	2016.0568	2.94	2	(30)	0.017	1	U	L.LVQA
8691	1009.0396	2016.0647	2016.0568	3.91	2	36	0.0041	1	U	L.LVQA

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52. 2::sp|P0A855|TOLB_ECOLI **Mass:** 45927 **Score:** 182 **Matches:** 8(7) **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	Peptid
4464	611.2973	1220.5800	1220.5786	1.21	0	(27)	0.04	1	U	F.TSDQ
4465	611.2974	1220.5802	1220.5786	1.31	0	28	0.031	1	U	F.TSDQ
6227	720.3518	1438.6889	1438.6841	3.37	1	24	0.094	1	U	L.AFTS
7647	842.3586	1682.7026	1682.7020	0.36	0	(50)	8.7e-05	1	U	W.EGSQ
7648	842.3596	1682.7046	1682.7020	1.53	0	65	2.9e-06	1	U	W.EGSQ
8029	894.4436	1786.8726	1786.8738	-0.63	0	30	0.025	1	U	L.GIDA
8758	1030.0211	2058.0277	2058.0270	0.34	1	36	0.0057	1	U	W.SALG
8759	1030.0240	2058.0335	2058.0270	3.19	1	(27)	0.043	1	U	W.SALG

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53. 2::sp|P0AEK4|FABI_ECOLI **Mass:** 28074 **Score:** 175 **Matches:** 3(3) **Sequences:** 3

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	Peptid
2032	496.7625	991.5104	991.5087	1.72	0	36	0.004	1	U	Y.VNAV
6157	715.8489	1429.6832	1429.6838	-0.41	0	61	1.5e-05	1	U	L.SAGI
8703	1012.4758	2022.9370	2022.9283	4.29	2	80	2.1e-07	1	U	F.APGD

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54. 2::sp|P0ABB0|ATPA_ECOLI **Mass:** 55416 **Score:** 170 **Matches:** 9(8) **Sequences:** 5

ATP synthase subunit alpha OS=Escherichia coli (strain K12) OX=83333 GN=atpA 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
145	390.2185	778.4225	778.4225	0.03	1	35	0.0034	1	U	L.KGILD
5003	639.8513	1277.6881	1277.6867	1.08	2	(41)	0.00093	1	U	Y.LADVE
5004	639.8522	1277.6899	1277.6867	2.51	2	44	0.0005	1	U	Y.LADVE
7237	803.8998	1605.7850	1605.7821	1.82	1	(32)	0.016	1	U	L.NLERD
7296	811.8959	1621.7772	1621.7770	0.11	1	(40)	0.0027	1	U	L.NLERD

7297	811.8976	1621.7807	1621.7770	2.29	1	40	0.0024	1	U	L.NLERD
7539	555.2817	1662.8232	1662.8213	1.16	2	23	0.12	1	U	F.RDRGE
9122	838.7661	2513.2765	2513.2762	0.13	0	29	0.021	1	U	F.SAVEA
9123	838.7696	2513.2871	2513.2762	4.35	0	(26)	0.036	1	U	F.SAVEA

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55. 2::sp|P08390|USG_ECOLI **Mass:** 36456 **Score:** 170 **Matches:** 6(6) **Sequences:** 5(5

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
1168	454.2351	906.4556	906.4559	-0.36	0	30	0.018	1	U	W.SVADN
1875	490.2272	978.4398	978.4406	-0.87	0	(25)	0.038	1	U	L.AAEEA
1876	490.2275	978.4405	978.4406	-0.12	0	45	0.00034	1	U	L.AAEEA
4792	629.8247	1257.6347	1257.6313	2.75	1	25	0.051	3	U	Y.ALARN
5522	668.8415	1335.6685	1335.6671	1.12	0	41	0.0018	1	U	F.GGKTI
7457	826.4220	1650.8294	1650.8253	2.50	1	28	0.04	1	U	L.ETLAE

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56. 2::sp|P07913|TDH_ECOLI **Mass:** 37557 **Score:** 169 **Matches:** 9(8) **Sequences:** 3(3

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
2662	528.7535	1055.4924	1055.4924	0.02	1	45	0.00039	1	U	F.SIDDF
2663	528.7538	1055.4930	1055.4924	0.59	1	(39)	0.0019	1	U	F.SIDDF
6065	709.3877	1416.7608	1416.7613	-0.32	0	81	1.3e-07	1	U	Y.VGEVV
6066	709.3883	1416.7621	1416.7613	0.54	0	(65)	5.7e-06	1	U	Y.VGEVV
6067	709.3903	1416.7661	1416.7613	3.37	0	(48)	0.00028	1	U	Y.VGEVV
7436	825.4143	1648.8141	1648.8131	0.61	2	(33)	0.012	1	U	W.MTDVP
7437	825.4155	1648.8165	1648.8131	2.09	2	(39)	0.0037	1	U	W.MTDVP
7553	833.4139	1664.8132	1664.8080	3.14	2	42	0.0016	1	U	W.MTDVP
7554	833.4145	1664.8145	1664.8080	3.94	2	(22)	0.17	1	U	W.MTDVP

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57. 2::sp|P02943|LAMB_ECOLI **Mass:** 49995 **Score:** 168 **Matches:** 8(7) **Sequences:** 5(

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
336	402.7162	803.4178	803.4178	0.02	0	26	0.033	1	U	F.GKAVP
337	402.7165	803.4185	803.4178	0.91	0	(23)	0.061	1	U	F.GKAVP
1940	493.2514	984.4882	984.4876	0.63	0	26	0.028	1	U	F.TAEHT
1969	494.2846	986.5545	986.5549	-0.36	1	35	0.0032	1	U	Y.KITLA
1970	494.2852	986.5559	986.5549	1.00	1	(31)	0.01	1	U	Y.KITLA
4275	602.3101	1202.6057	1202.6044	1.08	1	(30)	0.022	1	U	Y.RLVDG
4276	602.3106	1202.6065	1202.6044	1.80	1	45	0.00071	1	U	Y.RLVDG
7953	589.9357	1766.7854	1766.7820	1.93	0	39	0.0022	1	U	Y.DNVES

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58. 2::sp|P24182|ACCC_ECOLI **Mass:** 49745 **Score:** 165 **Matches:** 8(8) **Sequences:** 4(

Biotin carboxylase OS=Escherichia coli (strain K12) OX=83333 GN=accC PE=1 SV=2

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2363	511.7483	1021.4821	1021.4829	-0.76	0	(42)	0.0012	1	U	F.AEQVE
2365	511.7496	1021.4847	1021.4829	1.81	0	54	7.6e-05	1	U	F.AEQVE
3063	549.3377	1096.6607	1096.6604	0.30	0	35	0.00084	1	U	F.IGPKA
3064	549.3386	1096.6627	1096.6604	2.07	0	(31)	0.0022	1	U	F.IGPKA
4232	600.8450	1199.6754	1199.6761	-0.63	0	(38)	0.0018	1	U	L.IIDGI
4233	600.8472	1199.6798	1199.6761	3.03	0	43	0.00046	1	U	L.IIDGI
6284	723.9069	1445.7992	1445.7990	0.09	1	34	0.0042	1	U	Y.LENPR
6285	723.9075	1445.8005	1445.7990	1.01	1	(23)	0.053	1	U	Y.LENPR

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59. 2::sp|P00509|AAT_ECOLI **Mass:** 43831 **Score:** 164 **Matches:** 6(6) **Sequences:** 4(4

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
2437	514.7925	1027.5704	1027.5702	0.18	1	24	0.039	1	U	L.SVEKG
3743	580.2836	1158.5526	1158.5517	0.81	1	34	0.0069	1	U	F.ARGLE
4482	612.8094	1223.6042	1223.6033	0.72	2	44	0.00086	1	U	Y.LLENE
4483	612.8097	1223.6048	1223.6033	1.21	2	(39)	0.0027	1	U	Y.LLENE
5017	640.8114	1279.6082	1279.6044	2.97	0	(64)	7.1e-06	1	U	L.VAADS
5018	640.8116	1279.6087	1279.6044	3.36	0	65	5.9e-06	1	U	L.VAADS

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60. 2::sp|P27248|GCST_ECOLI **Mass:** 40235 **Score:** 164 **Matches:** 9(6) **Sequences:** 5

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
1625	478.7924	955.5702	955.5702	-0.04	2	32	0.0031	1	U	Y.LLAND
1626	478.7927	955.5708	955.5702	0.59	2	(31)	0.0036	1	U	Y.LLAND
3401	565.8057	1129.5968	1129.5979	-1.00	0	(34)	0.0067	1	U	F.GIEIT
3402	565.8063	1129.5981	1129.5979	0.20	0	46	0.00037	1	U	F.GIEIT
5395	660.8143	1319.6140	1319.6146	-0.47	1	(21)	0.17	1	U	W.TIAWE
5396	660.8148	1319.6150	1319.6146	0.27	1	25	0.058	1	U	W.TIAWE
6674	752.3762	1502.7379	1502.7405	-1.74	1	(22)	0.14	1	U	Y.EIALP
6675	752.3792	1502.7439	1502.7405	2.24	1	23	0.11	1	U	Y.EIALP
7969	888.4138	1774.8130	1774.8122	0.42	0	40	0.0021	1	U	F.TDAQG

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61. 2::sp|P00960|SYGA_ECOLI **Mass:** 35037 **Score:** 162 **Matches:** 8(7) **Sequences:** 5

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
14	380.2341	758.4536	758.4538	-0.25	2	(26)	0.025	1	U	Y.LGSLKE
16	380.2341	758.4537	758.4538	-0.10	2	28	0.016	1	U	Y.LGSLKE
4588	617.7713	1233.5280	1233.5262	1.51	0	32	0.0047	1	U	F.HQNEVE
5140	648.8109	1295.6073	1295.6067	0.40	0	22	0.13	1	U	L.ECKPVT
7876	871.9700	1741.9254	1741.9250	0.20	1	40	0.0017	1	U	F.QVVIKP
7877	871.9717	1741.9289	1741.9250	2.24	1	(36)	0.0035	1	U	F.QVVIKP

8359	939.9671	1877.9196	1877.9193	0.17	1	(42)	0.0018	1	U	F.QQVGGL
8360	939.9679	1877.9212	1877.9193	1.02	1	43	0.0013	1	U	F.QQVGGL

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62. 2::sp|P00926|SDHD_ECOLI **Mass:** 48155 **Score:** 158 **Matches:** 6(4) **Sequences:** 4(
D-serine dehydratase OS=Escherichia coli (strain K12) OX=83333 GN=dsdA PE=1 SV=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1526	474.2628	946.5111	946.5124	-1.36	1	21	0.11	1	U	L.VALKE
1527	474.2637	946.5129	946.5124	0.56	1	(21)	0.12	1	U	L.VALKE
6797	763.4152	1524.8159	1524.8147	0.76	2	67	2.6e-06	1	U	W.LAQEE
6798	763.4163	1524.8180	1524.8147	2.12	2	(42)	0.00078	1	U	W.LAQEE
7459	551.2845	1650.8318	1650.8326	-0.44	1	36	0.0055	1	U	Y.VGLTE
8087	902.9725	1803.9305	1803.9254	2.82	0	36	0.0048	1	U	L.AKAFP

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63. 2::sp|P0AGE9|SUCD_ECOLI **Mass:** 30044 **Score:** 155 **Matches:** 6(6) **Sequences:** 3(
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
1352	465.2687	928.5229	928.5229	0.01	0	42	0.00079	1	U	L.EAIDA
1353	465.2689	928.5232	928.5229	0.27	0	(32)	0.0085	1	U	L.EAIDA
2648	527.7559	1053.4973	1053.4978	-0.53	0	42	0.001	1	U	Y.EAVKQ
2649	527.7570	1053.4995	1053.4978	1.56	0	(41)	0.0011	1	U	Y.EAVKQ
8055	897.4744	1792.9343	1792.9319	1.33	0	(46)	0.00043	1	U	F.NTVRE
8056	897.4758	1792.9371	1792.9319	2.90	0	71	1.3e-06	1	U	F.NTVRE

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64. 2::sp|P33232|LLDD_ECOLI **Mass:** 42872 **Score:** 149 **Matches:** 6(4) **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	Peptid
2694	529.7895	1057.5645	1057.5842	-18.55	0	20	0.14	3	U	W.DGPM
3007	546.7822	1091.5498	1091.5499	-0.09	2	(32)	0.013	1	U	Y.LGKP
3008	546.7838	1091.5529	1091.5499	2.81	2	32	0.012	1	U	Y.LGKP
4706	625.2953	1248.5760	1248.5775	-1.18	2	(22)	0.13	1	U	W.LGNN
4707	625.2953	1248.5761	1248.5775	-1.08	2	34	0.0082	1	U	W.LGNN
4893	635.3637	1268.7129	1268.7088	3.18	2	62	3.8e-06	1	U	Y.ALAT

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65. 2::sp|P0AE08|AHPC_ECOLI **Mass:** 20862 **Score:** 148 **Matches:** 9(7) **Sequences:** 4(
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	Peptide
2235	506.8071	1011.5997	1011.5964	3.23	2	(36)	0.001	1	U	L.APSLD
2236	506.8091	1011.6037	1011.5964	7.21	2	42	0.00026	1	U	L.APSLD
7921	585.9250	1754.7531	1754.7530	0.10	1	(32)	0.008	1	U	F.DNMRE
7922	585.9263	1754.7572	1754.7530	2.39	1	38	0.0018	1	U	F.DNMRE

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  8250  923.9117  1845.8089  1845.8091  -0.09  2  (35)  0.0039  1     U    F.VCPTE
  8251  923.9158  1845.8170  1845.8091   4.28  2   38   0.0023  1     U    F.VCPTE
  8748  684.6725  2050.9956  2050.9960  -0.15  1   30    0.028  1     U    F.KNGEF
  8749  513.7571  2050.9992  2050.9960   1.59  1  (26)   0.069  1     U    F.KNGEF
  8751  684.6746  2051.0020  2050.9960   2.96  1  (20)    0.25  1     U    F.KNGEF
```

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66.   2::sp|P27434|RODZ_ECOLI     Mass: 36283    Score: 145    Matches: 6(5)   Sequences: 5
      Cytoskeleton protein RodZ OS=Escherichia coli (strain K12) OX=83333 GN=rodZ PE=1 SV=
      Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank Unique   Peptide
      2127  501.2722  1000.5299  1000.5301  -0.25   0   (36) 0.0035   1     U    L.SQQAVA
      2128  501.2723  1000.5301  1000.5301  -0.01   0    43  0.0007   1     U    L.SQQAVA
      2686  529.7592  1057.5039  1057.5040  -0.09   1    29   0.015   1     U    L.TLNAEQ
      3926  586.3270  1170.6395  1170.6357   3.28   1    25   0.041   1     U    L.GLSQQA
      5404  441.2505  1320.7296  1320.7289   0.55   2    22   0.055   1     U    W.LEVTDA
      8674  671.3739  2011.0999  2011.0990   0.46   2    26   0.026   1     U    L.VHIPEE
```

```
67.   2::sp|P77774|BAMB_ECOLI     Mass: 41918    Score: 141    Matches: 9(7)   Sequences: 5
      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
      1541  475.2590   948.5034   948.5029   0.61   0   (23)   0.05   1     U    F.IVDGNR
      1542  475.2592   948.5038   948.5029   0.95   0    25   0.032   1     U    F.IVDGNR
      3281  560.2757  1118.5368  1118.5357   1.05   0    38  0.0028   1     U    L.SGGVTV
      3282  560.2764  1118.5383  1118.5357   2.35   0   (35) 0.0061   1     U    L.SGGVTV
      3436  567.7749  1133.5352  1133.5353  -0.05   1    31   0.014   1     U    Y.ALNTSD
      3437  567.7758  1133.5371  1133.5353   1.57   1   (22)   0.13   1     U    Y.ALNTSD
      3537  571.3324  1140.6502  1140.6503  -0.03   1    26   0.016   1     U    L.SRPVVS
      3538  571.3326  1140.6507  1140.6503   0.39   1   (24)  0.029   1     U    L.SRPVVS
      7841  865.4557  1728.8969  1728.8682   16.6   2    20    0.21   1     U    L.QALNEA
```

```
68.   2::sp|P37095|PEPB_ECOLI     Mass: 46436    Score: 140    Matches: 6(5)   Sequences: 4
      Peptidase B OS=Escherichia coli (strain K12) OX=83333 GN=pepB PE=1 SV=2
      Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score  Expect Rank Unique   Peptide
       758  423.2477   844.4808   844.4807   0.17   1    21    0.081   2     U    W.RLPLA
      7022  522.2740  1563.8003  1563.8005  -0.11   1    34   0.0082   1     U    Y.RITKG
      7023  522.2749  1563.8029  1563.8005   1.52   1   (32)   0.014   1     U    Y.RITKG
      7468  826.8963  1651.7780  1651.7729   3.09   2    35   0.0066   1     U    L.ALDYN
      8105  905.4717  1808.9289  1808.9268   1.17   1   (52) 0.00013   1     U    W.VRDTI
      8106  905.4745  1808.9344  1808.9268   4.21   1    55  6.3e-05   1     U    W.VRDTI
```

```
69.   2::sp|P52643|LDHD_ECOLI     Mass: 36854    Score: 140    Matches: 5(5)   Sequences: 3
      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
3302	561.7776	1121.5407	1121.5393	1.28	1	(26)	0.054	1	U	L.AFDPY
3303	561.7778	1121.5411	1121.5393	1.61	1	48	0.00035	1	U	L.AFDPY
6244	721.8596	1441.7047	1441.7049	-0.13	1	62	1.2e-05	1	U	F.VNDDG
7570	835.8805	1669.7465	1669.7472	-0.37	1	(28)	0.029	1	U	F.FEDKS
7571	835.8837	1669.7528	1669.7472	3.37	1	32	0.011	1	U	F.FEDKS

---

70. 2::sp|P15034|AMPP_ECOLI **Mass:** 50012 **Score:** 139 **Matches:** 6(4) **Sequences:** 4(
Xaa-Pro aminopeptidase OS=Escherichia coli (strain K12) OX=83333 GN=pepP PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2201	504.7589	1007.5033	1007.5036	-0.32	0	23	0.091	1	U	F.TQAQR
2695	529.7895	1057.5645	1057.5655	-0.93	1	33	0.0072	1	U	L.GILKG
4052	593.8085	1185.6024	1185.6030	-0.53	2	(53)	7.8e-05	1	U	W.LGLDV
4054	593.8098	1185.6051	1185.6030	1.73	2	54	4.9e-05	1	U	W.LGLDV
7489	828.3835	1654.7525	1654.7475	3.07	0	29	0.023	1	U	F.AAPEV
7490	828.3848	1654.7550	1654.7475	4.55	0	(24)	0.07	1	U	F.AAPEV

---

71. 2::sp|P0AGJ9|SYY_ECOLI **Mass:** 47896 **Score:** 133 **Matches:** 5(4) **Sequences:** 3(2
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
1896	490.7744	979.5343	979.5338	0.43	0	(30)	0.0082	1	U	L.ITKAD
1897	490.7746	979.5346	979.5338	0.76	0	30	0.0076	1	U	L.ITKAD
2781	533.2522	1064.4898	1064.4887	1.10	0	22	0.1	1	U	L.NREDQ
6925	772.4041	1542.7937	1542.7889	3.07	1	(76)	4.3e-07	1	U	L.VAQVT
6926	772.4042	1542.7939	1542.7889	3.24	1	80	1.7e-07	1	U	L.VAQVT

---

72. 2::sp|P24180|ACRE_ECOLI **Mass:** 41350 **Score:** 128 **Matches:** 8(5) **Sequences:** 3(
Multidrug export protein AcrE OS=Escherichia coli (strain K12) OX=83333 GN=acrE PE=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
8236	921.4739	1840.9333	1840.9294	2.12	1	(22)	0.13	2	U	L.RAVF
8238	921.4764	1840.9382	1840.9294	4.77	1	22	0.12	2	U	L.RAVF
8950	747.3643	2239.0710	2239.0645	2.89	2	(58)	3.5e-05	1		L.ATVQ
8951	1120.5433	2239.0721	2239.0645	3.40	2	(35)	0.0084	1		L.ATVQ
8952	747.3647	2239.0724	2239.0645	3.55	2	(55)	7.9e-05	1		L.ATVQ
8953	1120.5436	2239.0726	2239.0645	3.63	2	(50)	0.00025	1		L.ATVQ
8954	1120.5441	2239.0736	2239.0645	4.07	2	86	5.9e-08	1		L.ATVQ
9157	867.1114	2598.3125	2598.3112	0.52	0	22	0.11	1	U	L.IVND

---

73. 2::sp|P00954|SYW_ECOLI **Mass:** 37642 **Score:** 127 **Matches:** 4(4) **Sequences:** 3(3
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
6323	725.8672	1449.7198	1449.7174	1.70	1	42	0.0017	1	U	Y.LACGI
7201	533.6428	1597.9066	1597.8675	24.5	2	23	0.035	1	U	Y.DVQNK
7358	817.4257	1632.8369	1632.8359	0.61	1	(52)	0.00015	1	U	L.SAVTG
7359	817.4259	1632.8372	1632.8359	0.83	1	65	7.1e-06	1	U	L.SAVTG

---

74. 2::sp|P23721|SERC_ECOLI **Mass:** 39986 **Score:** 126 **Matches:** 6(4) **Sequences:** 3(
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
1878	490.2579	978.5012	978.5022	-0.99	1	28	0.031	1	U	L.EGVKA
1879	490.2589	978.5033	978.5022	1.08	1	(20)	0.17	1	U	L.EGVKA
4328	605.8005	1209.5864	1209.5877	-1.09	1	70	1.9e-06	1	U	L.NILGD
4329	605.8027	1209.5909	1209.5877	2.63	1	(61)	1.6e-05	1	U	L.NILGD
7535	831.9204	1661.8263	1661.8260	0.14	1	33	0.013	1	U	F.IQVAE
7536	831.9233	1661.8321	1661.8260	3.67	1	(24)	0.099	1	U	F.IQVAE

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75. 2::sp|P0A7V3|RS3_ECOLI **Mass:** 25967 **Score:** 124 **Matches:** 4(4) **Sequences:** 2(2
30S ribosomal protein S3 OS=Escherichia coli (strain K12) OX=83333 GN=rpsC PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1379	467.2482	932.4819	932.4815	0.46	0	55	5.1e-05	1	U	L.VADSI
1380	467.2484	932.4823	932.4815	0.85	0	(53)	8.9e-05	1	U	L.VADSI
7129	793.8535	1585.6925	1585.6896	1.81	2	69	1.9e-06	1	U	F.ANTKE
7130	793.8544	1585.6942	1585.6896	2.88	2	(52)	9.9e-05	1	U	F.ANTKE

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76. 2::sp|P0A7A9|IPYR_ECOLI **Mass:** 19805 **Score:** 118 **Matches:** 5(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
3153	554.7795	1107.5444	1107.5448	-0.34	1	(22)	0.14	1	U	Y.EIDKE
3154	554.7802	1107.5459	1107.5448	0.98	1	24	0.085	1	U	Y.EIDKE
6160	715.8610	1429.7075	1429.7089	-0.98	0	28	0.033	1	U	L.NVPAG
6912	771.4340	1540.8534	1540.8501	2.14	0	(56)	2.4e-05	1	U	Y.VVIEI
6913	771.4346	1540.8547	1540.8501	3.01	0	66	2.3e-06	1	U	Y.VVIEI

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77. 2::sp|P0A8J8|RHLB_ECOLI **Mass:** 47325 **Score:** 116 **Matches:** 6(4) **Sequences:** 3(
ATP-dependent RNA helicase RhlB OS=Escherichia coli (strain K12) OX=83333 GN=rhlB 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
1517	473.7555	945.4964	945.4953	1.10	0	(22)	0.12	1	U	L.IMAPT

1518	473.7555	945.4964	945.4953	1.10	0	22	0.097	1	U	L.IMAPT
3123	552.8021	1103.5896	1103.5862	3.01	1	(52)	9.2e-05	1	U	Y.ALNLP
3124	552.8021	1103.5897	1103.5862	3.12	1	53	7.5e-05	1	U	Y.ALNLP
7733	853.4426	1704.8706	1704.8682	1.38	1	(32)	0.014	1	U	L.AVQIH
7734	853.4443	1704.8741	1704.8682	3.45	1	40	0.0021	1	U	L.AVQIH

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78. 2::sp|P0A6F5|CH60_ECOLI **Mass:** 57464 **Score:** 114 **Matches:** 5(4) **Sequences:** 3(

60 kDa chaperonin OS=Escherichia coli (strain K12) OX=83333 GN=groL PE=1 SV=2

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5367	659.3564	1316.6983	1316.6976	0.57	1	40	0.0016	1	U	Y.FINKP
5369	659.3582	1316.7019	1316.6976	3.26	1	(36)	0.0038	1	U	Y.FINKP
7990	889.4544	1776.8943	1776.8934	0.49	2	52	0.00017	1	U	Y.FINKP
7991	889.4567	1776.8989	1776.8934	3.10	2	(50)	0.00025	1	U	Y.FINKP
8512	647.3430	1939.0072	1939.0123	-2.60	1	23	0.082	1	U	L.ADLRG

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79. 2::sp|P0ABK5|CYSK_ECOLI **Mass:** 34525 **Score:** 111 **Matches:** 4(4) **Sequences:** 3(

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
2624	526.7673	1051.5200	1051.5186	1.35	1	33	0.0088	1	U	M.SKIFE
8009	891.4860	1780.9575	1780.9571	0.23	1	(40)	0.0012	1	U	L.KPGVE
8010	891.4864	1780.9583	1780.9571	0.71	1	48	0.00016	1	U	L.KPGVE
8041	597.3314	1788.9723	1788.9734	-0.63	0	30	0.014	1	U	F.TNKNI

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80. 2::sp|P0AG67|RS1_ECOLI **Mass:** 61235 **Score:** 111 **Matches:** 4(4) **Sequences:** 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
4604	618.7963	1235.5781	1235.5782	-0.08	0	48	0.00034	1	U	W.NVAGE
4605	618.7967	1235.5788	1235.5782	0.51	0	(36)	0.0059	1	U	W.NVAGE
5104	646.8408	1291.6670	1291.6660	0.76	1	(52)	0.00011	1	U	L.VLSVG
5105	646.8417	1291.6688	1291.6660	2.17	1	63	1e-05	1	U	L.VLSVG

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81. 2::sp|P0A9K9|SLYD_ECOLI **Mass:** 21182 **Score:** 109 **Matches:** 6(5) **Sequences:** 3(

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
2249	507.2722	1012.5299	1012.5077	21.9	0	(22)	0.059	1	U	L.VDES
2250	507.2725	1012.5305	1012.5077	22.5	0	22	0.063	1	U	L.VDES
7717	850.9386	1699.8626	1699.8628	-0.09	0	(46)	0.00053	1	U	F.NVEV
7718	850.9415	1699.8684	1699.8628	3.28	0	55	6.5e-05	1	U	F.NVEV
8670	1006.0229	2010.0312	2010.0270	2.12	1	(32)	0.011	1	U	Y.QVRT
8671	1006.0234	2010.0322	2010.0270	2.61	1	32	0.01	1	U	Y.QVRT

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82. 2::sp|P67910|HLDD_ECOLI **Mass:** 34985 **Score:** 104 **Matches:** 4(3) **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
2963	**544.2744**	**1086.5341**	**1086.5346**	**-0.41**	**1**	**21**	**0.11**	**1**	**U**	**Y.VGDVA**
3048	**548.7794**	**1095.5442**	**1095.5448**	**-0.58**	**0**	**40**	**0.0015**	**1**	**U**	**F.KTVAE**
7574	**835.9662**	**1669.9179**	**1669.9151**	**1.68**	**0**	**(32)**	**0.0068**	**1**	**U**	**Y.VRQIL**
7575	**835.9686**	**1669.9226**	**1669.9151**	**4.46**	**0**	**43**	**0.00049**	**1**	**U**	**Y.VRQIL**

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83. 2::sp|P0ABU2|YCHF_ECOLI **Mass:** 39984 **Score:** 104 **Matches:** 4(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
1531	474.7667	947.5189	947.5301	-11.81	0	20	0.11	2	U	L.NRVIR
7183	**798.3520**	**1594.6895**	**1594.6899**	**-0.25**	**1**	**56**	**3e-05**	**1**	**U**	**Y.IANVN**
7184	**798.3555**	**1594.6965**	**1594.6899**	**4.12**	**1**	**(37)**	**0.0024**	**1**	**U**	**Y.IANVN**
9239	**916.7942**	**2747.3607**	**2747.3613**	**-0.22**	**0**	**28**	**0.03**	**1**	**U**	**F.ENDNI**

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84. 2::sp|P03841|MALM_ECOLI **Mass:** 31981 **Score:** 103 **Matches:** 6(6) **Sequences:** 3

Maltose operon 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
2956	**543.8113**	**1085.6081**	**1085.6080**	**0.09**	**2**	**(26)**	**0.03**	**1**	**U**	**L.KLLDE**
2959	**543.8118**	**1085.6090**	**1085.6080**	**0.88**	**2**	**33**	**0.0057**	**1**	**U**	**L.KLLDE**
3221	**557.3119**	**1112.6092**	**1112.6077**	**1.35**	**1**	**28**	**0.014**	**1**	**U**	**Y.SVPAN**
3222	**557.3126**	**1112.6106**	**1112.6077**	**2.55**	**1**	**(25)**	**0.032**	**1**	**U**	**Y.SVPAN**
6278	**723.8750**	**1445.7354**	**1445.7362**	**-0.52**	**0**	**(39)**	**0.003**	**1**	**U**	**W.TPVDQ**
6279	**723.8763**	**1445.7381**	**1445.7362**	**1.33**	**0**	**45**	**0.00081**	**1**	**U**	**W.TPVDQ**

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85. 2::sp|P0AB77|KBL_ECOLI **Mass:** 43432 **Score:** 102 **Matches:** 4(4) **Sequences:** 3(3

2-amino-3-ketobutyrate coenzyme A ligase 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
4164	**398.8910**	**1193.6512**	**1193.6517**	**-0.36**	**0**	**23**	**0.044**	**1**	**U**	**L.NHASI**
4314	**603.8289**	**1205.6432**	**1205.6404**	**2.30**	**1**	**34**	**0.0056**	**1**	**U**	**F.ARELQ**
6207	**718.8542**	**1435.6938**	**1435.6943**	**-0.33**	**2**	**45**	**0.00073**	**1**	**U**	**L.TNDLE**
6208	**718.8547**	**1435.6948**	**1435.6943**	**0.35**	**2**	**(42)**	**0.0015**	**1**	**U**	**L.TNDLE**

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86. 2::sp|P0A717|KPRS_ECOLI **Mass:** 34425 **Score:** 96 **Matches:** 4(4) **Sequences:** 2

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
1370	466.2639	930.5133	930.5135	-0.18	0	(42)	0.00094	1	U	L.SSVGV
1371	466.2643	930.5141	930.5135	0.66	0	58	2.2e-05	1	U	L.SSVGV
3021	547.2859	1092.5573	1092.5564	0.89	1	(32)	0.012	1	U	Y.TSLGD
3022	547.2862	1092.5578	1092.5564	1.32	1	37	0.0035	1	U	Y.TSLGD

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87. 2::sp|P21507|SRMB_ECOLI **Mass:** 49998 **Score:** 96 **Matches:** 6(4) **Sequences:** 3(
ATP-dependent RNA helicase SrmB OS=Escherichia coli (strain K12) OX=83333 GN=srmB 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
1031	444.7430	887.4715	887.4712	0.26	0	22	0.12	4	U	L.TEGRVN
1032	444.7430	887.4715	887.4712	0.26	0	(21)	0.13	3	U	L.TEGRVN
1165	454.2292	906.4439	906.4447	-0.88	1	(30)	0.017	1	U	L.EALQDK
1166	454.2303	906.4461	906.4447	1.55	1	33	0.01	1	U	L.EALQDK
4027	591.2935	1180.5724	1180.5724	-0.04	0	41	0.0016	1	U	L.GSAPTG
4028	591.2946	1180.5746	1180.5724	1.82	0	(38)	0.0034	1	U	L.GSAPTG

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88. 2::sp|P60422|RL2_ECOLI **Mass:** 29956 **Score:** 95 **Matches:** 5(2) **Sequences:** 3(1
50S ribosomal protein L2 OS=Escherichia coli (strain K12) OX=83333 GN=rplB PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
462	408.7273	815.4400	815.4402	-0.21	0	(20)	0.14	1	U	L.GKAGA
463	408.7273	815.4401	815.4402	-0.11	0	22	0.1	1	U	L.GKAGA
3000	546.2955	1090.5765	1090.5771	-0.55	0	(49)	0.00019	1	U	Y.VQIVA
3001	546.2974	1090.5802	1090.5771	2.81	0	51	0.00013	1	U	Y.VQIVA
5732	681.8386	1361.6626	1361.6575	3.72	1	23	0.13	1	U	L.EYDPN

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89. 2::sp|P0AGJ5|YFIF_ECOLI **Mass:** 37989 **Score:** 95 **Matches:** 3(3) **Sequences:** 2(
Uncharacterized tRNA/rRNA methyltransferase YfiF 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
5576	673.8633	1345.7120	1345.7089	2.29	0	61	1.4e-05	1	U	Y.TVVTT
5577	673.8634	1345.7122	1345.7089	2.47	0	(61)	1.6e-05	1	U	Y.TVVTT
5852	691.8324	1381.6502	1381.6474	2.09	0	34	0.0088	1	U	Y.EGLPD

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90. 2::sp|P39099|DEGQ_ECOLI **Mass:** 47176 **Score:** 94 **Matches:** 5(5) **Sequences:** 3(
Periplasmic pH-dependent serine endoprotease DegQ 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
1696	482.7403	963.4660	963.4881	-23.02	0	(26)	0.045	2	U	-.MKKQT
1697	482.7408	963.4670	963.4881	-21.94	0	33	0.0073	2	U	-.MKKQT
3959	587.8187	1173.6228	1173.6241	-1.13	0	33	0.0089	1	U	L.TQIAI

3960	587.8201	1173.6256	1173.6241	1.27	0	(27)	0.036	1	U	L.TQIAI
7593	837.4374	1672.8602	1672.8519	4.95	2	30	0.02	1	U	F.DAKLI

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91. 2::sp|P03023|LACI_ECOLI **Mass:** 38737 **Score:** 94 **Matches:** 4(3) **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
367	404.7133	807.4121	807.4201	-9.80	1	24	0.048	1	U	M.KPVTL
1981	494.7744	987.5343	987.5349	-0.65	1	21	0.12	1	U	L.GQTSV
4942	636.8632	1271.7118	1271.7125	-0.61	1	51	8.5e-05	1	U	Y.IPPLT
4943	636.8635	1271.7125	1271.7125	-0.03	1	(41)	0.00084	1	U	Y.IPPLT

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92. 2::sp|P0A9S3|GATD_ECOLI **Mass:** 37822 **Score:** 93 **Matches:** 3(3) **Sequences:** 3

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

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2795	533.7980	1065.5814	1065.5819	-0.45	2	33	0.0035	1	U	L.ALVGTL
2825	537.2374	1072.4602	1072.4614	-1.14	0	22	0.048	1	U	Y.SSPWPG
3135	553.3042	1104.5938	1104.5927	1.00	0	37	0.0028	1	U	L.AVEIAG

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93. 2::sp|P0A7V0|RS2_ECOLI **Mass:** 26784 **Score:** 91 **Matches:** 4(3) **Sequences:** 3(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
5771	684.8196	1367.6247	1367.6205	3.09	1	28	0.03	1	U	L.KDLETQ
6424	732.8290	1463.6434	1463.6416	1.20	0	38	0.0019	1	U	F.AIVDTN
6425	732.8308	1463.6471	1463.6416	3.70	0	(34)	0.0052	1	U	F.AIVDTN
8257	925.4516	1848.8886	1848.8928	-2.22	2	27	0.056	1	U	L.ENSLGG

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94. 2::sp|P0A9K3|PHOL_ECOLI **Mass:** 39129 **Score:** 90 **Matches:** 5(4) **Sequences:** 3

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

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3901	585.8274	1169.6403	1169.6404	-0.05	0	(25)	0.033	1	U	L.TRPAV
3902	585.8279	1169.6412	1169.6404	0.68	0	31	0.0083	1	U	L.TRPAV
4740	626.8658	1251.7170	1251.7187	-1.32	0	(32)	0.0028	1	U	L.IERNV
4741	626.8686	1251.7226	1251.7187	3.17	0	39	0.00051	1	U	L.IERNV
4918	636.3351	1270.6556	1270.6557	-0.11	1	21	0.11	1	U	Y.IANIL

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95. 2::sp|P0A9A6|FTSZ_ECOLI **Mass:** 40299 **Score:** 88 **Matches:** 3(3) **Sequences:** 2

Cell division protein FtsZ OS=Escherichia coli (strain K12) OX=83333 GN=ftsZ 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
1683	481.2898	960.5650	960.5644	0.61	0	(36)	0.0014	1	U	L.TVAVV
1684	481.2901	960.5657	960.5644	1.32	0	37	0.00099	1	U	L.TVAVV
5684	679.3725	1356.7304	1356.7249	4.10	2	51	0.00012	1	U	L.LEDID

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96. 2::sp|P0AGG8|TLDD_ECOLI **Mass:** 51446 **Score:** 88 **Matches:** 3(2) **Sequences:** 2

Metalloprotease TldD OS=Escherichia coli (strain K12) OX=83333 GN=tldD PE=1 SV=1

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2045	497.2651	992.5156	992.5178	-2.25	2	21	0.15	1	U	F.AYADQ
7178	797.8951	1593.7757	1593.7787	-1.89	1	67	5.3e-06	1	U	Y.APNFG
7182	797.8975	1593.7804	1593.7787	1.02	1	(35)	0.0087	1	U	Y.APNFG

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97. 2::sp|P36672|PTTBC_ECOLI **Mass:** 51389 **Score:** 87 **Matches:** 2(2) **Sequences:**

PTS system trehalose-specific EIIBC component 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
5456	664.3289	1326.6433	1326.6456	-1.74	1	32	0.011	1	U	F.QVVIG
7346	815.9148	1629.8150	1629.8145	0.35	0	55	7.5e-05	1	U	F.RNVIG

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98. 2::sp|P30845|EPTA_ECOLI **Mass:** 62369 **Score:** 86 **Matches:** 4(4) **Sequences:** 2

Phosphoethanolamine transferase EptA OS=Escherichia coli (strain K12) OX=83333 GN=ep

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4469	611.8076	1221.6006	1221.5990	1.32	0	(39)	0.0024	1	U	L.IVGET
4471	611.8084	1221.6023	1221.5990	2.71	0	49	0.00025	1	U	L.IVGET
4748	627.8564	1253.6982	1253.6980	0.20	1	(25)	0.026	1	U	Y.INNLQ
4750	627.8568	1253.6991	1253.6980	0.89	1	37	0.0016	1	U	Y.INNLQ

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99. 2::sp|P25553|ALDA_ECOLI **Mass:** 52411 **Score:** 85 **Matches:** 4(4) **Sequences:** 2

Lactaldehyde dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=aldA 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
6453	735.8532	1469.6917	1469.6933	-1.02	0	47	0.00043	1	U	F.GNPAE
6454	735.8535	1469.6925	1469.6933	-0.52	0	(40)	0.0019	1	U	F.GNPAE
7559	835.4236	1668.8326	1668.8318	0.46	0	41	0.0017	1	U	Y.EGEII
7561	835.4241	1668.8336	1668.8318	1.04	0	(35)	0.006	1	U	Y.EGEII

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100. 2::sp|P37773|MPL_ECOLI **Mass:** 50298 **Score:** 85 **Matches:** 4(3) **Sequences:** 2(2

UDP-N-acetylmuramate--L-alanyl-gamma-D-glutamyl-meso-2,6-diaminoheptandioate ligase

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2841	537.8087	1073.6029	1073.6022	0.65	2	(21)	0.093	1	U	F.LLQPA
2842	537.8096	1073.6046	1073.6022	2.24	2	44	0.00049	1	U	F.LLQPA
7212	534.2905	1599.8498	1599.8508	-0.66	2	(36)	0.0038	1	U	W.EVLLD
7213	534.2906	1599.8499	1599.8508	-0.55	2	41	0.0013	1	U	W.EVLLD

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101. 2::sp|P21599|KPYK2_ECOLI **Mass:** 51553 **Score:** 83 **Matches:** 5(5) **Sequences:** 3

Pyruvate kinase II OS=Escherichia coli (strain K12) OX=83333 GN=pykA PE=1 SV=3

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2435	514.7908	1027.5670	1027.5662	0.76	2	28	0.016	1	U	L.LLDDGR
5119	647.3743	1292.7341	1292.7340	0.08	0	28	0.0075	1	U	Y.KGLPAD
5120	647.3745	1292.7343	1292.7340	0.26	0	(25)	0.017	1	U	Y.KGLPAD
6671	752.3491	1502.6836	1502.6849	-0.86	0	(27)	0.033	1	U	F.DSANDG
6672	752.3505	1502.6864	1502.6849	1.00	0	29	0.021	1	U	F.DSANDG

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102. 2::sp|P0A858|TPIS_ECOLI **Mass:** 27126 **Score:** 83 **Matches:** 4(4) **Sequences:** 2

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
239	397.2133	792.4121	792.4130	-1.07	0	28	0.018	1	U	L.KTQGA
241	397.2135	792.4124	792.4130	-0.76	0	(28)	0.019	1	U	L.KTQGA
4896	635.3811	1268.7476	1268.7452	1.93	0	(54)	2e-05	1	U	F.AVIVK
4897	635.3819	1268.7492	1268.7452	3.20	0	54	1.5e-05	1	U	F.AVIVK

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103. 2::sp|P07012|RF2_ECOLI **Mass:** 41339 **Score:** 82 **Matches:** 3(2) **Sequences:** 2(

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
6852	766.8835	1531.7525	1531.7552	-1.75	2	32	0.016	1	U	L.DQMKQ
6853	766.8850	1531.7555	1531.7552	0.17	2	(26)	0.067	1	U	L.DQMKQ
6944	774.3508	1546.6870	1546.6900	-1.93	1	50	0.00014	1	U	Y.LDIQA

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104. 2::sp|P21888|SYC_ECOLI **Mass:** 52454 **Score:** 80 **Matches:** 3(2) **Sequences:** 2(

Cysteine--tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=cysS PE=1 SV=2

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3417	566.7806	1131.5467	1131.5448	1.72	2	38	0.003	1	U	L.GLLEQE
6513	738.8756	1475.7367	1475.7369	-0.13	0	(22)	0.16	1	U	L.RGTDKT
6514	738.8780	1475.7414	1475.7369	3.09	0	42	0.0015	1	U	L.RGTDKT

105. 2::sp|P0AC38|ASPA_ECOLI **Mass:** 52950 **Score:** 79 **Matches:** 4(3) **Sequences:** 2(
Aspartate ammonia-lyase OS=Escherichia coli (strain K12) OX=83333 GN=aspA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5338	658.3456	1314.6766	1314.6779	-0.98	1	51	0.00015	1	U	M.SNNIR
5339	658.3479	1314.6812	1314.6779	2.55	1	(41)	0.0013	1	U	M.SNNIR
5830	688.8582	1375.7019	1375.6983	2.60	0	29	0.03	1	U	Y.ISNNK
5831	688.8607	1375.7068	1375.6983	6.14	0	(24)	0.082	1	U	Y.ISNNK

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106. 2::sp|P0A9J6|RBSK_ECOLI **Mass:** 32328 **Score:** 79 **Matches:** 3(2) **Sequences:** 2(
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
6415	732.3768	1462.7391	1462.7416	-1.72	0	25	0.078	1	U	F.RVQAV
7923	878.4745	1754.9344	1754.9302	2.43	1	(47)	0.00022	1	U	L.ALVDI
7924	878.4778	1754.9411	1754.9302	6.25	1	54	4.1e-05	1	U	L.ALVDI

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107. 2::sp|P62707|GPMA_ECOLI **Mass:** 28539 **Score:** 77 **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
3471	569.7740	1137.5334	1137.5342	-0.70	2	31	0.019	1	U	Y.EFDEN
3472	569.7756	1137.5366	1137.5342	2.08	2	(27)	0.048	1	U	Y.EFDEN
4689	623.3315	1244.6485	1244.6500	-1.15	1	47	0.00039	1	U	L.SEKEL
4690	623.3336	1244.6527	1244.6500	2.19	1	(30)	0.018	1	U	L.SEKEL

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108. 2::sp|P00448|SODM_ECOLI **Mass:** 23083 **Score:** 77 **Matches:** 4(2) **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
5733	454.9047	1361.6924	1361.6939	-1.09	1	24	0.087	1	U	L.QGDLK
5734	454.9051	1361.6934	1361.6939	-0.41	1	(24)	0.095	1	U	L.QGDLK
5905	696.3401	1390.6656	1390.6629	1.93	1	(44)	0.00084	1	U	W.NVVNW
5906	696.3409	1390.6673	1390.6629	3.15	1	53	0.00012	1	U	W.NVVNW

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109. 2::sp|P0A9D8|DAPD_ECOLI **Mass:** 30044 **Score:** 77 **Matches:** 2(2) **Sequences:** 2(
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
1947	493.7144	985.4142	985.4141	0.06	1	36	0.0017	1	U	F.ADYDEA
4238	601.3210	1200.6274	1200.6251	1.92	0	41	0.0015	1	U	L.RVAEKI

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110. 2::sp|P0A6Y8|DNAK_ECOLI **Mass:** 69130 **Score:** 76 **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
3942	587.2997	1172.5849	1172.5826	2.02	0	33	0.0069	1	U	F.KIIAAD
7370	818.8939	1635.7733	1635.7740	-0.44	0	42	0.0012	1	U	L.ENAEGD
7371	818.8966	1635.7787	1635.7740	2.85	0	(36)	0.0057	1	U	L.ENAEGD

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111. 2::sp|P31120|GLMM_ECOLI **Mass:** 47799 **Score:** 75 **Matches:** 4(4) **Sequences:** 2(
Phosphoglucosamine mutase OS=Escherichia coli (strain K12) OX=83333 GN=glmM 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
115	386.2396	770.4646	770.4650	-0.58	0	(27)	0.014	1	U	Y.IIARE
116	386.2400	770.4655	770.4650	0.62	0	28	0.0097	1	U	Y.IIARE
5287	655.8257	1309.6369	1309.6336	2.51	0	50	0.00023	1	U	L.KIVVD
5288	655.8268	1309.6391	1309.6336	4.19	0	(46)	0.00049	1	U	L.KIVVD

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112. 2::sp|P0A7L0|RL1_ECOLI **Mass:** 24714 **Score:** 75 **Matches:** 2(2) **Sequences:** 1(1
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
6479	736.8711	1471.7276	1471.7266	0.67	0	75	6.1e-07	1	U	F.TQGAN
6480	736.8718	1471.7291	1471.7266	1.68	0	(64)	7.5e-06	1	U	F.TQGAN

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113. 2::sp|P0AFK9|POTD_ECOLI **Mass:** 38842 **Score:** 75 **Matches:** 4(3) **Sequences:** 2(
Spermidine/putrescine-binding periplasmic protein 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
2101	500.2794	998.5443	998.5437	0.66	2	(41)	0.00058	1	U	Y.VPPGL
2102	500.2797	998.5449	998.5437	1.26	2	46	0.00018	1	U	Y.VPPGL
2783	533.2635	1064.5124	1064.5138	-1.33	1	29	0.028	1	U	L.LTDDA
2784	533.2643	1064.5140	1064.5138	0.16	1	(21)	0.19	1	U	L.LTDDA

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114. 2::sp|P0ABJ1|CYOA_ECOLI **Mass:** 34946 **Score:** 75 **Matches:** 4(4) **Sequences:** 2(
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
349	403.7234	805.4323	805.4334	-1.37	0	45	0.00031	1	U	F.ADVINKF
350	403.7236	805.4326	805.4334	-0.93	0	(27)	0.021	1	U	F.ADVINKF
1288	460.2477	918.4808	918.4811	-0.30	1	(28)	0.021	1	U	F.SNVKPDL
1289	460.2477	918.4808	918.4811	-0.30	1	32	0.0095	1	U	F.SNVKPDL

115. 2::sp|P16095|SDHL_ECOLI **Mass:** 49388 **Score:** 74 **Matches:** 4(2) **Sequences:** 3
L-serine dehydratase 1 OS=Escherichia coli (strain K12) OX=83333 GN=sdaA 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
32	**381.2242**	**760.4337**	**760.4330**	**0.93**	**1**	**24**	**0.045**	**1**	**U**	**F.KSATEL**
620	**417.2122**	**832.4098**	**832.4113**	**-1.75**	**0**	**21**	**0.14**	**1**	**U**	**L.AIKVQC**
6087	**711.3326**	**1420.6507**	**1420.6511**	**-0.24**	**1**	**30**	**0.021**	**1**	**U**	**Y.DHFIES**
6088	**711.3343**	**1420.6540**	**1420.6511**	**2.09**	**1**	**(24)**	**0.078**	**1**	**U**	**Y.DHFIES**

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116. 2::sp|P0ADR8|PPNN_ECOLI **Mass:** 51281 **Score:** 71 **Matches:** 4(4) **Sequences:** 2
Pyrimidine/purine nucleotide 5'-monophosphate nucleosidase OS=Escherichia coli (stra
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4833	**632.8068**	**1263.5990**	**1263.5943**	**3.73**	**1**	**(35)**	**0.0068**	**1**	**U**	**L.NSGSLT**
4834	**632.8079**	**1263.6013**	**1263.5943**	**5.57**	**1**	**40**	**0.0026**	**1**	**U**	**L.NSGSLT**
5179	**650.8611**	**1299.7076**	**1299.7074**	**0.13**	**1**	**32**	**0.0099**	**1**	**U**	**L.KLYPDQ**
5180	**650.8626**	**1299.7107**	**1299.7074**	**2.48**	**1**	**(31)**	**0.012**	**1**	**U**	**L.KLYPDQ**

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117. 2::sp|P0A7S9|RS13_ECOLI **Mass:** 13148 **Score:** 70 **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
5876	**693.8777**	**1385.7409**	**1385.7402**	**0.56**	**0**	**(64)**	**6.3e-06**	**1**	**U**	**L.AAAGI**
5877	**693.8795**	**1385.7445**	**1385.7402**	**3.11**	**0**	**70**	**1.5e-06**	**1**	**U**	**L.AAAGI**

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118. 2::sp|P39336|YJGL_ECOLI **Mass:** 69819 **Score:** 70 **Matches:** 4(3) **Sequences:** 3
Uncharacterized protein YjgL OS=Escherichia coli (strain K12) OX=83333 GN=yjgL 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
738	**422.7346**	**843.4546**	**843.4701**	**-18.46**	**2**	**(24)**	**0.055**	**1**	**U**	**L.QKLNN**
741	**422.7353**	**843.4560**	**843.4701**	**-16.73**	**2**	**26**	**0.028**	**1**	**U**	**L.QKLNN**
897	**436.2479**	**870.4812**	**870.4698**	**13.0**	**0**	**24**	**0.028**	**3**	**U**	**F.NEVPV**
6244	721.8596	1441.7047	1441.7161	-7.89	2	21	0.18	2	U	L.NNNQE

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119. 2::sp|P08660|AK3_ECOLI **Mass:** 48787 **Score:** 70 **Matches:** 3(3) **Sequences:** 2(2
Lysine-sensitive aspartokinase 3 OS=Escherichia coli (strain K12) OX=83333 GN=lysC 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
4381	**607.3500**	**1212.6854**	**1212.6867**	**-1.03**	**0**	**44**	**0.00044**	**1**	**U**	**L.LPAVR**

4382	607.3514	1212.6883	1212.6867	1.37	0	(28)	0.016	1	U	L.LPAVR
5878	694.3647	1386.7148	1386.7143	0.37	2	27	0.046	3	U	L.VALAE

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120. 2::sp|P05459|PDXB_ECOLI **Mass:** 41684 **Score:** 70 **Matches:** 5(3) **Sequences:** 3(
Erythronate-4-phosphate dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=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
437	407.7430	813.4713	813.4708	0.62	0	(21)	0.055	3	U	L.VQRADI
438	407.7431	813.4716	813.4708	0.92	0	25	0.024	3	U	L.VQRADI
786	424.7345	847.4544	847.4626	-9.60	0	20	0.097	2	U	L.AGKPIK
3927	586.3283	1170.6421	1170.6244	15.1	1	(23)	0.064	2	U	L.DELVQR
3928	586.3293	1170.6440	1170.6244	16.7	1	28	0.02	1	U	L.DELVQR

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121. 2::sp|P37349|DHAM_ECOLI **Mass:** 51872 **Score:** 69 **Matches:** 2(2) **Sequences:** 2(
Protein-lysine deacetylase OS=Escherichia coli (strain K12) OX=83333 GN=dhaM 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
6393	729.8965	1457.7784	1457.7766	1.27	1	33	0.0083	1	U	L.IAKGPE
8245	923.4851	1844.9557	1844.9520	2.00	1	38	0.003	1	U	L.TQTKEE

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122. 2::sp|P0A6B7|ISCS_ECOLI **Mass:** 45232 **Score:** 69 **Matches:** 3(3) **Sequences:** 2(
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
221	396.2233	790.4320	790.4337	-2.19	0	37	0.0022	1	U	L.AIKGAA
222	396.2233	790.4321	790.4337	-2.03	0	(37)	0.0022	1	U	L.AIKGAA
5071	644.8324	1287.6502	1287.6459	3.37	1	34	0.008	1	U	Y.KQGVDL

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123. 2::sp|P60723|RL4_ECOLI **Mass:** 22073 **Score:** 68 **Matches:** 4(4) **Sequences:** 2(2
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
210	395.2389	788.4632	788.4643	-1.49	1	(29)	0.0098	1	U	L.KSILSEL.
212	395.2392	788.4638	788.4643	-0.70	1	34	0.0038	1	U	L.KSILSEL.
1485	472.7739	943.5332	943.5338	-0.62	1	(31)	0.0091	1	U	L.VLKDAQSA
1486	472.7740	943.5334	943.5338	-0.49	1	35	0.0039	1	U	L.VLKDAQSA

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124. 2::sp|P24181|ACRF_ECOLI **Mass:** 111554 **Score:** 68 **Matches:** 3(2) **Sequences:** 2(
Multidrug export protein AcrF OS=Escherichia coli (strain K12) OX=83333 GN=acrF 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
5796	686.3784	1370.7423	1370.7405	1.30	1	44	0.00064	2	U	F.KLEVD
5797	686.3792	1370.7439	1370.7405	2.45	1	(41)	0.0011	2	U	F.KLEVD
6419	732.3800	1462.7454	1462.7490	-2.40	1	25	0.081	1	U	L.MENLA

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125. 2::sp|P0A6N4|EFP_ECOLI **Mass:** 20635 **Score:** 68 **Matches:** 3(3) **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
1793	485.7999	969.5853	969.5859	-0.60	0	34	0.0015	1	U	L.STGAVV
1794	485.8002	969.5859	969.5859	0.02	0	(32)	0.0026	1	U	L.STGAVV
8931	738.3825	2212.1257	2212.1223	1.52	1	34	0.0073	1	U	L.EIVDTD

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126. 2::sp|P0C018|RL18_ECOLI **Mass:** 12762 **Score:** 68 **Matches:** 2(2) **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
6155	715.3987	1428.7828	1428.7824	0.30	0	68	2.3e-06	1	U	L.VAAST
6156	715.4006	1428.7867	1428.7824	3.03	0	(61)	1e-05	1	U	L.VAAST

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127. 2::sp|P77300|YAGI_ECOLI **Mass:** 27878 **Score:** 67 **Matches:** 3(0) **Sequences:** 3

Uncharacterized HTH-type transcriptional regulator YagI OS=Escherichia coli (strain

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1553	476.2262	950.4379	950.4345	3.58	1	23	0.068	1	U	L.FNEQA
2766	532.7606	1063.5067	1063.5332	-24.89	1	21	0.17	4	U	L.ASREA
7333	814.9484	1627.8823	1627.8855	-1.93	1	23	0.059	1	U	-.MPIIQ

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128. 2::sp|P07004|PROA_ECOLI **Mass:** 45001 **Score:** 67 **Matches:** 1(1) **Sequences:** 1

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
5785	685.8669	1369.7193	1369.7201	-0.59	0	67	2.6e-06	1	U	Y.EARPN

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129. 2::sp|P0A7V8|RS4_ECOLI **Mass:** 23512 **Score:** 67 **Matches:** 4(3) **Sequences:** 2(2

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

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
786	424.7345	847.4544	847.4552	-0.89	1	25	0.028	1	U	Y.GVLERQ
787	424.7348	847.4551	847.4552	-0.11	1	(22)	0.065	1	U	Y.GVLERQ

6741	758.3879	1514.7613	1514.7616	-0.21	2	41	0.0014	1	U	L.SADINE
6742	758.3881	1514.7616	1514.7616	-0.05	2	(28)	0.032	1	U	L.SADINE

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130. 2::sp|P76373|UDG_ECOLI **Mass:** 43744 **Score:** 67 **Matches:** 3(3) **Sequences:** 2(2

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
1962	494.2651	986.5157	986.5185	-2.83	1	27	0.033	1	U	F.LQSDKI
5435	662.8350	1323.6555	1323.6558	-0.23	1	43	0.0012	1	U	F.TDSTEA
5436	662.8355	1323.6563	1323.6558	0.42	1	(35)	0.0069	1	U	F.TDSTEA

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131. 2::sp|P0A6Y5|HSLO_ECOLI **Mass:** 32856 **Score:** 66 **Matches:** 5(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
2535	521.7818	1041.5490	1041.5495	-0.42	1	(21)	0.078	1	U	L.TLPAN
2536	521.7821	1041.5496	1041.5495	0.16	1	25	0.032	1	U	L.TLPAN
6413	732.3739	1462.7332	1462.7668	-22.91	0	(24)	0.088	1	U	Y.VVITI
6420	732.3931	1462.7716	1462.7668	3.30	0	(38)	0.0026	1	U	Y.VVITI
6421	732.3942	1462.7738	1462.7668	4.81	0	41	0.0014	1	U	Y.VVITI

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132. 2::sp|P0ACB2|HEM2_ECOLI **Mass:** 35944 **Score:** 66 **Matches:** 2(2) **Sequences:** 1(

Delta-aminolevulinic acid dehydratase OS=Escherichia coli (strain K12) OX=83333 GN=h

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
7350	816.4239	1630.8333	1630.8315	1.15	1	66	5.7e-06	1	U	L.ENLGK
7351	816.4257	1630.8369	1630.8315	3.32	1	(52)	0.00014	1	U	L.ENLGK

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133. 2::sp|P05042|FUMC_ECOLI **Mass:** 50856 **Score:** 65 **Matches:** 3(3) **Sequences:** 2(

Fumarate hydratase class II OS=Escherichia coli (strain K12) OX=83333 GN=fumC 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
1998	495.7481	989.4817	989.4818	-0.08	1	(36)	0.0046	1	U	L.TLGQEI
1999	495.7486	989.4826	989.4818	0.78	1	36	0.0046	1	U	L.TLGQEI
7777	858.9421	1715.8697	1715.8689	0.46	0	30	0.024	1	U	L.SEEKAS

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134. 2::sp|P39371|NANM_ECOLI **Mass:** 39548 **Score:** 64 **Matches:** 3(3) **Sequences:** 2(

N-acetylneuraminate epimerase OS=Escherichia coli (strain K12) OX=83333 GN=nanM 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
6743	758.3922	1514.7699	1514.7729	-2.01	1	42	0.0011	1	U	W.NKLAPV

6744	758.3934	1514.7722	1514.7729	-0.48	1	(38)	0.0028	1	U	W.NKLAPV
7142	794.4354	1586.8563	1586.8516	2.98	0	26	0.038	1	U	L.IIGGET

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135. 2::sp|P0A7G6|RECA_ECOLI **Mass:** 38121 **Score:** 62 **Matches:** 3(2) **Sequences:** 2

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
1856	488.7509	975.4871	975.4873	-0.14	0	(41)	0.0015	1	U	Y.GPESSG
1857	488.7511	975.4877	975.4873	0.43	0	41	0.0013	1	U	Y.GPESSG
3391	565.3140	1128.6135	1128.6138	-0.30	0	21	0.11	1	U	M.AIDENK

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136. 2::sp|P39406|RSMC_ECOLI **Mass:** 37829 **Score:** 62 **Matches:** 3(3) **Sequences:** 2

Ribosomal RNA small subunit methyltransferase C 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
3612	573.7919	1145.5692	1145.5677	1.32	1	25	0.054	1	U	F.SRDGLD
5038	642.3345	1282.6544	1282.6517	2.08	1	36	0.0035	1	U	F.AGDLQD
5039	642.3358	1282.6571	1282.6517	4.19	1	(34)	0.006	1	U	F.AGDLQD

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137. 2::sp|P37759|RMLB1_ECOLI **Mass:** 40704 **Score:** 62 **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
4745	627.8157	1253.6169	1253.6140	2.36	0	(52)	0.00012	1	U	Y.TVVTE
4746	627.8164	1253.6181	1253.6140	3.35	0	62	1.1e-05	1	U	Y.TVVTE

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138. 2::sp|P0A6J5|DADA_ECOLI **Mass:** 47919 **Score:** 61 **Matches:** 3(2) **Sequences:** 2

D-amino acid dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=dadA 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
2175	503.7687	1005.5228	1005.5244	-1.54	1	36	0.0039	1	U	L.AVRLDG
2177	503.7698	1005.5251	1005.5244	0.71	1	(31)	0.015	1	U	L.AVRLDG
8188	916.9569	1831.8991	1831.8952	2.16	1	25	0.08	1	U	Y.ENATRD

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139. 2::sp|P0AG48|RL21_ECOLI **Mass:** 11557 **Score:** 61 **Matches:** 2(2) **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
3659	576.3196	1150.6246	1150.6234	1.05	1	33	0.0051	1	U	W.FTDVKI
6677	752.3987	1502.7829	1502.7803	1.76	0	28	0.032	1	U	L.MIANGE

140. 2::sp|P0AFK0|PMBA_ECOLI **Mass:** 48625 **Score:** 60 **Matches:** 3(2) **Sequences:** 2

Metalloprotease PmbA OS=Escherichia coli (strain K12) OX=83333 GN=pmbA PE=1 SV=1

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
506	410.7302	819.4458	819.4491	-4.01	1	21	0.063	1	U	L.KGLAST
4224	600.8215	1199.6284	1199.6299	-1.25	1	(32)	0.0083	1	U	F.GHLVGA
4226	600.8220	1199.6295	1199.6299	-0.33	1	38	0.0021	1	U	F.GHLVGA

141. 2::sp|P0ADA3|NLPD_ECOLI **Mass:** 40181 **Score:** 58 **Matches:** 4(3) **Sequences:** 2

Murein hydrolase activator NlpD OS=Escherichia coli (strain K12) OX=83333 GN=nlpD 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
451	408.2343	814.4541	814.4549	-0.98	1	(24)	0.048	1	U	Y.ALNVGQTL
452	408.2347	814.4548	814.4549	-0.07	1	28	0.018	1	U	Y.ALNVGQTL
613	416.7425	831.4704	831.4715	-1.29	1	30	0.0088	1	U	L.RYLPQR.-
614	416.7425	831.4705	831.4715	-1.21	1	(21)	0.064	1	U	L.RYLPQR.-

142. 2::sp|P39173|YEAD_ECOLI **Mass:** 32874 **Score:** 57 **Matches:** 2(2) **Sequences:** 2

Putative glucose-6-phosphate 1-epimerase 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
516	411.7450	821.4755	821.4759	-0.50	2	23	0.017	1	U	F.ALQGAH
6158	715.8532	1429.6919	1429.6878	2.87	2	34	0.0075	1	U	L.SWKPAG

143. 2::sp|P0A6F1|CARA_ECOLI **Mass:** 41633 **Score:** 56 **Matches:** 3(3) **Sequences:** 2

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
550	413.2638	824.5131	824.5120	1.42	0	31	0.0015	1	U	L.VIRDLP
551	413.2640	824.5135	824.5120	1.81	0	(23)	0.0082	1	U	L.VIRDLP
2909	541.7721	1081.5296	1081.5291	0.46	0	26	0.042	1	U	L.AKEVTT

144. 2::sp|P0AEZ3|MIND_ECOLI **Mass:** 29710 **Score:** 55 **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
5094	646.3298	1290.6450	1290.6456	-0.47	1	(46)	0.00054	1	U	Y.DFVNV
5095	646.3319	1290.6493	1290.6456	2.84	1	55	6.7e-05	1	U	Y.DFVNV

145. 2::sp|P27837|YIFK_ECOLI **Mass:** 50651 **Score:** 55 **Matches:** 3(1) **Sequences:** 2(
Probable transport protein YifK OS=Escherichia coli (strain K12) OX=83333 GN=yifK 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
55	382.7178	763.4210	763.4228	-2.40	1	31	0.0085	1	U	L.ISQLRF
56	382.7180	763.4214	763.4228	-1.90	1	(21)	0.086	2	U	L.ISQLRF
2698	529.7953	1057.5760	1057.5630	12.3	2	24	0.058	2	U	L.KWAGPS

146. 2::sp|P0A908|MIPA_ECOLI **Mass:** 27813 **Score:** 55 **Matches:** 1(1) **Sequences:** 1(
MltA-interacting protein OS=Escherichia coli (strain K12) OX=83333 GN=mipA 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
5048	642.8332	1283.6518	1283.6510	0.63	1	55	4.7e-05	1	U	F.SLGAG

147. 2::sp|P0AC41|SDHA_ECOLI **Mass:** 65008 **Score:** 54 **Matches:** 2(2) **Sequences:** 2(
Succinate dehydrogenase flavoprotein subunit 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
1019	442.7635	883.5124	883.5127	-0.30	0	21	0.04	1	U	L.ESRLPG
4871	634.3433	1266.6721	1266.6721	-0.00	1	33	0.0055	1	U	W.QFHPTG

148. 2::sp|P08312|SYFA_ECOLI **Mass:** 36866 **Score:** 54 **Matches:** 1(1) **Sequences:** 1(
Phenylalanine--tRNA ligase alpha subunit 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
7740	854.3782	1706.7419	1706.7424	-0.29	1	54	4.9e-05	1	U	F.TVATG

149. 2::sp|P25522|MNME_ECOLI **Mass:** 49258 **Score:** 54 **Matches:** 2(1) **Sequences:** 2(
tRNA modification GTPase MnmE OS=Escherichia coli (strain K12) OX=83333 GN=mnmE 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
4237	601.3204	1200.6262	1200.5986	23.0	0	23	0.082	1	U	W.QEIEQA
5580	674.3490	1346.6834	1346.6830	0.32	1	33	0.01	1	U	W.QEIEQA

150. 2::sp|P75876|RLMI_ECOLI **Mass:** 44671 **Score:** 53 **Matches:** 1(1) **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
7518	830.9329	1659.8512	1659.8468	2.63	0	53	0.00011	1	U	L.IAGES

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151. 2::sp|P23908|ARGE_ECOLI **Mass:** 42777 **Score:** 52 **Matches:** 2(1) **Sequences:** 2

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
2682	529.3032	1056.5919	1056.5815	9.82	2	21	0.084	1	U	L.ASIGQG
7765	857.9009	1713.7872	1713.7879	-0.42	1	31	0.016	1	U	Y.ILATAD

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152. 2::sp|P39382|YJIK_ECOLI **Mass:** 32107 **Score:** 52 **Matches:** 3(1) **Sequences:** 2

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
3166	555.2952	1108.5758	1108.5652	9.56	1	(22)	0.1	1	U	F.VKDLET
3167	555.2957	1108.5767	1108.5652	10.4	1	23	0.07	1	U	F.VKDLET
3965	588.3094	1174.6042	1174.6081	-3.29	2	28	0.033	1	U	Y.KVNGLL

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153. 1::sp|cRAP087|P02769|ALBU_BOVIN **Mass:** 71244 **Score:** 51 **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
4023	590.8274	1179.6403	1179.6400	0.27	2	51	7.2e-05	1	U	Y.GFQNA
4024	590.8291	1179.6436	1179.6400	3.07	2	(40)	0.001	1	U	Y.GFQNA

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154. 2::sp|P0A903|BAMC_ECOLI **Mass:** 36877 **Score:** 51 **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
5374	659.8339	1317.6533	1317.6525	0.62	0	53	0.0001	1	U	Y.TITQR
5375	659.8348	1317.6550	1317.6525	1.93	0	(51)	0.00018	1	U	Y.TITQR

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155. 2::sp|P36683|ACNB_ECOLI **Mass:** 94009 **Score:** 50 **Matches:** 2(2) **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
5279	655.3368	1308.6590	1308.6562	2.19	0	(50)	0.0002	1	U	Y.VAQVD
5280	655.3381	1308.6616	1308.6562	4.15	0	50	0.00018	1	U	Y.VAQVD

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156. 2::sp|P0A7W7|RS8_ECOLI **Mass:** 14175 **Score:** 50 **Matches:** 2(2) **Sequences:** 2(2
30S ribosomal protein S8 OS=Escherichia coli (strain K12) OX=83333 GN=rpsH PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
564	**414.2706**	**826.5266**	**826.5276**	**-1.25**	**0**	**22**	**0.012**	**1**	**U**	**L.KVAIAN**
3209	**557.2583**	**1112.5020**	**1112.5026**	**-0.49**	**1**	**28**	**0.023**	**1**	**U**	**L.KEEGFI**

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157. 2::sp|P25744|MDTG_ECOLI **Mass:** 44067 **Score:** 50 **Matches:** 2(2) **Sequences:** 2(
Multidrug resistance protein MdtG OS=Escherichia coli (strain K12) OX=83333 GN=mdtG
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2908	**541.3409**	**1080.6672**	**1080.6543**	**11.9**	**2**	**28**	**0.0025**	**1**	**U**	**Y.VQTPLQ**
5921	**698.4155**	**1394.8164**	**1394.8245**	**-5.83**	**1**	**22**	**0.021**	**2**	**U**	**L.GKLGDR**

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158. 2::sp|P62623|ISPH_ECOLI **Mass:** 34981 **Score:** 49 **Matches:** 2(1) **Sequences:** 2(
4-hydroxy-3-methylbut-2-enyl diphosphate reductase 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
5853	**692.3735**	**1382.7324**	**1382.7293**	**2.24**	**0**	**23**	**0.073**	**1**	**U**	**F.IEQISE**
6497	**737.8590**	**1473.7035**	**1473.6987**	**3.23**	**1**	**26**	**0.053**	**1**	**U**	**F.LIDDAK**

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159. 2::sp|P37653|BCSA_ECOLI **Mass:** 100348 **Score:** 49 **Matches:** 3(3) **Sequences:** 2(
Cellulose synthase catalytic subunit [UDP-forming] OS=Escherichia coli (strain K12)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
200	394.7471	787.4796	787.4877	-10.27	2	25	0.012	2	U	L.MLIVLSL
201	394.7474	787.4803	787.4877	-9.40	2	(24)	0.014	3	U	L.MLIVLSL
1550	**475.7704**	**949.5263**	**949.5233**	**3.18**	**0**	**24**	**0.038**	**1**	**U**	**L.NVVKNTI**

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160. 2::sp|P0ADK0|YIAF_ECOLI **Mass:** 25761 **Score:** 48 **Matches:** 2(1) **Sequences:** 2(
Uncharacterized protein YiaF OS=Escherichia coli (strain K12) OX=83333 GN=yiaF 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
1014	442.2172	882.4198	882.4195	0.34	0	20	0.13	2	U	L.QADAA
2293	**508.2626**	**1014.5106**	**1014.5345**	**-23.54**	**1**	**28**	**0.019**	**1**	**U**	**L.AQQLQ**

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161. 2::sp|P09832|GLTD_ECOLI **Mass:** 52609 **Score:** 48 **Matches:** 2(1) **Sequences:** 2(
Glutamate synthase [NADPH] small chain 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
4424	608.8611	1215.7076	1215.7009	5.49	0	28	0.0097	2	U	F.VSMEGK
5640	**452.2429**	**1353.7068**	**1353.6785**	**20.9**	**0**	**23**	**0.081**	**1**	**U**	**L.QRVDPP**

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162. 1::sp|cRAP008|P00722|BGAL_ECOLI **Mass:** 117321 **Score:** 48 **Matches:** 2(1) **Seque**
Beta-galactosidase OS=Escherichia coli (strain K12) GN=lacZ PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3444	**568.2747**	**1134.5348**	**1134.5305**	**3.72**	**0**	**26**	**0.046**	**1**	**U**	**Y.GQDSRL**
6470	**736.3832**	**1470.7518**	**1470.7467**	**3.49**	**2**	**22**	**0.12**	**1**	**U**	**W.LGLGPQ**

Proteins matching the same set of peptides:
2::sp|P00722|BGAL_ECOLI **Mass:** 117321 **Score:** 48 **Matches:** 2(1) **Sequences:** 2(
Beta-galactosidase OS=Escherichia coli (strain K12) OX=83333 GN=lacZ PE=1 SV=2

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163. 2::sp|P33353|YEHQ_ECOLI **Mass:** 68657 **Score:** 48 **Matches:** 2(1) **Sequences:** 2(
Putative uncharacterized protein YehQ 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
446	**408.2278**	**814.4409**	**814.4436**	**-3.28**	**1**	**22**	**0.077**	**1**	**U**	**L.TPQALTA**
1465	**472.2873**	**942.5600**	**942.5750**	**-15.85**	**0**	**25**	**0.027**	**1**	**U**	**L.VAKGITI**

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164. 2::sp|P69924|RIR2_ECOLI **Mass:** 43775 **Score:** 48 **Matches:** 1(1) **Sequences:** 1(
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
6966	**776.3583**	**1550.7021**	**1550.7001**	**1.30**	**1**	**48**	**0.00028**	**1**	**U**	**F.VQAAQ**

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165. 2::sp|P0ADN0|VIAA_ECOLI **Mass:** 56214 **Score:** 46 **Matches:** 3(1) **Sequences:** 2(
Protein ViaA OS=Escherichia coli (strain K12) OX=83333 GN=viaA 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
816	**426.2473**	**850.4801**	**850.4623**	**21.0**	**1**	**28**	**0.0099**	**1**	**U**	**Y.QLIVKY**
3166	555.2952	1108.5758	1108.5652	9.56	2	(20)	0.15	2	U	L.ATLGIT
3167	555.2957	1108.5767	1108.5652	10.4	2	22	0.095	2	U	L.ATLGIT

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166. 2::sp|P76083|PAAH_ECOLI **Mass:** 52042 **Score:** 46 **Matches:** 2(1) **Sequences:** 2(
3-hydroxyadipyl-CoA dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=paaH
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
225	**396.7029**	**791.3913**	**791.3814**	**12.6**	**0**	**25**	**0.048**	**1**	**U**	**L.IGQDVNF.**
1300	461.7658	921.5171	921.4994	19.3	1	21	0.067	2	U	L.EVKKALF.

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167. 2::sp|P0ABH0|FTSA_ECOLI **Mass:** 45815 **Score:** 45 **Matches:** 1(1) **Sequences:** 1

Cell division protein FtsA OS=Escherichia coli (strain K12) OX=83333 GN=ftsA 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
6748	**758.9045**	**1515.7945**	**1515.7933**	**0.82**	**1**	**45**	**0.00053**	**1**	**U**	**Y.AIDYQ**

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168. 2::sp|P28904|TREC_ECOLI **Mass:** 64082 **Score:** 45 **Matches:** 2(2) **Sequences:** 2

Trehalose-6-phosphate hydrolase OS=Escherichia coli (strain K12) OX=83333 GN=treC 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
3701	578.3543	1154.6941	1154.7023	-7.09	1	23	0.025	3	U	L.IALRKQ
4791	**629.3630**	**1256.7114**	**1256.7162**	**-3.84**	**2**	**23**	**0.049**	**1**	**U**	**W.KGQTLL**

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169. 2::sp|P0AFG3|ODO1_ECOLI **Mass:** 105566 **Score:** 45 **Matches:** 1(1) **Sequences:** 1

2-oxoglutarate dehydrogenase E1 component OS=Escherichia coli (strain K12) OX=83333

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6045	**707.8704**	**1413.7263**	**1413.7252**	**0.73**	**0**	**45**	**0.00052**	**1**	**U**	**F.QQLPG**

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170. 2::sp|P76269|YEBQ_ECOLI **Mass:** 48519 **Score:** 45 **Matches:** 2(0) **Sequences:** 2

Uncharacterized transporter YebQ OS=Escherichia coli (strain K12) OX=83333 GN=yebQ

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5210	**651.8494**	**1301.6843**	**1301.6939**	**-7.38**	**2**	**22**	**0.12**	**1**	**U**	**L.GTARLL**
6900	**770.9223**	**1539.8300**	**1539.8193**	**6.97**	**2**	**23**	**0.059**	**1**	**U**	**L.LTPWPL**

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171. 2::sp|P76658|HLDE_ECOLI **Mass:** 51247 **Score:** 45 **Matches:** 2(2) **Sequences:** 1

Bifunctional protein HldE OS=Escherichia coli (strain K12) OX=83333 GN=hldE PE=1 SV=

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4417	**608.8266**	**1215.6386**	**1215.6347**	**3.23**	**0**	**45**	**0.00062**	**1**	**U**	**Y.DVTGA**
4418	**608.8268**	**1215.6390**	**1215.6347**	**3.53**	**0**	**(34)**	**0.0069**	**1**	**U**	**Y.DVTGA**

172. 2::sp|P0A862|TPX_ECOLI **Mass:** 17995 **Score:** 45 **Matches:** 1(1) **Sequences:** 1(1
Thiol peroxidase OS=Escherichia coli (strain K12) OX=83333 GN=tpx PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4977	637.8663	1273.7181	1273.7129	4.06	2	45	0.00033	1	U	F.TLVAK

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173. 2::sp|P0AEW6|INGK_ECOLI **Mass:** 48817 **Score:** 44 **Matches:** 2(2) **Sequences:** 1
Inosine-guanosine kinase OS=Escherichia coli (strain K12) OX=83333 GN=gsk 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
7195	799.9246	1597.8347	1597.8311	2.24	0	44	0.00057	1	U	L.RAESI
7196	799.9255	1597.8364	1597.8311	3.31	0	(40)	0.0015	1	U	L.RAESI

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174. 2::sp|P0A6L4|NANA_ECOLI **Mass:** 32801 **Score:** 44 **Matches:** 2(1) **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
474	408.7449	815.4752	815.4575	21.8	0	25	0.028	1	U	Y.QGIVKA
7363	818.4255	1634.8364	1634.8338	1.60	0	21	0.16	1	U	Y.RAIIDS

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175. 2::sp|P0AAX8|YBIS_ECOLI **Mass:** 33418 **Score:** 44 **Matches:** 2(0) **Sequences:** 2
Probable L,D-transpeptidase YbiS OS=Escherichia coli (strain K12) OX=83333 GN=ybiS
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
512	411.2296	820.4445	820.4443	0.31	0	22	0.075	1	U	Y.IEVHNP
7989	593.2917	1776.8534	1776.8530	0.24	0	22	0.17	1	U	F.IDEPVK

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176. 2::sp|P0AF08|APBC_ECOLI **Mass:** 40084 **Score:** 43 **Matches:** 1(1) **Sequences:** 1
Iron-sulfur cluster carrier protein OS=Escherichia coli (strain K12) OX=83333 GN=mrp
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6685	753.3980	1504.7815	1504.7773	2.77	1	43	0.0011	1	U	L.AAEGAK

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177. 2::sp|P76464|YFAS_ECOLI **Mass:** 151134 **Score:** 43 **Matches:** 2(0) **Sequences:** 2
Putative UPF0192 protein YfaS OS=Escherichia coli (strain K12) OX=83333 GN=yfaS 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
2298	508.2871	1014.5595	1014.5532	6.26	0	21	0.1	3	U	L.KGKPVS
2685	529.7590	1057.5034	1057.5040	-0.55	0	21	0.084	1	U	W.DKAANS

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178.  2::sp|P0ACC7|GLMU_ECOLI     Mass: 49388     Score: 43      Matches: 2(2)   Sequences: 1(
      Bifunctional protein GlmU OS=Escherichia coli (strain K12) OX=83333 GN=glmU 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
      3155  554.7804  1107.5462  1107.5448   1.29    1    43  0.0011   1     U    L.TVKLDD
      3156  554.7805  1107.5464  1107.5448   1.40    1   (30)  0.019   1     U    L.TVKLDD

179.  2::sp|P0ABD5|ACCA_ECOLI     Mass: 35333     Score: 42      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
      5156  433.5858  1297.7357  1297.7354   0.26    0   (37)  0.0014   1     U    Y.ADDKA
      5158  433.5859  1297.7359  1297.7354   0.40    0    42  0.00042   1     U    Y.ADDKA

180.  2::sp|P0A6K6|DEOB_ECOLI     Mass: 44684     Score: 42      Matches: 2(2)   Sequences: 1(
      Phosphopentomutase OS=Escherichia coli (strain K12) OX=83333 GN=deoB PE=1 SV=1
      Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank Unique  Peptide
      3842  583.2789  1164.5432  1164.5411   1.79    0    42  0.0011   1     U    F.GIGATE
      3843  583.2797  1164.5449  1164.5411   3.25    0   (32)  0.013   1     U    F.GIGATE

181.  2::sp|P60438|RL3_ECOLI     Mass: 22230     Score: 42      Matches: 3(0)   Sequences: 2(0
      50S ribosomal protein L3 OS=Escherichia coli (strain K12) OX=83333 GN=rplC PE=1 SV=1
      Check to include this hit in error tolerant search or archive report

     Query  Observed   Mr(expt)   Mr(calc)    ppm  Miss Score Expect Rank Unique  Peptide
      4206  600.2925  1198.5705  1198.5691   1.22    0   (20)   0.13   1     U    F.RTQDAT
      4207  600.2933  1198.5721  1198.5691   2.54    0    22   0.095   1     U    F.RTQDAT
      4385  405.5593  1213.6562  1213.6567  -0.47    1    20    0.14   1     U    F.AKAGVE

182.  2::sp|P0A9W3|ETTA_ECOLI     Mass: 62518     Score: 42      Matches: 3(1)   Sequences: 2(
      Energy-dependent translational throttle protein EttA 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
      1496  473.2482  944.4818  944.5001 -19.38    2    25  0.047   1     U    L.LQVGGNM
      1499  473.2537  944.4928  944.5001  -7.75    2    22   0.11   1     U    L.QVGGNML
      1500  473.2537  944.4928  944.5001  -7.75    2   (23) 0.082   1     U    L.LQVGGNM

183.  2::sp|P37344|PSPF_ECOLI     Mass: 37134     Score: 42      Matches: 3(0)   Sequences: 2(
```

Psp operon transcriptional activator OS=Escherichia coli (strain K12) OX=83333 GN=ps
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1364	466.2460	930.4774	930.4770	0.48	0	(21)	0.12	3	U	Y.NQKRAA
1365	466.2461	930.4776	930.4770	0.61	0	21	0.12	3	U	Y.NQKRAA
4379	**607.3445**	**1212.6744**	**1212.6826**	**-6.74**	**2**	**21**	**0.091**	**1**	**U**	**Y.NQKRAA**

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184. 2::sp|P62399|RL5_ECOLI **Mass:** 20346 **Score:** 41 **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
1020	**442.7636**	**883.5127**	**883.5127**	**0.04**	**0**	**41**	**0.00037**	**1**	**U**	**L.AAISGQK**
1022	**442.7639**	**883.5132**	**883.5127**	**0.60**	**0**	**(33)**	**0.0028**	**1**	**U**	**L.AAISGQK**

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185. 2::sp|P11880|MURF_ECOLI **Mass:** 47646 **Score:** 41 **Matches:** 2(0) **Sequences:** 2(
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase OS=Escherichia coli (stra
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3944	587.3106	1172.6065	1172.6077	-0.99	1	20	0.15	5	U	L.FPIQL
6484	**491.5890**	**1471.7451**	**1471.7704**	**-17.19**	**2**	**21**	**0.16**	**1**	**U**	**L.NNDIG**

---

186. 2::sp|P75882|GFCD_ECOLI **Mass:** 78923 **Score:** 41 **Matches:** 3(0) **Sequences:** 2(
Uncharacterized lipoprotein GfcD OS=Escherichia coli (strain K12) OX=83333 GN=gfcD 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
2109	500.7402	999.4659	999.4549	11.0	1	21	0.089	2	U	L.DGGIFT
2112	**500.7406**	**999.4667**	**999.4549**	**11.8**	**1**	**(20)**	**0.11**	**1**	**U**	**L.DGGIFT**
4041	592.2583	1182.5020	1182.5015	0.43	2	20	0.1	2	U	L.YMSGQQ

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187. 2::sp|P23482|HYFB_ECOLI **Mass:** 73048 **Score:** 41 **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
2105	**500.2852**	**998.5559**	**998.5437**	**12.2**	**2**	**41**	**0.00059**	**1**	**U**	**L.LAQTGLP**
2106	**500.2853**	**998.5559**	**998.5437**	**12.3**	**2**	**(31)**	**0.0068**	**1**	**U**	**L.LAQTGLP**

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188. 2::sp|P77455|PAAZ_ECOLI **Mass:** 73527 **Score:** 41 **Matches:** 2(0) **Sequences:** 2(
Bifunctional protein PaaZ OS=Escherichia coli (strain K12) OX=83333 GN=paaZ 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
1414	**469.2530**	**936.4914**	**936.4739**	**18.7**	**2**	**21**	**0.11**	**1**	**U**	**-.MQQLASFL**
1822	487.2696	972.5246	972.5128	12.1	0	20	0.14	3	U	W.VDIEGGIG

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189. 2::sp|P0AEG4|DSBA_ECOLI **Mass:** 23204 **Score:** 41 **Matches:** 1(1) **Sequences:** 1

Thiol:disulfide interchange protein DsbA 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
3018	**547.2792**	**1092.5439**	**1092.5451**	**-1.08**	**0**	**41**	**0.0017**	**1**	**U**	**F.INAGIK**

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190. 2::sp|P0A7B5|PROB_ECOLI **Mass:** 39204 **Score:** 40 **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
1255	**458.2968**	**914.5791**	**914.5801**	**-1.04**	**1**	**40**	**0.00016**	**1**	**U**	**L.VVKLGTS**
1256	**458.2977**	**914.5808**	**914.5801**	**0.78**	**1**	**(33)**	**0.00072**	**1**	**U**	**L.VVKLGTS**

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191. 2::sp|P0A7J3|RL10_ECOLI **Mass:** 17757 **Score:** 39 **Matches:** 2(2) **Sequences:** 1

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
6295	**724.3931**	**1446.7716**	**1446.7718**	**-0.15**	**1**	**(37)**	**0.0034**	**1**	**U**	**L.ATLPTY**
6296	**724.3959**	**1446.7772**	**1446.7718**	**3.72**	**1**	**39**	**0.0022**	**1**	**U**	**L.ATLPTY**

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192. 2::sp|P0AEP3|GALU_ECOLI **Mass:** 33206 **Score:** 38 **Matches:** 2(2) **Sequences:** 1

UTP--glucose-1-phosphate uridylyltransferase 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
1853	**488.2783**	**974.5420**	**974.5437**	**-1.75**	**1**	**(36)**	**0.0037**	**1**	**U**	**L.VDKPLIQY**
1854	**488.2805**	**974.5464**	**974.5437**	**2.77**	**1**	**38**	**0.0019**	**1**	**U**	**L.VDKPLIQY**

---

193. 2::sp|P46474|YHDP_ECOLI **Mass:** 139081 **Score:** 38 **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
2547	**522.2512**	**1042.4879**	**1042.4819**	**5.79**	**0**	**(34)**	**0.005**	**1**	**U**	**L.DDPQIN**
2548	**522.2515**	**1042.4884**	**1042.4819**	**6.25**	**0**	**38**	**0.0019**	**1**	**U**	**L.DDPQIN**

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194. 2::sp|P0ABP8|DEOD_ECOLI **Mass:** 26161 **Score:** 37 **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
1730	483.7608	965.5070	965.5070	0.09	1	(28)	0.02	1	U	Y.TKELITDF
1731	483.7618	965.5089	965.5070	2.06	1	37	0.0025	1	U	Y.TKELITDF

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195. 2::sp|P06616|ERA_ECOLI **Mass:** 33846 **Score:** 37 **Matches:** 1(1) **Sequences:** 1(1
GTPase Era OS=Escherichia coli (strain K12) OX=83333 GN=era 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
2880	540.2895	1078.5645	1078.5659	-1.23	0	37	0.0029	1	U	Y.SVTVEI

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196. 2::sp|P76372|WZZB_ECOLI **Mass:** 36432 **Score:** 37 **Matches:** 2(2) **Sequences:** 1(
Chain length determinant protein OS=Escherichia coli (strain K12) OX=83333 GN=wzzB 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
6377	728.8859	1455.7572	1455.7569	0.18	1	(31)	0.012	1	U	Y.GQAAPK
6378	728.8881	1455.7617	1455.7569	3.28	1	37	0.003	1	U	Y.GQAAPK

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197. 2::sp|P77690|ARNB_ECOLI **Mass:** 42439 **Score:** 36 **Matches:** 1(1) **Sequences:** 1(
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
6587	743.8822	1485.7498	1485.7464	2.35	0	36	0.0051	1	U	Y.GIAVIE

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198. 2::sp|P62620|ISPG_ECOLI **Mass:** 40943 **Score:** 36 **Matches:** 2(2) **Sequences:** 1(
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
1212	456.7608	911.5070	911.5076	-0.62	0	36	0.0013	1	U	L.AKQIDQPL
1213	456.7613	911.5080	911.5076	0.39	0	(34)	0.0018	1	U	L.AKQIDQPL

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199. 2::sp|P06720|AGAL_ECOLI **Mass:** 51308 **Score:** 35 **Matches:** 2(2) **Sequences:** 1(
Alpha-galactosidase OS=Escherichia coli (strain K12) OX=83333 GN=melA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2153	502.7919	1003.5693	1003.5702	-0.92	1	(33)	0.0046	1	U	F.VKNILG
2154	502.7931	1003.5716	1003.5702	1.33	1	35	0.0021	1	U	F.VKNILG

```
200.   2::sp|P0A9L5|PPIC_ECOLI     Mass: 10340     Score: 35     Matches: 2(2)   Sequences: 1
       Peptidyl-prolyl cis-trans isomerase C OS=Escherichia coli (strain K12) OX=83333 GN=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
        141  388.7126  775.4105  775.4262 -20.16    0    35  0.0033   1     U     -.MAKTAAA
        142  388.7131  775.4116  775.4262 -18.82    0   (35) 0.0041   1     U     -.MAKTAAA


201.   2::sp|P75697|YAIX_ECOLI     Mass: 25201     Score: 35     Matches: 1(1)   Sequences: 1
       Putative uncharacterized acetyltransferase YaiX 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
       4141  398.5796  1192.7170  1192.7179  -0.74    2    35  0.00044   1     U    W.KRQPL


202.   2::sp|P0ABD8|BCCP_ECOLI     Mass: 16733     Score: 34     Matches: 1(1)   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
       5793  686.3779  1370.7413  1370.7406   0.55    0    34  0.0052   1     U    F.IEVGQK


203.   2::sp|P63284-2|CLPB_ECOLI     Mass: 79935     Score: 34     Matches: 1(1)   Sequences:
       Isoform ClpB-3 of Chaperone protein ClpB 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
        426  407.2633  812.5120  812.5007  13.9    2    34  0.0012   1     U    F.NILLQVL.


       Proteins matching the same set of peptides:
       2::sp|P63284|CLPB_ECOLI     Mass: 95697     Score: 34     Matches: 1(1)   Sequences: 1
       Chaperone protein ClpB OS=Escherichia coli (strain K12) OX=83333 GN=clpB PE=1 SV=1

204.   2::sp|P31446|YIDI_ECOLI     Mass: 15833     Score: 34     Matches: 1(1)   Sequences: 1
       Inner membrane protein YidI OS=Escherichia coli (strain K12) OX=83333 GN=yidI 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
       3563  572.3225  1142.6303  1142.6183   10.6    1    34  0.0044   1     U    L.NQSGIA


205.   2::sp|P69797|PTNAB_ECOLI     Mass: 35026     Score: 34     Matches: 1(1)   Sequences: 1
       PTS system mannose-specific EIIAB component 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
217	396.2066	790.3986	790.4007	-2.61	0	34	0.0052	1	U	Y.AGERVML.

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206. 2::sp|P60716|LIPA_ECOLI **Mass:** 36505 **Score:** 34 **Matches:** 1(1) **Sequences:** 1

Lipoyl synthase OS=Escherichia coli (strain K12) OX=83333 GN=lipA 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
7186	798.8614	1595.7083	1595.7025	3.67	1	34	0.0064	1	U	Y.VSPDEF

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207. 2::sp|P27243|RFAL_ECOLI **Mass:** 47076 **Score:** 34 **Matches:** 1(1) **Sequences:** 1

O-antigen ligase OS=Escherichia coli (strain K12) OX=83333 GN=rfaL 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
2520	520.3116	1038.6086	1038.6324	-22.95	1	34	0.0016	1	U	Y.NIKNL

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208. 2::sp|P0A7W1|RS5_ECOLI **Mass:** 17592 **Score:** 33 **Matches:** 4(2) **Sequences:** 1(1

30S ribosomal protein S5 OS=Escherichia coli (strain K12) OX=83333 GN=rpsE 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
3988	589.3010	1176.5875	1176.5888	-1.08	0	33	0.011	1	U	L.TVVGDG
3989	589.3024	1176.5903	1176.5888	1.30	0	(31)	0.017	1	U	L.TVVGDG
3993	589.7946	1177.5747	1177.5728	1.62	0	(21)	0.19	1	U	L.TVVGDG
3994	589.7949	1177.5753	1177.5728	2.13	0	(23)	0.1	1	U	L.TVVGDG

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209. 2::sp|P09151|LEU1_ECOLI **Mass:** 57604 **Score:** 32 **Matches:** 1(1) **Sequences:** 1

2-isopropylmalate synthase OS=Escherichia coli (strain K12) OX=83333 GN=leuA 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
717	421.7390	841.4635	841.4657	-2.70	1	32	0.0034	1	U	L.NQIQLNL.

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210. 2::sp|P31068|FLIH_ECOLI **Mass:** 25149 **Score:** 32 **Matches:** 2(2) **Sequences:** 1

Flagellar assembly protein FliH OS=Escherichia coli (strain K12) OX=83333 GN=fliH 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
902	436.2717	870.5289	870.5174	13.2	0	32	0.003	1	U	L.IKQIQQL.
903	436.2718	870.5291	870.5174	13.4	0	(30)	0.0046	1	U	L.IKQIQQL.

211. 2::sp|P46855|YHHZ_ECOLI **Mass:** 44375 **Score:** 32 **Matches:** 2(2) **Sequences:** 1
Uncharacterized protein YhhZ OS=Escherichia coli (strain K12) OX=83333 GN=yhhZ PE=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
129	387.2291	772.4437	772.4331	13.8	0	(28)	0.024	1	U	L.IDKSTPL.
130	387.2292	772.4438	772.4331	13.9	0	32	0.0094	1	U	L.IDKSTPL.

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212. 2::sp|Q46851|GPR_ECOLI **Mass:** 38922 **Score:** 32 **Matches:** 2(2) **Sequences:** 1(1
L-glyceraldehyde 3-phosphate reductase OS=Escherichia coli (strain K12) OX=83333 GN=
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1548	475.7686	949.5227	949.5233	-0.55	2	32	0.0066	1	U	L.AQGLLTGK
1549	475.7688	949.5231	949.5233	-0.17	2	(25)	0.028	1	U	L.AQGLLTGK

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213. 2::sp|O52982|YFJS_ECOLI **Mass:** 16895 **Score:** 32 **Matches:** 2(1) **Sequences:** 1
Lipoprotein YfjS OS=Escherichia coli (strain K12) OX=83333 GN=yfjS 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
5833	689.3286	1376.6427	1376.6679	-18.35	1	34	0.0073	1	U	L.MNALC
5834	689.3309	1376.6472	1376.6679	-15.06	1	(24)	0.083	1	U	L.MNALC

Proteins matching the same set of peptides:
2::sp|P77365|YAFY_ECOLI **Mass:** 16975 **Score:** 30 **Matches:** 2(1) **Sequences:** 1
Lipoprotein YafY OS=Escherichia coli (strain K12) OX=83333 GN=yafY PE=1 SV=2

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214. 2::sp|P69441|KAD_ECOLI **Mass:** 23628 **Score:** 31 **Matches:** 2(2) **Sequences:** 1(1
Adenylate kinase OS=Escherichia coli (strain K12) OX=83333 GN=adk PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4100	595.3035	1188.5924	1188.5887	3.06	0	(30)	0.019	1	U	L.GAPGAG
4101	595.3046	1188.5947	1188.5887	5.02	0	31	0.015	1	U	L.GAPGAG

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215. 2::sp|P24183|FDNG_ECOLI **Mass:** 113634 **Score:** 31 **Matches:** 1(1) **Sequences:** 1
Formate dehydrogenase, nitrate-inducible, major subunit OS=Escherichia coli (strain
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
658	419.2265	836.4384	836.4280	12.4	1	34	0.0064	1	U	L.LSTSLPGY

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216. 2::sp|P04128|FIMA1_ECOLI **Mass:** 18214 **Score:** 31 **Matches:** 2(2) **Sequences:** 1

Type-1 fimbrial protein, A chain OS=Escherichia coli (strain K12) OX=83333 GN=fimA 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
4963	637.3722	1272.7298	1272.7549	-19.72	1	31	0.0057	1	U	M.KIKTL
4964	637.3731	1272.7315	1272.7549	-18.37	1	(26)	0.02	1	U	M.KIKTL

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217. 2::sp|P0A6V1|GLGC_ECOLI **Mass:** 49180 **Score:** 30 **Matches:** 1(1) **Sequences:** 1
Glucose-1-phosphate adenylyltransferase 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
3074	550.3112	1098.6078	1098.6073	0.38	1	30	0.0076	1	U	Y.VVILAG

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218. 2::sp|P15639|PUR9_ECOLI **Mass:** 57692 **Score:** 30 **Matches:** 2(2) **Sequences:** 1(
Bifunctional purine biosynthesis protein PurH 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
1483	472.7647	943.5149	943.5273	-13.13	1	(30)	0.016	1	U	F.KRVNGGL
1484	472.7648	943.5151	943.5273	-12.94	1	30	0.015	1	U	F.KRVNGGL

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219. 2::sp|P0AFB8|NTRC_ECOLI **Mass:** 52336 **Score:** 30 **Matches:** 1(1) **Sequences:** 1(
DNA-binding transcriptional regulator NtrC 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
3627	574.8058	1147.5971	1147.5795	15.4	1	30	0.021	1	U	W.LTVMAA

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220. 2::sp|P25552|GPPA_ECOLI **Mass:** 55293 **Score:** 30 **Matches:** 1(1) **Sequences:** 1(
Guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase OS=Escherichia coli (strain
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5281	655.8113	1309.6081	1309.6051	2.31	2	30	0.021	1	U	Y.FADRNL

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221. 2::sp|P09053|AVTA_ECOLI **Mass:** 47080 **Score:** 30 **Matches:** 2(2) **Sequences:** 1(
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	Peptide
7566	835.4495	1668.8845	1668.8835	0.59	1	(24)	0.052	1	U	F.VSARPN
7567	835.4501	1668.8856	1668.8835	1.25	1	30	0.016	1	U	F.VSARPN

222. 2::sp|P0AAB6|GALF_ECOLI **Mass:** 32979 **Score:** 29 **Matches:** 2(2) **Sequences:** 1

UTP--glucose-1-phosphate uridylyltransferase 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
867	434.2867	866.5587	866.5589	-0.21	0	29	0.0012	1	U	L.KAVIPVAG
868	434.2868	866.5590	866.5589	0.14	0	(23)	0.0046	1	U	L.KAVIPVAG

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223. 2::sp|P0A6R0|FABH_ECOLI **Mass:** 33779 **Score:** 29 **Matches:** 2(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
11	380.2337	758.4528	758.4538	-1.25	0	29	0.011	1	U	F.KVAVTEL.
17	380.2341	758.4537	758.4538	-0.12	0	(20)	0.084	1	U	F.KVAVTEL.

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224. 2::sp|P0AE48|YTFP_ECOLI **Mass:** 12858 **Score:** 29 **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
321	401.7180	801.4214	801.4344	-16.25	0	(26)	0.041	1	U	Y.RIDNATL
322	401.7184	801.4222	801.4344	-15.27	0	29	0.018	1	U	Y.RIDNATL

---

225. 2::sp|P77454|GLSA1_ECOLI **Mass:** 33168 **Score:** 29 **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
2523	521.2707	1040.5268	1040.5502	-22.48	1	29	0.015	1	U	L.GATLA

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226. 2::sp|P0AC33|FUMA_ECOLI **Mass:** 60774 **Score:** 29 **Matches:** 1(1) **Sequences:** 1

Fumarate hydratase class I, aerobic OS=Escherichia coli (strain K12) OX=83333 GN=fum

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
7972	888.4625	1774.9105	1774.9101	0.21	1	29	0.027	1	U	Y.KEVNTG

Proteins matching the same set of peptides:

2::sp|P14407|FUMB_ECOLI **Mass:** 60581 **Score:** 29 **Matches:** 1(1) **Sequences:** 1

Fumarate hydratase class I, anaerobic OS=Escherichia coli (strain K12) OX=83333 GN=f

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227. 2::sp|P77171|YDCI_ECOLI **Mass:** 33552 **Score:** 29 **Matches:** 3(2) **Sequences:** 1

Uncharacterized HTH-type transcriptional regulator YdcI OS=Escherichia coli (strain

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2290	**508.2563**	**1014.4980**	**1014.5206**	**-22.28**	**0**	**29**	**0.017**	**1**	**U**	**F.ERGRQ**
2292	**508.2616**	**1014.5086**	**1014.5206**	**-11.81**	**0**	**(23)**	**0.051**	**1**	**U**	**F.ERGRQ**
2293	508.2626	1014.5106	1014.5206	-9.84	0	(21)	0.1	2	U	F.ERGRQ

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228. 2::sp|P0A7K2|RL7_ECOLI **Mass:** 12288 **Score:** 29 **Matches:** 2(1) **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
4813	**631.3177**	**1260.6208**	**1260.6197**	**0.87**	**0**	**29**	**0.029**	**1**	**U**	**L.KEGVSK**
4814	**631.3182**	**1260.6218**	**1260.6197**	**1.64**	**0**	**(26)**	**0.057**	**1**	**U**	**L.KEGVSK**

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229. 2::sp|P0ADE8|YGFZ_ECOLI **Mass:** 36185 **Score:** 28 **Matches:** 1(1) **Sequences:** 1

tRNA-modifying protein YgfZ OS=Escherichia coli (strain K12) OX=83333 GN=ygfZ 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
8531	**648.6947**	**1943.0623**	**1943.0575**	**2.46**	**0**	**28**	**0.017**	**1**	**U**	**F.SELPSK**

---

230. 2::sp|P0AG55|RL6_ECOLI **Mass:** 18949 **Score:** 28 **Matches:** 1(1) **Sequences:** 1(1

50S ribosomal protein L6 OS=Escherichia coli (strain K12) OX=83333 GN=rplF PE=1 SV=2

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6132	**713.3534**	**1424.6922**	**1424.6896**	**1.87**	**0**	**28**	**0.032**	**1**	**U**	**L.NDAVEV**

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231. 2::sp|P77173|ZIPA_ECOLI **Mass:** 36452 **Score:** 28 **Matches:** 1(1) **Sequences:** 1

Cell division protein ZipA OS=Escherichia coli (strain K12) OX=83333 GN=zipA 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
3011	**546.7875**	**1091.5605**	**1091.5499**	**9.77**	**2**	**28**	**0.032**	**1**	**U**	**L.LLNSIQ**

---

232. 2::sp|P52612|FLII_ECOLI **Mass:** 49342 **Score:** 28 **Matches:** 2(1) **Sequences:** 1

Flagellum-specific ATP synthase OS=Escherichia coli (strain K12) OX=83333 GN=fliI 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
6005	**705.3906**	**1408.7666**	**1408.7748**	**-5.85**	**2**	**28**	**0.016**	**1**	**U**	**L.QSGKQL**
6006	**705.3906**	**1408.7666**	**1408.7748**	**-5.85**	**2**	**(21)**	**0.081**	**1**	**U**	**L.QSGKQL**

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233. 2::sp|P37640|YHJB_ECOLI **Mass:** 22704 **Score:** 28 **Matches:** 1(1) **Sequences:** 1
Putative HTH-type transcriptional regulator YhjB 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
5837	689.8453	1377.6761	1377.6711	3.67	1	28	0.043	1	U	L.ITATDC

---

234. 2::sp|P23841|XAPR_ECOLI **Mass:** 33663 **Score:** 27 **Matches:** 2(2) **Sequences:** 1
HTH-type transcriptional regulator XapR 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
450	408.2343	814.4540	814.4661	-14.80	1	(27)	0.027	1	U	L.LERREL.
453	408.2347	814.4549	814.4661	-13.67	1	27	0.024	1	U	L.LERREL.

Proteins matching the same set of peptides:
2::sp|Q46938|KDUI_ECOLI **Mass:** 31341 **Score:** 27 **Matches:** 2(2) **Sequences:** 1
4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase OS=Escherichia coli (strain K1

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235. 2::sp|P77260|YDFI_ECOLI **Mass:** 53879 **Score:** 27 **Matches:** 2(1) **Sequences:** 1
Uncharacterized oxidoreductase YdfI OS=Escherichia coli (strain K12) OX=83333 GN=ydf
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
767	423.7284	845.4422	845.4317	12.5	0	(21)	0.13	1	U	L.KVQGVDL.
768	423.7285	845.4425	845.4317	12.8	0	27	0.032	1	U	L.KVQGVDL.

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236. 2::sp|P37663|YHJY_ECOLI **Mass:** 25935 **Score:** 27 **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
6892	770.8486	1539.6826	1539.6994	-10.90	2	27	0.033	1	U	L.RPWAQ
6893	770.8492	1539.6838	1539.6994	-10.11	2	(25)	0.047	1	U	L.RPWAQ

---

237. 2::sp|P30176|RIBX_ECOLI **Mass:** 18658 **Score:** 27 **Matches:** 2(1) **Sequences:** 1
N-glycosidase YbiA OS=Escherichia coli (strain K12) OX=83333 GN=ybiA PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1284	459.7486	917.4826	917.4640	20.3	1	(24)	0.063	1	U	L.MELREQL.
1285	459.7489	917.4833	917.4640	21.0	1	27	0.037	1	U	L.MELREQL.

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238. 2::sp|P52143|YPJA_ECOLI **Mass:** 157576 **Score:** 27 **Matches:** 1(1) **Sequences:** 1

```
       Uncharacterized outer membrane protein YpjA 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
       1349  465.2461  928.4777  928.4865  -9.54   2    27   0.022   1     U    L.ENGGNLLV

239.   2::sp|P69801|PTNC_ECOLI     Mass: 27732     Score: 27      Matches: 1(1)   Sequences: 1
       PTS system mannose-specific EIIC 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
        800  425.2472  848.4799  848.4643  18.3    1    27   0.021   1     U    Y.IQLSPKY.

240.   2::sp|P15723|DGTP_ECOLI     Mass: 59688     Score: 27      Matches: 1(1)   Sequences: 1
       Deoxyguanosinetriphosphate triphosphohydrolase OS=Escherichia coli (strain K12) OX=8
       Check to include this hit in error tolerant search or archive report

      Query  Observed  Mr(expt)  Mr(calc)    ppm  Miss Score Expect Rank Unique  Peptide
       1497  473.2485  944.4825  944.4967  -15.04   1    27   0.036   1     U    L.TWAQVGG

241.   2::sp|P76224|YNJC_ECOLI     Mass: 56434     Score: 27      Matches: 2(2)   Sequences: 1
       Inner membrane ABC transporter permease protein YnjC 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
        425  407.2631  812.5116  812.5007  13.4    1    27  0.0072   1     U    L.LQQVIVL.
        426  407.2633  812.5120  812.5007  13.9    1   (27) 0.0073   2     U    L.LQQVIVL.

242.   2::sp|P76403|YEGQ_ECOLI     Mass: 51446     Score: 27      Matches: 1(1)   Sequences: 1
       Uncharacterized protease YegQ OS=Escherichia coli (strain K12) OX=83333 GN=yegQ PE=3
       Check to include this hit in error tolerant search or archive report

      Query  Observed   Mr(expt)   Mr(calc)   ppm  Miss Score Expect Rank Unique  Peptide
       5708  453.9174  1358.7303  1358.7306  -0.21   0    27   0.039   1     U    Y.RKAIDD

243.   2::sp|P06983|HEM3_ECOLI     Mass: 34059     Score: 26      Matches: 1(1)   Sequences: 1
       Porphobilinogen deaminase OS=Escherichia coli (strain K12) OX=83333 GN=hemC 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
       2257  507.3155  1012.6164  1012.6168  -0.45   2    26   0.011   1     U    F.VKELEV

244.   2::sp|P0ABC3|HFLC_ECOLI     Mass: 37626     Score: 26      Matches: 2(2)   Sequences: 1
```

Modulator of FtsH protease HflC OS=Escherichia coli (strain K12) OX=83333 GN=hflC 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
1675	481.2424	960.4703	960.4705	-0.22	2	(25)	0.046	1	U	L.VYEPGLHF
1676	481.2425	960.4704	960.4705	-0.10	2	26	0.035	1	U	L.VYEPGLHF

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245. 2::sp|P64481|YDJM_ECOLI **Mass:** 22564 **Score:** 26 **Matches:** 2(2) **Sequences:** 1
Inner membrane protein YdjM OS=Escherichia coli (strain K12) OX=83333 GN=ydjM 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
1017	442.7511	883.4876	883.4763	12.8	0	26	0.012	1	U	L.VPQKGNQL
1018	442.7512	883.4878	883.4763	13.0	0	(26)	0.012	1	U	L.VPQKGNQL

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246. 2::sp|P0ABF6|CDD_ECOLI **Mass:** 31805 **Score:** 26 **Matches:** 2(2) **Sequences:** 1(1
Cytidine deaminase OS=Escherichia coli (strain K12) OX=83333 GN=cdd PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
897	436.2479	870.4812	870.4698	13.0	1	26	0.015	1	U	L.QSALEPIL
898	436.2479	870.4813	870.4698	13.2	1	(22)	0.039	1	U	L.QSALEPIL

---

247. 2::sp|P0AA25|THIO_ECOLI **Mass:** 11913 **Score:** 26 **Matches:** 2(1) **Sequences:** 1
Thioredoxin 1 OS=Escherichia coli (strain K12) OX=83333 GN=trxA 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
5360	659.3243	1316.6340	1316.6361	-1.56	0	26	0.047	1	U	L.NIDQNP
5363	659.3289	1316.6432	1316.6361	5.46	0	(24)	0.074	1	U	L.NIDQNP

---

248. 2::sp|P37649|PDEK_ECOLI **Mass:** 74733 **Score:** 26 **Matches:** 1(1) **Sequences:** 1
Probable cyclic di-GMP phosphodiesterase PdeK 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
728	422.2414	842.4683	842.4498	22.0	2	26	0.03	1	U	Y.NLNQQLL.

---

249. 2::sp|P75682|YAGE_ECOLI **Mass:** 32681 **Score:** 26 **Matches:** 1(1) **Sequences:** 1
Putative 2-dehydro-3-deoxy-D-gluconate aldolase YagE 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
4059	396.2225	1185.6457	1185.6679	-18.73	0	26	0.035	1	U	F.VNVIK

```
250.  2::sp|P63020|NFUA_ECOLI     Mass: 21212     Score: 25      Matches: 1(1)   Sequences: 1
      Fe/S biogenesis protein NfuA OS=Escherichia coli (strain K12) OX=83333 GN=nfuA 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
      2697  529.7953  1057.5760  1057.6019  -24.45    1    25   0.041    1      U    L.KEGIE
```

```
251.  2::sp|P0A8H3|ZUPT_ECOLI     Mass: 26524     Score: 25      Matches: 1(0)   Sequences: 1
      Zinc transporter ZupT OS=Escherichia coli (strain K12) OX=83333 GN=zupT 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
       947  438.2267  874.4387  874.4292   10.9    0    25   0.063    1      U    L.MEMLPAAL
```

```
252.  2::sp|Q46836|PPPA_ECOLI     Mass: 29846     Score: 25      Matches: 2(1)   Sequences: 1
      Leader peptidase PppA OS=Escherichia coli (strain K12) OX=83333 GN=pppA 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
      3813  582.2823  1162.5501  1162.5692  -16.43    0   (25)  0.063    1      U    F.QQYPT
      3815  582.2828  1162.5510  1162.5692  -15.69    0    25   0.057    1      U    F.QQYPT
```

```
253.  2::sp|P00861|DCDA_ECOLI     Mass: 46377     Score: 25      Matches: 2(2)   Sequences: 1
      Diaminopimelate decarboxylase OS=Escherichia coli (strain K12) OX=83333 GN=lysA 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
       757  423.2475  844.4804  844.4807  -0.33    1    25    0.03    1      U    L.LRLPAEF.
       758  423.2477  844.4808  844.4807   0.17    1   (25)  0.035    1      U    L.LRLPAEF.
```

```
254.  2::sp|P76425|RCNA_ECOLI     Mass: 30514     Score: 25      Matches: 2(1)   Sequences: 1
      Nickel/cobalt efflux system RcnA OS=Escherichia coli (strain K12) OX=83333 GN=rcnA
      Check to include this hit in error tolerant search or archive report

     Query  Observed  Mr(expt)  Mr(calc)    ppm  Miss Score Expect Rank Unique   Peptide
        22  380.7194  759.4243  759.4200   5.59    1    25    0.04    1      U    L.LICIQL.K
        24  380.7200  759.4255  759.4200   7.19    1   (21)    0.1    1      U    L.LICIQL.K
```

```
255.  2::sp|P76204|YDIV_ECOLI     Mass: 27371     Score: 25      Matches: 1(1)   Sequences: 1
      Putative anti-FlhC(2)FlhD(4) factor YdiV 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
      3213  557.2831  1112.5516  1112.5502   1.28    1    25   0.042    1      U    L.LINENY
```

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256. 2::sp|P36999|RLMA_ECOLI **Mass:** 30855 **Score:** 25 **Matches:** 2(1) **Sequences:** 1

23S rRNA (guanine(745)-N(1))-methyltransferase 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
2247	507.2671	1012.5196	1012.4978	21.6	2	25	0.037	1	U	F.LDAGHY
2248	507.2676	1012.5207	1012.4978	22.6	2	(21)	0.085	1	U	F.LDAGHY

---

257. 2::sp|P0A9C5|GLN1B_ECOLI **Mass:** 52099 **Score:** 25 **Matches:** 2(0) **Sequences:** 1

Glutamine synthetase OS=Escherichia coli (strain K12) OX=83333 GN=glnA 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
1113	451.7492	901.4839	901.5055	-24.00	0	25	0.054	1	U	L.IIRCDIL
1114	451.7502	901.4857	901.5055	-21.92	0	(21)	0.14	4	U	L.IIRCDIL

---

258. 2::sp|P08839|PT1_ECOLI **Mass:** 63750 **Score:** 25 **Matches:** 1(1) **Sequences:** 1(1

Phosphoenolpyruvate-protein phosphotransferase 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
775	424.2021	846.3897	846.3971	-8.71	0	25	0.039	1	U	L.TPSETAQL

---

259. 2::sp|P0AB24|EFEO_ECOLI **Mass:** 41226 **Score:** 25 **Matches:** 1(0) **Sequences:** 1

Iron uptake system component EfeO OS=Escherichia coli (strain K12) OX=83333 GN=efeO

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4563	616.3180	1230.6215	1230.6204	0.93	1	25	0.066	1	U	Y.DKLTDA

---

260. 2::sp|P42620|YQJG_ECOLI **Mass:** 37477 **Score:** 25 **Matches:** 1(1) **Sequences:** 1

Glutathionyl-hydroquinone reductase YqjG 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
2749	531.8019	1061.5892	1061.6089	-18.57	1	25	0.035	1	U	L.IMRKL

---

261. 2::sp|P39321|TAMB_ECOLI **Mass:** 136923 **Score:** 25 **Matches:** 2(2) **Sequences:** 1

Translocation and assembly module subunit TamB 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

1940	493.2514	984.4882	984.4917	-3.46	1	(24)	0.045	2	U	F.QTPVGPWS
1941	493.2515	984.4884	984.4917	-3.34	1	25	0.035	1	U	F.QTPVGPWS

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262. 2::sp|P66948|BEPA_ECOLI **Mass:** 53874 **Score:** 25 **Matches:** 2(1) **Sequences:** 1
Beta-barrel assembly-enhancing protease OS=Escherichia coli (strain K12) OX=83333 GN
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3897	585.8129	1169.6112	1169.6292	-15.37	2	27	0.027	1	U	L.RTNPV
3898	585.8143	1169.6141	1169.6292	-12.87	2	(22)	0.087	1	U	L.RTNPV

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263. 2::sp|P77674|ABDH_ECOLI **Mass:** 51197 **Score:** 24 **Matches:** 3(3) **Sequences:** 1
Gamma-aminobutyraldehyde dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1078	450.2452	898.4757	898.4760	-0.28	1	27	0.015	1	U	Y.NPATGDVL
1079	450.2508	898.4870	898.4760	12.3	1	(22)	0.037	1	U	Y.NPATGDVL
1080	450.2508	898.4871	898.4760	12.3	1	(22)	0.037	1	U	Y.NPATGDVL

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264. 2::sp|P15006|MCRC_ECOLI **Mass:** 40792 **Score:** 24 **Matches:** 2(0) **Sequences:** 1
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
6115	712.8492	1423.6839	1423.7055	-15.17	1	(22)	0.14	1	U	L.NSTIR
6117	712.8503	1423.6861	1423.7055	-13.62	1	24	0.079	1	U	L.NSTIR

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265. 2::sp|P00490|PHSM_ECOLI **Mass:** 90865 **Score:** 24 **Matches:** 1(1) **Sequences:** 1
Maltodextrin phosphorylase OS=Escherichia coli (strain K12) OX=83333 GN=malP 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
5659	678.8487	1355.6828	1355.7157	-24.23	0	24	0.056	1	U	L.RAEQQ

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266. 2::sp|P33011|YEEA_ECOLI **Mass:** 40158 **Score:** 24 **Matches:** 1(1) **Sequences:** 1
Inner membrane protein YeeA OS=Escherichia coli (strain K12) OX=83333 GN=yeeA 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
4387	405.5666	1213.6779	1213.7030	-20.67	1	24	0.048	1	U	F.ERIGG

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267. 2::sp|P17115|GUTQ_ECOLI **Mass:** 34181 **Score:** 24 **Matches:** 2(1) **Sequences:** 1
Arabinose 5-phosphate isomerase GutQ OS=Escherichia coli (strain K12) OX=83333 GN=gu

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1507	473.2757	944.5369	944.5291	8.28	2	(20)	0.11	2	U	L.ELSRTGLG
1508	**473.2761**	**944.5376**	**944.5291**	**9.05**	**2**	**24**	**0.042**	**1**	**U**	**L.ELSRTGLG**

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268. 2::sp|P08202|ARAA_ECOLI **Mass:** 56437 **Score:** 24 **Matches:** 2(0) **Sequences:** 1(
L-arabinose isomerase OS=Escherichia coli (strain K12) OX=83333 GN=araA PE=1 SV=3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5206	**651.8373**	**1301.6600**	**1301.6723**	**-9.44**	**2**	**(22)**	**0.11**	**1**	**U**	**W.INGLTM**
5208	**651.8383**	**1301.6620**	**1301.6723**	**-7.94**	**2**	**24**	**0.078**	**1**	**U**	**W.INGLTM**

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269. 2::sp|P08722|PTV3B_ECOLI **Mass:** 66896 **Score:** 24 **Matches:** 2(1) **Sequences:** 1
PTS system beta-glucoside-specific EIIBCA component OS=Escherichia coli (strain K12)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
473	**408.7448**	**815.4749**	**815.4939**	**-23.20**	**2**	**(20)**	**0.096**	**1**	**U**	**L.KGMLALA**
474	408.7449	815.4752	815.4939	-22.83	2	24	0.037	3	U	L.KGMLALA

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270. 2::sp|P16525|TUS_ECOLI **Mass:** 35875 **Score:** 24 **Matches:** 1(0) **Sequences:** 1(
DNA replication terminus site-binding protein 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
7743	**570.2854**	**1707.8344**	**1707.8250**	**5.48**	**0**	**24**	**0.1**	**1**	**U**	**Y.KGDQKQ**

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271. 2::sp|P75916|YCDZ_ECOLI **Mass:** 17291 **Score:** 24 **Matches:** 1(0) **Sequences:** 1(
Inner membrane protein YcdZ OS=Escherichia coli (strain K12) OX=83333 GN=ycdZ 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
5259	**654.3220**	**1306.6294**	**1306.6335**	**-3.14**	**2**	**27**	**0.056**	**1**	**U**	**F.LMCIQA**

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      : 9340
```

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