

locus	log2ratio	lowerCI	upperCI	quantified_description
sp_P0A6X3_HFQ_ECOLI	4.5	4	5	7 Protein hfq OS=Escheri
sp_P0AG67_RS1_ECOLI	3.4	3.1	3.7	22 30S ribosomal protein S
sp_P0A7V8_RS4_ECOLI	3.1	2.5	3.8	4 30S ribosomal protein S
sp_P0A6P9_ENO_ECOLI	2.3	1.7	2.9	7 Enolase OS=Escherichia
sp_P30850_RNB_ECOLI	2.2	1.5	3	3 Exoribonuclease 2 OS=E
sp_P02359_RS7_ECOLI	2.1	1.5	2.7	6 30S ribosomal protein S
sp_P0A7D4_PURA_ECOLI	2	1.4	2.5	9 Adenylosuccinate synth
sp_P0A7L0_RL1_ECOLI	2	0.8	2.8	4 50S ribosomal protein L
sp_P67910_HLDD_ECOLI	1.9	1.6	2.1	40 ADP-L-glycero-D-manno
sp_P0A6X7_IHFA_ECOLI	1.8	0.9	2.6	2 Integration host factor :
sp_P0A7X3_RS9_ECOLI	1.8	-2.3	2.9	2 30S ribosomal protein S
sp_P0ABD8_BCCP_ECOLI	1.5	0.9	2	7 Biotin carboxyl carrier p
sp_P25665_METE_ECOLI	1.4	0.9	1.9	7 5-methyltetrahydropter
sp_P0A7Z4_RPOA_ECOLI	1.1	0.8	1.4	15 DNA-directed RNA poly
sp_P09373_PFLB_ECOLI	1	0.2	1.9	2 Formate acetyltransfera
sp_P0A8R0_RRAA_ECOLI	1	0.5	1.6	4 Regulator of ribonuclea
sp_P0A9K9_SLYD_ECOLI	1	0.6	1.4	8 FKBP-type peptidyl-pro
sp_P30126_LEUD_ECOLI	1	-0.1	2.2	2 3-isopropylmalate dehy
sp_P36683_ACON2_ECOLI	0.9	0.6	1.3	12 Aconitate hydratase 2 C
sp_P64476_YDIH_ECOLI	0.9	0	1.9	2 Uncharacterized protei
sp_P0ACF0_DBHA_ECOLI	0.7	-0.3	1.6	2 DNA-binding protein H
sp_P0A8J4_YBED_ECOLI	0.6	-0.3	1.6	2 UPF0250 protein ybeD
sp_P0ABK5_CYSK_ECOLI	0.5	0.2	0.7	33 Cysteine synthase A OS
sp_P0ADE8_YGFZ_ECOLI	0.5	-0.2	1.1	7 tRNA-modifying proteir
sp_P0A8T7_RPOC_ECOLI	0.4	0.2	0.7	48 DNA-directed RNA poly
sp_P0A8V2_RPOB_ECOLI	0.4	0.2	0.6	61 DNA-directed RNA poly
sp_P0AFF6_NUSA_ECOLI	0.4	-0.1	0.8	7 Transcription elongatio
sp_P21889_SYD_ECOLI	0.4	-0.5	1.2	2 Aspartyl-tRNA syntheta
sp_P06989_HIS2_ECOLI	0.3	-0.6	1.3	2 Histidine biosynthesis b
sp_P0AEP3_GALU_ECOLI	0.3	-0.6	1	8 UTP--glucose-1-phosph
sp_P68066_GRCA_ECOLI	0.3	-0.5	1.1	3 Autonomous glycy radi
sp_P76539_YPEA_ECOLI	0.3	-0.7	1.2	2 Acetyltransferase ypeA
sp_P0A6A6_LEUC_ECOLI	0.2	-0.5	1	4 3-isopropylmalate dehy
sp_P0AE08_AHPC_ECOLI	0.2	-0.8	1.1	2 Alkyl hydroperoxide rec
sp_P0AEK4_FABI_ECOLI	0.1	-0.3	0.6	11 Enoyl-[acyl-carrier-prot
sp_P0ACF8_HNS_ECOLI	0	-0.8	0.9	2 DNA-binding protein H-
sp_P37188_PTKB_ECOLI	0	-0.8	0.8	2 Galactitol-specific phos
sp_P61889_MDH_ECOLI	0	-0.6	0.5	6 Malate dehydrogenase
sp_P0A6A3_ACKA_ECOLI	-0.1	-0.7	0.5	12 Acetate kinase OS=Esch
sp_P22634_MURI_ECOLI	-0.1	-0.9	0.8	2 Glutamate racemase O'
sp_P0A6H5_HSLU_ECOLI	-0.2	-1	0.6	4 ATP-dependent proteas
sp_P0A6M8_EFG_ECOLI	-0.3	-0.7	0	17 Elongation factor G OS=
sp_P69441_KAD_ECOLI	-0.3	-0.8	0.2	7 Adenylate kinase OS=Es
sp_P69783_PTGA_ECOLI	-0.3	-1	0.3	3 Glucose-specific phosph
sp_P05791_ILVD_ECOLI	-0.4	-1.1	0.4	2 Dihydroxy-acid dehydra
sp_P08660_AK3_ECOLI	-0.4	-0.8	0.1	8 Lysine-sensitive aspartc
sp_P08839_PT1_ECOLI	-0.4	-0.8	0.1	12 Phosphoenolpyruvate- π

sp_POAAB6_GALF_ECOLI	-0.4	-0.9	0	11 UTP--glucose-1-phosph
sp_POAF08_MRP_ECOLI	-0.4	-1.3	0.6	2 Protein mrp OS=Escher
sp_POAC69_GLRX4_ECOLI	-0.5	-1.4	0.4	2 Glutaredoxin-4 OS=Escl
sp_P22106_ASNB_ECOLI	-0.5	-1.1	0	5 Asparagine synthetase
sp_POA887_UBIE_ECOLI	-0.6	-1.5	0.3	3 Ubiquinone/menaquinc
sp_P24186_FOLD_ECOLI	-0.6	-1.7	2.9	2 Bifunctional protein fol
sp_P00934_THRC_ECOLI	-0.7	-0.9	-0.4	31 Threonine synthase OS:
sp_P02413_RL15_ECOLI	-0.7	-1.4	0.1	4 50S ribosomal protein L
sp_POA7D7_PUR7_ECOLI	-0.7	-1.1	-0.2	8 Phosphoribosylaminoin
sp_POAEK2_FABG_ECOLI	-0.7	-1.8	0.3	2 3-oxoacyl-[acyl-carrier-
sp_POAGK8_ISCR_ECOLI	-0.7	-1.2	-0.2	9 HTH-type transcription:
sp_P09053_AVTA_ECOLI	-0.8	-1.4	-0.3	6 Valine--pyruvate amino
sp_POAED0_USPA_ECOLI	-0.8	-1.3	-0.4	10 Universal stress protein
sp_P23893_GSA_ECOLI	-0.8	-1.4	-0.1	3 Glutamate-1-semialdeh
sp_P33221_PURT_ECOLI	-0.8	-1.2	-0.3	9 Phosphoribosylglycinan
REVERSE_sp_P13809_RPI_ECOLI	-0.9	-1.5	-0.2	3 Reverse sequence, was
sp_POA7E5_PYRG_ECOLI	-0.9	-1.6	-0.2	4 CTP synthase OS=Esche
sp_POA7J7_RL11_ECOLI	-0.9	-1.7	-0.1	2 50S ribosomal protein L
sp_POA9M2_HPRT_ECOLI	-0.9	-1.5	-0.3	6 Hypoxanthine phospho
sp_POAC41_DHSA_ECOLI	-0.9	-1.3	-0.4	8 Succinate dehydrogena
sp_P60595_HIS5_ECOLI	-0.9	-1.9	0.1	2 Imidazole glycerol phos
sp_P00561_AK1H_ECOLI	-1	-1.2	-0.8	39 Bifunctional aspartokin.
sp_P08244_PYRF_ECOLI	-1	-1.5	-0.6	8 Orotidine 5'-phosphate
sp_POA6N4_EFP_ECOLI	-1	-2.3	0.2	2 Elongation factor P OS=
sp_POA734_MINE_ECOLI	-1	-2	-0.1	2 Cell division topological
sp_POA8F0_UPP_ECOLI	-1	-1.3	-0.7	22 Uracil phosphoribosyltr
sp_POAB80_ILVE_ECOLI	-1	-1.9	0	2 Branched-chain-amino-
sp_P37903_USPF_ECOLI	-1	-1.6	-0.3	3 Universal stress protein
sp_POA7R5_RS10_ECOLI	-1.1	-1.5	-0.6	8 30S ribosomal protein S
sp_P00547_KHSE_ECOLI	-1.2	-1.9	-0.6	3 Homoserine kinase OS=
sp_P00961_SYGB_ECOLI	-1.2	-1.5	-0.8	15 Glycyl-tRNA synthetase
sp_POA6Z1_HSCA_ECOLI	-1.2	-1.6	-0.8	8 Chaperone protein hsc/
sp_POA9Q1_ARCA_ECOLI	-1.2	-1.7	-0.6	9 Aerobic respiration con
sp_P24182_ACCC_ECOLI	-1.2	-2	-0.4	3 Biotin carboxylase OS=f
sp_P36680_YACF_ECOLI	-1.2	-1.8	-0.6	6 UPF0289 protein yacF C
sp_P09151_LEU1_ECOLI	-1.3	-1.8	-0.7	8 2-isopropylmalate syntl
sp_POA749_MURA_ECOLI	-1.3	-1.7	-0.9	11 UDP-N-acetylglucosami
sp_POA953_FABB_ECOLI	-1.3	-2.1	-0.5	3 3-oxoacyl-[acyl-carrier-
sp_POAGG0_THIL_ECOLI	-1.3	-1.9	-0.7	4 Thiamine-monophosph
sp_P23538_PPSA_ECOLI	-1.3	-1.6	-1	20 Phosphoenolpyruvate s
sp_P24203_YJIA_ECOLI	-1.4	-2.2	-0.7	3 Uncharacterized GTP-bi
sp_P77364_GLXK1_ECOLI	-1.4	-2.1	-0.7	3 Glycerate kinase 1 OS=f
sp_POA6H1_CLPX_ECOLI	-1.5	-2	-1	8 ATP-dependent Clp pro
sp_POA9B2_G3P1_ECOLI	-1.5	-2.2	-0.9	4 Glyceraldehyde-3-phos
sp_P07639_AROB_ECOLI	-1.6	-2.1	-1.2	9 3-dehydroquinat syntl
sp_POA9X4_MREB_ECOLI	-1.6	-2.1	-1.1	11 Rod shape-determining
sp_POAAB8_USPD_ECOLI	-1.6	-2.5	-0.9	4 Universal stress protein
sp_POAEZ1_METF_ECOLI	-1.6	-1.9	-1.3	20 5,10-methylenetetrahy

sp_P24193_HYPE_ECOLI	-1.6	-2.9	-0.2	2 Hydrogenase isoenzyme
sp_P27833_RFFA_ECOLI	-1.6	-2.6	-0.6	2 Lipopolysaccharide biosynthesis
sp_P37440_UCPA_ECOLI	-1.6	-2.3	-1	5 Oxidoreductase ucpA O
sp_P69407_RCSB_ECOLI	-1.6	-2.1	-1.2	8 Capsular synthesis regulator
sp_P76423_THIM_ECOLI	-1.6	-2.2	-1	6 Hydroxyethylthiazole kinase
sp_P05852_GCP_ECOLI	-1.7	-7	-0.5	3 Probable O-sialoglycoproteinase
sp_P0A825_GLYA_ECOLI	-1.7	-2.1	-1.3	9 Serine hydroxymethyltransferase
sp_P0A9Q9_DHAS_ECOLI	-1.7	-2.7	3.5	4 Aspartate-semialdehyde dehydrogenase
sp_P32132_TYPA_ECOLI	-1.7	-2	-1.5	21 GTP-binding protein tyf
sp_P0A6E1_AROL_ECOLI	-1.8	-7	-0.7	2 Shikimate kinase 2 OS=Escherichia coli
sp_P0A817_METK_ECOLI	-1.8	-2.2	-1.4	12 S-adenosylmethionine synthetase
sp_P0AAI5_FABF_ECOLI	-1.8	-2.3	-1.2	4 3-oxoacyl-[acyl-carrier-protein] synthase 3
sp_P0AAV4_YBGJ_ECOLI	-1.8	-2.5	-1.1	3 Uncharacterized protein
sp_P16659_SYP_ECOLI	-1.8	-2.1	-1.5	17 Prolyl-tRNA synthetase
sp_P31677_OTSA_ECOLI	-1.8	-2.7	-1	3 Alpha,alpha-trehalose synthase
sp_P76658_HLDE_ECOLI	-1.8	-2.1	-1.5	33 Bifunctional protein hld
sp_P0A6F1_CARA_ECOLI	-1.9	-2.3	-1.5	9 Carbamoyl-phosphate synthase
sp_P0A720_KTHY_ECOLI	-1.9	-3.1	-0.9	2 Thymidylate kinase OS=Escherichia coli
sp_P0A9W3_YJKK_ECOLI	-1.9	-2.4	-1.3	7 Uncharacterized ABC transporter
sp_P0AFG0_NUSG_ECOLI	-1.9	-2.5	-1.4	4 Transcription antitermination factor
sp_P16456_SELD_ECOLI	-1.9	-2.3	-1.6	10 Selenide, water dikinase
sp_P08390_USG_ECOLI	-2	-2.8	-1.2	2 USG-1 protein OS=Escherichia coli
sp_P00895_TRPE_ECOLI	-2.1	-2.9	-1.3	2 Anthranilate synthase component 2
sp_P08142_ILVB_ECOLI	-2.1	-2.4	-1.9	26 Acetolactate synthase i
sp_P0A6F5_CH60_ECOLI	-2.1	-2.4	-1.7	11 60 kDa chaperonin OS=Escherichia coli
sp_P0ABB0_ATPA_ECOLI	-2.1	-2.7	-1.4	5 ATP synthase subunit alpha
sp_P0AGA6_UHPA_ECOLI	-2.1	-2.9	-1.3	2 Transcriptional regulator
sp_P10371_HIS4_ECOLI	-2.1	-2.5	-1.8	19 1-(5-phosphoribosyl)-5-phosphoribosyl transferase
sp_P62620_ISPG_ECOLI	-2.1	-2.4	-1.8	17 4-hydroxy-3-methylbutyrate dehydrogenase
sp_P00968_CARB_ECOLI	-2.2	-2.4	-2	62 Carbamoyl-phosphate synthase
sp_P08178_PUR5_ECOLI	-2.2	-2.6	-1.8	9 Phosphoribosylformylglycinamido transferase
sp_P0AEI4_RIMO_ECOLI	-2.2	-2.9	-1.6	4 Ribosomal protein S12
sp_P0AF24_NAGD_ECOLI	-2.2	-2.5	-1.9	14 Protein nagD OS=Escherichia coli
sp_P23909_MUTS_ECOLI	-2.2	-2.7	-1.7	7 DNA mismatch repair protein
sp_P60757_HIS1_ECOLI	-2.2	-2.6	-1.8	8 ATP phosphoribosyltransferase
sp_P10121_FTSY_ECOLI	-2.3	-3.2	-1.1	6 Cell division protein ftsY
sp_P60785_LEPA_ECOLI	-2.3	-2.7	-2	11 GTP-binding protein lep
sp_P0A7G6_RECA_ECOLI	-2.4	-2.8	-1.9	14 Protein recA OS=Escherichia coli
sp_P0A8S1_ICIA_ECOLI	-2.4	-2.9	-1.8	7 Chromosome initiation
sp_P0AG14_SOHB_ECOLI	-2.4	-7	-1.2	2 Probable protease sohE
sp_P0A6B7_ISCS_ECOLI	-2.5	-2.9	-2.1	25 Cysteine desulfurase O
sp_P0A9A6_FTSZ_ECOLI	-2.5	-2.8	-2.2	28 Cell division protein ftsZ
sp_P0A9B6_E4PD_ECOLI	-2.5	-4.9	-1.5	3 D-erythrose-4-phosphate dehydrogenase
sp_P30137_THIE_ECOLI	-2.5	-2.9	-2	8 Thiamine-phosphate pyrophosphorylase
sp_P37351_RPIB_ECOLI	-2.5	-3.5	-1.6	2 Ribose-5-phosphate isomerase
sp_P00960_SYGA_ECOLI	-2.6	-3.3	-2	6 Glycyl-tRNA synthetase
sp_P0A9Q7_ADHE_ECOLI	-2.6	-3.3	-1.9	4 Aldehyde-alcohol dehydrogenase
sp_P0AED5_UVRY_ECOLI	-2.7	-3.5	-1.9	2 Response regulator uvr

sp_P13009_METH_ECOLI	-2.7	-3	-2.3	22 Methionine synthase O
sp_P00894_ILVH_ECOLI	-2.8	-3.2	-2.4	10 Acetolactate synthase i
sp_P30139_THIG_ECOLI	-2.8	-3.3	-2.4	8 Thiazole synthase OS=E
sp_P60716_LIPA_ECOLI	-2.8	-3.4	-2.1	5 Lipoyl synthase OS=Escl
sp_P21170_SPEA_ECOLI	-2.9	-3.3	-2.5	12 Biosynthetic arginine de
sp_P21177_FADB_ECOLI	-2.9	-3.3	-2.5	10 Fatty acid oxidation cor
sp_P43337_NUDL_ECOLI	-2.9	-3.5	-2.3	4 Uncharacterized Nudix
sp_P0A879_TRPB_ECOLI	-3	-3.4	-2.7	24 Tryptophan synthase br
sp_P64581_YQJD_ECOLI	-3	-4.1	-2.2	2 Uncharacterized protei
sp_P75745_YBGK_ECOLI	-3	-7	-2.1	3 Uncharacterized protei
sp_P0AEI1_MIAB_ECOLI	-3.2	-7	-2	3 (Dimethylallyl)adenosin
sp_P31802_NARP_ECOLI	-3.2	-7	-0.8	2 Nitrate/nitrite respons
sp_P69828_PTKA_ECOLI	-3.4	-3.8	-3	12 Galactitol-specific phos
sp_P0A6U5_RSMG_ECOLI	-3.5	-3.9	-3.1	7 Ribosomal RNA small su
sp_P76034_YCIT_ECOLI	-3.5	-4	-2.9	9 Uncharacterized HTH-ty
sp_P0A6C8_ARGB_ECOLI	-3.7	-4.1	-3	32 Acetylglutamate kinase
sp_P0A8F4_URK_ECOLI	-3.7	-4.2	-3.1	7 Uridine kinase OS=Esch
sp_P0ACJ0_LRP_ECOLI	-3.7	-4.9	-2.4	2 Leucine-responsive regi
sp_P0AEZ3_MIND_ECOLI	-3.7	-4	-0.7	36 Septum site-determinir
sp_P76027_OPPD_ECOLI	-3.7	-4.5	-2.9	2 Oligopeptide transport
sp_P0A959_YFBQ_ECOLI	-3.8	-4.4	-3.1	4 Uncharacterized amino
sp_P23845_CYSN_ECOLI	-3.9	-4.4	-3.4	12 Sulfate adenylyltransfer
sp_P28635_METQ_ECOLI	-3.9	-4.4	-3.3	7 D-methionine-binding I
sp_P0ABB4_ATPB_ECOLI	-4	-4.4	-3.6	20 ATP synthase subunit b
sp_P76422_THID_ECOLI	-4	-5.4	-3.4	6 Hydroxymethylpyrimidi
sp_P04968_THD1_ECOLI	-4.1	-5.2	-3.1	3 Threonine dehydratase
sp_P22523_MUKB_ECOLI	-4.2	-4.7	-3.7	7 Chromosome partition
sp_P0ABA0_ATPF_ECOLI	-4.6	-5.1	-4	4 ATP synthase subunit b
sp_P0A6C5_ARGA_ECOLI	-4.8	-5.5	-4	5 Amino-acid acetyltransi
sp_P0A7F3_PYRI_ECOLI	-4.8	-5.4	-4.2	7 Aspartate carbamoyltra
sp_P0ACP1_FRUR_ECOLI	-4.8	-6.1	-4.1	6 Fructose repressor OS=
sp_P00893_ILVI_ECOLI	-4.9	-5.4	-3.7	10 Acetolactate synthase i
sp_P30138_THIF_ECOLI	-4.9	-5.6	-4.4	10 Sulfur carrier protein T
sp_P0A9L5_PPIC_ECOLI	-5.1	-5.8	-4.4	4 Peptidyl-prolyl cis-trans
sp_P0A698_UVRA_ECOLI	-5.5	-6.3	-4.8	3 UvrABC system protein
sp_P0AG30_RHO_ECOLI	-6	-6.3	-5.6	28 Transcription terminati
sp_P00936_CYAA_ECOLI	-6.1	-7	-1.4	3 Adenylate cyclase OS=E
sp_P62399_RL5_ECOLI	-6.7	-7	-5.9	2 50S ribosomal protein L
sp_P00562_AK2H_ECOLI	-6.8	-7	-6.5	23 Bifunctional aspartokin
sp_P39274_YJDJ_ECOLI	-6.9	-7	-6.6	17 Uncharacterized protei
sp_P06971_FHUA_ECOLI	-7	-7	-6.2	2 Ferrichrome-iron recep
sp_P0A6Y5_HSLO_ECOLI	-7	-7	-6.4	8 33 kDa chaperonin OS=

chia coli (strain K12) GN=hfq PE=1 SV=2 [MASS=11166]
51 OS=Escherichia coli (strain K12) GN=rpsA PE=1 SV=1 [MASS=61158]
54 OS=Escherichia coli (strain K12) GN=rpsD PE=1 SV=2 [MASS=23469]
1 coli (strain K12) GN=eno PE=1 SV=2 [MASS=45655]
Escherichia coli (strain K12) GN=rnb PE=1 SV=3 [MASS=72491]
57 OS=Escherichia coli (strain K12) GN=rpsG PE=1 SV=3 [MASS=20019]
etase OS=Escherichia coli (strain K12) GN=purA PE=1 SV=2 [MASS=47345]
.1 OS=Escherichia coli (strain K12) GN=rplA PE=1 SV=2 [MASS=24730]
o-heptose-6-epimerase OS=Escherichia coli (strain K12) GN=hldD PE=1 SV=1 [MASS=34893]
subunit alpha OS=Escherichia coli (strain K12) GN=ihfA PE=1 SV=1 [MASS=11354]
59 OS=Escherichia coli (strain K12) GN=rpsI PE=1 SV=2 [MASS=14856]
rotein of acetyl-CoA carboxylase OS=Escherichia coli (strain K12) GN=accB PE=1 SV=1 [MASS=16687]
royltriglutamate--homocysteine methyltransferase OS=Escherichia coli (strain K12) GN=metE PE=1 SV=6 [M
'merase subunit alpha OS=Escherichia coli (strain K12) GN=rpoA PE=1 SV=1 [MASS=36512]
ase 1 OS=Escherichia coli (strain K12) GN=pf1B PE=1 SV=2 [MASS=85357]
ise activity A OS=Escherichia coli (strain K12) GN=rraA PE=1 SV=1 [MASS=17360]
yl cis-trans isomerase slyD OS=Escherichia coli (strain K12) GN=slyD PE=1 SV=1 [MASS=20853]
/dratase small subunit OS=Escherichia coli (strain K12) GN=leuD PE=1 SV=3 [MASS=22487]
OS=Escherichia coli (strain K12) GN=acnB PE=1 SV=3 [MASS=93498]
n ydiH OS=Escherichia coli (strain K12) GN=ydiH PE=4 SV=2 [MASS=7266]
U-alpha OS=Escherichia coli (strain K12) GN=hupA PE=1 SV=1 [MASS=9535]
OS=Escherichia coli (strain K12) GN=ybeD PE=1 SV=1 [MASS=9827]
=Escherichia coli (strain K12) GN=cysK PE=1 SV=2 [MASS=34490]
1 ygfZ OS=Escherichia coli (strain K12) GN=ygfZ PE=1 SV=2 [MASS=36094]
'merase subunit beta' OS=Escherichia coli (strain K12) GN=rpoC PE=1 SV=1 [MASS=155160]
'merase subunit beta OS=Escherichia coli (strain K12) GN=rpoB PE=1 SV=1 [MASS=150632]
n protein nusA OS=Escherichia coli (strain K12) GN=nusA PE=1 SV=1 [MASS=54871]
ise OS=Escherichia coli (strain K12) GN=aspS PE=1 SV=1 [MASS=65913]
ifunctional protein hisI OS=Escherichia coli (strain K12) GN=hisI PE=3 SV=3 [MASS=22756]
ate uridylyltransferase OS=Escherichia coli (strain K12) GN=galU PE=1 SV=2 [MASS=32942]
ical cofactor OS=Escherichia coli (strain K12) GN=grcA PE=1 SV=1 [MASS=14284]
OS=Escherichia coli (strain K12) GN=ypeA PE=3 SV=2 [MASS=16312]
/dratase large subunit OS=Escherichia coli (strain K12) GN=leuC PE=1 SV=2 [MASS=49882]
ductase subunit C OS=Escherichia coli (strain K12) GN=ahpC PE=1 SV=2 [MASS=20761]
ein] reductase [NADH] OS=Escherichia coli (strain K12) GN=fabI PE=1 SV=2 [MASS=27864]
-NS OS=Escherichia coli (strain K12) GN=hns PE=1 SV=2 [MASS=15540]
photransferase enzyme IIB component OS=Escherichia coli (strain K12) GN=gatB PE=1 SV=2 [MASS=10222]
OS=Escherichia coli (strain K12) GN=mdh PE=1 SV=1 [MASS=32337]
erichia coli (strain K12) GN=ackA PE=1 SV=1 [MASS=43290]
S=Escherichia coli (strain K12) GN=murI PE=1 SV=2 [MASS=31002]
se ATPase subunit HslU OS=Escherichia coli (strain K12) GN=hslU PE=1 SV=1 [MASS=49594]
=Escherichia coli (strain K12) GN=fusA PE=1 SV=2 [MASS=77581]
scherichia coli (strain K12) GN=adk PE=1 SV=1 [MASS=23586]
hotransferase enzyme IIA component OS=Escherichia coli (strain K12) GN=crr PE=1 SV=2 [MASS=18251]
atase OS=Escherichia coli (strain K12) GN=ilvD PE=1 SV=5 [MASS=65532]
okinase 3 OS=Escherichia coli (strain K12) GN=lysC PE=1 SV=2 [MASS=48532]
protein phosphotransferase OS=Escherichia coli (strain K12) GN=ptsI PE=1 SV=1 [MASS=63562]

ate uridylyltransferase OS=Escherichia coli (strain K12) GN=galF PE=1 SV=1 [MASS=32829]
ichia coli (strain K12) GN=mrp PE=3 SV=1 [MASS=39938]
herichia coli (strain K12) GN=grxD PE=1 SV=1 [MASS=12879]
B [glutamine-hydrolyzing] OS=Escherichia coli (strain K12) GN=asnB PE=1 SV=3 [MASS=62659]
one biosynthesis methyltransferase ubiE OS=Escherichia coli (strain K12) GN=ubiE PE=1 SV=1 [MASS=28073]
D OS=Escherichia coli (strain K12) GN=foLD PE=1 SV=4 [MASS=31044]
=Escherichia coli (strain K12) GN=thrC PE=1 SV=1 [MASS=47114]
.15 OS=Escherichia coli (strain K12) GN=rplO PE=1 SV=1 [MASS=14980]
nidazole-succinocarboxamide synthase OS=Escherichia coli (strain K12) GN=purC PE=1 SV=1 [MASS=26995]
protein] reductase OS=Escherichia coli (strain K12) GN=fabG PE=1 SV=1 [MASS=25560]
al regulator iscR OS=Escherichia coli (strain K12) GN=iscR PE=1 SV=1 [MASS=17337]
transferase OS=Escherichia coli (strain K12) GN=avtA PE=3 SV=3 [MASS=46711]
A OS=Escherichia coli (strain K12) GN=uspA PE=1 SV=2 [MASS=16066]
yde 2,1-aminomutase OS=Escherichia coli (strain K12) GN=hemL PE=1 SV=2 [MASS=45366]
nide formyltransferase 2 OS=Escherichia coli (strain K12) GN=purT PE=1 SV=3 [MASS=42434]
Protein D OS=Escherichia coli GN=D PE=4 SV=1 [MASS=15756]
erichia coli (strain K12) GN=pyrG PE=1 SV=2 [MASS=60374]
.11 OS=Escherichia coli (strain K12) GN=rplK PE=1 SV=2 [MASS=14875]
ribosyltransferase OS=Escherichia coli (strain K12) GN=hpt PE=1 SV=1 [MASS=20115]
se flavoprotein subunit OS=Escherichia coli (strain K12) GN=sdhA PE=1 SV=1 [MASS=64422]
osphate synthase subunit hisH OS=Escherichia coli (strain K12) GN=hisH PE=1 SV=1 [MASS=21653]
ase/homoserine dehydrogenase 1 OS=Escherichia coli (strain K12) GN=thrA PE=1 SV=2 [MASS=89120]
decarboxylase OS=Escherichia coli (strain K12) GN=pyrF PE=1 SV=1 [MASS=26350]
Escherichia coli (strain K12) GN=efp PE=1 SV=2 [MASS=20591]
l specificity factor OS=Escherichia coli (strain K12) GN=minE PE=1 SV=1 [MASS=10235]
ransferase OS=Escherichia coli (strain K12) GN=upp PE=1 SV=1 [MASS=22533]
acid aminotransferase OS=Escherichia coli (strain K12) GN=ilvE PE=1 SV=2 [MASS=34094]
F OS=Escherichia coli (strain K12) GN=uspF PE=1 SV=2 [MASS=16017]
510 OS=Escherichia coli (strain K12) GN=rpsJ PE=1 SV=1 [MASS=11736]
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beta subunit OS=Escherichia coli (strain K12) GN=glyS PE=1 SV=4 [MASS=76813]
A OS=Escherichia coli (strain K12) GN=hscA PE=1 SV=1 [MASS=65652]
ontrol protein ArcA OS=Escherichia coli (strain K12) GN=arcA PE=1 SV=1 [MASS=27292]
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hase OS=Escherichia coli (strain K12) GN=leuA PE=1 SV=5 [MASS=57298]
ine 1-carboxyvinyltransferase OS=Escherichia coli (strain K12) GN=murA PE=1 SV=1 [MASS=44818]
protein] synthase 1 OS=Escherichia coli (strain K12) GN=fabB PE=1 SV=1 [MASS=42613]
ate kinase OS=Escherichia coli (strain K12) GN=thiL PE=3 SV=1 [MASS=35071]
ynthase OS=Escherichia coli (strain K12) GN=ppsA PE=1 SV=5 [MASS=87435]
inding protein yjiA OS=Escherichia coli (strain K12) GN=yjiA PE=1 SV=3 [MASS=35660]
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tease ATP-binding subunit clpX OS=Escherichia coli (strain K12) GN=clpX PE=1 SV=2 [MASS=46356]
phate dehydrogenase A OS=Escherichia coli (strain K12) GN=gapA PE=1 SV=2 [MASS=35532]
hase OS=Escherichia coli (strain K12) GN=aroB PE=3 SV=1 [MASS=38881]
; protein mreB OS=Escherichia coli (strain K12) GN=mreB PE=1 SV=1 [MASS=36952]
D OS=Escherichia coli (strain K12) GN=uspD PE=2 SV=1 [MASS=16293]
drofolate reductase OS=Escherichia coli (strain K12) GN=metF PE=1 SV=1 [MASS=33103]

es formation protein hypE OS=Escherichia coli (strain K12) GN=hypE PE=1 SV=2 [MASS=35092]
synthesis protein rffA OS=Escherichia coli (strain K12) GN=rffA PE=3 SV=2 [MASS=41901]
S=Escherichia coli (strain K12) GN=ucpA PE=1 SV=3 [MASS=27850]
ilator component B OS=Escherichia coli (strain K12) GN=rcsB PE=1 SV=1 [MASS=23671]
inase OS=Escherichia coli (strain K12) GN=thiM PE=3 SV=1 [MASS=27339]
rotein endopeptidase OS=Escherichia coli (strain K12) GN=gcp PE=3 SV=2 [MASS=36008]
ransferase OS=Escherichia coli (strain K12) GN=glyA PE=1 SV=1 [MASS=45317]
e dehydrogenase OS=Escherichia coli (strain K12) GN=asd PE=1 SV=1 [MASS=40018]
α/BipA OS=Escherichia coli (strain K12) GN=typA PE=1 SV=2 [MASS=67355]
Escherichia coli (strain K12) GN=aroL PE=1 SV=3 [MASS=19151]
synthase OS=Escherichia coli (strain K12) GN=metK PE=1 SV=2 [MASS=41952]
protein] synthase 2 OS=Escherichia coli (strain K12) GN=fabF PE=1 SV=2 [MASS=43046]
n ybgJ OS=Escherichia coli (strain K12) GN=ybgJ PE=4 SV=1 [MASS=23947]
OS=Escherichia coli (strain K12) GN=proS PE=1 SV=4 [MASS=63693]
phosphate synthase [UDP-forming] OS=Escherichia coli (strain K12) GN=otsA PE=1 SV=3 [MASS=53611]
lE OS=Escherichia coli (strain K12) GN=hldE PE=1 SV=1 [MASS=51051]
synthase small chain OS=Escherichia coli (strain K12) GN=carA PE=1 SV=1 [MASS=41431]
=Escherichia coli (strain K12) GN=tmk PE=1 SV=1 [MASS=23783]
ransporter ATP-binding protein yjjK OS=Escherichia coli (strain K12) GN=yjjK PE=1 SV=2 [MASS=62443]
nation protein nusG OS=Escherichia coli (strain K12) GN=nusG PE=1 SV=2 [MASS=20532]
e OS=Escherichia coli (strain K12) GN=selD PE=1 SV=1 [MASS=36687]
erichia coli (strain K12) GN=usg PE=1 SV=1 [MASS=36364]
omponent 1 OS=Escherichia coli (strain K12) GN=trpE PE=1 SV=2 [MASS=57494]
sozyme 1 large subunit OS=Escherichia coli (strain K12) GN=ilvB PE=1 SV=1 [MASS=60441]
Escherichia coli (strain K12) GN=groL PE=1 SV=2 [MASS=57329]
lpha OS=Escherichia coli (strain K12) GN=atpA PE=1 SV=1 [MASS=55222]
ory protein uhpA OS=Escherichia coli (strain K12) GN=uhpA PE=1 SV=1 [MASS=20889]
-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase OS=Escherichia coli (str
-2-en-1-yl diphosphate synthase OS=Escherichia coli (strain K12) GN=ispG PE=1 SV=1 [MASS=40684]
synthase large chain OS=Escherichia coli (strain K12) GN=carB PE=1 SV=2 [MASS=117842]
lycinamide cyclo-ligase OS=Escherichia coli (strain K12) GN=purM PE=1 SV=3 [MASS=36854]
methylthiotransferase rimO OS=Escherichia coli (strain K12) GN=rimO PE=1 SV=1 [MASS=49582]
erichia coli (strain K12) GN=nagD PE=1 SV=1 [MASS=27163]
rotein mutS OS=Escherichia coli (strain K12) GN=mutS PE=1 SV=1 [MASS=95247]
nsferase OS=Escherichia coli (strain K12) GN=hisG PE=1 SV=1 [MASS=33367]
Y OS=Escherichia coli (strain K12) GN=ftsY PE=1 SV=1 [MASS=54513]
α OS=Escherichia coli (strain K12) GN=lepA PE=1 SV=1 [MASS=66570]
erichia coli (strain K12) GN=recA PE=1 SV=2 [MASS=37973]
inhibitor OS=Escherichia coli (strain K12) GN=iciA PE=1 SV=1 [MASS=33472]
3 OS=Escherichia coli (strain K12) GN=sohB PE=1 SV=1 [MASS=39366]
S=Escherichia coli (strain K12) GN=iscS PE=1 SV=1 [MASS=45089]
Z OS=Escherichia coli (strain K12) GN=ftsZ PE=1 SV=1 [MASS=40324]
te dehydrogenase OS=Escherichia coli (strain K12) GN=epd PE=1 SV=2 [MASS=37299]
rophosphorylase OS=Escherichia coli (strain K12) GN=thiE PE=1 SV=1 [MASS=23015]
merase B OS=Escherichia coli (strain K12) GN=rpiB PE=1 SV=2 [MASS=16073]
: alpha subunit OS=Escherichia coli (strain K12) GN=glyQ PE=1 SV=2 [MASS=34774]
drogenase OS=Escherichia coli (strain K12) GN=adhE PE=1 SV=2 [MASS=96127]
Y OS=Escherichia coli (strain K12) GN=uvrY PE=1 SV=1 [MASS=23893]

S=Escherichia coli (strain K12) GN=metH PE=1 SV=5 [MASS=135997]
sozyme 3 small subunit OS=Escherichia coli (strain K12) GN=ilvH PE=1 SV=3 [MASS=17977]
Escherichia coli (strain K12) GN=thiG PE=1 SV=3 [MASS=26896]
Escherichia coli (strain K12) GN=lipA PE=1 SV=1 [MASS=36072]
isocitrate dehydrogenase OS=Escherichia coli (strain K12) GN=speA PE=1 SV=2 [MASS=73898]
sigma factor 70 OS=Escherichia coli (strain K12) GN=fadB PE=1 SV=2 [MASS=79594]
phosphatase OS=Escherichia coli (strain K12) GN=nudL PE=3 SV=1 [MASS=21436]
beta chain OS=Escherichia coli (strain K12) GN=trpB PE=1 SV=2 [MASS=42983]
sigma factor 54 OS=Escherichia coli (strain K12) GN=yqjD PE=4 SV=1 [MASS=11051]
sigma factor 32 OS=Escherichia coli (strain K12) GN=ybgK PE=4 SV=1 [MASS=34386]
lysine tRNA methyltransferase miaB OS=Escherichia coli (strain K12) GN=miaB PE=1 SV=1 [MASS=53663]
sigma factor 24 OS=Escherichia coli (strain K12) GN=narP PE=3 SV=1 [MASS=23575]
phosphotransferase enzyme IIA component OS=Escherichia coli (strain K12) GN=gatA PE=4 SV=1 [MASS=16907]
sigma factor 54 subunit methyltransferase G OS=Escherichia coli (strain K12) GN=rsmG PE=1 SV=1 [MASS=23431]
sigma factor 54 type transcriptional regulator yciT OS=Escherichia coli (strain K12) GN=yciT PE=4 SV=1 [MASS=27603]
sigma factor 54 OS=Escherichia coli (strain K12) GN=argB PE=1 SV=1 [MASS=27160]
Escherichia coli (strain K12) GN=udk PE=3 SV=1 [MASS=24353]
sigma factor 24 regulatory protein OS=Escherichia coli (strain K12) GN=lrp PE=1 SV=2 [MASS=18887]
sigma factor 54 protein minD OS=Escherichia coli (strain K12) GN=minD PE=1 SV=2 [MASS=29614]
sigma factor 54 ATP-binding protein oppD OS=Escherichia coli (strain K12) GN=oppD PE=3 SV=2 [MASS=37188]
sigma factor 54 transferase yfbQ OS=Escherichia coli (strain K12) GN=yfbQ PE=1 SV=1 [MASS=45517]
sigma factor 54 kinase subunit 1 OS=Escherichia coli (strain K12) GN=cysN PE=1 SV=1 [MASS=52558]
sigma factor 54 lipoprotein metQ OS=Escherichia coli (strain K12) GN=metQ PE=1 SV=2 [MASS=29432]
sigma factor 54 eta OS=Escherichia coli (strain K12) GN=atpD PE=1 SV=2 [MASS=50325]
sigma factor 54 threonine/phosphomethylpyrimidine kinase OS=Escherichia coli (strain K12) GN=thiD PE=1 SV=1 [MASS=28634]
sigma factor 54 biosynthetic OS=Escherichia coli (strain K12) GN=ilvA PE=1 SV=1 [MASS=56195]
sigma factor 54 protein mukB OS=Escherichia coli (strain K12) GN=mukB PE=1 SV=2 [MASS=170230]
sigma factor 54 OS=Escherichia coli (strain K12) GN=atpF PE=1 SV=1 [MASS=17264]
sigma factor 54 transferase OS=Escherichia coli (strain K12) GN=argA PE=1 SV=1 [MASS=49195]
sigma factor 54 transferase regulatory chain OS=Escherichia coli (strain K12) GN=pyrI PE=1 SV=2 [MASS=17121]
Escherichia coli (strain K12) GN=fruR PE=1 SV=1 [MASS=37999]
sigma factor 54 sozyme 3 large subunit OS=Escherichia coli (strain K12) GN=ilvI PE=1 SV=2 [MASS=62984]
sigma factor 54 threonine adenylyltransferase OS=Escherichia coli (strain K12) GN=thiF PE=1 SV=2 [MASS=26970]
sigma factor 54 isomerase C OS=Escherichia coli (strain K12) GN=ppiC PE=1 SV=2 [MASS=10232]
sigma factor 54 A OS=Escherichia coli (strain K12) GN=uvrA PE=1 SV=1 [MASS=103868]
sigma factor 54 sigma factor rho OS=Escherichia coli (strain K12) GN=rho PE=1 SV=1 [MASS=47004]
Escherichia coli (strain K12) GN=cyaA PE=3 SV=5 [MASS=97586]
sigma factor 54 OS=Escherichia coli (strain K12) GN=rpIE PE=1 SV=2 [MASS=20302]
sigma factor 54 aspartate/homoserine dehydrogenase 2 OS=Escherichia coli (strain K12) GN=metL PE=1 SV=3 [MASS=88888]
sigma factor 54 sigma factor 54 OS=Escherichia coli (strain K12) GN=yjdJ PE=4 SV=1 [MASS=10468]
sigma factor 54 sigma factor 54 OS=Escherichia coli (strain K12) GN=fhuA PE=1 SV=2 [MASS=82182]
Escherichia coli (strain K12) GN=hsIO PE=1 SV=1 [MASS=32534]

MASS=84674]

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rain K12) GN=hisA PE=1 SV=2 [MASS=26033]

