locus	log2ratio	lowerCI	upperCI	quantified_	description
sp_P39274_YJDJ_ECOLI	6.7	6.2	7	6	Uncharacte
sp_P0A8R0_RRAA_ECOLI	5	4.2	5.7	2	Regulator o
sp_P69913_CSRA_ECOLI	5	4.2	5.8	2	Carbon stor
sp_P76539_YPEA_ECOLI	3.7	3.1	4.2	6	Acetyltrans
sp_P75838_YCAO_ECOLI	3.5	2.9	4.2	5	UPF0142 pr
sp_P64476_YDIH_ECOLI	2.9	2.1	3.6	3	Uncharacte
sp_P0A6X3_HFQ_ECOLI	2.6	2	3.2	5	Protein hfq
sp_P67910_HLDD_ECOLI	2.5	2.3	2.7	52	ADP-L-glyce
sp_P30138_THIF_ECOLI	2.2	1.6	3.1	5	Sulfur carrie
sp_P0A7L0_RL1_ECOLI	1.7	1	2.5	4	50S ribosom
sp_P0A9K9_SLYD_ECOLI	1.5	0.9	2	6	FKBP-type
sp_P0AEZ3_MIND_ECOLI	1.1	0.7	1.5	16	Septum site
sp_P0A6C8_ARGB_ECOLI	0.9	0.4	1.3	9	Acetylgluta
sp_P0AFG0_NUSG_ECOLI	0.9	-0.1	1.8	2	Transcriptio
sp_P0A7Z4_RPOA_ECOLI	0.5	0.2	0.9	17	DNA-directe
sp_P0AED0_USPA_ECOLI	0.2	-0.3	0.7	5	Universal st
sp_P0A8T7_RPOC_ECOLI	-0.1	-0.3	0.1	41	DNA-directe
sp_P0AG67_RS1_ECOLI	-0.1	-0.5	0.4	10	30S ribosom
sp_P36680_YACF_ECOLI	-0.1	-1.3	1.1	2	UPF0289 pr
sp_P0AG30_RHO_ECOLI	-0.2	-0.9	0.7	6	Transcriptio
sp_P0A8V2_RPOB_ECOLI	-0.3	-0.5	-0.1	42	DNA-directe
sp_P0A9B2_G3P1_ECOLI	-0.4	-1.1	0.3	3	Glyceraldeh
sp_P0ACF8_HNS_ECOLI	-0.4	-1.3	0.5	2	DNA-bindin
sp_P61889_MDH_ECOLI	-0.4	-0.9	0	7	Malate deh
sp_P0A953_FABB_ECOLI	-0.6	-1.7	0.5	2	3-oxoacyl-[
sp_P08178_PUR5_ECOLI	-0.7	-1.1	-0.3	8	Phosphorib
sp_P0AGK8_ISCR_ECOLI	-0.7	-1.3	-0.1	5	HTH-type tr
sp_P0A7D7_PUR7_ECOLI	-0.8	-1.7	0.1	2	Phosphorib
sp_P0AAB8_USPD_ECOLI	-0.8	-1.5	0	3	Universal st
sp_P0A9B6_E4PD_ECOLI	-0.9	-1.9	0.1	2	D-erythrose
sp_P0A6S7_GPDA_ECOLI	-1	-1.9	0	2	Glycerol-3-
sp_P0A850_TIG_ECOLI	-1	-2.2	0	3	Trigger fact
sp_P27833_RFFA_ECOLI	-1	-1.8	-0.2	4	Lipopolysac
sp_P0A734_MINE_ECOLI	-1.1	-1.8	-0.4	3	Cell division
sp_P0AEK4_FABI_ECOLI	-1.1	-2.5	0.2	2	Enoyl-[acyl-
sp_P37903_USPF_ECOLI	-1.1	-1.8	-0.4	3	Universal st
sp_P08390_USG_ECOLI	-1.2	-2.2	-0.4	4	USG-1 prote
sp_P0AAB6_GALF_ECOLI	-1.2	-1.8	-0.6	4	UTP--glucos
sp_P10371_HIS4_ECOLI	-1.2	-2.5	0	2	1-(5-phosph
sp_P23893_GSA_ECOLI	-1.2	-1.8	-0.7	5	Glutamate-
sp_P69828_PTKA_ECOLI	-1.2	-1.7	-0.7	8	Galactitol-s
sp_P60757_HIS1_ECOLI	-1.3	-1.7	-0.8	7	ATP phosph
sp_P08839_PT1_ECOLI	-1.4	-2	-0.8	8	Phosphoen
sp_P0A6F1_CARA_ECOLI	-1.4	-1.8	-0.9	7	Carbamoyl-
sp_P0A8S1_ICIA_ECOLI	-1.4	-2.1	-0.7	3	Chromosom
sp_P16456_SELD_ECOLI	-1.4	-1.8	-1	11	Selenide, w
sp_P24182_ACCC_ECOLI	-1.4	-2.1	-0.7	3	Biotin carbo

sp_P0AB80_ILVE_ECOLI	-1.5	-2.3	-0.7	2	Branched-c
sp_P0ACP1_FRUR_ECOLI	-1.5	-2.4	-0.6	2	Fructose re
sp_P0AG14_SOHB_ECOLI	-1.5	-2.6	-0.5	2	Probable pr
sp_P62399_RL5_ECOLI	-1.5	-2.5	-0.5	2	50S riboson
sp_P00960_SYGA_ECOLI	-1.7	-2.4	-1	3	Glycyl-tRNA
sp_P0A799_PGK_ECOLI	-1.7	-2.5	-1.1	4	Phosphogly
sp_P60716_LIPA_ECOLI	-1.7	-3	-0.8	2	Lipoyl synth
sp_P09053_AVTA_ECOLI	-1.8	-2.5	-1.1	4	Valine--pyru
sp_P0A6H1_CLPX_ECOLI	-1.8	-2.5	-1.1	3	ATP-depend
sp_P76034_YCIT_ECOLI	-1.8	-2.4	-1	4	Uncharacte
sp_P00561_AK1H_ECOLI	-1.9	-3	-0.8	2	Bifunctiona
sp_P02413_RL15_ECOLI	-1.9	-2.6	-1.3	4	50S riboson
sp_P0A836_SUCC_ECOLI	-1.9	-2.7	-1	5	Succinyl-Co
sp_P0AF24_NAGD_ECOLI	-1.9	-2.4	-1.5	8	Protein nag
sp_P13009_METH_ECOLI	-1.9	-2.6	-1.2	4	Methionine
sp_P62620_ISPG_ECOLI	-1.9	-2.3	-1.6	16	4-hydroxy-3
sp_P08660_AK3_ECOLI	-2	-2.4	-1.5	10	Lysine-sens
sp_P0A9A6_FTSZ_ECOLI	-2	-2.3	-1.7	21	Cell division
sp_P77364_GLXK1_ECOLI	-2	-3.1	-0.9	3	Glycerate ki
sp_P0A7G6_RECA_ECOLI	-2.1	-3	-1.5	7	Protein rec
sp_P21889_SYD_ECOLI	-2.1	-3.1	-1.2	5	Aspartyl-tR
sp_P60785_LEPA_ECOLI	-2.1	-2.5	-1.7	14	GTP-binding
sp_P76422_THID_ECOLI	-2.1	-7	-0.9	2	Hydroxyme
sp_P00547_KHSE_ECOLI	-2.2	-2.8	-1.5	3	Homoserine
sp_P02359_RS7_ECOLI	-2.2	-3	-1.4	2	30S riboson
sp_P00934_THRC_ECOLI	-2.3	-2.5	-2	36	Threonine s
sp_P0A879_TRPB_ECOLI	-2.3	-2.6	-2	14	Tryptophan
sp_P0A9A9_FUR_ECOLI	-2.3	-3.4	-1.2	2	Ferric uptak
sp_P0A6P1_EFTS_ECOLI	-2.4	-3.2	-1.6	2	Elongation
sp_P07639_AROB_ECOLI	-2.5	-2.9	-2.1	15	3-dehydroq
sp_P22634_MURI_ECOLI	-2.5	-3	-1.9	6	Glutamate
sp_P0A6B7_ISCS_ECOLI	-2.6	-3.2	-1.8	5	Cysteine de
sp_P0A959_YFBQ_ECOLI	-2.6	-7	-1.7	2	Uncharacte
sp_P0AGG0_THIL_ECOLI	-2.6	-3.1	-2	5	Thiamine-m
sp_P08142_ILVB_ECOLI	-2.7	-3.2	-2.2	15	Acetolactat
sp_P0A749_MURA_ECOLI	-2.7	-3.1	-2.3	12	UDP-N-acet
sp_P0A887_UBIE_ECOLI	-2.7	-3.8	-1.9	2	Ubiquinone
sp_P0A6A3_ACKA_ECOLI	-2.8	-3.2	-2.4	10	Acetate kin
sp_P0A7R5_RS10_ECOLI	-2.8	-3.2	-2.3	9	30S riboson
sp_P0AEP3_GALU_ECOLI	-2.8	-3.6	-2	2	UTP--glucos
sp_P69441_KAD_ECOLI	-2.8	-3.3	-2.4	10	Adenylate k
sp_P0AAI5_FABF_ECOLI	-2.9	-3.5	-2.3	4	3-oxoacyl-[
sp_P0AC41_DHSA_ECOLI	-2.9	-3.3	-2.4	6	Succinate d
sp_P33221_PURT_ECOLI	-2.9	-3.4	-2.5	13	Phosphorib
sp_P00893_ILVI_ECOLI	-3	-7	-1.8	2	Acetolactat
sp_P76423_THIM_ECOLI	-3.1	-3.7	-2.5	4	Hydroxyeth
sp_P0AEZ1_METF_ECOLI	-3.2	-3.6	-2.9	21	5,10-methy
sp_P24203_YJIA_ECOLI	-3.2	-3.7	-2.7	5	Uncharacte

sp_P32132_TYPA_ECOLI	-3.2	-3.5	-2.9	22	GTP-bindin
sp_P0A7E5_PYRG_ECOLI	-3.3	-7	-2.2	2	CTP synthas
sp_P0A8F0_UPP_ECOLI	-3.3	-3.9	-2.6	4	Uracil phos
sp_P05791_ILVD_ECOLI	-3.4	-3.9	-2.9	5	Dihydroxy-
sp_P0A8M0_SYN_ECOLI	-3.4	-4.2	-2.6	3	Asparaginyl
sp_P16659_SYP_ECOLI	-3.6	-3.9	-3.4	29	Prolyl-tRNA
sp_P22106_ASNB_ECOLI	-3.6	-4.4	-2.7	9	Asparagine
sp_P0A825_GLYA_ECOLI	-3.9	-4.3	-3.6	17	Serine hydr
sp_P0ABK5_CYSK_ECOLI	-3.9	-4.1	-3.7	46	Cysteine sy
sp_P24186_FOLD_ECOLI	-3.9	-4.7	-3.1	3	Bifunctiona
sp_P0A6P9_ENO_ECOLI	-4.2	-4.8	-3.7	9	Enolase OS
sp_P21170_SPEA_ECOLI	-4.3	-4.7	-3.9	11	Biosyntheti
sp_P76658_HLDE_ECOLI	-4.3	-4.9	-3.7	11	Bifunctiona
sp_P0A817_METK_ECOLI	-4.4	-4.8	-4	17	S-adenosyl
sp_P0ADP0_YIGB_ECOLI	-4.6	-5.7	-3.5	2	Uncharacte
sp_P0A7D4_PURA_ECOLI	-5	-5.4	-4.6	24	Adenylosuc
sp_P0A9W3_YJJK_ECOLI	-5	-5.6	-4.4	10	Uncharacte
sp_P07023_TYRA_ECOLI	-5.4	-6.5	-4.3	4	T-protein O
sp_P0A8L1_SYS_ECOLI	-5.4	-6.5	-4.3	2	Seryl-tRNA
sp_P0A9C9_GLPX_ECOLI	-5.5	-6.3	-4.7	3	Fructose-1,
sp_P0A796_K6PF1_ECOLI	-5.9	-6.7	-5.2	6	6-phosphof
sp_P0A6Y5_HSLO_ECOLI	-6.7	-7	-6.1	7	33 kDa cha
sp_P0A8M3_SYT_ECOLI	-6.7	-7	-6.2	7	Threonyl-t
sp_P27550_ACSA_ECOLI	-7	-7	-5.9	2	Acetyl-coen

rized protein yjdJ OS=Escherichia coli (strain K12) GN=yjdJ PE=4 SV=1 [MASS=10468]
f ribonuclease activity A OS=Escherichia coli (strain K12) GN=rraA PE=1 SV=1 [MASS=17360]
rage regulator OS=Escherichia coli (strain K12) GN=csrA PE=1 SV=1 [MASS=6856]
ferase ypeA OS=Escherichia coli (strain K12) GN=ypeA PE=3 SV=2 [MASS=16312]
rotein ycaO OS=Escherichia coli (strain K12) GN=ycaO PE=3 SV=2 [MASS=65652]
rized protein ydiH OS=Escherichia coli (strain K12) GN=ydiH PE=4 SV=2 [MASS=7266]
OS=Escherichia coli (strain K12) GN=hfq PE=1 SV=2 [MASS=11166]
ero-D-manno-heptose-6-epimerase OS=Escherichia coli (strain K12) GN=hldD PE=1 SV=1 [MASS=34893]
er protein ThiS adenylyltransferase OS=Escherichia coli (strain K12) GN=thiF PE=1 SV=2 [MASS=26970]
nal protein L1 OS=Escherichia coli (strain K12) GN=rplA PE=1 SV=2 [MASS=24730]
eptidyl-prolyl cis-trans isomerase slyD OS=Escherichia coli (strain K12) GN=slyD PE=1 SV=1 [MASS=20853]
-determining protein minD OS=Escherichia coli (strain K12) GN=minD PE=1 SV=2 [MASS=29614]
mate kinase OS=Escherichia coli (strain K12) GN=argB PE=1 SV=1 [MASS=27160]
n antitermination protein nusG OS=Escherichia coli (strain K12) GN=nusG PE=1 SV=2 [MASS=20532]
ed RNA polymerase subunit alpha OS=Escherichia coli (strain K12) GN=rpoA PE=1 SV=1 [MASS=36512]
tress protein A OS=Escherichia coli (strain K12) GN=uspA PE=1 SV=2 [MASS=16066]
ed RNA polymerase subunit beta' OS=Escherichia coli (strain K12) GN=rpoC PE=1 SV=1 [MASS=155160]
nal protein S1 OS=Escherichia coli (strain K12) GN=rpsA PE=1 SV=1 [MASS=61158]
rotein yacF OS=Escherichia coli (strain K12) GN=yacF PE=3 SV=2 [MASS=28292]
n termination factor rho OS=Escherichia coli (strain K12) GN=rho PE=1 SV=1 [MASS=47004]
ed RNA polymerase subunit beta OS=Escherichia coli (strain K12) GN=rpoB PE=1 SV=1 [MASS=150632]
hyde-3-phosphate dehydrogenase A OS=Escherichia coli (strain K12) GN=gapA PE=1 SV=2 [MASS=35532]
g protein H-NS OS=Escherichia coli (strain K12) GN=hns PE=1 SV=2 [MASS=15540]
ydrogenase OS=Escherichia coli (strain K12) GN=mdh PE=1 SV=1 [MASS=32337]
acyl-carrier-protein] synthase 1 OS=Escherichia coli (strain K12) GN=fabB PE=1 SV=1 [MASS=42613]
osylformylglycinamidine cyclo-ligase OS=Escherichia coli (strain K12) GN=purM PE=1 SV=3 [MASS=36854]
ranscriptional regulator iscR OS=Escherichia coli (strain K12) GN=iscR PE=1 SV=1 [MASS=17337]
osylaminoimidazole-succinocarboxamide synthase OS=Escherichia coli (strain K12) GN=purC PE=1 SV=1 [M
tress protein D OS=Escherichia coli (strain K12) GN=uspD PE=2 SV=1 [MASS=16293]
-4-phosphate dehydrogenase OS=Escherichia coli (strain K12) GN=epd PE=1 SV=2 [MASS=37299]
phosphate dehydrogenase [NAD(P)+] OS=Escherichia coli (strain K12) GN=gpsA PE=3 SV=1 [MASS=36362]
or OS=Escherichia coli (strain K12) GN=tig PE=1 SV=1 [MASS=48193]
charide biosynthesis protein rffA OS=Escherichia coli (strain K12) GN=rffA PE=3 SV=2 [MASS=41901]
topological specificity factor OS=Escherichia coli (strain K12) GN=minE PE=1 SV=1 [MASS=10235]
-carrier-protein] reductase [NADH] OS=Escherichia coli (strain K12) GN=fabI PE=1 SV=2 [MASS=27864]
tress protein F OS=Escherichia coli (strain K12) GN=uspF PE=1 SV=2 [MASS=16017]
ein OS=Escherichia coli (strain K12) GN=usg PE=1 SV=1 [MASS=36364]
se-1-phosphate uridylyltransferase OS=Escherichia coli (strain K12) GN=galF PE=1 SV=1 [MASS=32829]
horibosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase OS=Escheri
1-semialdehyde 2,1-aminomutase OS=Escherichia coli (strain K12) GN=hemL PE=1 SV=2 [MASS=45366]
pecific phosphotransferase enzyme IIA component OS=Escherichia coli (strain K12) GN=gatA PE=4 SV=1 [M
horibosyltransferase OS=Escherichia coli (strain K12) GN=hisG PE=1 SV=1 [MASS=33367]
olpyruvate-protein phosphotransferase OS=Escherichia coli (strain K12) GN=ptsI PE=1 SV=1 [MASS=63562]
-phosphate synthase small chain OS=Escherichia coli (strain K12) GN=carA PE=1 SV=1 [MASS=41431]
ne initiation inhibitor OS=Escherichia coli (strain K12) GN=iciA PE=1 SV=1 [MASS=33472]
ater dikinase OS=Escherichia coli (strain K12) GN=selD PE=1 SV=1 [MASS=36687]
xylase OS=Escherichia coli (strain K12) GN=accC PE=1 SV=2 [MASS=49321]

hain-amino-acid aminotransferase OS=Escherichia coli (strain K12) GN=ilvE PE=1 SV=2 [MASS=34094]
pressor OS=Escherichia coli (strain K12) GN=fruR PE=1 SV=1 [MASS=37999]
otease sohB OS=Escherichia coli (strain K12) GN=sohB PE=1 SV=1 [MASS=39366]
nal protein L5 OS=Escherichia coli (strain K12) GN=rplE PE=1 SV=2 [MASS=20302]
synthetase alpha subunit OS=Escherichia coli (strain K12) GN=glyQ PE=1 SV=2 [MASS=34774]
cerate kinase OS=Escherichia coli (strain K12) GN=pgk PE=1 SV=2 [MASS=41118]
ase OS=Escherichia coli (strain K12) GN=lipA PE=1 SV=1 [MASS=36072]
uvate aminotransferase OS=Escherichia coli (strain K12) GN=avtA PE=3 SV=3 [MASS=46711]
dent Clp protease ATP-binding subunit clpX OS=Escherichia coli (strain K12) GN=clpX PE=1 SV=2 [MASS=463
rized HTH-type transcriptional regulator yciT OS=Escherichia coli (strain K12) GN=yciT PE=4 SV=1 [MASS=27
l aspartokinase/homoserine dehydrogenase 1 OS=Escherichia coli (strain K12) GN=thrA PE=1 SV=2 [MASS=
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A ligase [ADP-forming] subunit beta OS=Escherichia coli (strain K12) GN=sucC PE=1 SV=1 [MASS=41393]
D OS=Escherichia coli (strain K12) GN=nagD PE=1 SV=1 [MASS=27163]
synthase OS=Escherichia coli (strain K12) GN=metH PE=1 SV=5 [MASS=135997]
3-methylbut-2-en-1-yl diphosphate synthase OS=Escherichia coli (strain K12) GN=ispG PE=1 SV=1 [MASS=4
itive aspartokinase 3 OS=Escherichia coli (strain K12) GN=lysC PE=1 SV=2 [MASS=48532]
protein ftsZ OS=Escherichia coli (strain K12) GN=ftsZ PE=1 SV=1 [MASS=40324]
inase 1 OS=Escherichia coli (strain K12) GN=glxK PE=1 SV=1 [MASS=38734]
A OS=Escherichia coli (strain K12) GN=recA PE=1 SV=2 [MASS=37973]
NA synthetase OS=Escherichia coli (strain K12) GN=aspS PE=1 SV=1 [MASS=65913]
g protein lepA OS=Escherichia coli (strain K12) GN=lepA PE=1 SV=1 [MASS=66570]
thylpyrimidine/phosphomethylpyrimidine kinase OS=Escherichia coli (strain K12) GN=thiD PE=1 SV=1 [MAS
e kinase OS=Escherichia coli (strain K12) GN=thrB PE=1 SV=2 [MASS=33624]
nal protein S7 OS=Escherichia coli (strain K12) GN=rpsG PE=1 SV=3 [MASS=20019]
ynthase OS=Escherichia coli (strain K12) GN=thrC PE=1 SV=1 [MASS=47114]
synthase beta chain OS=Escherichia coli (strain K12) GN=trpB PE=1 SV=2 [MASS=42983]
e regulation protein OS=Escherichia coli (strain K12) GN=fur PE=1 SV=1 [MASS=16795]
factor Ts OS=Escherichia coli (strain K12) GN=tsf PE=1 SV=2 [MASS=30423]
uinate synthase OS=Escherichia coli (strain K12) GN=aroB PE=3 SV=1 [MASS=38881]
racemase OS=Escherichia coli (strain K12) GN=murI PE=1 SV=2 [MASS=31002]
sulfurase OS=Escherichia coli (strain K12) GN=iscS PE=1 SV=1 [MASS=45089]
rized aminotransferase yfbQ OS=Escherichia coli (strain K12) GN=yfbQ PE=1 SV=1 [MASS=45517]
onophosphate kinase OS=Escherichia coli (strain K12) GN=thiL PE=3 SV=1 [MASS=35071]
e synthase isozyme 1 large subunit OS=Escherichia coli (strain K12) GN=ilvB PE=1 SV=1 [MASS=60441]
tylglucosamine 1-carboxyvinyltransferase OS=Escherichia coli (strain K12) GN=murA PE=1 SV=1 [MASS=448
/menaquinone biosynthesis methyltransferase ubiE OS=Escherichia coli (strain K12) GN=ubiE PE=1 SV=1 [
ase OS=Escherichia coli (strain K12) GN=ackA PE=1 SV=1 [MASS=43290]
nal protein S10 OS=Escherichia coli (strain K12) GN=rpsJ PE=1 SV=1 [MASS=11736]
se-1-phosphate uridylyltransferase OS=Escherichia coli (strain K12) GN=galU PE=1 SV=2 [MASS=32942]
inase OS=Escherichia coli (strain K12) GN=adk PE=1 SV=1 [MASS=23586]
acyl-carrier-protein] synthase 2 OS=Escherichia coli (strain K12) GN=fabF PE=1 SV=2 [MASS=43046]
ehydrogenase flavoprotein subunit OS=Escherichia coli (strain K12) GN=sdhA PE=1 SV=1 [MASS=64422]
osylglycinamide formyltransferase 2 OS=Escherichia coli (strain K12) GN=purT PE=1 SV=3 [MASS=42434]
e synthase isozyme 3 large subunit OS=Escherichia coli (strain K12) GN=ilvI PE=1 SV=2 [MASS=62984]
ylthiazole kinase OS=Escherichia coli (strain K12) GN=thiM PE=3 SV=1 [MASS=27339]
lenetetrahydrofolate reductase OS=Escherichia coli (strain K12) GN=metF PE=1 SV=1 [MASS=33103]
rized GTP-binding protein yjiA OS=Escherichia coli (strain K12) GN=yjiA PE=1 SV=3 [MASS=35660]

g protein typA/BipA OS=Escherichia coli (strain K12) GN=typA PE=1 SV=2 [MASS=67355]
se OS=Escherichia coli (strain K12) GN=pyrG PE=1 SV=2 [MASS=60374]
phoribosyltransferase OS=Escherichia coli (strain K12) GN=upp PE=1 SV=1 [MASS=22533]
acid dehydratase OS=Escherichia coli (strain K12) GN=ilvD PE=1 SV=5 [MASS=65532]
l-tRNA synthetase OS=Escherichia coli (strain K12) GN=asnS PE=1 SV=2 [MASS=52570]
synthetase OS=Escherichia coli (strain K12) GN=proS PE=1 SV=4 [MASS=63693]
synthetase B [glutamine-hydrolyzing] OS=Escherichia coli (strain K12) GN=asnB PE=1 SV=3 [MASS=62659]
roxymethyltransferase OS=Escherichia coli (strain K12) GN=glyA PE=1 SV=1 [MASS=45317]
nthase A OS=Escherichia coli (strain K12) GN=cysK PE=1 SV=2 [MASS=34490]
l protein folD OS=Escherichia coli (strain K12) GN=folD PE=1 SV=4 [MASS=31044]
=Escherichia coli (strain K12) GN=eno PE=1 SV=2 [MASS=45655]
c arginine decarboxylase OS=Escherichia coli (strain K12) GN=speA PE=1 SV=2 [MASS=73898]
l protein hldE OS=Escherichia coli (strain K12) GN=hldE PE=1 SV=1 [MASS=51051]
methionine synthase OS=Escherichia coli (strain K12) GN=metK PE=1 SV=2 [MASS=41952]
rized protein yigB OS=Escherichia coli (strain K12) GN=yigB PE=4 SV=1 [MASS=27122]
cinate synthetase OS=Escherichia coli (strain K12) GN=purA PE=1 SV=2 [MASS=47345]
rized ABC transporter ATP-binding protein yjjK OS=Escherichia coli (strain K12) GN=yjjK PE=1 SV=2 [MASS=
S=Escherichia coli (strain K12) GN=tyrA PE=1 SV=1 [MASS=42043]
synthetase OS=Escherichia coli (strain K12) GN=serS PE=1 SV=1 [MASS=48414]
6-bisphosphatase class 2 OS=Escherichia coli (strain K12) GN=glpX PE=1 SV=1 [MASS=35852]
ructokinase isozyme 1 OS=Escherichia coli (strain K12) GN=pfkA PE=1 SV=1 [MASS=34842]
peronin OS=Escherichia coli (strain K12) GN=hslO PE=1 SV=1 [MASS=32534]
RNA synthetase OS=Escherichia coli (strain K12) GN=thrS PE=1 SV=1 [MASS=74014]
nzyme A synthetase OS=Escherichia coli (strain K12) GN=acs PE=1 SV=2 [MASS=72094]

ASS=26995]

chia coli (strain K12) GN=hisA PE=1 SV=2 [MASS=26033]

ASS=16907]

56]
7603]
89120]

684]

S=28634]

18]
ASS=28073]

62443]