

locus	log2ratio	lowerCI	upperCI	quantified_	description
sp_P39274_YJDJ_ECOLI	6.9	6.5	7	8	Uncharacte
sp_P77293_GTRB_ECOLI	4.8	4	5.6	2	Bactopreno
sp_P76539_YPEA_ECOLI	3.6	2.4	7	2	Acetyltrans
sp_P00579_RPOD_ECOLI	3.2	2.6	3.9	4	RNA polym
REVERSE_sp_POA6A0_UBIB_ECOLI	3	1.7	7	2	Reverse sec
sp_POAA43_RSUA_ECOLI	3	2.4	3.7	5	Ribosomal s
sp_P69913_CSRA_ECOLI	3	2.3	3.6	3	Carbon stor
sp_POA6X3_HFQ_ECOLI	2.6	2.1	3	10	Protein hfq
sp_POA7Z4_RPOA_ECOLI	2.6	2.3	3	12	DNA-direct
sp_POAFF6_NUSA_ECOLI	2.4	1.9	3	11	Transcripti
sp_POA8T7_RPOC_ECOLI	2.3	2.1	2.5	47	DNA-direct
sp_POA9K9_SLYD_ECOLI	2.3	1.9	2.7	9	FKBP-type β
sp_POA887_UBIE_ECOLI	2.1	1.3	2.9	2	Ubiquinone
sp_P21499_RNR_ECOLI	2	1.3	2.8	6	Ribonuclea
sp_P25714_OXAA_ECOLI	2	1.1	3.1	2	Inner mem
sp_P07001_PNTA_ECOLI	1.7	1.2	2.3	6	NAD(P) trar
sp_POABA0_ATPF_ECOLI	1.6	0.9	2.4	3	ATP syntha
sp_P02359_RS7_ECOLI	1.5	1.2	1.9	15	30S riboson
sp_POADZ7_YAJC_ECOLI	1.5	0.7	2.3	2	UPF0092 m
sp_P21513_RNE_ECOLI	1.5	0.8	2.3	4	Ribonuclea
sp_POA7S9_RS13_ECOLI	1.4	0.7	2.2	3	30S riboson
sp_POA8V2_RPOB_ECOLI	1.4	1.1	1.6	45	DNA-direct
sp_P60438_RL3_ECOLI	1.4	0.6	2.1	6	50S riboson
sp_POA7L3_RL20_ECOLI	1.3	0.2	2.6	2	50S riboson
sp_POABB0_ATPA_ECOLI	1.3	0.9	1.7	13	ATP syntha
sp_POABB4_ATPB_ECOLI	1.3	1	1.6	18	ATP syntha
sp_P28635_METQ_ECOLI	1.3	1	1.6	17	D-methioni
sp_P0C0S1_MSCS_ECOLI	1.2	0.6	1.7	5	Small-condi
sp_POAAI3_FTSH_ECOLI	1.1	0.1	2.1	2	Cell division
sp_POAC41_DHSA_ECOLI	1.1	0.2	2.1	2	Succinate d
sp_POA7K2_RL7_ECOLI	1	0.2	1.8	3	50S riboson
sp_POA7T3_RS16_ECOLI	1	0.4	1.5	5	30S riboson
sp_P60422_RL2_ECOLI	0.7	-0.1	1.6	3	50S riboson
sp_POADZ4_RS15_ECOLI	0.6	0	1.3	4	30S riboson
sp_POA7W1_RS5_ECOLI	0.4	-0.4	1.2	2	30S riboson
sp_POADY7_RL16_ECOLI	0.4	-0.5	1.4	2	50S riboson
sp_P25526_GABD_ECOLI	0.4	-0.6	1.5	2	Succinate-s
sp_POA7V8_RS4_ECOLI	0.2	-0.1	0.6	13	30S riboson
sp_P67910_HLDD_ECOLI	0.2	-0.1	0.4	30	ADP-L-glyce
sp_POA7L0_RL1_ECOLI	0.1	-0.2	0.5	13	50S riboson
sp_POAG55_RL6_ECOLI	0	-0.6	0.7	5	50S riboson
sp_POAG67_RS1_ECOLI	0	-0.3	0.3	31	30S riboson
sp_POAGK8_ISCR_ECOLI	-0.2	-1.2	0.9	2	HTH-type tr
sp_P04968_THD1_ECOLI	-0.5	-1.5	0.5	2	Threonine c
sp_POA7R9_RS11_ECOLI	-0.5	-1.4	0.2	3	30S riboson
sp_POAA10_RL13_ECOLI	-0.5	-1.3	0.3	4	50S riboson
sp_POABD8_BCCP_ECOLI	-0.5	-1	-0.1	8	Biotin carb

sp_POA8F0_UPP_ECOLI	-0.6	-1.5	0.2	2 Uracil phosj
sp_POAAI5_FABF_ECOLI	-0.6	-1.2	0.1	3 3-oxoacyl-[ε
sp_P06996_OMPC_ECOLI	-0.7	-1.5	0.1	2 Outer mem
sp_POA910_OMPA_ECOLI	-0.7	-2.1	0.6	2 Outer mem
sp_P62399_RL5_ECOLI	-0.7	-1.3	-0.1	5 50S riboson
sp_P76423_THIM_ECOLI	-0.7	-1.2	-0.2	7 Hydroxyeth
sp_POA6Y8_DNAK_ECOLI	-0.8	-1.7	0.2	2 Chaperone
sp_P11458_NADA_ECOLI	-0.8	-1.6	0	4 Quinolinate
sp_P69783_PTGA_ECOLI	-0.8	-1.6	0	2 Glucose-spe
sp_POAF24_NAGD_ECOLI	-1	-1.4	-0.6	9 Protein nag
sp_POA7J7_RL11_ECOLI	-1.1	-1.8	-0.4	3 50S riboson
sp_POA7V3_RS3_ECOLI	-1.1	-1.4	-0.7	13 30S riboson
sp_POABK5_CYSK_ECOLI	-1.1	-1.8	-0.2	6 Cysteine syi
sp_P00934_THRC_ECOLI	-1.2	-2.5	-0.3	4 Threonine s
sp_POA7D7_PUR7_ECOLI	-1.2	-2	-0.4	2 Phosphorib
sp_POA8C1_YBJQ_ECOLI	-1.2	-1.9	-0.6	3 UPF0145 pr
sp_POA9Q1_ARCA_ECOLI	-1.2	-1.9	-0.4	5 Aerobic resj
sp_POAEJ6_EUTB_ECOLI	-1.2	-1.8	-0.5	4 Ethanolami
sp_POA698_UVRA_ECOLI	-1.3	-1.8	-0.8	8 UvrABC syst
sp_POAEZ3_MIND_ECOLI	-1.3	-2.6	-0.2	2 Septum site
sp_P23538_PPSA_ECOLI	-1.5	-1.8	-1.1	13 Phosphoeni
sp_POA7R5_RS10_ECOLI	-1.6	-2	-1.2	13 30S riboson
sp_POAAV4_YBGJ_ECOLI	-1.6	-2.6	-0.5	2 Uncharacte
sp_P12758_UDP_ECOLI	-1.6	-7	-0.1	3 Uridine pho
sp_P60595_HIS5_ECOLI	-1.6	-2.6	-0.7	3 Imidazole g
sp_P60723_RL4_ECOLI	-1.6	-2	-1.1	8 50S riboson
sp_P62620_ISPG_ECOLI	-1.6	-2.3	-1	5 4-hydroxy-ε
sp_P77444_SUFS_ECOLI	-1.6	-2.5	-0.8	2 Cysteine de
sp_P08178_PUR5_ECOLI	-1.7	-2.2	-1.1	5 Phosphorib
sp_P25665_METE_ECOLI	-1.8	-2.2	-1.4	14 5-methyltet
sp_P30139_THIG_ECOLI	-1.8	-7	-0.8	2 Thiazole syr
sp_P00968_CARB_ECOLI	-1.9	-2.1	-1.7	32 Carbamoyl-
sp_POA879_TRPB_ECOLI	-1.9	-2.3	-1.5	22 Tryptophan
sp_P68919_RL25_ECOLI	-1.9	-2.6	-1.2	4 50S riboson
sp_POA6M8_EFG_ECOLI	-2	-2.4	-1.6	11 Elongation i
sp_P42641_OBG_ECOLI	-2	-7	-1.1	2 GTPase obg
sp_P76658_HLDE_ECOLI	-2	-7	-0.1	2 Bifunctiona
sp_POA6F1_CARA_ECOLI	-2.1	-3	-1	3 Carbamoyl-
sp_POAG48_RL21_ECOLI	-2.1	-2.9	-0.9	3 50S riboson
sp_P08244_PYRF_ECOLI	-2.2	-2.7	-1.6	6 Orotidine 5'
sp_POAEJ2_ENTC_ECOLI	-2.2	-2.8	-1.6	6 Isochorisma
sp_P60757_HIS1_ECOLI	-2.2	-2.9	-1.6	3 ATP phosph
sp_POA734_MINE_ECOLI	-2.3	-2.9	-1.8	5 Cell division
sp_POA817_METK_ECOLI	-2.4	-2.7	-2.2	40 S-adenosylr
sp_POADZ0_RL23_ECOLI	-2.4	-3.2	-1.7	2 50S riboson
sp_POA7K6_RL19_ECOLI	-2.5	-3.2	-1.7	4 50S riboson
sp_POAEP3_GALU_ECOLI	-2.8	-3.4	-2.3	5 UTP--glucos
sp_POA6P9_ENO_ECOLI	-2.9	-3.6	-2.4	4 Enolase OS-

sp_P0A9Q7_ADHE_ECOLI	-2.9	-4	-1.8	2 Aldehyde-a
sp_P0AG30_RHO_ECOLI	-3.3	-4.1	-2.5	3 Transcriptic
sp_P08779_K1C16_HUMAN	-3.4	-7	-2.8	4 Keratin, typ
sp_P0A6B7_ISCS_ECOLI	-3.6	-4.7	-2.2	2 Cysteine de
sp_P21170_SPEA_ECOLI	-3.6	-4.1	-3.1	10 Biosyntheti
sp_P02533_K1C14_HUMAN	-3.7	-4.8	-2.8	4 Keratin, typ
sp_P0A850_TIG_ECOLI	-3.7	-4.8	-2.6	3 Trigger fact
sp_P0A825_GLYA_ECOLI	-4.1	-4.5	-3.7	13 Serine hydr
REVERSE_sp_P19778_YI23_ECOLX	-5.1	-5.8	-4.6	16 Reverse sec
sp_P35908_K22E_HUMAN	-5.1	-6.7	-4.3	12 Keratin, typ
sp_P13645_K1C10_HUMAN	-5.3	-5.9	-4.5	27 Keratin, typ
sp_P0A6Y5_HSLO_ECOLI	-5.5	-6	-5.1	15 33 kDa chaç
sp_P00761_TRYP_PIG	-5.6	-5.9	-5.3	59 Trypsin OS=
sp_P35527_K1C9_HUMAN	-5.9	-6.3	-5.5	28 Keratin, typ
sp_P04264_K2C1_HUMAN	-6	-6.3	-5.7	51 Keratin, typ
sp_P67762_YHBP_ECOLI	-6	-6.8	-4.9	3 UPF0306 pr
sp_P16659_SYP_ECOLI	-7	-7	-3.1	6 Prolyl-tRNA

urized protein yjdJ OS=Escherichia coli (strain K12) GN=yjdJ PE=4 SV=1 [MASS=10468]
glucosyl transferase homolog from prophage CPS-53 OS=Escherichia coli (strain K12) GN=yfdH PE=1 SV=1
ferase ypeA OS=Escherichia coli (strain K12) GN=ypeA PE=3 SV=2 [MASS=16312]
erase sigma factor rpoD OS=Escherichia coli (strain K12) GN=rpoD PE=1 SV=2 [MASS=70263]
quence, was Probable ubiquinone biosynthesis protein ubiB OS=Escherichia coli (strain K12) GN=ubiB PE=1
small subunit pseudouridine synthase A OS=Escherichia coli (strain K12) GN=rsuA PE=1 SV=1 [MASS=25865]
rage regulator OS=Escherichia coli (strain K12) GN=csrA PE=1 SV=1 [MASS=6856]
OS=Escherichia coli (strain K12) GN=hfq PE=1 SV=2 [MASS=11166]
ed RNA polymerase subunit alpha OS=Escherichia coli (strain K12) GN=rpoA PE=1 SV=1 [MASS=36512]
on elongation protein nusA OS=Escherichia coli (strain K12) GN=nusA PE=1 SV=1 [MASS=54871]
ed RNA polymerase subunit beta' OS=Escherichia coli (strain K12) GN=rpoC PE=1 SV=1 [MASS=155160]
eptidyl-prolyl cis-trans isomerase slyD OS=Escherichia coli (strain K12) GN=slyD PE=1 SV=1 [MASS=20853]
y/menaquinone biosynthesis methyltransferase ubiE OS=Escherichia coli (strain K12) GN=ubiE PE=1 SV=1 [M
se R OS=Escherichia coli (strain K12) GN=rnr PE=1 SV=2 [MASS=92109]
brane protein oxaA OS=Escherichia coli (strain K12) GN=oxaA PE=1 SV=2 [MASS=61526]
rshydrogenase subunit alpha OS=Escherichia coli (strain K12) GN=pntA PE=1 SV=2 [MASS=54623]
se subunit b OS=Escherichia coli (strain K12) GN=atpF PE=1 SV=1 [MASS=17264]
nal protein S7 OS=Escherichia coli (strain K12) GN=rpsG PE=1 SV=3 [MASS=20019]
embrane protein yajC OS=Escherichia coli (strain K12) GN=yajC PE=1 SV=1 [MASS=11887]
se E OS=Escherichia coli (strain K12) GN=rne PE=1 SV=6 [MASS=118197]
nal protein S13 OS=Escherichia coli (strain K12) GN=rpsM PE=1 SV=2 [MASS=13099]
ed RNA polymerase subunit beta OS=Escherichia coli (strain K12) GN=rpoB PE=1 SV=1 [MASS=150632]
nal protein L3 OS=Escherichia coli (strain K12) GN=rpIC PE=1 SV=1 [MASS=22244]
nal protein L20 OS=Escherichia coli (strain K12) GN=rpIT PE=1 SV=2 [MASS=13497]
se subunit alpha OS=Escherichia coli (strain K12) GN=atpA PE=1 SV=1 [MASS=55222]
se subunit beta OS=Escherichia coli (strain K12) GN=atpD PE=1 SV=2 [MASS=50325]
ne-binding lipoprotein metQ OS=Escherichia coli (strain K12) GN=metQ PE=1 SV=2 [MASS=29432]
uctance mechanosensitive channel OS=Escherichia coli (strain K12) GN=mscS PE=1 SV=1 [MASS=30896]
r protease ftsH OS=Escherichia coli (strain K12) GN=ftsH PE=1 SV=1 [MASS=70708]
ehydrogenase flavoprotein subunit OS=Escherichia coli (strain K12) GN=sdhA PE=1 SV=1 [MASS=64422]
nal protein L7/L12 OS=Escherichia coli (strain K12) GN=rpIL PE=1 SV=2 [MASS=12295]
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nal protein S4 OS=Escherichia coli (strain K12) GN=rpsD PE=1 SV=2 [MASS=23469]
ero-D-manno-heptose-6-epimerase OS=Escherichia coli (strain K12) GN=hldD PE=1 SV=1 [MASS=34893]
nal protein L1 OS=Escherichia coli (strain K12) GN=rpIA PE=1 SV=2 [MASS=24730]
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oxyl carrier protein of acetyl-CoA carboxylase OS=Escherichia coli (strain K12) GN=accB PE=1 SV=1 [MASS=1

phoribosyltransferase OS=Escherichia coli (strain K12) GN=upp PE=1 SV=1 [MASS=22533]
acyl-carrier-protein] synthase 2 OS=Escherichia coli (strain K12) GN=fabF PE=1 SV=2 [MASS=43046]
lbrane protein C OS=Escherichia coli (strain K12) GN=ompC PE=1 SV=1 [MASS=40368]
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ylthiazole kinase OS=Escherichia coli (strain K12) GN=thiM PE=3 SV=1 [MASS=27339]
protein dnaK OS=Escherichia coli (strain K12) GN=dnaK PE=1 SV=2 [MASS=69115]
 synthase A OS=Escherichia coli (strain K12) GN=nadA PE=1 SV=3 [MASS=38241]
pecific phosphotransferase enzyme IIA component OS=Escherichia coli (strain K12) GN=crr PE=1 SV=2 [MASS
D OS=Escherichia coli (strain K12) GN=nagD PE=1 SV=1 [MASS=27163]
nal protein L11 OS=Escherichia coli (strain K12) GN=rpLK PE=1 SV=2 [MASS=14875]
nal protein S3 OS=Escherichia coli (strain K12) GN=rpsC PE=1 SV=2 [MASS=25983]
nthase A OS=Escherichia coli (strain K12) GN=cysK PE=1 SV=2 [MASS=34490]
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osylaminoimidazole-succinocarboxamide synthase OS=Escherichia coli (strain K12) GN=purC PE=1 SV=1 [M
rotein ybjQ OS=Escherichia coli (strain K12) GN=ybjQ PE=1 SV=1 [MASS=11437]
puration control protein ArcA OS=Escherichia coli (strain K12) GN=arcA PE=1 SV=1 [MASS=27292]
ne ammonia-lyase heavy chain OS=Escherichia coli (strain K12) GN=eutB PE=1 SV=1 [MASS=49403]
tem protein A OS=Escherichia coli (strain K12) GN=uvrA PE=1 SV=1 [MASS=103868]
e-determining protein minD OS=Escherichia coli (strain K12) GN=minD PE=1 SV=2 [MASS=29614]
olpyruvate synthase OS=Escherichia coli (strain K12) GN=ppsA PE=1 SV=5 [MASS=87435]
nal protein S10 OS=Escherichia coli (strain K12) GN=rpsJ PE=1 SV=1 [MASS=11736]
rized protein ybgJ OS=Escherichia coli (strain K12) GN=ybgJ PE=4 SV=1 [MASS=23947]
osphorylase OS=Escherichia coli (strain K12) GN=udp PE=1 SV=3 [MASS=27159]
lycerol phosphate synthase subunit hisH OS=Escherichia coli (strain K12) GN=hisH PE=1 SV=1 [MASS=2165
nal protein L4 OS=Escherichia coli (strain K12) GN=rpID PE=1 SV=1 [MASS=22087]
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sulfurase OS=Escherichia coli (strain K12) GN=sufS PE=1 SV=1 [MASS=44434]
osylformylglycinamidine cyclo-ligase OS=Escherichia coli (strain K12) GN=purM PE=1 SV=3 [MASS=36854]
trahydropteroyltryglutamate--homocysteine methyltransferase OS=Escherichia coli (strain K12) GN=metE P
nthase OS=Escherichia coli (strain K12) GN=thiG PE=1 SV=3 [MASS=26896]
hosphate synthase large chain OS=Escherichia coli (strain K12) GN=carB PE=1 SV=2 [MASS=117842]
 synthase beta chain OS=Escherichia coli (strain K12) GN=trpB PE=1 SV=2 [MASS=42983]
nal protein L25 OS=Escherichia coli (strain K12) GN=rpLY PE=1 SV=1 [MASS=10693]
factor G OS=Escherichia coli (strain K12) GN=fusA PE=1 SV=2 [MASS=77581]
E/cgtA OS=Escherichia coli (strain K12) GN=obgE PE=1 SV=1 [MASS=43286]
l protein hldE OS=Escherichia coli (strain K12) GN=hldE PE=1 SV=1 [MASS=51051]
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nal protein L21 OS=Escherichia coli (strain K12) GN=rpIU PE=1 SV=1 [MASS=11564]
-phosphate decarboxylase OS=Escherichia coli (strain K12) GN=pyrF PE=1 SV=1 [MASS=26350]
ate synthase entC OS=Escherichia coli (strain K12) GN=entC PE=1 SV=1 [MASS=42932]
oribosyltransferase OS=Escherichia coli (strain K12) GN=hisG PE=1 SV=1 [MASS=33367]
 topological specificity factor OS=Escherichia coli (strain K12) GN=minE PE=1 SV=1 [MASS=10235]
methionine synthase OS=Escherichia coli (strain K12) GN=metK PE=1 SV=2 [MASS=41952]
nal protein L23 OS=Escherichia coli (strain K12) GN=rpIW PE=1 SV=1 [MASS=11199]
nal protein L19 OS=Escherichia coli (strain K12) GN=rpIS PE=1 SV=2 [MASS=13133]
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lcohol dehydrogenase OS=Escherichia coli (strain K12) GN=adhE PE=1 SV=2 [MASS=96127]
on termination factor rho OS=Escherichia coli (strain K12) GN=rho PE=1 SV=1 [MASS=47004]
ie I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 [MASS=51268]
sulfurase OS=Escherichia coli (strain K12) GN=iscS PE=1 SV=1 [MASS=45089]
c arginine decarboxylase OS=Escherichia coli (strain K12) GN=speA PE=1 SV=2 [MASS=73898]
ie I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 [MASS=51561]
or OS=Escherichia coli (strain K12) GN=tig PE=1 SV=1 [MASS=48193]
oxymethyltransferase OS=Escherichia coli (strain K12) GN=glyA PE=1 SV=1 [MASS=45317]
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ie II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 [MASS=65433]
ie I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 [MASS=58827]
peronin OS=Escherichia coli (strain K12) GN=hsIO PE=1 SV=1 [MASS=32534]
-Sus scrofa PE=1 SV=1 [MASS=24409]
ie I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 [MASS=62064]
ie II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 [MASS=66039]
rotein yhbP OS=Escherichia coli (strain K12) GN=yhbP PE=3 SV=1 [MASS=16776]
c synthetase OS=Escherichia coli (strain K12) GN=proS PE=1 SV=4 [MASS=63693]

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E=1 SV=6 [MASS=84674]

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