

| locus | log2ratio | lowerCI | upperCI | quantified_ | description |
|----------------------|-----------|---------|---------|-------------|--------------|
| sp_P67762_YHBP_ECOLI | 4.3 | 3.6 | 4.9 | 3 | UPF0306 pr |
| sp_POA6X7_IHFA_ECOLI | 3.6 | 2.8 | 7 | 2 | Integration |
| sp_P21499_RNR_ECOLI | 3.3 | 2.9 | 3.8 | 15 | Ribonucleas |
| sp_P69913_CSRA_ECOLI | 3.1 | -0.7 | 4.2 | 2 | Carbon stor |
| sp_POA7L0_RL1_ECOLI | 3 | 2.6 | 3.5 | 19 | 50S riboson |
| sp_POA8R0_RRAA_ECOLI | 2.8 | 1.7 | 7 | 2 | Regulator o |
| sp_POAEJ2_ENTC_ECOLI | 2.8 | 2.2 | 3.6 | 5 | Isochorisma |
| sp_POA6X3_HFQ_ECOLI | 2.3 | 1.8 | 2.8 | 5 | Protein hfq |
| sp_POA7V8_RS4_ECOLI | 2.1 | 1.7 | 2.5 | 9 | 30S riboson |
| sp_POAG67_RS1_ECOLI | 2.1 | 1.8 | 2.4 | 30 | 30S riboson |
| sp_P37765_RLUB_ECOLI | 2.1 | 1.4 | 7 | 3 | Ribosomal l |
| sp_P76550_YFFS_ECOLI | 1.8 | 0.2 | 7 | 2 | Uncharacte |
| sp_PO0888_AROF_ECOLI | 1.7 | 0.7 | 3 | 2 | Phospho-2- |
| sp_POADZ4_RS15_ECOLI | 1.6 | 1 | 2.2 | 4 | 30S riboson |
| sp_POACF0_DBHA_ECOLI | 1.5 | 1 | 2.2 | 6 | DNA-bindin |
| sp_POA8C1_YBJQ_ECOLI | 0.9 | 0 | 1.8 | 3 | UPF0145 pr |
| sp_POAGJ5_YFIF_ECOLI | 0.9 | -0.3 | 2.3 | 2 | Uncharacte |
| sp_POA7V3_RS3_ECOLI | 0.7 | 0.1 | 1.4 | 4 | 30S riboson |
| sp_POA7W1_RS5_ECOLI | 0.7 | 0.3 | 1.2 | 12 | 30S riboson |
| sp_POA6R3_FIS_ECOLI | 0.6 | -0.3 | 1.5 | 2 | DNA-bindin |
| sp_POA7S9_RS13_ECOLI | 0.5 | 0 | 0.9 | 9 | 30S riboson |
| sp_P10908_UGPQ_ECOLI | 0.5 | -0.5 | 1.4 | 2 | Glyceropho |
| sp_POA6B7_ISCS_ECOLI | 0.4 | -0.4 | 1.3 | 5 | Cysteine de |
| sp_P60422_RL2_ECOLI | 0.4 | -0.8 | 1.6 | 2 | 50S riboson |
| sp_POA7W7_RS8_ECOLI | 0.3 | -0.9 | 1.5 | 2 | 30S riboson |
| sp_POA6A3_ACKA_ECOLI | 0.2 | -0.6 | 1.1 | 2 | Acetate kin |
| sp_P60723_RL4_ECOLI | 0.2 | -0.3 | 0.7 | 9 | 50S riboson |
| sp_P02359_RS7_ECOLI | 0 | -0.5 | 0.7 | 8 | 30S riboson |
| sp_POA707_IF3_ECOLI | 0 | -0.7 | 0.7 | 3 | Translation |
| sp_POA7R1_RL9_ECOLI | 0 | -0.8 | 0.7 | 3 | 50S riboson |
| sp_P02413_RL15_ECOLI | -0.1 | -1.4 | 0.7 | 4 | 50S riboson |
| sp_POA7Z4_RPOA_ECOLI | -0.2 | -1 | 0.7 | 2 | DNA-directe |
| sp_POAG48_RL21_ECOLI | -0.2 | -1 | 0.8 | 4 | 50S riboson |
| sp_POAG55_RL6_ECOLI | -0.2 | -0.9 | 0.5 | 7 | 50S riboson |
| sp_POA9K9_SLYD_ECOLI | -0.3 | -1.2 | 0.5 | 3 | FKBP-type p |
| sp_P76539_YPEA_ECOLI | -0.3 | -1.2 | 0.6 | 2 | Acetyltransi |
| sp_POA7L3_RL20_ECOLI | -0.4 | -0.9 | 0.1 | 6 | 50S riboson |
| sp_POABD8_BCCP_ECOLI | -0.4 | -0.8 | 0.1 | 7 | Biotin carbc |
| sp_POAGK8_ISCR_ECOLI | -0.4 | -1.5 | 0.7 | 4 | HTH-type tr |
| sp_POABK5_CYSK_ECOLI | -0.5 | -1 | 0 | 6 | Cysteine sy |
| sp_P67910_HLDD_ECOLI | -0.5 | -0.8 | -0.2 | 19 | ADP-L-glyce |
| sp_P76423_THIM_ECOLI | -0.5 | -1.1 | 0.2 | 4 | Hydroxyeth |
| sp_POA6C8_ARGB_ECOLI | -0.6 | -1.3 | 0 | 5 | Acetylgluta |
| sp_POA7K2_RL7_ECOLI | -0.6 | -1.5 | 0.3 | 2 | 50S riboson |
| sp_POADY7_RL16_ECOLI | -0.6 | -1.3 | 0.1 | 4 | 50S riboson |
| sp_POAFG0_NUSG_ECOLI | -0.6 | -1.2 | 0.1 | 3 | Transcriptic |
| sp_POA7R9_RS11_ECOLI | -0.7 | -1.1 | -0.2 | 12 | 30S riboson |

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|----------------------|------|------|------|-----------------|
| sp_POA9Q1_ARCA_ECOLI | -0.7 | -1.4 | -0.1 | 6 Aerobic res |
| sp_P60624_RL24_ECOLI | -0.7 | -1.7 | 0.3 | 2 50S riboson |
| sp_POA910_OMPA_ECOLI | -0.9 | -1.8 | 0.1 | 2 Outer mem |
| sp_P00959_SYM_ECOLI | -1 | -2 | -0.2 | 3 Methionyl-t |
| sp_POA7T3_RS16_ECOLI | -1 | -1.6 | -0.3 | 3 30S riboson |
| sp_P62620_ISPG_ECOLI | -1 | -1.9 | -0.1 | 2 4-hydroxy-3 |
| sp_POAED0_USPA_ECOLI | -1.1 | -1.8 | -0.5 | 3 Universal st |
| sp_POA7J3_RL10_ECOLI | -1.2 | -2.1 | -0.3 | 2 50S riboson |
| sp_P60595_HIS5_ECOLI | -1.2 | -2.2 | -0.3 | 3 Imidazole g |
| sp_P06996_OMPC_ECOLI | -1.4 | -2.1 | -0.6 | 3 Outer mem |
| sp_POA7X3_RS9_ECOLI | -1.4 | -2 | -0.8 | 5 30S riboson |
| sp_P18196_MINC_ECOLI | -1.4 | -2.2 | -0.6 | 2 Septum site |
| sp_POA7J7_RL11_ECOLI | -1.5 | -2.5 | -0.6 | 2 50S riboson |
| sp_POAF24_NAGD_ECOLI | -1.5 | -1.9 | -1.1 | 8 Protein nag |
| sp_P11458_NADA_ECOLI | -1.5 | -2.2 | -0.8 | 3 Quinolinate |
| sp_POA734_MINE_ECOLI | -1.6 | -2.1 | -1.1 | 5 Cell division |
| sp_POABB0_ATPA_ECOLI | -1.6 | -2 | -1.3 | 11 ATP synthas |
| sp_POAG99_SECG_ECOLI | -1.6 | -2.4 | -0.9 | 3 Protein-exp |
| sp_POAAI5_FABF_ECOLI | -1.7 | -2.4 | -1 | 3 3-oxoacyl-[ε |
| sp_POABB4_ATPB_ECOLI | -1.7 | -2 | -1.3 | 16 ATP synthas |
| sp_P60757_HIS1_ECOLI | -1.7 | -2.4 | -1.1 | 4 ATP phosph |
| sp_P68919_RL25_ECOLI | -1.7 | -2.4 | -0.9 | 3 50S riboson |
| sp_P77804_YDGA_ECOLI | -1.7 | -2.5 | -0.9 | 3 Protein ydg |
| sp_P00934_THRC_ECOLI | -1.8 | -2.5 | -1.1 | 3 Threonine s |
| sp_POABA0_ATPF_ECOLI | -1.8 | -2.6 | -1 | 2 ATP synthas |
| sp_POAC41_DHSA_ECOLI | -1.8 | -3.1 | -0.9 | 2 Succinate d |
| sp_POADZ7_YAJC_ECOLI | -1.8 | -2.5 | -1.1 | 3 UPF0092 m |
| sp_POC0S1_MSCS_ECOLI | -1.8 | -2.4 | -1.1 | 4 Small-condu |
| sp_P00968_CARB_ECOLI | -1.9 | -2.2 | -1.6 | 26 Carbamoyl- |
| sp_P08178_PUR5_ECOLI | -1.9 | -2.4 | -1.5 | 8 Phosphorib |
| sp_POA9M8_PTA_ECOLI | -1.9 | -2.8 | -1 | 2 Phosphate : |
| sp_POA6F5_CH60_ECOLI | -2 | -2.8 | -1.2 | 3 60 kDa chap |
| sp_POAEP3_GALU_ECOLI | -2 | -3.1 | -1.2 | 3 UTP--glucos |
| sp_POA7R5_RS10_ECOLI | -2.1 | -2.5 | -1.7 | 11 30S riboson |
| sp_POAA10_RL13_ECOLI | -2.1 | -3.1 | -1.3 | 3 50S riboson |
| sp_POAEI4_RIMO_ECOLI | -2.1 | -7 | -1.2 | 2 Ribosomal p |
| sp_P28635_METQ_ECOLI | -2.1 | -2.5 | -1.8 | 15 D-methionii |
| sp_P07001_PNTA_ECOLI | -2.2 | -2.7 | -1.6 | 6 NAD(P) trar |
| sp_POA698_UVRA_ECOLI | -2.2 | -2.8 | -1.5 | 4 UvrABC syst |
| sp_POA9P0_DLDH_ECOLI | -2.2 | -7 | -0.7 | 2 Dihydrolipo |
| sp_POA7V0_RS2_ECOLI | -2.3 | -3.1 | -1.5 | 2 30S riboson |
| sp_P25665_METE_ECOLI | -2.3 | -2.7 | -1.9 | 16 5-methyltet |
| sp_P04968_THD1_ECOLI | -2.4 | -3.2 | -1.6 | 4 Threonine c |
| sp_POA7E1_PYRD_ECOLI | -2.4 | -7 | -1.5 | 2 Dihydrooro |
| sp_POA879_TRPB_ECOLI | -2.4 | -2.8 | -2.1 | 19 Tryptophan |
| sp_POADY3_RL14_ECOLI | -2.4 | -3.1 | -1.7 | 3 50S riboson |
| sp_P62399_RL5_ECOLI | -2.4 | -3.1 | -1.7 | 6 50S riboson |
| sp_POA825_GLYA_ECOLI | -2.5 | -3.1 | -1.8 | 3 Serine hydr |

| | | | | |
|----------------------|------|------|------|-----------------|
| sp_POA6P9_ENO_ECOLI | -2.6 | -3.1 | -2.1 | 8 Enolase OS- |
| sp_POAAV4_YBGJ_ECOLI | -2.6 | -3.8 | -1.3 | 2 Uncharacte |
| sp_POA817_METK_ECOLI | -2.8 | -3.1 | -2.6 | 28 S-adenosylr |
| sp_P76536_YFEX_ECOLI | -2.9 | -7 | -1.8 | 2 Uncharacte |
| sp_POAGG8_TLDD_ECOLI | -3 | -7 | -0.9 | 2 Protein tldC |
| sp_POA6M8_EFG_ECOLI | -3.1 | -3.5 | -2.6 | 13 Elongation f |
| sp_P23538_PPSA_ECOLI | -3.1 | -3.5 | -2.7 | 12 Phosphoen |
| sp_P60438_RL3_ECOLI | -3.4 | -4.2 | -2.7 | 3 50S riboson |
| sp_POADZ0_RL23_ECOLI | -3.8 | -4.9 | -2.7 | 2 50S riboson |
| sp_POA7K6_RL19_ECOLI | -4 | -4.7 | -3.4 | 7 50S riboson |
| sp_POA850_TIG_ECOLI | -4 | -5.2 | -3.3 | 5 Trigger fact |
| sp_P76316_DCYD_ECOLI | -4 | -5.1 | -0.9 | 2 D-cysteine c |
| sp_POAEJ6_EUTB_ECOLI | -4.3 | -5.4 | -3.2 | 4 Ethanolami |
| sp_P21170_SPEA_ECOLI | -5.5 | -6 | -4.8 | 13 Biosyntheti |
| sp_P77293_GTRB_ECOLI | -5.9 | -7 | -3.9 | 2 Bactopreno |
| sp_P39274_YJDJ_ECOLI | -6.7 | -7 | -6.3 | 9 Uncharacte |
| sp_POA6Y5_HSLO_ECOLI | -7 | -7 | -6.4 | 11 33 kDa çap |
| sp_POAFF6_NUSA_ECOLI | -7 | -7 | -5.9 | 3 Transcriptic |

rotein yhbP OS=Escherichia coli (strain K12) GN=yhbP PE=3 SV=1 [MASS=16776]
host factor subunit alpha OS=Escherichia coli (strain K12) GN=ihfA PE=1 SV=1 [MASS=11354]
se R OS=Escherichia coli (strain K12) GN=rnr PE=1 SV=2 [MASS=92109]
rage regulator OS=Escherichia coli (strain K12) GN=csrA PE=1 SV=1 [MASS=6856]
nal protein L1 OS=Escherichia coli (strain K12) GN=rplA PE=1 SV=2 [MASS=24730]
f ribonuclease activity A OS=Escherichia coli (strain K12) GN=rraA PE=1 SV=1 [MASS=17360]
ate synthase entC OS=Escherichia coli (strain K12) GN=entC PE=1 SV=1 [MASS=42932]
OS=Escherichia coli (strain K12) GN=hfq PE=1 SV=2 [MASS=11166]
nal protein S4 OS=Escherichia coli (strain K12) GN=rpsD PE=1 SV=2 [MASS=23469]
nal protein S1 OS=Escherichia coli (strain K12) GN=rpsA PE=1 SV=1 [MASS=61158]
large subunit pseudouridine synthase B OS=Escherichia coli (strain K12) GN=rluB PE=1 SV=2 [MASS=32711]
rized protein yffS OS=Escherichia coli (strain K12) GN=yffS PE=4 SV=2 [MASS=29751]
dehydro-3-deoxyheptonate aldolase, Tyr-sensitive OS=Escherichia coli (strain K12) GN=aroF PE=1 SV=1 [M/
nal protein S15 OS=Escherichia coli (strain K12) GN=rpsO PE=1 SV=2 [MASS=10269]
ig protein HU-alpha OS=Escherichia coli (strain K12) GN=hupA PE=1 SV=1 [MASS=9535]
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nal protein S3 OS=Escherichia coli (strain K12) GN=rpsC PE=1 SV=2 [MASS=25983]
nal protein S5 OS=Escherichia coli (strain K12) GN=rpsE PE=1 SV=2 [MASS=17603]
ig protein fis OS=Escherichia coli (strain K12) GN=fis PE=1 SV=1 [MASS=11240]
nal protein S13 OS=Escherichia coli (strain K12) GN=rpsM PE=1 SV=2 [MASS=13099]
sphoryl diester phosphodiesterase OS=Escherichia coli (strain K12) GN=ugpQ PE=1 SV=1 [MASS=27410]
sulfurase OS=Escherichia coli (strain K12) GN=iscS PE=1 SV=1 [MASS=45089]
nal protein L2 OS=Escherichia coli (strain K12) GN=rplB PE=1 SV=2 [MASS=29860]
nal protein S8 OS=Escherichia coli (strain K12) GN=rpsH PE=1 SV=2 [MASS=14127]
ase OS=Escherichia coli (strain K12) GN=ackA PE=1 SV=1 [MASS=43290]
nal protein L4 OS=Escherichia coli (strain K12) GN=rplD PE=1 SV=1 [MASS=22087]
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nal protein L9 OS=Escherichia coli (strain K12) GN=rplI PE=1 SV=1 [MASS=15769]
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eptidyl-prolyl cis-trans isomerase slyD OS=Escherichia coli (strain K12) GN=slyD PE=1 SV=1 [MASS=20853]
ferase ypeA OS=Escherichia coli (strain K12) GN=ypeA PE=3 SV=2 [MASS=16312]
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xyl carrier protein of acetyl-CoA carboxylase OS=Escherichia coli (strain K12) GN=accB PE=1 SV=1 [MASS=1
ranscriptional regulator iscR OS=Escherichia coli (strain K12) GN=iscR PE=1 SV=1 [MASS=17337]
nthase A OS=Escherichia coli (strain K12) GN=cysK PE=1 SV=2 [MASS=34490]
ero-D-manno-heptose-6-epimerase OS=Escherichia coli (strain K12) GN=hldD PE=1 SV=1 [MASS=34893]
ylthiazole kinase OS=Escherichia coli (strain K12) GN=thiM PE=3 SV=1 [MASS=27339]
mate kinase OS=Escherichia coli (strain K12) GN=argB PE=1 SV=1 [MASS=27160]
nal protein L7/L12 OS=Escherichia coli (strain K12) GN=rplL PE=1 SV=2 [MASS=12295]
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on antitermination protein nusG OS=Escherichia coli (strain K12) GN=nusG PE=1 SV=2 [MASS=20532]
nal protein S11 OS=Escherichia coli (strain K12) GN=rpsK PE=1 SV=2 [MASS=13845]

piration control protein ArcA OS=Escherichia coli (strain K12) GN=arcA PE=1 SV=1 [MASS=27292]
nal protein L24 OS=Escherichia coli (strain K12) GN=rpIX PE=1 SV=2 [MASS=11316]
brane protein A OS=Escherichia coli (strain K12) GN=ompA PE=1 SV=1 [MASS=37201]
tRNA synthetase OS=Escherichia coli (strain K12) GN=metG PE=1 SV=2 [MASS=76255]
nal protein S16 OS=Escherichia coli (strain K12) GN=rpsP PE=1 SV=1 [MASS=9191]
3-methylbut-2-en-1-yl diphosphate synthase OS=Escherichia coli (strain K12) GN=ispG PE=1 SV=1 [MASS=40666]
ress protein A OS=Escherichia coli (strain K12) GN=uspA PE=1 SV=2 [MASS=16066]
nal protein L10 OS=Escherichia coli (strain K12) GN=rpIJ PE=1 SV=2 [MASS=17712]
lycerol phosphate synthase subunit hisH OS=Escherichia coli (strain K12) GN=hisH PE=1 SV=1 [MASS=21656]
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e-determining protein minC OS=Escherichia coli (strain K12) GN=minC PE=1 SV=1 [MASS=24776]
nal protein L11 OS=Escherichia coli (strain K12) GN=rpLK PE=1 SV=2 [MASS=14875]
D OS=Escherichia coli (strain K12) GN=nagD PE=1 SV=1 [MASS=27163]
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topological specificity factor OS=Escherichia coli (strain K12) GN=minE PE=1 SV=1 [MASS=10235]
se subunit alpha OS=Escherichia coli (strain K12) GN=atpA PE=1 SV=1 [MASS=55222]
ort membrane protein secG OS=Escherichia coli (strain K12) GN=secG PE=1 SV=1 [MASS=11365]
acyl-carrier-protein] synthase 2 OS=Escherichia coli (strain K12) GN=fabF PE=1 SV=2 [MASS=43046]
se subunit beta OS=Escherichia coli (strain K12) GN=atpD PE=1 SV=2 [MASS=50325]
oribosyltransferase OS=Escherichia coli (strain K12) GN=hisG PE=1 SV=1 [MASS=33367]
nal protein L25 OS=Escherichia coli (strain K12) GN=rpLY PE=1 SV=1 [MASS=10693]
A OS=Escherichia coli (strain K12) GN=ydgA PE=1 SV=1 [MASS=54689]
ynthase OS=Escherichia coli (strain K12) GN=thrC PE=1 SV=1 [MASS=47114]
se subunit b OS=Escherichia coli (strain K12) GN=atpF PE=1 SV=1 [MASS=17264]
ehydrogenase flavoprotein subunit OS=Escherichia coli (strain K12) GN=sdhA PE=1 SV=1 [MASS=64422]
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uctance mechanosensitive channel OS=Escherichia coli (strain K12) GN=mscS PE=1 SV=1 [MASS=30896]
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acetyltransferase OS=Escherichia coli (strain K12) GN=pta PE=1 SV=2 [MASS=77172]
peronin OS=Escherichia coli (strain K12) GN=groL PE=1 SV=2 [MASS=57329]
se-1-phosphate uridylyltransferase OS=Escherichia coli (strain K12) GN=galU PE=1 SV=2 [MASS=32942]
nal protein S10 OS=Escherichia coli (strain K12) GN=rpsJ PE=1 SV=1 [MASS=11736]
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protein S12 methylthiotransferase rimO OS=Escherichia coli (strain K12) GN=rimO PE=1 SV=1 [MASS=49582]
ne-binding lipoprotein metQ OS=Escherichia coli (strain K12) GN=metQ PE=1 SV=2 [MASS=29432]
hydrogenase subunit alpha OS=Escherichia coli (strain K12) GN=pntA PE=1 SV=2 [MASS=54623]
tem protein A OS=Escherichia coli (strain K12) GN=uvrA PE=1 SV=1 [MASS=103868]
yl dehydrogenase OS=Escherichia coli (strain K12) GN=lpdA PE=1 SV=2 [MASS=50688]
nal protein S2 OS=Escherichia coli (strain K12) GN=rpsB PE=1 SV=2 [MASS=26744]
trahydropteroyltryglutamate--homocysteine methyltransferase OS=Escherichia coli (strain K12) GN=metE P
dehydratase biosynthetic OS=Escherichia coli (strain K12) GN=ilvA PE=1 SV=1 [MASS=56195]
tate dehydrogenase OS=Escherichia coli (strain K12) GN=pyrD PE=1 SV=1 [MASS=36775]
i synthase beta chain OS=Escherichia coli (strain K12) GN=trpB PE=1 SV=2 [MASS=42983]
nal protein L14 OS=Escherichia coli (strain K12) GN=rpIN PE=1 SV=1 [MASS=13541]
nal protein L5 OS=Escherichia coli (strain K12) GN=rpIE PE=1 SV=2 [MASS=20302]
oxymethyltransferase OS=Escherichia coli (strain K12) GN=glyA PE=1 SV=1 [MASS=45317]

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methionine synthase OS=Escherichia coli (strain K12) GN=metK PE=1 SV=2 [MASS=41952]
rized protein yfeX OS=Escherichia coli (strain K12) GN=yfeX PE=3 SV=2 [MASS=33052]
OS=Escherichia coli (strain K12) GN=tldD PE=1 SV=1 [MASS=51364]
factor G OS=Escherichia coli (strain K12) GN=fusA PE=1 SV=2 [MASS=77581]
olpyruvate synthase OS=Escherichia coli (strain K12) GN=ppsA PE=1 SV=5 [MASS=87435]
nal protein L3 OS=Escherichia coli (strain K12) GN=rplC PE=1 SV=1 [MASS=22244]
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or OS=Escherichia coli (strain K12) GN=tig PE=1 SV=1 [MASS=48193]
desulfhydrase OS=Escherichia coli (strain K12) GN=dcyD PE=1 SV=4 [MASS=35153]
ne ammonia-lyase heavy chain OS=Escherichia coli (strain K12) GN=eutB PE=1 SV=1 [MASS=49403]
c arginine decarboxylase OS=Escherichia coli (strain K12) GN=speA PE=1 SV=2 [MASS=73898]
l glucosyl transferase homolog from prophage CPS-53 OS=Escherichia coli (strain K12) GN=yfdH PE=1 SV=1
rized protein yjdJ OS=Escherichia coli (strain K12) GN=yjdJ PE=4 SV=1 [MASS=10468]
peronin OS=Escherichia coli (strain K12) GN=hsIO PE=1 SV=1 [MASS=32534]
n elongation protein nusA OS=Escherichia coli (strain K12) GN=nusA PE=1 SV=1 [MASS=54871]

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