

EggNOG alignment									
gene	name	function	PDBID	length	# seqs	# pos	frac pos	COG	uniprot ID
cydA	cytochrome d terminal oxidase, subunit I	aerobic respiratory chain	N/A	522	1321	394	0.75	COG1271C	P0ABJ9
cydB	cytochrome d terminal oxidase, subunit II	aerobic respiratory chain	N/A	379	1138	301	0.79	COG1294C	P0ABK2
nrpA	ribonucleoside diphosphate reductase I, alpha subunit	biosynthesis of deoxyribonucleotides	2X0X	761	1697	504	0.66	COG0209F	P00452
nrpB	ribonucleoside diphosphate reductase I, beta subunit	biosynthesis of deoxyribonucleotides	1BIQ	376	1003	290	0.77	COG0208F	P69924
fliG	flagellar motor switching and energizing component	flagellar motility	3HJL	331	793	315	0.95	COG1536N	P0ABZ1
fliM	flagellar motor switching and energizing component	flagellar motility	4FHR (partial)	334	681	307	0.92	COG1868N	P06974
fliN	flagellar motor switching and energizing component	flagellar motility	1YAB	137	769	87	0.64	COG1886NU	P15070
trpA	tryptophan synthase alpha subunit	tryptophan synthesis from chorismate	1V7Y	268	1347	246	0.92	COG0159E	P0A877
trpB	tryptophan synthase beta subunit	tryptophan synthesis from chorismate	2DH5	397	1509	382	0.96	COG0133E	P0A879
folA	dihydrofolate reductase	folate metabolism	1RX2	159	1183	142	0.89	COG0262H	P0ABQ4
thyA	thymidylate synthase	folate metabolism	1BID	264	1113	253	0.96	COG0207F	P0A884
purE	N5-carboxyaminoimidazole ribonucleotide mutase	purine metabolism	1QCZ	169	1556	157	0.93	COG0041F	P0AG18
purK	N5-carboxyaminoimidazole ribonucleotide synthetase	purine metabolism	1B6R	355	1120	322	0.91	COG0026F	P09029
purC	phosphoribosylaminoimidazole-succinocarboxamide synthetase	purine metabolism	2GQR	237	1163	180	0.76	COG0152F	P0A7D7
ilvC	ketol-acid reductoisomerase NAD(P) binding	branched chain amino acid biosynthesis	1YRL	491	1391	327	0.67	COG0059EH	P05793
ilvN	acetolactate synthase I, small subunit	branched chain amino acid biosynthesis	2LVW	96	67	95	0.99	COG0440E	P0ADF8
ilvB	acetolactate synthase I, large subunit	branched chain amino acid biosynthesis	1OZF	562	3055	508	0.90	COG0028EH	P08142
glgA	glycogen synthase	glycogen biosynthesis	2QZS	477	985	432	0.91	COG0297G	P0A6U8
glgC	glucose 1 phosphate adenyltransferase	glycogen biosynthesis	1M7X	728	598	386	0.53	COG0448G	P07762