

-3.80	64.47	0	0	dihydropteroate synthase
-2.85	37.16	4.10E-94	5.89E-91	phosphoglucosamine mutase
1.20	140.64	6.87E-30	6.57E-27	phage/plasmid replication protein, gene II/X family
1.04	64.56	1.15E-11	8.26E-09	Acidobacterial duplicated orphan permease
1.04	35.96	4.88E-10	2.80E-07	U2 snRNP auxiliary factor, large subunit, splicing factor
0.80	48.41	1.31E-07	6.28E-05	protein TolA
-0.74	80.93	7.20E-07	0.000295	scaffolding protein
21.86	13.50	1.29E-05	0.004627	carbon-monoxide dehydrogenase, large subunit
0.99	28.69	2.99E-05	0.009437	methionine synthase
-1.01	42.28	3.29E-05	0.009437	radical SAM enzyme, Cfr family
2.05	28.49	7.14E-05	0.018616	VWFA-related Acidobacterial domain
-19.92	21.58	9.13E-05	0.021837	phospholipid-translocating P-type ATPase, flippase
1.01	25.02	0.000414	0.091362	splicing factor, CC1-like family
1.23	29.57	0.000454	0.093133	nickel ABC transporter, periplasmic nickel-binding protein
21.41	12.18	0.000502	0.093861	probable F420-dependent oxidoreductase, Rv2161c family
1.70	24.37	0.000523	0.093861	cytochrome c oxidase, subunit II
-1.03	27.08	0.000557	0.09407	type I site-specific deoxyribonuclease, HsdR family