

Pathway Function	Gene	gene	Pfam	BLAST score
sulfate reduction	Sulfite reductase, dissimilatory-type subunit beta	dsrAB	PF01077	E-value: 4.3E-84 Score: 666 Ident.: 56.5%
sulfate reduction	Sulfite reductase, dissimilatory-type subunit alpha	dsrAB	PF03460	E-value: 3.2E-45 Score: 436 Ident.: 27.7%
sulfate reduction	Phosphoadesine phosphosulfate reductase	aps	PF01507	E-value: 310E-105 Score: 789 Ident.: 62.9%
sulfide oxidation	Thioredoxin reductase	soxF	PF07992	E-value: 13E-93 Score: 727 Ident.: 47.8%
sulfide oxidation	Thioredoxin-2	soxW	PF13098	E-value: 460E-51 Score: 398 Ident.: 71.2%
sulfide oxidation	Pyridine nucleotide-disulphide oxidoreductase	sqr	PF07992	E-value: 1.2E-72 Score: 600 Ident.: 45.0%
methanogenesis from	CO2 & H2 Formate dehydrogenase subunit alpha	fwdB	PF00384	E-value: 340E-177 Score: 1,398 Ident.: 33.6%
methanogenesis from	methanol Methylated-thiol--coenzyme M methyltransferase	mtaB	PF12176	E-value: 1.3E-84 Score: 682 Ident.: 50.9%
methanogenesis from	acetate Phosphate acetyltransferase	pta	PF01515	E-value: 460E-114 Score: 872 Ident.: 60.2%
methanogenesis from	acetate Acetate kinase	ackA	PF00871	E-value: 27E-102 Score: 800 Ident.: 46.3%
Denitrification	Multicopper oxidase	nirK	PF00394	E-value: 780E-108 Score: 848 Ident.: 38.4%
Denitrification	Copper-containing nitrite reductase		PF07732	E-value: 5.6E-36 Score: 361 Ident.: 34.8%
			PF00310,	PF04898, PF0164,
ammonia assimilation	cycle II, energy metabolism	gltB	PF014935	E-value: 0.0 Score: 4,229 Ident.: 54.9%
reductive acetyl-CoA	Ferredoxin-dependent glutamate synthase	CdhC	PF03598	E-value: 430E-162 Score: 1,223 Ident.: 56.0%
Glucose fermentation	pathway CO dehydrogenase/acetyl-CoA synthase complex beta subunit	pgi	PF00342	E-value: 0.0 Score: 1,992 Ident.: 70.0%
Glucose fermentation	glucose-6-phosphate isomerase	PFk	PF00365	E-value: 1.2E-150 Score: 1,178 Ident.: 43.9%
Glucose fermentation	6-phosphofructokinase	fda	PF01791	E-value: 210E-96 Score: 729 Ident.: 59.8%
Glucose fermentation	fructose-bisphosphate aldolase	fbaA	PF01116	E-value: 0.0 Score: 1,580 Ident.: 85.3%
Carbohydrate metabolism	fructose-bisphosphate aldolase	pgk/tpi	PF00162	E-value: 0.0 Score: 1,655 Ident.: 82.3%
Carbohydrate metabolism	phosphoglycerate kinase	gpmA	PF00300	E-value: 4.1E-129 Score: 948 Ident.: 85.3%
Carbohydrate metabolism	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	rbsK	PF00294	E-value: 74E-48 Score: 419 Ident.: 37.0%
Carbohydrate metabolism	ribokinase	porC	PF01558	E-value: 3.7E-30 Score: 282 Ident.: 43.4%
Pyruvate to acetyl-CoA	pyruvate ferredoxin oxidoreductase, gamma subunit	hypA	PF01155	E-value: 250E-57 Score: 442 Ident.: 68.1%
Hydrogenase activity	hydrogenase accessory protein HypA	hypC	PF01455	E-value: 5.4E-18 Score: 176 Ident.: 50.0%
Hydrogenase activity	hydrogenase expression/formation protein	hypD	PF01924	E-value: 0.0 Score: 1,768 Ident.: 87.0%
Hydrogenase activity	hydrogenase expression/formation protein	hypF	PF07503	E-value: 0.0 Score: 2,489 Ident.: 64.7%
Hydrogenase activity	hydrogenase expression regulatory protein	nifH	PF00142	
Nitrogen fixation	4Fe-4S iron sulfur cluster binding proteins	NifeSe	PF00374	
Nitrogen fixation	Nickel-dependent hydrogenase	nifU	PF01106	
Nitrogen fixation	NifU-like domain	nifU	PF01592	
Nitrogen fixation	NifU-like N terminal domain			