

Pathway Function Gene	PFam BLAST score			
sulfate reduction	Sulfite reductase, dissimilatory-type	dsrAB	PF01077, PF03460	E-value: 0.0 Score: 1,579 Ident.: 72.0%
sulfate reduction	Phosphoadesine phosphosulfate reductase	aps	PF01507	E-value: 2.7e-68 Score: 553 Ident.: 49.0%
sulfate reduction	Cytochrome subunit of sulfide dehydrogenase	soxD	PF00034	E-value: 4.2e-32 Score: 302 Ident.: 37.0%
sulfate reduction	Thioredoxin reductase	soxF	PF07992, PF00355	E-value: 1.3e-85 Score: 659 Ident.: 62.0%
sulfate reduction	Thiol:disulfide interchange protein	DsbD soxV, DsbD	PF02683	E-value: 8.3e-141 Score: 1,086 Ident.: 51.0%
sulfate reduction	Thioredoxin-2	soxW	PF13098	E-value: 6.1e-26 Score: 247 Ident.: 53.0%
methagenesis from CO2 & H2	Formate dehydrogenase subunit alpha	fwdB	PF00384	E-value: 340e-177 Score: 1,398 Ident.: 33.6%
methagenesis from methanol	Methylated-thiol-coenzyme M methyltransferase	mtaA	PF01208	E-value: 1.7e-48 Score: 436 Ident.: 35.0%
methagenesis from acetate	Phosphate acetyltransferase, subunit A	pta	PF07085	E-value: 6.5e-166 Score: 1,289 Ident.: 41.0%
methagenesis from acetate	Phosphate acetyltransferase, subunit B	pta	PF01515	E-value: 8e-152 Score: 1,126 Ident.: 63.0%
methagenesis from acetate	Acetate kinase	ackA	PF00871	E-value: 3.4e-154 Score: 1,153 Ident.: 58.0%
ammonia assimilation cycle	Ferredoxin-dependent glutamate synthase	gltB	PF00310	E-value: 0.0 Score: 4,185 Ident.: 54.0%
ammonia assimilation cycle	Ferredoxin-dependent glutamate synthase	gltB	PF04898	E-value: 0.0 Score: 4,175 Ident.: 54.0%
ammonia assimilation cycle	Ferredoxin-dependent glutamate synthase	gltB	PF01645	E-value: 0.0 Score: 4,185 Ident.: 54.0%
ammonia assimilation cycle	Ferredoxin-dependent glutamate synthase	gltB	PF01493	E-value: 0.0 Score: 4,175 Ident.: 54.0%
Nitrogen fixation	Nitrite reductase	nirK	PF07732	E-value: 6.4e-97 Score: 777 Ident.: 51.0%
reductive acetyl-CoA	pathway CO dehydrogenase/acetyl-CoA synthase complex beta subunit	CdhC	PF03598	E-value: 0.0 Score: 1,581 Ident.: 46.0%
Glucose fermentation	glucose-6-phosphate isomerase	pgi	PF00342	E-value: 1.3e-55, score 499, ident: 40%
Glucose fermentation	6-phosphofructokinase	Pfk	PF00365	E-value: 9.00e-98 Score: 298, Ident: 45.86
Glucose fermentation	fructose-bisphosphate aldolase	fda	PF01791	E-value:8.00e-171 score:484, Ident:63.82
Glucose fermentation	fructose-bisphosphate aldolase	fbaA	PF01116	E-value: 0.0, Score: 1,506, Ident.: 84.0%
Glucose fermentation	phosphoglycerate kinase	pgk/tpi	PF00162	E-value: 0.0, Score: 2,001, Ident.: 100.0%
Glucose fermentation	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	gpmA	PF00300	E-value: 4e-88, Score: 679, Ident.: 83.0%
pyruvate fermentation to acetate and lactate	pyruvate ferredoxin oxidoreductase, gamma subunit	porC	PF01558	E-value: 0.0 Score: 2,629 Ident.: 100.0%
pyruvate fermentation to acetate and lactate	pyruvate ferredoxin oxidoreductase, delta subunit	porD	PF00037	E-value: 0.0 Score: 3,258 Ident.: 66.0%
Carbohydrate metabolism	ribokinase	rbsK	PF00294	E-value: 0.0 Score: 1,618 Ident.: 100.0%
Carbohydrate metabolism	glycogen debranching enzyme	malQ	PF02446	E-value: 0.0 Score: 3,441 Ident.: 100.0%
Carbohydrate metabolism	starch phosphorylase	glgA	PF08323	E-value: 0.0 Score: 2,279 Ident.: 100.0%
Carbohydrate metabolism	starch phosphorylase	glgA	PF00534	E-value: 0.0 Score: 1,509 Ident.: 74.0%
Carbohydrate metabolism	glycogen(starch) synthase, 2 copies	Rv3032	PF13579	E-value: 0.0 Score: 2,279 Ident.: 100.0%
Carbohydrate metabolism	glycogen(starch) synthase, 2 copies	Rv3032	PF00534	E-value: 0.0 Score: 1,509 Ident.: 74.0%
Hydrogenase activity	hydrogenase expression/formation protein HypC	hypC	PF01455	E-value: 9.1e-58 Score: 467 Ident.: 100.0%
Hydrogenase activity	hydrogenase expression/formation protein HypD	hypD	PF01924	E-value: 0.0 Score: 1,453 Ident.: 100.0%
Hydrogenase activity	hydrogenase expression regulatory protein HypF	HypF	PF00708	E-value: 0.0 Score: 2,489 Ident.: 64.7%
Hydrogenase activity	hydrogenase expression regulatory protein HypF	HypF	PF01300	E-value: 0.0 Score: 2,489 Ident.: 64.7%
Hydrogenase activity	hydrogenase expression regulatory protein HypF	HypF	PF07503	E-value: 0.0 Score: 2,489 Ident.: 64.7%
Nitrogen fixation	4Fe-4S iron sulfur cluster binding proteins	nifH	PF00142	
Nitrogen fixation	Nickel-dependent hydrogenase	NifeSe	PF00374	
Nitrogen fixation	NifU-like domain	nifU	PF01106	
Nitrogen fixation	NifU-like N terminal domain	nifU	PF01592	