Cycle	Step	KEGG	Gene
CARBON	**Aerobic C fixation***(Calvin cycle) (K00855+K01602)/2	K00855	phosphoribulokinase
		K01602	RuBisCO small chain
	Aerobic CH4 oxidation	K08684	methane monooxygenase
	Aerobic respiration (K02256+K02262)/2+(K02274+ K02276)/2	K02256	cytochrome c oxidase subunit I (coxI)
		K02262	cytochrome c oxidase subunit III (coxIII)
		K02274	cytochrome c oxidase subunit I (coxA)
		K02276	cytochrome c oxidase subunit III (coxC)
	Anaerobic C fixation (Arnon: K00174,K00175,K00244, K01648. Reductive Acetil-CoA: K00194,K00197) (K00174+K00175+K00244+ K01648)/4+(K00194+K00197)/2	K00174	2-oxoglutarate:ferredoxin oxidoreductase subunit alpha
		K00175	2-oxoglutarate:ferredoxin oxidoreductase subunit beta
		K00244	frdA; fumarate reductase flavoprotein subunit
		K01648	adenosinetriphosphate (ATP) citrate lyase
		K00194	CO dehydrogenase subunit delta
		K00197	CO dehydrogenase subunit gamma
	CO oxidation (K03518+K03519+K03520)/3	K03518	CO dehydrogenase small subunit (coxS)
		K03519	cutM, coxM; carbon-monoxide dehydrogenase medium subunit
		K03520	cutL, coxL; carbon-monoxide dehydrogenase large subunit
	Fermentation	K00016	L-lactate dehydrogenase
	Methanogenesis (K00400+K00401)/2	K00400	coenzyme M methyl reductase beta subunit (mcrB)
		K00401	methyl coenzyme M reductase system, component A2
NITROGEN	**Ammonification** K05904+K03385	K03385	formate-dependent nitrite reductase periplasmic cytochrome c552 (nrfA)
		K05904	cytochrome c nitrite reductase (nrfA)
	Anammox (SRAO)	K10535	hydroxylamine oxidoreductase/hydrazine oxidoreducatse (hao/hzo)
	Denitrification (K02305+K04561+K00376)/3	K00376	nitrous oxide reductase (nosZ)
		K02305	nitric-oxide reductase (norC)
		K04561	nitric-oxide reductase (norB)
	Nitrate reduction + Nitrite oxidation (K00370+K00371)/2	K00370	nitrate reductase alpha & nitrite oxidoreductase (narG/nxrA)
		K00371	nitrate reductase beta & nitrite oxidoreductase (narH/nxrB)
	Nitrate reduction (K02567+K02568)/2	K02567	periplasmic nitrate reductase (napA)
		K02568	cytochrome c-type protein (napB)
	Nitrification (K10944+K10945+K10946)/3	K10944	ammonia monooxygenase subunit A (amoA)
		K10945	ammonia monooxygenase subunit B (amoB)
		K10946	ammonia monooxygenase subunit C (amoC)
	Nitrogen assimilation (K00360+K00367+K01915+ K00265+K00284)/3	K00265	glutamate synthase (NADPH/NADH) large chain (gltB)
		K00284	glutamate synthase (ferredoxin-dependent) (gltS)
		K00360	assimilatory nitrate reductase
		K00367	assimilatory nitrate reductase
		K01915	glutamine synthetase (glnA)
	Nitrogen Fixation (K00531+K02586+K02588+ K02591)/4	K00531	nitrogenase
		K02586	nitrogenase molybdenum-iron protein alpha chain (nifD)
		K02588	nitrogenase iron protein (nifH)
		K02591	nitrogenase molybdenum-iron protein beta chain (nifK)
	Nitrogen Mineralization K00260+K00261+K00262	K00260	glutamate dehydrogenase
		K00261	glutamate dehydrogenase
		K00262	glutamate dehydrogenase
SULFUR	**Assimilatory sulfate reduction** (K00860+K00956+K00957)/3	K00860	adenylylsulfate kinase (cysC)
		K00956	sulfate adenylyltransferase subunit 1 (cysN)
		K00957	sulfate adenylyltransferase subunit 2 (cysD)
	Dissimilatory sulfate reduction and sulfide oxidation** (K00394+K00395+K11180)/3	K00394	adenylylsulfate reductase subunit A (aprA)
		K00395	adenylylsulfate reductase subunit B (aprB)
		K11180	sulfite reductase (dsrA)
	Sulfur Mineralization K00456+K01011	K00456	cysteine dioxygenase
		K01011	3-mercaptopyruvate sulfurtransferase
	Polysulfide reduction	K08352	polysulfide reductase chain A (psrA)

*: *Chromatiales*: anoxygenic phototrophy through the Calvin cycle.
**: As marker genes K00394, K00395, K11180 can operate in both an oxidative and a reductive way. They were assigned to the sulfate reduction or sulfide oxidation step if they had a best match within KEGG to an ortholog from a sulfate-reducing or sulfur-oxidizing clade.