

**Supplemental Table 1.** Complete list of the 392 EC1 homologs identified through a manually refined search of all KEGG (Kyoto Encyclopedia of Genes and Genomes, <http://www.genome.jp/kegg/>) pathways directly involved in redox reactions of biogeochemical interest.

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
A	Ammonification	Cytochrome c type protein NapC	no EC	K02569	Cytochrome c type protein NapC	heme
A	Ammonification	Ferredoxin-Type protein NapG	no EC	K02573	Ferredoxin-Type protein NapG	ferredoxin
A	Ammonification	Ferredoxin-Type protein NapH	no EC	K02574	Ferredoxin-Type protein NapH	ferredoxin
A	Ammonification	nitrate reductase	1.7.99.4	K00370	nitrate reductase alpha subunit	molybdopterin, 4Fe-4S
A	Ammonification	nitrate reductase	1.7.99.4	K00371	nitrate reductase beta subunit	4Fe-4S, 3Fe-4S
A	Ammonification	nitrate reductase	1.7.99.4	K00374	nitrate reductase gamma subunit	heme
A	Ammonification	nitrate reductase	1.7.99.4	K02567	periplasmic nitrate reductase NapA	molybdopterin, 4Fe-4S
A	Ammonification	nitrate reductase	1.7.99.4	K02568	cytochrome c-type protein NapB	heme
A	Ammonification	nitrite reductase (cytochrome; ammonia-forming)	1.7.2.2	K03385	nitrite reductase (cytochrome c-552)	heme
A	Ammonification	nitrite reductase (NADH)	1.7.1.15	K00362	nitrite reductase (NADH) large subunit	4Fe-4S, heme, flavoprotein
A	Ammonification	nitrite reductase (NADH)	1.7.1.15	K00363	nitrite reductase (NADH) small subunit	2Fe-2S, NAD
A	Ammonification	nitrite reductase (NADH)	1.7.1.15	K15876	cytochrome c nitrite reductase small subunit	heme
A	Nitrogen Assimilation	ferredoxin-nitrate reductase	1.7.7.2	K00367	ferredoxin-nitrate reductase	molybdopterin, 4Fe-4S
A	Nitrogen Assimilation	ferredoxin-nitrite reductase	1.7.7.1	K00366	ferredoxin-nitrite reductase	4Fe-4S, heme
A	Nitrogen Assimilation	nitrate reductase (NADH)	1.7.1.1	K10534	nitrate reductase (NAD(P)H)(also 1.7.1.2 and 1.7.1.3)	molybdopterin, heme, flavoprotein
A	Nitrogen Assimilation	nitrite reductase [NAD(P)H]	1.7.1.4	K17877	nitrite reductase (NAD(P)H)	4Fe-4S, 2Fe-2S, heme, flavoprotein
AP	Anoxygenic Photosynthesis	Type I Photosystem	1.97.1.12	K08940	photosystem P840 reaction center large subunit	

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
AP	Anoxygenic Photosynthesis	Type I Photosystem	1.97.1.12	K08941	photosystem P840 reaction center iron-sulfur protein	
AP	Anoxygenic Photosynthesis	Type I Photosystem	1.97.1.12	K08942	photosystem P840 reaction center cytochrome c551	heme
AP	Anoxygenic Photosynthesis	Type I Photosystem	1.97.1.12	K08943	photosystem P840 reaction center protein PscD	
AP	Anoxygenic Photosynthesis	Type II Photosystem	no EC	K08928	photosynthetic reaction center L subunit	magnesium, iron
AP	Anoxygenic Photosynthesis	Type II Photosystem	no EC	K08929	photosynthetic reaction center M subunit	magnesium, iron
AP	Anoxygenic Photosynthesis	Type II Photosystem	no EC	K13991	photosynthetic reaction center H subunit	magnesium, quinone, ubiquinone
AP	Anoxygenic Photosynthesis	Type II Photosystem	no EC	K13994	photosynthetic reaction center PufX protein	
AP	Anoxygenic Photosynthesis	Type II Photosystem	no EC	K13992	photosynthetic reaction center cytochrome c subunit	heme
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K00404	cytochrome c oxidase cbb3-type subunit I	heme, copper
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K00405	cytochrome c oxidase cbb3-type subunit II	
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K00406	cytochrome c oxidase cbb3-type subunit III	heme
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K00407	cytochrome c oxidase cbb3-type subunit IV	
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02256	cytochrome c oxidase subunit 1	heme, copper
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02261	cytochrome c oxidase subunit 2	copper, magnesium
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02262	cytochrome c oxidase subunit 3	
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02263	cytochrome c oxidase subunit 4	
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02264	cytochrome c oxidase subunit 5a	heme
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02265	cytochrome c oxidase subunit 5b	zinc
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02266	cytochrome c oxidase subunit 6a	
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02267	cytochrome c oxidase subunit 6b	

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02268	cytochrome c oxidase subunit 6c	
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02269	cytochrome c oxidase subunit 7	
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02270	cytochrome c oxidase subunit 7a	
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02271	cytochrome c oxidase subunit 7b	
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02272	cytochrome c oxidase subunit 7c	
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02273	cytochrome c oxidase subunit 8	
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02274	cytochrome c oxidase subunit I	heme, copper
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02275	cytochrome c oxidase subunit II	heme, copper
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02276	cytochrome c oxidase subunit III	
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K02277	cytochrome c oxidase subunit IV	heme, copper
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K15408	cytochrome c oxidase subunit I+III	heme, copper
AR	Oxidative Phosphorylation	cytochrome-c oxidase	1.9.3.1	K15862	cytochrome c oxidase cbb3-type subunit I/II	
AU	3-Hydroxypropionate bi-cycle	3-hydroxypropionate dehydrogenase (NADP+)	1.1.1.298	K15039	3-hydroxypropionate dehydrogenase (NADP+)	
AU	3-Hydroxypropionate bi-cycle	3-hydroxypropionate dehydrogenase (NADP+)	1.2.1.75	K14468	malonyl-CoA reductase / 3-hydroxypropionate dehydrogenase (NADP+)	
AU	3-Hydroxypropionate bi-cycle	acryloyl-coenzyme A reductase	1.3.1.84	K14469	acrylyl-CoA reductase (NADPH) / 3-hydroxypropionyl-CoA dehydratase / 3-hydroxypropionyl-CoA synthetase	
AU	3-Hydroxypropionate bi-cycle	acryloyl-coenzyme A reductase	1.3.1.84	K15020	acryloyl-coenzyme A reductase	zinc, NAD(P)
AU	3-Hydroxypropionate bi-cycle	fumarate reductase	1.3.5.4	K00244	fumarate reductase flavoprotein subunit	Heme, flavoprotein

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
AU	3-Hydroxypropionate bi-cycle	fumarate reductase	1.3.5.4	K00245	fumarate reductase iron-sulfur subunit	4Fe-4S, 2Fe-2S, 3Fe-4S
AU	3-Hydroxypropionate bi-cycle	fumarate reductase	1.3.5.4	K00246	fumarate reductase subunit C	heme
AU	3-Hydroxypropionate bi-cycle	fumarate reductase	1.3.5.4	K00247	fumarate reductase subunit D	
AU	3-Hydroxypropionate bi-cycle	malonyl-CoA/succinyl-CoA reductase (NADPH)	1.2.1.75; 1.2.1.76	K15017	malonyl-CoA/succinyl-CoA reductase (NADPH)	NADP, NAD, Mg(2+), Mn(2+)
AU	3-Hydroxypropionate bi-cycle	succinate dehydrogenase	1.3.5.1	K00239	succinate dehydrogenase flavoprotein subunit succinate	FAD, Flavoprotein
AU	3-Hydroxypropionate bi-cycle	succinate dehydrogenase	1.3.5.1	K00240	succinate dehydrogenase iron-sulfur subunit	4Fe-4S, 2Fe-2S, 3Fe-4S
AU	3-Hydroxypropionate bi-cycle	succinate dehydrogenase	1.3.5.1	K00241	succinate dehydrogenase cytochrome b556 subunit	heme
AU	3-Hydroxypropionate bi-cycle	succinate dehydrogenase	1.3.5.1	K00242	succinate dehydrogenase membrane anchor subunit	heme
AU	Carbon fixation pathways in prokaryotes	fumarate reductase (CoM/CoB)	1.3.4.1	K18209	fumarate reductase (CoM/CoB) subunit A	
AU	Carbon fixation pathways in prokaryotes	fumarate reductase (CoM/CoB)	1.3.4.1	K18210	fumarate reductase (CoM/CoB) subunit B	
AU	Carbon fixation pathways in prokaryotes	fumarate reductase (NADH)	1.3.1.6	K18556	NADH-dependent fumarate reductase subunit A	
AU	Carbon fixation pathways in prokaryotes	fumarate reductase (NADH)	1.3.1.6	K18557	NADH-dependent fumarate reductase subunit B	
AU	Dicarboxylate-hydroxybutyrate cycle	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K15016	enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase	
AU	Dicarboxylate-hydroxybutyrate cycle	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K01782	3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase	FAD, NAD
AU	Dicarboxylate-hydroxybutyrate cycle	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K01825	3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase	FAD, NAD

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
AU	Dicarboxylate-hydroxybutyrate cycle	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K07516	3-hydroxyacyl-CoA dehydrogenase	
AU	Dicarboxylate-hydroxybutyrate cycle	fumarate reductase	1.3.5.4	K00244	fumarate reductase flavoprotein subunit	FAD, Flavoprotein, heme, Fe(3+)
AU	Dicarboxylate-hydroxybutyrate cycle	fumarate reductase	1.3.5.4	K00245	fumarate reductase iron-sulfur subunit	4Fe-4S, 2Fe-2S, 3Fe-4S
AU	Dicarboxylate-hydroxybutyrate cycle	fumarate reductase	1.3.5.4	K00246	fumarate reductase subunit C	heme
AU	Dicarboxylate-hydroxybutyrate cycle	fumarate reductase	1.3.5.4	K00247	fumarate reductase subunit D	
AU	Dicarboxylate-hydroxybutyrate cycle	malate dehydrogenase	1.1.1.37	K00024	malate dehydrogenase	NAD, NADP
AU	Dicarboxylate-hydroxybutyrate cycle	malonyl-CoA/succinyl-CoA reductase (NADPH)	1.2.1.75 1.2.1.76	K15017	malonyl-CoA/succinyl-CoA reductase (NADPH)	NADP, NAD, Mg(2+), Mn(2+)
AU	Dicarboxylate-hydroxybutyrate cycle	pyruvate ferredoxin oxidoreductase	1.2.7.1	K00169	pyruvate ferredoxin oxidoreductase, alpha subunit [EC:]	
AU	Dicarboxylate-hydroxybutyrate cycle	pyruvate ferredoxin oxidoreductase	1.2.7.1	K00170	pyruvate ferredoxin oxidoreductase, beta subunit [EC:1.2.7.1]	4Fe-4S
AU	Dicarboxylate-hydroxybutyrate cycle	pyruvate ferredoxin oxidoreductase	1.2.7.1	K00171	pyruvate ferredoxin oxidoreductase, delta subunit [EC:1.2.7.1]	4Fe-4S
AU	Dicarboxylate-hydroxybutyrate cycle	pyruvate ferredoxin oxidoreductase	1.2.7.1	K00172	pyruvate ferredoxin oxidoreductase, gamma subunit [EC:1.2.7.1]	4Fe-4S
AU	Dicarboxylate-hydroxybutyrate cycle	pyruvate-flavodoxin oxidoreductase	1.2.7.-	K03737	putative pyruvate-flavodoxin oxidoreductase	4Fe-4S
AU	Dicarboxylate-hydroxybutyrate cycle	succinate dehydrogenase	1.3.5.1	K00239	succinate dehydrogenase flavoprotein subunit	FAD, Flavoprotein
AU	Dicarboxylate-hydroxybutyrate cycle	succinate dehydrogenase	1.3.5.1	K00240	succinate dehydrogenase iron-sulfur subunit	4Fe-4S, 2Fe-2S, 3Fe-4S
AU	Dicarboxylate-hydroxybutyrate cycle	succinate dehydrogenase	1.3.5.1	K00241	succinate dehydrogenase cytochrome b556 subunit	heme
AU	Dicarboxylate-hydroxybutyrate cycle	succinate dehydrogenase	1.3.5.1	K00242	succinate dehydrogenase membrane anchor subunit	heme
AU	Dicarboxylate-hydroxybutyrate cycle	succinate semialdehyde reductase	1.1.1.-	K14465	succinate semialdehyde reductase (NADPH)	Zinc, NADP, NAD

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
AU	Dicarboxylate-hydroxybutyrate cycle	succinyl-CoA reductase	1.2.1.76	K15038	succinyl-CoA reductase	
AU	Hydroxypropionate-hydroxybutylate cycle	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K15016	enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase	
AU	Hydroxypropionate-hydroxybutylate cycle	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K01782	3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase	FAD, NAD
AU	Hydroxypropionate-hydroxybutylate cycle	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K01825	3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase	FAD, NAD
AU	Hydroxypropionate-hydroxybutylate cycle	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K07516	3-hydroxyacyl-CoA dehydrogenase	
AU	Hydroxypropionate-hydroxybutylate cycle	3-hydroxypropionate dehydrogenase (NADP+)	1.2.1.76; 1.2.1.75; 1.1.1.298	K14468	malonyl-CoA reductase / 3-hydroxypropionate dehydrogenase (NADP+)	
AU	Hydroxypropionate-hydroxybutylate cycle	3-hydroxypropionate dehydrogenase (NADP+)	1.2.1.76; 1.2.1.75; 1.1.1.298	K15039	3-hydroxypropionate dehydrogenase (NADP+)	
AU	Hydroxypropionate-hydroxybutylate cycle	acryloyl-coenzyme A reductase	1.3.1.84	K14469	acrylyl-CoA reductase (NADPH) / 3-hydroxypropionyl-CoA dehydratase / 3-hydroxypropionyl-CoA synthetase	
AU	Hydroxypropionate-hydroxybutylate cycle	acryloyl-coenzyme A reductase	1.3.1.84	K15020	acryloyl-coenzyme A reductase	Zinc, NADP, NAD
AU	Hydroxypropionate-hydroxybutylate cycle	malonyl-CoA/succinyl-CoA reductase (NADPH)	1.2.1.75	K15017	malonyl-CoA/succinyl-CoA reductase (NADPH)	NADP, NAD, Mg(2+), Mn(2+)
AU	Hydroxypropionate-hydroxybutylate cycle	succinate semialdehyde reductase	1.1.1.-	K14465	succinate semialdehyde reductase (NADPH) [EC:1.1.1.-]	Zinc, NADP, NAD
AU	Hydroxypropionate-hydroxybutylate cycle	succinyl-CoA reductase	1.2.1.76	K15038	succinyl-CoA reductase	

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
AU	Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	carbon-monoxide dehydrogenase	1.2.99.2; 1.2.7.4	K00198	carbon-monoxide dehydrogenase catalytic subunit	4Fe-4S, nickel, Ni-Fe-S
AU	Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	carbon-monoxide dehydrogenase	1.2.99.2; 1.2.7.4	no KO		
AU	Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	formate dehydrogenase	1.2.1.43	K05299	formate dehydrogenase alpha subunit	4Fe-4S, 2Fe-2S, Fe(3+), NADP, NAD
AU	Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	formate dehydrogenase	1.2.1.43	K15022	formate dehydrogenase beta subunit [EC:1.2.1.43]	4Fe-4S, Fe(3+), Flavoprotein
AU	Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	methylenetetrahydrofolate dehydrogenase (NADP+)	1.5.1.5	K01491	methylenetetrahydrofolate dehydrogenase (NADP+)	NADP, NAD
AU	Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	methylenetetrahydrofolate reductase (NADPH)	1.5.1.20	K00297	methylenetetrahydrofolate reductase (NADPH)	Flavoprotein
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	2-oxoglutarate ferredoxin oxidoreductase	1.2.7.3	K00174	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	2-oxoglutarate ferredoxin oxidoreductase	1.2.7.3	K00175	2-oxoglutarate ferredoxin oxidoreductase subunit beta	Mg(2+), Magnesium
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	2-oxoglutarate ferredoxin oxidoreductase	1.2.7.3	K00177	2-oxoglutarate ferredoxin oxidoreductase subunit gamma	
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	2-oxoglutarate ferredoxin oxidoreductase	1.2.7.3	K00176	2-oxoglutarate ferredoxin oxidoreductase subunit delta	4Fe-4S
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	fumarate reductase	1.3.5.4	K00244	fumarate reductase flavoprotein subunit	Flavoprotein, heme, Fe(3+)
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	fumarate reductase	1.3.5.4	K00245	fumarate reductase iron-sulfur subunit	4Fe-4S, 2Fe-2S, 3Fe-4S, Iron-sulfur, iron-sulfur, Iron, iron, Metal-binding
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	fumarate reductase	1.3.5.4	K00246	fumarate reductase subunit C	heme

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	fumarate reductase	1.3.5.4	K00247	fumarate reductase subunit D	
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	isocitrate dehydrogenase	1.1.1.42	K00031	isocitrate dehydrogenase	Mg(2+), Mn(2+), NADP, NAD
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	malate dehydrogenase	1.1.1.37	K00024	malate dehydrogenase	NAD, NADP
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	putative pyruvate-flavodoxin oxidoreductase	1.2.7.-	K03737	putative pyruvate-flavodoxin oxidoreductase	4Fe-4S
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	pyruvate ferredoxin oxidoreductase	1.2.7.1	K00169	pyruvate ferredoxin oxidoreductase, alpha subunit	
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	pyruvate ferredoxin oxidoreductase	1.2.7.1	K00170	pyruvate ferredoxin oxidoreductase, beta subunit	4Fe-4S
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	pyruvate ferredoxin oxidoreductase	1.2.7.1	K00171	pyruvate ferredoxin oxidoreductase, delta subunit	4Fe-4S
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	pyruvate ferredoxin oxidoreductase	1.2.7.1	K00172	pyruvate ferredoxin oxidoreductase, gamma subunit	4Fe-4S
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	succinate dehydrogenase	1.3.5.1	K00239	succinate dehydrogenase flavoprotein subunit	FAD, Flavoprotein
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	succinate dehydrogenase	1.3.5.1	K00240	succinate dehydrogenase iron-sulfur subunit	4Fe-4S, 2Fe-2S, 3Fe-4S
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	succinate dehydrogenase	1.3.5.1	K00241	succinate dehydrogenase cytochrome b556 subunit	heme
AU	Reductive citrate cycle (Arnon-Buchanan cycle)	succinate dehydrogenase	1.3.5.1	K00242	succinate dehydrogenase membrane anchor subunit	heme
AU	Reductive pentose phosphate cycle (Calvin cycle)	glyceraldehyde 3-phosphate dehydrogenase	1.2.1.12	K00134	glyceraldehyde 3-phosphate dehydrogenase	NAD, NADP
AU	Reductive pentose phosphate cycle (Calvin cycle)	glyceraldehyde-3-phosphate dehydrogenase (NAD(P))	1.2.1.59	K00150	glyceraldehyde-3-phosphate dehydrogenase (NAD(P))	NADP, NAD, Mg(2+), Magnesium
AU	Reductive pentose phosphate cycle (Calvin cycle)	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating)	1.2.1.13	K05298	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating)	NADP, NAD



Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
D	Denitrification	Cytochrome c type protein NapC	no EC	K02569	Cytochrome c type protein NapC	Heme
D	Denitrification	Ferredoxin-Type protein NapG	no EC	K02573	Ferredoxin-Type protein NapG	Ferredoxin
D	Denitrification	Ferredoxin-Type protein NapH	no EC	K02574	Ferredoxin-Type protein NapH	Ferredoxin
D	Denitrification	nitrate reductase	1.7.99.4	K00360	assimilatory nitrate reductase electron transfer subunit	
D	Denitrification	nitrate reductase	1.7.99.4	K00370	nitrate reductase alpha subunit	molybdopterin, 4Fe-4S
D	Denitrification	nitrate reductase	1.7.99.4	K00371	nitrate reductase beta subunit	4Fe-4S, 3Fe-4S
D	Denitrification	nitrate reductase	1.7.99.4	K00372	assimilatory nitrate reductase catalytic subunit	molybdopterin, 4Fe-4S
D	Denitrification	nitrate reductase	1.7.99.4	K00374	nitrate reductase gamma subunit	heme
D	Denitrification	nitrate reductase	1.7.99.4	K02567	periplasmic nitrate reductase NapA	molybdopterin, 4Fe-4S
D	Denitrification	nitrate reductase	1.7.99.4	K02568	cytochrome c-type protein NapB	heme
D	Denitrification	nitric oxide reductase (cytochrome c)	1.7.2.5	K04561	nitric oxide reductase subunit B	heme
D	Denitrification	nitric oxide reductase (menaquinol)	1.7.5.2	no KO		
D	Denitrification	nitrite reductase (cytochrome; ammonia-forming)	1.7.2.2	K03385	nitrite reductase (cytochrome c-552)	heme
D	Denitrification	nitrite reductase (cytochrome; ammonia-forming)	1.7.2.2	K05904	nitrite reductase (cytochrome c-552)	
D	Denitrification	nitrite reductase (cytochrome; ammonia-forming)	1.7.2.2	K02305	nitric oxide reductase subunit C	heme
D	Denitrification	nitrite reductase (NADH)	1.7.1.15	K00362	nitrite reductase (NADH) large subunit	4Fe-4S, heme, flavoprotein
D	Denitrification	nitrite reductase (NADH)	1.7.1.15	K00363	nitrite reductase (NADH) small subunit	2Fe-2S, NAD
D	Denitrification	nitrite reductase (NADH)	1.7.1.15	K15876	cytochrome c nitrite reductase small subunit	heme

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
D	Denitrification	nitrite reductase (NO-forming)	1.7.2.1	K00368	nitrite reductase (NO-forming)	Cu(2+), FAD, Flavoprotein
D	Denitrification	nitrite reductase (NO-forming)	1.7.2.1	K15864	nitrite reductase (NO-forming) / hydroxylamine reductase	heme
D	Denitrification	nitrous-oxide reductase	1.7.2.4	K00376	nitrous-oxide reductase	copper
H	Fatty acid degradation	acyl-CoA dehydrogenase	1.3.8.7	K00249	acyl-CoA dehydrogenase	FAD, Flavoprotein
H	Fatty acid degradation	long-chain acyl-CoA dehydrogenase	1.3.8.8	K00255	long-chain-acyl-CoA dehydrogenase	FAD, Flavoprotein
H	Fatty acid degradation	very-long-chain acyl-CoA dehydrogenase	1.3.8.9	K09479	very long chain acyl-CoA dehydrogenase	FAD, Flavoprotein
H	Fatty acid degradation/Toluene degradation	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K00022	3-hydroxyacyl-CoA dehydrogenase	NAD
H	Fatty acid degradation/Toluene degradation	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K01782	3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase	FAD, NAD
H	Fatty acid degradation/Toluene degradation	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K01825	3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase / 3-hydroxybutyryl-CoA epimerase / enoyl-CoA isomerase	FAD, NAD
H	Fatty acid degradation/Toluene degradation	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K07514	enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase / 3,2-trans-enoyl-CoA isomerase	NAD
H	Fatty acid degradation/Toluene degradation	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K07516	3-hydroxyacyl-CoA dehydrogenase	
H	Fatty acid degradation/Toluene degradation	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K07547	2-[hydroxy(phenyl)methyl]-succinyl-CoA dehydrogenase BbsC subunit	
H	Fatty acid degradation/Toluene degradation	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K07548	2-[hydroxy(phenyl)methyl]-succinyl-CoA dehydrogenase BbsD subunit	

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
H	Fatty acid degradation/Toluene degradation	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K08683	3-hydroxyacyl-CoA dehydrogenase / 3-hydroxy-2-methylbutyryl-CoA dehydrogenase	NAD
H	Fatty acid degradation/Toluene degradation	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K10527	enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase	NAD
H	Fatty acid degradation/Toluene degradation	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K12405	3-hydroxyacyl-CoA dehydrogenase / 3a,7a,12a-trihydroxy-5b-cholest-24-enoyl-CoA hydratase	NAD
H	Fatty acid degradation/Toluene degradation	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	K15016	enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase	
H	Glycerophospholipid metabolism	aldehyde reductase	1.1.1.21	K00011	aldehyde reductase	NADP, NAD
H	Glycerophospholipid metabolism	glycerol 2-dehydrogenase (NADP+)	1.1.1.156	K18097	glycerol 2-dehydrogenase (NADP+)	NADP, NAD
H	Glycerophospholipid metabolism	glycerol dehydrogenase	1.1.1.6	K00005	glycerol dehydrogenase	zinc, NAD
H	Glycerophospholipid metabolism	glycerol-3-phosphate dehydrogenase (NAD+)	1.1.1.8	K00006	glycerol-3-phosphate dehydrogenase (NAD+)	NAD
H	Glycerophospholipid metabolism	glycolate oxidase	1.1.3.15	K00104	glycolate oxidase	FAD, Flavoprotein
H	Glycerophospholipid metabolism	glycolate oxidase	1.1.3.15	K11517	(S)-2-hydroxy-acid oxidase	Flavoprotein, FMN
H	Glycerophospholipid metabolism	thioredoxin-disulfide reductase	1.8.1.9	K00384	thioredoxin reductase (NADPH)	FAD, Flavoprotein, NADP, NAD, Selenocysteine
H	Glycolysis / Gluconeogenesis	alcohol dehydrogenase (NADP+)	1.1.1.2	K00002	alcohol dehydrogenase (NADP+)	NADP, NAD, Zinc
H	Glycolysis / Gluconeogenesis	glyceraldehyde-3-P-dehydrogenase	1.2.1.12	K00134	glyceraldehyde 3-phosphate dehydrogenase	NAD, NADP
H	Glycolysis / Gluconeogenesis	glyceraldehyde-3-P-dehydrogenase	1.2.1.12	K10705	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	NAD
H	Glycolysis / Gluconeogenesis	glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) (phosphorylating)	1.2.1.59	K00150	glyceraldehyde-3-phosphate dehydrogenase (NAD(P))	NADP, NAD, Mg(2+), Magnesium

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
H	Glycolysis / Gluconeogenesis	glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) (phosphorylating)	1.2.1.59	K00140	malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase	NAD
H	Glycolysis / Gluconeogenesis	hydrogen dehydrogenase	1.12.1.2	K00436	NAD-reducing hydrogenase large subunit	Ni(2+), FMN, NAD
H	Glycolysis / Gluconeogenesis	L-lactate dehydrogenase	1.1.1.27	K00016	L-lactate dehydrogenase	NAD
H	Glycolysis/Gluconeogenesis/Fatty acid degradation	alcohol dehydrogenase	1.1.1.1	K00001	alcohol dehydrogenase	Zinc, NAD
H	Glycolysis/Gluconeogenesis/Fatty acid degradation	alcohol dehydrogenase	1.1.1.1	K00121	S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase	Zinc, NAD, FAD
H	Glycolysis/Gluconeogenesis/Fatty acid degradation	alcohol dehydrogenase	1.1.1.1	K04072	acetaldehyde dehydrogenase / alcohol dehydrogenase	Iron, NAD
H	Glycolysis/Gluconeogenesis/Fatty acid degradation	alcohol dehydrogenase	1.1.1.1	K11440	choline dehydrogenase	NAD
H	Glycolysis/Gluconeogenesis/Fatty acid degradation	alcohol dehydrogenase	1.1.1.1	K13951	alcohol dehydrogenase 1/7	Zinc, NAD
H	Glycolysis/Gluconeogenesis/Fatty acid degradation	alcohol dehydrogenase	1.1.1.1	K13952	alcohol dehydrogenase 6	Zinc, NAD
H	Glycolysis/Gluconeogenesis/Fatty acid degradation	alcohol dehydrogenase	1.1.1.1	K13953	alcohol dehydrogenase, propanol-preferring	Zinc, NAD
H	Glycolysis/Gluconeogenesis/Fatty acid degradation	alcohol dehydrogenase	1.1.1.1	K13954	alcohol dehydrogenase	NAD, Fe(2+), zinc
H	Glycolysis/Gluconeogenesis/Fatty acid degradation	alcohol dehydrogenase	1.1.1.1	K13980	alcohol dehydrogenase 4	Zinc, NAD
H	Glycolysis/Gluconeogenesis/Fatty acid degradation	alcohol dehydrogenase	1.1.1.1	K18857	alcohol dehydrogenase class-P	
H	Glycolysis/Gluconeogenesis/Fatty acid	aldehyde dehydrogenase (NAD+)	1.2.1.3	K00128	aldehyde dehydrogenase (NAD+)	NAD, NADP, Potassium, Mg(2+),

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
	degradation					Magnesium
H	Glycolysis/Gluconeogenesis/Fatty acid degradation	aldehyde dehydrogenase (NAD <sup>+</sup> )	1.2.1.3	K00149	aldehyde dehydrogenase family 9 member A1	NAD
H	Glycolysis/Gluconeogenesis/Fatty acid degradation	aldehyde dehydrogenase (NAD <sup>+</sup> )	1.2.1.3	K14085	aldehyde dehydrogenase family 7 member A1	NAD
H	Glycolysis/Gluconeogenesis/Methane metabolism	methanol dehydrogenase (cytochrome c)	1.1.2.7	K14028	methanol dehydrogenase (cytochrome c) subunit 1	quinone, Metal-binding
H	Glycolysis/Gluconeogenesis/Methane metabolism	methanol dehydrogenase (cytochrome c)	1.1.2.7	K14029	methanol dehydrogenase (cytochrome c) subunit 2	
H	Glycolysis/Gluconeogenesis/Pentose Phosphate	glyceraldehyde-3-phosphate dehydrogenase (NADP <sup>+</sup> )	1.2.1.9	K00131	glyceraldehyde-3-phosphate dehydrogenase (NADP <sup>+</sup> )	NADP, NAD
H	Glycolysis/Gluconeogenesis/TC A Cycle	dihydrolipoyl dehydrogenase	1.8.1.4	K00382	dihydrolipoamide dehydrogenase	FAD, Flavoprotein, NAD, quinone
H	Glycolysis/Gluconeogenesis/TC A Cycle	Pyruvate dehydrogenase	1.2.4.1	K00161	pyruvate dehydrogenase E1 component alpha subunit	thiamine diphosphate, Mg(2+), Magnesium
H	Glycolysis/Gluconeogenesis/TC A Cycle	Pyruvate dehydrogenase	1.2.4.1	K00162	pyruvate dehydrogenase E1 component beta subunit	thiamine diphosphate
H	Glycolysis/Gluconeogenesis/TC A Cycle	Pyruvate dehydrogenase	1.2.4.1	K00163	pyruvate dehydrogenase E1 component	Mg(2+), Magnesium, thiamine diphosphate
H	Glycolysis/Gluconeogenesis/TC A Cycle/Methane Metabolism	Pyruvate Oxidoreductase	1.2.7.1	K00169	pyruvate ferredoxin oxidoreductase, alpha subunit	
H	Glycolysis/Gluconeogenesis/TC A Cycle/Methane Metabolism	Pyruvate Oxidoreductase	1.2.7.1	K00170	pyruvate ferredoxin oxidoreductase, beta subunit	4Fe-4S
H	Glycolysis/Gluconeogenesis/TC A Cycle/Methane Metabolism	Pyruvate Oxidoreductase	1.2.7.1	K00171	pyruvate ferredoxin oxidoreductase, delta subunit	4Fe-4S
H	Glycolysis/Gluconeogenesis/TC A Cycle/Methane Metabolism	Pyruvate Oxidoreductase	1.2.7.1	K00172	pyruvate ferredoxin oxidoreductase, gamma subunit	4Fe-4S

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
H	Pentose Phosphate	glucose-6-phosphate dehydrogenase	1.1.1.49	K00036	glucose-6-phosphate 1-dehydrogenase	NADP, NAD
H	TCA Cycle	isocitrate dehydrogenase (NAD <sup>+</sup> )	1.1.1.41	K00030	isocitrate dehydrogenase (NAD <sup>+</sup> )	Mg(2+), Mn(2+), NAD
H	TCA Cycle	isocitrate--homoisocitrate dehydrogenase	1.1.1.286	K17753	isocitrate--homoisocitrate dehydrogenase	Mg(2+), Mn(2+), NAD
H	TCA Cycle	malate dehydrogenase (quinone)	1.1.5.4	K00116	malate dehydrogenase (quinone)	quinone, FAD, Flavoprotein
H	TCA Cycle	oxoglutarate dehydrogenase (succinyl-transferring)	1.2.4.2	K00164	2-oxoglutarate dehydrogenase E1 component	thiamine diphosphate, Metal-binding, Mg(2+), Magnesium
H	TCA Cycle	oxoglutarate dehydrogenase (succinyl-transferring)	1.2.4.2	K15791	probable 2-oxoglutarate dehydrogenase E1 component DHKTD1	thiamine diphosphate
H	TCA Cycle/Oxidative Phosphorylation/Reverse TCA Cycle	succinate dehydrogenase	1.3.5.1	K00234	succinate dehydrogenase (ubiquinone) flavoprotein subunit	quinone, ubiquinone, FAD, Flavoprotein
H	TCA Cycle/Oxidative Phosphorylation/Reverse TCA Cycle	succinate dehydrogenase	1.3.5.1	K00235	succinate dehydrogenase (ubiquinone) iron-sulfur subunit	4Fe-4S, 2Fe-2S, 3Fe-4S, quinone, ubiquinone
H	TCA Cycle/Oxidative Phosphorylation/Reverse TCA Cycle	succinate dehydrogenase	1.3.5.1	K00236	succinate dehydrogenase (ubiquinone) cytochrome b560 subunit	heme, quinone, ubiquinone
H	TCA Cycle/Oxidative Phosphorylation/Reverse TCA Cycle	succinate dehydrogenase	1.3.5.1	K00237	succinate dehydrogenase (ubiquinone) membrane anchor subunit	heme, quinone, ubiquinone
H	TCA Cycle/Oxidative Phosphorylation/Reverse TCA Cycle	succinate dehydrogenase	1.3.5.1	K00239	succinate dehydrogenase / fumarate reductase, flavoprotein subunit	FAD, Flavoprotein
H	TCA Cycle/Oxidative Phosphorylation/Reverse TCA Cycle	succinate dehydrogenase	1.3.5.1	K00240	succinate dehydrogenase / fumarate reductase, iron-sulfur subunit	4Fe-4S, 2Fe-2S, 3Fe-4S
H	TCA Cycle/Oxidative Phosphorylation/Reverse TCA Cycle	succinate dehydrogenase	1.3.5.1	K00241	succinate dehydrogenase / fumarate reductase, cytochrome b subunit	heme

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
H	TCA Cycle/Oxidative Phosphorylation/ Reverse TCA Cycle	succinate dehydrogenase	1.3.5.1	K00242	succinate dehydrogenase / fumarate reductase, membrane anchor subunit	heme
H	TCA Cycle/Oxidative Phosphorylation/ Reverse TCA Cycle	succinate dehydrogenase	1.3.5.1	K18859	succinate dehydrogenase / fumarate reductase, subunit D	
H	TCA Cycle/Oxidative Phosphorylation/ Reverse TCA Cycle	succinate dehydrogenase	1.3.5.1	K18860	putative succinate dehydrogenase / fumarate reductase, subunit D	
H	TCA Cycle/Reverse TCA Cycle	2-oxoglutarate synthase	1.2.7.3	K00174	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	
H	TCA Cycle/Reverse TCA Cycle	2-oxoglutarate synthase	1.2.7.3	K00175	2-oxoglutarate ferredoxin oxidoreductase subunit beta	Mg(2+), Magnesium
H	TCA Cycle/Reverse TCA Cycle	2-oxoglutarate synthase	1.2.7.3	K00176	2-oxoglutarate ferredoxin oxidoreductase subunit delta	4Fe-4S
H	TCA Cycle/Reverse TCA Cycle	2-oxoglutarate synthase	1.2.7.3	K00177	2-oxoglutarate ferredoxin oxidoreductase subunit gamma	
H	TCA Cycle/Reverse TCA Cycle	fumarate reductase	1.3.5.4	K00239	succinate dehydrogenase / fumarate reductase, flavoprotein subunit	FAD, Flavoprotein
H	TCA Cycle/Reverse TCA Cycle	fumarate reductase	1.3.5.4	K00240	succinate dehydrogenase / fumarate reductase, iron-sulfur subunit	4Fe-4S, 2Fe-2S, 3Fe-4S
H	TCA Cycle/Reverse TCA Cycle	fumarate reductase	1.3.5.4	K00244	fumarate reductase flavoprotein subunit	FAD, Flavoprotein, heme, Fe(3+)
H	TCA Cycle/Reverse TCA Cycle	fumarate reductase	1.3.5.4	K00245	fumarate reductase iron-sulfur subunit	4Fe-4S, 2Fe-2S, 3Fe-4S
H	TCA Cycle/Reverse TCA Cycle	isocitrate dehydrogenase (NADP+)	1.1.1.42	K00031	isocitrate dehydrogenase	Mg(2+), Mn(2+), NADP, NAD
H	TCA Cycle/Reverse TCA Cycle/Methane metabolism	malate dehydrogenase	1.1.1.37	K00024	malate dehydrogenase	NAD, NADP
H	TCA Cycle/Reverse TCA Cycle/Methane metabolism	malate dehydrogenase	1.1.1.37	K00025	malate dehydrogenase	NAD

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
H	TCA Cycle/Reverse TCA	malate dehydrogenase	1.1.1.37	K00026	malate dehydrogenase	NAD
H	Cycle/Methane metabolism TCA Cycle/Reverse TCA	malate dehydrogenase [NAD(P)+]	no EC	no KO		
HO	Hydrogen Oxidation	hydrogen dehydrogenase	1.12.1.2	K18005	[NiFe] hydrogenase diaphorase moiety large subunit	4Fe-4S, Flavoprotein, FMN, NAD
HO	Hydrogen Oxidation	hydrogen dehydrogenase	1.12.1.2	K18006	[NiFe] hydrogenase diaphorase moiety small subunit	4Fe-4S, Flavoprotein, FMN, NAD
HO	Hydrogen Oxidation	hydrogen dehydrogenase	1.12.1.2	K18007	NAD-reducing hydrogenase small subunit	4Fe-4S, 2Fe-2S, 3Fe-4S, Ni(2+), FMN, NAD
HO	Hydrogen Oxidation	hydrogen dehydrogenase (NADP+)	1.12.1.3	K17992	NADP-reducing hydrogenase subunit HndB	
HO	Hydrogen Oxidation	hydrogen dehydrogenase (NADP+)	1.12.1.3	K17993	sulphydrogenase subunit alpha	Ni(2+), iron, NADP, NAD
HO	Hydrogen Oxidation	hydrogen dehydrogenase (NADP+)	1.12.1.3	K17994	sulphydrogenase subunit delta	4Fe-4S, 3Fe-4S, Nickel, Ni(2+), NADP, NAD
HO	Hydrogen Oxidation	hydrogen dehydrogenase (NADP+)	1.12.1.3	K18330	NADP-reducing hydrogenase subunit HndA	
HO	Hydrogen Oxidation	hydrogen dehydrogenase (NADP+)	1.12.1.3	K18331	NADP-reducing hydrogenase subunit HndC	
HO	Hydrogen Oxidation	hydrogen dehydrogenase (NADP+)	1.12.1.3	K18332	NADP-reducing hydrogenase subunit HndD	
HO	Hydrogen Oxidation	hydrogen dehydrogenase [NAD(P)+]	1.12.1.5	K17993	sulphydrogenase subunit alpha	Ni(2+), iron, NADP, NAD
HO	Hydrogen Oxidation	hydrogen dehydrogenase [NAD(P)+]	1.12.1.5	K17994	sulphydrogenase subunit delta	4Fe-4S, 3Fe-4S, Nickel, Ni(2+), NADP, NAD
Intra	Na Translocating	NADH:ubiquinone reductase (Na+-transporting)	1.6.5.8	no KO		
Intra	Other	catalase	1.11.1.6	K03781	catalase	heme, NADP, NAD
Intra	Other	catalase-peroxidase	1.11.1.21	K03782	catalase-peroxidase	heme, NADP, NAD
Intra	Other	eosinophil peroxidase	1.11.1.18	K10788	eosinophil peroxidase	heme, NADP, NAD
Intra	Other	lactoperoxidase	1.11.1.7	K12550	lactoperoxidase	heme, NADP, NAD
Intra	Other	peroxidase	1.11.1.7	K00430	peroxidase	heme, NADP,



Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
						NAD
Intra	Other	peroxiredoxin 6, 1-Cys peroxiredoxin	1.11.1.7 1.11.1.15	K11188	peroxiredoxin 6, 1-Cys peroxiredoxin	
Intra	Oxidative Phosphorylation	caldariellaquinol oxidase (H+-transporting)	1.10.3.13	no KO		
Intra	Oxidative Phosphorylation	cytochrome-c peroxidase	1.11.1.5	K00428	cytochrome c peroxidase	heme, Zinc, Zinc-finger
Intra	Oxidative Phosphorylation	menaquinol oxidase (H+-transporting)	1.10.3.12	K02826	cytochrome aa3-600 menaquinol oxidase subunit II	
Intra	Oxidative Phosphorylation	menaquinol oxidase (H+-transporting)	1.10.3.12	K02827	cytochrome aa3-600 menaquinol oxidase subunit I	heme, Cu(2+)
Intra	Oxidative Phosphorylation	menaquinol oxidase (H+-transporting)	1.10.3.12	K02828	cytochrome aa3-600 menaquinol oxidase subunit III	heme, Cu(2+)
Intra	Oxidative Phosphorylation	menaquinol oxidase (H+-transporting)	1.10.3.12	K02829	cytochrome aa3-600 menaquinol oxidase subunit IV	
Intra	Oxidative Phosphorylation	NADH dehydrogenase	1.6.99.3	K00356	NADH dehydrogenase	Flavoprotein, NADP, FMN, NAD
Intra	Oxidative Phosphorylation	NADH dehydrogenase	1.6.99.3	K03885	NADH dehydrogenase	FAD, Flavoprotein, NAD, quinone, Ubiquinone
Intra	Oxidative Phosphorylation	NADH dehydrogenase	1.6.99.3	K03934	NADH dehydrogenase (ubiquinone) Fe-S protein 1	4Fe-4S, 2Fe-2S, quinone, Ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH dehydrogenase	1.6.99.3	K03935	NADH dehydrogenase (ubiquinone) Fe-S protein 2	4Fe-4S, quinone, Ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH dehydrogenase	1.6.99.3	K03936	NADH dehydrogenase (ubiquinone) Fe-S protein 3	iron-sulfur, quinone, Ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH dehydrogenase	1.6.99.3	K03940	NADH dehydrogenase (ubiquinone) Fe-S protein 7	4Fe-4S, quinone, Ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH dehydrogenase	1.6.99.3	K03941	NADH dehydrogenase (ubiquinone) Fe-S protein 8	4Fe-4S, quinone, Ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH dehydrogenase	1.6.99.3	K03942	NADH dehydrogenase (ubiquinone) flavoprotein 1	4Fe-4S quinone, ubiquinone, Flavoprotein, FMN, NAD
Intra	Oxidative Phosphorylation	NADH dehydrogenase	1.6.99.3	K03943	NADH dehydrogenase (ubiquinone) flavoprotein 2	2Fe-2S, quinone, ubiquinone, NAD

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
Intra	Oxidative Phosphorylation	NADH dehydrogenase (quinone)	1.6.99.5	K05903	NADH dehydrogenase (quinone)	4Fe-4S, quinone, Ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K00329	NADH dehydrogenase	
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K00330	NADH-quinone oxidoreductase subunit A	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K00331	NADH-quinone oxidoreductase subunit B	4Fe-4S, quinone, Ubiquinone, NAD, FAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K00332	NADH-quinone oxidoreductase subunit C	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K00333	NADH-quinone oxidoreductase subunit D	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K00334	NADH-quinone oxidoreductase subunit E	2Fe-2S, quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K00335	NADH-quinone oxidoreductase subunit F	4Fe-4S, quinone, Ubiquinone, NAD, FAD, FMN
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K00336	NADH-quinone oxidoreductase subunit G	4Fe-4S, 2Fe-2S, quinone, Ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K00337	NADH-quinone oxidoreductase subunit H	4Fe-4S, quinone, Ubiquinone, NAD, FAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K00338	NADH-quinone oxidoreductase subunit I	4Fe-4S, quinone, Ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K00339	NADH-quinone oxidoreductase subunit J	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K00340	NADH-quinone oxidoreductase subunit K	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K00341	NADH-quinone oxidoreductase subunit L	quinone, ubiquinone, NAD

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K00342	NADH-quinone oxidoreductase subunit M	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K00343	NADH-quinone oxidoreductase subunit N	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K03878	NADH-ubiquinone oxidoreductase chain 1	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K03879	NADH-ubiquinone oxidoreductase chain 2	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K03880	NADH-ubiquinone oxidoreductase chain 3	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K03881	NADH-ubiquinone oxidoreductase chain 4	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K03882	NADH-ubiquinone oxidoreductase chain 4L	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K03883	NADH-ubiquinone oxidoreductase chain 5	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K03884	NADH-ubiquinone oxidoreductase chain 6	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K03934	NADH dehydrogenase (ubiquinone) Fe-S protein 1	4Fe-4S, 2Fe-2S, quinone, ubiquinone, NAD, iron-sulfur, iron
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K03935	NADH dehydrogenase (ubiquinone) Fe-S protein 2	4Fe-4S, quinone, Ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K03936	NADH dehydrogenase (ubiquinone) Fe-S protein 3	iron-sulfur, quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K03937	NADH dehydrogenase (ubiquinone) Fe-S protein 4	iron-sulfur, quinone, ubiquinone, NAD

<b>Pathway Abbreviation</b>	<b>Process</b>	<b>Enzyme Complex Name</b>	<b>EC number</b>	<b>KEGG Orthology</b>	<b>KEGG Enzyme Name</b>	<b>Cofactors</b>
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03938	NADH dehydrogenase (ubiquinone) Fe-S protein 5	iron-sulfur, quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03939	NADH dehydrogenase (ubiquinone) Fe-S protein 6	iron-sulfur, quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03940	NADH dehydrogenase (ubiquinone) Fe-S protein 7	4Fe-4S, quinone, Ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03941	NADH dehydrogenase (ubiquinone) Fe-S protein 8	4Fe-4S, quinone, Ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03942	NADH dehydrogenase (ubiquinone) flavoprotein 1	4Fe-4S, quinone, Ubiquinone, NAD, FMN
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03943	NADH dehydrogenase (ubiquinone) flavoprotein 2	2Fe-2S, quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03944	NADH dehydrogenase (ubiquinone) flavoprotein 3	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03945	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 1	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03946	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 2	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03947	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 3	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03948	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 4	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03949	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 5	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03950	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 6	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03951	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 7	quinone, ubiquinone, NAD

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03952	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 8	quinone, ubiquinone, NAD, iron-sulfur
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03953	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 9	quinone, ubiquinone, FAD, Flavoprotein, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03954	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 10	quinone, ubiquinone, FAD, Flavoprotein, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03955	NADH dehydrogenase (ubiquinone) 1 alpha/beta subcomplex 1	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03956	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 11	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K11352	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 12	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K11353	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 13	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03957	NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 1	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03958	NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 2	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03959	NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 3	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03960	NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 4	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03961	NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 5	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03962	NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 6	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H <sup>+</sup> -translocating)	1.6.5.3	K03963	NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 7	quinone, ubiquinone, NAD

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K03964	NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 8	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K03965	NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 9	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K03966	NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 10	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K11351	NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 11	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K03967	NADH dehydrogenase (ubiquinone) 1 subunit C1	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K03968	NADH dehydrogenase (ubiquinone) 1 subunit C2	quinone, ubiquinone, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K05572	NAD(P)H-quinone oxidoreductase subunit 1	quinone, NADP, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K05573	NAD(P)H-quinone oxidoreductase subunit 2	quinone, NADP, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K05574	NAD(P)H-quinone oxidoreductase subunit 3	quinone, NADP, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K05575	NAD(P)H-quinone oxidoreductase subunit 4	quinone, NADP, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K05576	NAD(P)H-quinone oxidoreductase subunit 4L	quinone, ubiquinone, NAD, NADP
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K05577	NAD(P)H-quinone oxidoreductase subunit 5	quinone, ubiquinone, NAD, NADP
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K05578	NAD(P)H-quinone oxidoreductase subunit 6	quinone, ubiquinone, NAD, NADP
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K05579	NAD(P)H-quinone oxidoreductase subunit H	quinone, ubiquinone, NAD, NADP

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K05580	NAD(P)H-quinone oxidoreductase subunit I	4Fe-4S, Iron-sulfur, Iron, Quinone, quinone, NADP, Metal-binding, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K05581	NAD(P)H-quinone oxidoreductase subunit J	quinone, ubiquinone, NAD, NADP
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K05582	NAD(P)H-quinone oxidoreductase subunit K	4Fe-4S, quinone, NADP, NAD
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K05583	NAD(P)H-quinone oxidoreductase subunit L	quinone, ubiquinone, NAD, NADP
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K05584	NAD(P)H-quinone oxidoreductase subunit M	quinone, ubiquinone, NAD, NADP
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K05585	NAD(P)H-quinone oxidoreductase subunit N	quinone, ubiquinone, NAD, NADP
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K05586	bidirectional [NiFe] hydrogenase diaphorase subunit	
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K05587	bidirectional [NiFe] hydrogenase diaphorase subunit	
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K05588	bidirectional [NiFe] hydrogenase diaphorase subunit	
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K13378	NADH-quinone oxidoreductase subunit C/D	quinone, ubiquinone, NAD, NADP
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K13380	NADH-quinone oxidoreductase subunit B/C/D	quinone, ubiquinone, NAD, NADP
Intra	Oxidative Phosphorylation	NADH:ubiquinone reductase (H+-translocating)	1.6.5.3	K15863	NADH-quinone oxidoreductase subunit L/M	
Intra	Oxidative Phosphorylation	quinol---cytochrome-c reductase	1.10.2.2	K00410	ubiquinol-cytochrome c reductase cytochrome b/c1 subunit	heme

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
Intra	Oxidative Phosphorylation	quinol---cytochrome-c reductase	1.10.2.2	K00411	ubiquinol-cytochrome c reductase iron-sulfur subunit	2Fe-2S
Intra	Oxidative Phosphorylation	quinol---cytochrome-c reductase	1.10.2.2	K00412	ubiquinol-cytochrome c reductase cytochrome b subunit	heme
Intra	Oxidative Phosphorylation	quinol---cytochrome-c reductase	1.10.2.2	K00413	ubiquinol-cytochrome c reductase cytochrome c1 subunit	heme
Intra	Oxidative Phosphorylation	quinol---cytochrome-c reductase	1.10.2.2	K00414	ubiquinol-cytochrome c reductase core subunit 1	
Intra	Oxidative Phosphorylation	quinol---cytochrome-c reductase	1.10.2.2	K00415	ubiquinol-cytochrome c reductase core subunit 2	
Intra	Oxidative Phosphorylation	quinol---cytochrome-c reductase	1.10.2.2	K00416	ubiquinol-cytochrome c reductase subunit 6	heme
Intra	Oxidative Phosphorylation	quinol---cytochrome-c reductase	1.10.2.2	K00417	ubiquinol-cytochrome c reductase subunit 7	
Intra	Oxidative Phosphorylation	quinol---cytochrome-c reductase	1.10.2.2	K00418	ubiquinol-cytochrome c reductase subunit 8	quinone, ubiquinone
Intra	Oxidative Phosphorylation	quinol---cytochrome-c reductase	1.10.2.2	K00419	ubiquinol-cytochrome c reductase subunit 9	heme
Intra	Oxidative Phosphorylation	quinol---cytochrome-c reductase	1.10.2.2	K00420	ubiquinol-cytochrome c reductase subunit 10	
Intra	Oxidative Phosphorylation	ubiquinol oxidase (electrogenic, non H <sup>+</sup> -transporting)	1.10.3.14	no KO		
Intra	Oxidative Phosphorylation	ubiquinol oxidase (H <sup>+</sup> -transporting)	1.10.3.10	no KO		
M	Methanogenesis	5,10-methenyltetrahydro methanopterin hydrogenase	1.12.98.2	K13942	5,10-methenyltetrahydromethanopterin hydrogenase	
M	Methanogenesis	5,10-methylenetetrahydro methanopterin reductase	1.5.98.2	K00320	5,10-methylenetetrahydromethanopterin reductase	
M	Methanogenesis	carbon-monoxide dehydrogenase (acceptor)	1.2.99.2	K00198	carbon-monoxide dehydrogenase catalytic subunit	4Fe-4S Nickel, Ni-Fe-S
M	Methanogenesis	carbon-monoxide dehydrogenase (acceptor)	1.2.99.2	K03518	carbon-monoxide dehydrogenase small subunit	2Fe-2S



Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
M	Methanogenesis	carbon-monoxide dehydrogenase (acceptor)	1.2.99.2	K03519	carbon-monoxide dehydrogenase medium subunit	FAD, Flavoprotein
M	Methanogenesis	carbon-monoxide dehydrogenase (acceptor)	1.2.99.2	K03520	carbon-monoxide dehydrogenase large subunit	molybdopterin, Copper
M	Methanogenesis	carbon-monoxide dehydrogenase (ferredoxin)	1.2.7.4	K00192	acetyl-CoA decarbonylase/synthase complex subunit alpha	4Fe-4S, Nickel, Ni-Fe-S
M	Methanogenesis	carbon-monoxide dehydrogenase (ferredoxin)	1.2.7.4	K00198	carbon-monoxide dehydrogenase catalytic subunit	4Fe-4S, Nickel, Ni-Fe-S
M	Methanogenesis	CoB-CoM heterodisulfide reductase	1.8.98.1	K03388	heterodisulfide reductase subunit A	4Fe-4S, FAD, Flavoprotein, Selenocysteine
M	Methanogenesis	CoB-CoM heterodisulfide reductase	1.8.98.1	K03389	heterodisulfide reductase subunit B	
M	Methanogenesis	CoB-CoM heterodisulfide reductase	1.8.98.1	K03390	heterodisulfide reductase subunit C	4Fe-4S
M	Methanogenesis	CoB-CoM heterodisulfide reductase	1.8.98.1	K08264	heterodisulfide reductase subunit D	4Fe-4S
M	Methanogenesis	CoB-CoM heterodisulfide reductase	1.8.98.1	K08265	heterodisulfide reductase subunit E	
M	Methanogenesis	coenzyme F420 hydrogenase	1.12.98.1	K00440	coenzyme F420 hydrogenase subunit alpha	Iron-sulfur, Ni(2+), FAD, Flavoprotein
M	Methanogenesis	coenzyme F420 hydrogenase	1.12.98.1	K00441	coenzyme F420 hydrogenase subunit beta	4Fe-4S, Ni(2+), FAD, heme
M	Methanogenesis	coenzyme F420 hydrogenase	1.12.98.1	K00443	coenzyme F420 hydrogenase subunit gamma	4Fe-4S, Ni(2+), FAD, heme
M	Methanogenesis	Formylmethanofuran Dehydrogenase	1.2.99.5	K00200	formylmethanofuran dehydrogenase subunit A	inc
M	Methanogenesis	Formylmethanofuran Dehydrogenase	1.2.99.5	K00201	formylmethanofuran dehydrogenase subunit B	tungsten, selenocysteine
M	Methanogenesis	Formylmethanofuran Dehydrogenase	1.2.99.5	K00202	formylmethanofuran dehydrogenase subunit C	molybdenum, tungsten
M	Methanogenesis	Formylmethanofuran Dehydrogenase	1.2.99.5	K00203	formylmethanofuran dehydrogenase subunit D	
M	Methanogenesis	Formylmethanofuran Dehydrogenase	1.2.99.5	K11261	formylmethanofuran dehydrogenase subunit E	

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
M	Methanogenesis	Formylmethanofuran Dehydrogenase	1.2.99.5	K00205	4Fe-4S ferredoxin	
M	Methanogenesis	Formylmethanofuran Dehydrogenase	1.2.99.5	K11260	4Fe-4S ferredoxin	
M	Methanogenesis	Formylmethanofuran Dehydrogenase	1.2.99.5	K00204	4Fe-4S ferredoxin	
M	Methanogenesis	methylenetetrahydropterin dehydrogenase	1.5.98.1	K00319	methylenetetrahydropterin dehydrogenase	
MO	Methane oxidation	alcohol oxidase	1.1.3.13	K17066	alcohol oxidase	FAD, Flavoprotein
MO	Methane oxidation	methane monooxygenase (soluble)	1.14.13.25	K16157	methane monooxygenase component A alpha chain	iron, NADP, NAD
MO	Methane oxidation	methane monooxygenase (soluble)	1.14.13.25	K16158	methane monooxygenase component A beta chain	NADP, NAD
MO	Methane oxidation	methane monooxygenase (soluble)	1.14.13.25	K16159	methane monooxygenase component A gamma chain	NADP, NAD
MO	Methane oxidation	methane monooxygenase (soluble)	1.14.13.25	K16161	methane monooxygenase component C	2Fe-2S, FAD, Flavoprotein, NADP, NAD
MO	Methane oxidation	methane monooxygenase (soluble)	1.14.13.25	K16162	methane monooxygenase component D	
MO	Methane oxidation	methane/ammonia monooxygenase	1.14.18.3 or 1.14.99.39	K10944	methane/ammonia monooxygenase subunit A	
MO	Methane oxidation	methane/ammonia monooxygenase	1.14.18.3 or 1.14.99.39	K10945	methane/ammonia monooxygenase subunit B	Cu(2+), NAD
MO	Methane oxidation	methane/ammonia monooxygenase	1.14.18.3 or 1.14.99.39	K10946	methane/ammonia monooxygenase subunit C	
N	Annamox	R10471	no EC	no KO		
N	Nitrification	hydroxylamine dehydrogenase	1.7.2.6	K10535	hydroxylamine dehydrogenase	heme
N	Nitrification	hydroxylamine oxidase (cytochrome)	1.7.3.6	no KO		
N	Nitrification	methane/ammonia monooxygenase	1.14.18.3 or 1.14.99.39	K10944	methane/ammonia monooxygenase subunit A	
N	Nitrification	methane/ammonia monooxygenase	1.14.18.3 or 1.14.99.39	K10945	methane/ammonia monooxygenase subunit B	Cu(2+), NAD
N	Nitrification	methane/ammonia monooxygenase	1.14.18.3 or 1.14.99.39	K10946	methane/ammonia monooxygenase subunit C	

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
NF	N-fixation	nitrogenase	1.18.6.1	K00531	nitrogenase delta subunit	
NF	N-fixation	nitrogenase	1.18.6.1	K02586	nitrogenase molybdenum-iron protein alpha chain	Molybdenum, iron-sulfur
NF	N-fixation	nitrogenase	1.18.6.1	K02588	nitrogenase iron protein NifH	4Fe-4S
NF	N-fixation	nitrogenase	1.18.6.1	K02591	nitrogenase molybdenum-iron protein beta chain	Molybdenum, iron-sulfur
NF	N-fixation	nitrogenase	1.19.6.1	no KO	nitrogenase(flavodoxin)	
OP	Oxygenic Photosynthesis	Cytochrome b6f complex	1.10.9.2	K02635	cytochrome b6	heme
OP	Oxygenic Photosynthesis	Cytochrome b6f complex	1.10.9.2	K02636	cytochrome b6-f complex iron-sulfur subunit	2Fe-2S, quinone
OP	Oxygenic Photosynthesis	Cytochrome b6f complex	1.10.9.2	K02637	cytochrome b6-f complex subunit 4	
OP	Oxygenic Photosynthesis	Cytochrome b6f complex	1.10.9.2	K02634	apocytochrome f	heme
OP	Oxygenic Photosynthesis	Cytochrome b6f complex	1.10.9.2	K02642	cytochrome b6-f complex subunit 6	
OP	Oxygenic Photosynthesis	Cytochrome b6f complex	1.10.9.2	K02643	cytochrome b6-f complex subunit 7	
OP	Oxygenic Photosynthesis	Cytochrome b6f complex	1.10.9.2	K03689	cytochrome b6-f complex subunit 8	
OP	Oxygenic Photosynthesis	Cytochrome b6f complex	1.10.9.2	K02640	cytochrome b6-f complex subunit 5	
OP	Oxygenic Photosynthesis	ferredoxin-NADP+ reductase	1.18.1.2	K02641	ferredoxin--NADP+ reductase	FAD, Flavoprotein, NADP, NAD
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02703	photosystem II P680 reaction center D1 protein	manganese, magnesium, Iron, quinone, heme
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02706	photosystem II P680 reaction center D2 protein	magnesium, iron, quinone, heme
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02705	photosystem II CP43 chlorophyll apoprotein	Manganese
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02704	photosystem II CP47 chlorophyll apoprotein	
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02707	photosystem II cytochrome b559 subunit alpha	heme
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02708	photosystem II cytochrome b559 subunit beta	heme
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02713	photosystem II PsbL protein	
OP	Oxygenic	Photosystem II	1.10.3.9	K02711	photosystem II PsbJ	

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
	Photosynthesis				protein	
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02712	photosystem II PsbK protein	
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02714	photosystem II PsbM protein	
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02709	photosystem II PsbH protein	
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02710	photosystem II PsbI protein	
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02716	photosystem II oxygen-evolving enhancer protein 1	Manganese
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02717	photosystem II oxygen-evolving enhancer protein 2	
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K08901	photosystem II oxygen-evolving enhancer protein 3	
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K03541	photosystem II 10kDa protein	
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K03542	photosystem II 22kDa protein	
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02718	photosystem II PsbT protein	
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02719	photosystem II PsbU protein	
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02720	photosystem II cytochrome c550	heme
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02721	photosystem II PsbW protein	
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02722	photosystem II PsbX protein	
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02723	photosystem II PsbY protein	Manganese
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K02724	photosystem II PsbZ protein	
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K08902	photosystem II Psb27 protein	
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K08903	photosystem II 13kDa protein	
OP	Oxygenic Photosynthesis	Photosystem II	1.10.3.9	K08904	photosystem II Psb28-2 protein	
OP	Oxygenic Photosynthesis	Photosytem I	1.97.1.12	K02689	photosystem I P700 chlorophyll a apoprotein A1	Magnesium, 4Fe-4S, quinone
OP	Oxygenic Photosynthesis	Photosytem I	1.97.1.12	K02690	photosystem I P700 chlorophyll a apoprotein A2	Magnesium, 4Fe-4S, quinone
OP	Oxygenic Photosynthesis	Photosytem I	1.97.1.12	K02691	photosystem I subunit VII	4Fe-4S

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
OP	Oxygenic Photosynthesis	Photosytem I	1.97.1.12	K02692	photosystem I subunit II	
OP	Oxygenic Photosynthesis	Photosytem I	1.97.1.12	K02693	photosystem I subunit IV	
OP	Oxygenic Photosynthesis	Photosytem I	1.97.1.12	K02694	photosystem I subunit III	
OP	Oxygenic Photosynthesis	Photosytem I	1.97.1.12	K08905	photosystem I subunit V	
OP	Oxygenic Photosynthesis	Photosytem I	1.97.1.12	K02695	photosystem I subunit VI	
OP	Oxygenic Photosynthesis	Photosytem I	1.97.1.12	K02696	photosystem I subunit VIII	
OP	Oxygenic Photosynthesis	Photosytem I	1.97.1.12	K02697	photosystem I subunit IX	
OP	Oxygenic Photosynthesis	Photosytem I	1.97.1.12	K02698	photosystem I subunit X	
OP	Oxygenic Photosynthesis	Photosytem I	1.97.1.12	K02699	photosystem I subunit XI	
OP	Oxygenic Photosynthesis	Photosytem I	1.97.1.12	K02700	photosystem I subunit XII	
OP	Oxygenic Photosynthesis	Photosytem I	1.97.1.12	K02701	photosystem I subunit PsaN	
OP	Oxygenic Photosynthesis	Photosytem I	1.97.1.12	K14332	photosystem I subunit PsaO	
OP	Oxygenic Photosynthesis	Photosytem I	1.97.1.12	K02702	photosystem I 4.8kDa protein	
SDO	Sulfide Oxidation	sulfide:quinone reductase	1.8.5.4	no KO		
SDO	Thiosulfate Oxidation	Thiosulfate dehydrogenase	1.8.2.2	no KO		
SDO	Thiosulfate Oxidation	thiosulfate dehydrogenase (quinone)	1.8.5.2	K16936	thiosulfate dehydrogenase [quinone] small subunit	
SDO	Thiosulfate Oxidation	Thiosulfate Oxidation (SOX)	no EC	K08738	cytochrome c	heme
SDO	Thiosulfate Oxidation	Thiosulfate Oxidation (SOX)	no EC	K17222	sulfur-oxidizing protein SoxA	Heme, Cu(2+)
SDO	Thiosulfate Oxidation	Thiosulfate Oxidation (SOX)	no EC	K17223	sulfur-oxidizing protein SoxX	heme
SDO	Thiosulfate Oxidation	Thiosulfate Oxidation (SOX)	no EC	K17224	sulfur-oxidizing protein SoxB	
SDO	Thiosulfate Oxidation	Thiosulfate Oxidation (SOX)	no EC	K17225	sulfane dehydrogenase subunit SoxC	
SDO	Thiosulfate Oxidation	Thiosulfate Oxidation (SOX)	no EC	K17226	sulfur-oxidizing protein SoxY	
SDO	Thiosulfate Oxidation	Thiosulfate Oxidation (SOX)	no EC	K17227	sulfur-oxidizing protein SoxZ	
SO	Sulfur Metabolism	sulfite dehydrogenase	1.8.2.1	K05301	sulfite dehydrogenase	
SO	Sulfur Metabolism	sulfite oxidase	1.8.3.1	K00387	sulfite oxidase	molybdopterin, heme

Pathway Abbreviation	Process	Enzyme Complex Name	EC number	KEGG Orthology	KEGG Enzyme Name	Cofactors
SR	Sulfur Metabolism	H <sub>2</sub> :polysulfide oxidoreductase	1.12.98.4	K17995	sulphydrogenase subunit gamma (sulfur reductase)	2Fe-2S, FAD, Flavoprotein,
SR	Sulfur Metabolism	H <sub>2</sub> :polysulfide oxidoreductase	1.12.98.4	K17996	sulphydrogenase subunit beta (sulfur reductase)	4Fe-4S
SR	Sulphydrogenase	hydrogen dehydrogenase [NAD(P)+]	1.12.1.5	K17993	sulphydrogenase subunit alpha	Iron, Ni(2+), NADP, NAD
SR	Sulphydrogenase	hydrogen dehydrogenase [NAD(P)+]	1.12.1.5	K17994	sulphydrogenase subunit delta	4Fe-4S, 3Fe-4S, Ni(2+), NADP, NAD
STR	Sulfate reduction	adenylyl-sulfate reductase	1.8.99.2	K00394	adenylylsulfate reductase, subunit A	
STR	Sulfate reduction	adenylyl-sulfate reductase	1.8.99.2	K00395	adenylylsulfate reductase, subunit B	
STR	Sulfate reduction	adenylyl-sulfate reductase (glutathione)	1.8.4.9	K05907	adenylyl-sulfate reductase (glutathione)	4Fe-4S
STR	Sulfate reduction	adenylyl-sulfate reductase (thioredoxin)	1.8.4.10	no KO		
STR	Sulfite reduction	sulfite reductase	1.8.99.1	K11180	sulfite reductase alpha subunit (and 1.8.99.3)	4Fe-4S, heme
STR	Sulfite reduction	sulfite reductase	1.8.99.1	K11181	sulfite reductase beta subunit (and 1.8.99.3)	4Fe-4S, heme
STR	Sulfur assimilation	phosphoadenylyl-sulfate reductase (thioredoxin)	1.8.4.8	K00390	phosphoadenosine phosphosulfate reductase	NADP, NAD
STR	Sulfur assimilation	sulfite reductase (ferredoxin)	1.8.7.1	K00392	sulfite reductase (ferredoxin)	4Fe-4S, heme
STR	Sulfur assimilation	sulfite reductase (NADPH)	1.8.1.2	K00380	sulfite reductase (NADPH) flavoprotein alpha-component	FAD, Flavoprotein, NADP, FMN, NAD
STR	Sulfur assimilation	sulfite reductase (NADPH)	1.8.1.2	K00381	sulfite reductase (NADPH) hemoprotein beta-component	4Fe-4S, heme, NADP, NAD
Ex	Arsenate reduction	arsenate reductase	1.20.4.1	K00537		
Ex	Arsenate reduction	arsenate reductase	1.20.4.1	K03741		
Ex	Selenate reduction	Putative selenate reductase	1.97.1.9	K12527		

<b>Pathway Abbreviation</b>	<b>Process</b>	<b>Enzyme Complex Name</b>	<b>EC number</b>	<b>KEGG Orthology</b>	<b>KEGG Enzyme Name</b>	<b>Cofactors</b>
Ex	Iron Reduction	Ferric iron reductase		K13255		
Ex	Mercuric reductase	Mercuric reductase	1.16.1.1	K00520		NAD, FAD

**Supplemental Table 2.** List of the taxa presented in Figure 2.1 and the sources used to survey their physiology and metabolism.

<b>Domain</b>	<b>Phylum</b>	<b>Class</b>	<b>Reference</b>
<b>Archaea</b>	<i>Euryarchaeota</i>		(6, 9, 15, 18, 21)
	<i>Crenarchaeota</i>		(6, 8, 18, 21, 24)
<b>Bacteria</b>	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	(6, 18, 21)
		<i>Betaproteobacteria</i>	
		<i>Alphaproteobacteria</i>	
		<i>Epsilonproteobacteria</i>	
		<i>Deltaproteobacteria</i>	
	<i>Chlorobi</i>		(6, 18, 21)
	<i>Nitrospirae</i>		(6, 16, 18, 21)
	<i>Cyanobacteria</i>		(6, 18, 21)
	<i>Chloroflexi</i>		
	<i>Firmicutes</i>		
	<i>Aquificae</i>		
<i>Thermodesulfobacteria</i>		(6, 12, 18, 21)	



**Supplemental Table 3.** A list of enzymes from Figure 3.1 and the sources for the midpoint potentials of their corresponding redox centers.

Enzyme Name	Organism	Redox Center (or couple)	Midpoint Potential	Reference
Selenate reductase	<i>Thauera selenatis</i>	[Fe <sub>3</sub> S <sub>4</sub> ]	+118	(7)
Formylmethanofuran dehydrogenase	<i>Methanobacterium thermoautotrophicum</i>	Molybdopterin dinucleotide cofactor	-530	(2)
Formate dehydrogenase	<i>Methanobacterium formicicum</i>	Mo(V)/Mo(IV)	-470	(1)
APS reductase	<i>Desulfovibrio gigas</i>	Center II (Fe <sub>4</sub> S <sub>4</sub> Ferredoxin)	-400	(14)
Sulfide-quinone reductase	<i>Acidithiobacillus ferrooxidans</i>	FAD Semiquinone	-139	(25)
p870 (primary e <sup>-</sup> acceptor)	<i>Rhodospseudomonas spheroides</i>	Bacteriochlorophyll reaction center	-45	(5)
Cytochrome C oxidase	mitochondrial	Cu	+340	(17)
Nitrate reductase	<i>Rhodobacter sphaeroides</i>	Mo(VI)/Mo(V)	+570	(4)
Assimilatory nitrate reductase	<i>Escherichia coli</i>	Mo(V)/Mo(VI)	+250	(19)
p700	<i>Synechocystis</i> sp. PCC 6803	p700	+260	(10)
p680	generic	p680	+1200	(11)
Arsenate reductase	<i>Synechocystis</i> sp. PCC 6803	Single disulfide	-165	(13)
Ferric iron reductase	<i>Geobacter sulfurreducens</i>	Heme (Cytochrome)	-167	(22)
Nitrite reductase	<i>Rhodobacter sphaeroides</i>	Type I (Cu)	+247	(20)
Nitric oxide reductase	<i>Paracoccus denitrificans</i>	Low-spin b heme	+345	(3)
Carbon monoxide dehydrogenase	<i>Rhodospirillum rubrum</i>	Ni-X-[Fe <sub>4</sub> S <sub>4</sub> ] (C-center)	-110	(23)

## Supplemental References

1. Barber, M.J., Siegel, L.M., Schauer, N.L., May, H.D. and Ferry, J.G. 1983. Formate dehydrogenase from *Methanobacterium formicicum*. Electron paramagnetic resonance spectroscopy of the molybdenum and iron-sulfur centers. *Journal of Biological Chemistry* 258: 10839-10845.
2. Bertram, Peter A., and Rudolf K. Thauer. 1994. Thermodynamics of the formylmethanofuran dehydrogenase reaction in *Methanobacterium thermoautotrophicum*. *European Journal of Biochemistry* 226(3): 811-818
3. Butland, G., Spiro, S., Watmough, N.J. and Richardson, D.J. 2001. Two conserved glutamates in the bacterial nitric oxide reductase are essential for activity but not assembly of the enzyme. *Journal of bacteriology* 183(1): 189-199
4. Dementin, S., Arnoux, P., Frangioni, B., Grosse, S., Léger, C., Burlat, B., Guigliarelli, B., Sabaty, M. and Pignol, D. 2007. Access to the active site of periplasmic nitrate reductase: insights from site-directed mutagenesis and zinc inhibition studies. *Biochemistry* 46(34): 9713-9721
5. Dutton, P. Leslie, John S. Leigh, and Cohn A. Wraight. 1973. Direct measurement of the midpoint potential of the primary electron acceptor in *Rhodospseudomonas spheroides in situ* and in the isolated state: some relationships with pH and o-phenanthroline. *FEBS letters* 36(2): 169-173
6. Dworkin, M. and Falkow, S. 2006. *The Prokaryotes a Handbook on the Biology of Bacteria*. 3rd ed. New York, Springer
7. Elizabeth, J.D., Watts, C.A., Jepson, B.J., Kirsty, L.I.N.E., Santini, J.M., Richardson, D.J. and Butler, C.S. 2007. Investigation of the redox centres of selenate reductase from *Thauera selenatis* by electron paramagnetic resonance spectroscopy. *Biochemical Journal* 408: 19-28.
8. Friedrich, C.G., Bardischewsky, F., Rother, D., Quentmeier, A. and Fischer, J. 2005. Prokaryotic sulfur oxidation. *Current opinion in microbiology*, 8(3): 253-259
9. Hafenbradl, D., Keller, M., Dirmeier, R., Rachel, R., Rossnagel, P., Burggraf, S., Huber, H. and Stetter, K.O. 1996. *Ferroglobus placidus* gen. nov., sp. nov., a novel hyperthermophilic archaeum that oxidizes Fe<sup>2+</sup> at neutral pH under anoxic conditions. *Archives of Microbiology*, 166(5): 308-314
10. Hamacher, E., Kruip, J., Rögner, M. and Mäntele, W. 1996. Characterization of the primary electron donor of photosystem I, P700, by electrochemistry and Fourier transform infrared (FTIR) difference spectroscopy. *Spectrochimica Acta Part A: Molecular and Biomolecular Spectroscopy* 52(1): 107-121

11. Hillier, Warwick, and Gerald T. Babcock. 2001. Photosynthetic reaction centers. *Plant physiology* 125(1): 33-37
12. Jeanthon, C., L'Haridon, S., Cueff, V., Banta, A., Reysenbach, A.L. and Prieur, D., 2002. *Thermodesulfobacterium hydrogeniphilum* sp. nov., a thermophilic, chemolithoautotrophic, sulfate-reducing bacterium isolated from a deep-sea hydrothermal vent at Guaymas Basin, and emendation of the genus *Thermodesulfobacterium*. *International Journal of Systematic and Evolutionary Microbiology*, 52(3): 765-772
13. Kim, S.G., Chung, J.S., Sutton, R.B., Lee, J.S., López-Maury, L., Lee, S.Y., Florencio, F.J., Lin, T., Zabet-Moghaddam, M., Wood, M.J. and Nayak, K. 2012. Redox, mutagenic and structural studies of the glutaredoxin/arsenate reductase couple from the cyanobacterium *Synechocystis* sp. PCC 6803. *Biochimica et Biophysica Acta -Proteins and Proteomics* 1824(2): 392-403
14. Lampreia, J., Moura, I., Teixeira, M., Peck, H.D., Legall, J., Huynh, B.H. and Moura, J.J. 1990. The active centers of adenylylsulfate reductase from *Desulfovibrio gigas*. *European Journal of Biochemistry* 188(3): 653-664
15. Leigh, J.A., 2000. Nitrogen fixation in methanogens: the archaeal perspective. *Current issues in molecular biology*, 2: 125-131
16. Lin, W., Deng, A., Wang, Z., Li, Y., Wen, T., Wu, L.F., Wu, M. and Pan, Y., 2014. Genomic insights into the uncultured genus 'Candidatus Magnetobacterium' in the phylum Nitrospirae. *The ISME journal*
17. Lindsay, J. G., C. S. Owen, and D. F. Wilson. 1975. The invisible copper of cytochrome c oxidase: pH and ATP dependence of its midpoint potential and its role in the oxygen reaction. *Archives of Biochemistry and Biophysics* 169(2): 492-505
18. Madigan, M.T., Martinko, J.M., Bender, K.S. and Buckley, D.H. 2014. Brock Biology of Microorganisms. 14th edition, Benjamin Cummings
19. Magalon, A., Asso, M., Guigliarelli, B., Rothery, R.A., Bertrand, P., Giordano, G. and Blasco, F. 1998. Molybdenum cofactor properties and [Fe-S] cluster coordination in *Escherichia coli* nitrate reductase A: Investigation by site-directed mutagenesis of the conserved His-50 residue in the NarG subunit. *Biochemistry* 37(20): 7363-7370
20. Olesen, K., Veselov, A., Zhao, Y., Wang, Y., Danner, B., Scholes, C.P. and Shapleigh, J.P. 1998. Spectroscopic, kinetic, and electrochemical characterization of heterologously expressed wild-type and mutant forms of copper-containing nitrite reductase from *Rhodobacter sphaeroides* 2.4. 3. *Biochemistry* 37(17): 6086-6094
21. Rosenberg, E., DeLong, E. F., Lory, S., Stackebrandt, E., Thompson, F.L. 2013. The Prokaryotes Prokaryotic Communities and Ecophysiology. Berlin, Heidelberg: Springer Berlin Heidelberg

22. Seeliger, Sabine, Ralf Cord-Ruwisch, and Bernhard Schink. 1998. A periplasmic and extracellular c-type cytochrome of *Geobacter sulfurreducens* acts as a ferric iron reductase and as an electron carrier to other acceptors or to partner bacteria. *Journal of Bacteriology* 180(14): 3686-3691
23. Spangler, N.J., Lindahl, P.A., Bandarian, V. and Ludden, P.W. 1996. Spectroelectrochemical characterization of the metal centers in carbon monoxide dehydrogenase (CODH) and nickel-deficient CODH from *Rhodospirillum rubrum*. *Journal of Biological Chemistry*, 271(14):7973-7977
24. Wuchter, C., Abbas, B., Coolen, M.J., Herfort, L., van Bleijswijk, J., Timmers, P., Strous, M., Teira, E., Herndl, G.J., Middelburg, J.J. and Schouten, S. 2006. Archaeal nitrification in the ocean. *Proceedings of the National Academy of Sciences*, 103(33): 12317-12322
25. Zhang, Yanfei, and Joel H. Weiner. 2014. Characterization of the kinetics and electron paramagnetic resonance spectroscopic properties of *Acidithiobacillus ferrooxidans* sulfide: quinone oxidoreductase (SQR). *Archives of biochemistry and biophysics* 56: 110-119