

SOM Table 4. Genes with known homologues involved in carbon metabolism

accoa¹ acetyl-CoA pathway (CO₂ fixation)

enzyme	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database
5-methyltetrahydrofolate-corrinoid FeS protein methyltransferase	kustd1538	<i>Clostridium tetani</i> (CTC01806:791/261 4-259 (30%))	<i>Thermoanaerobacter tengcongensis</i> (tte:TTE1803:803/261 4-259 (31%))
small subunit corrinoid iron-sulfur protein	kustd1539	<i>Moorella thermoacetica</i> (L07100:323/318 1-317 (51%))	<i>Dehalococcoides ethenogenes</i> _195 (det:DET0701:313/318 2-317 (42%))
carbon monoxide dehydrogenase/acetyl CoA synthetase, nickel insertion protein	kustd1540	<i>Methanosarcina acetivorans</i> (MA1013:232/256 22-244 (33%))	<i>Methanococcus maripaludis</i> _S2 (mmp:MMP0982:250/256 5-238 (42%))
Conserved hypothetical FeS protein	kustd1541	<i>Desulfovibrio vulgaris</i> (DVU0908:543/644 214-626 (25%))	<i>Dehalococcoides ethenogenes</i> _195 (det:DET0704:640/644 1-635 (36%))
large subunit corrinoid/iron-sulfur protein	kustd1542	<i>Moorella thermoacetica</i> (L07099:446/446 1-441 (46%))	<i>Dehalococcoides ethenogenes</i> _195 (det:DET0699:448/446 1-441 (43%))
carbon monoxide dehydrogenase/acetyl CoA synthetase, alpha subunit	kustd1545	<i>Methanosarcina mazei</i> (MM0686:469/727 318-722 (40%))	<i>Dehalococcoides ethenogenes</i> _195 (det:DET0700:733/727 1-726 (50%))
carbon monoxide dehydrogenase/acetyl CoA synthetase, beta subunit	kustd1546	<i>Methanosarcina mazei</i> (MM0121:628/653 10-627 (46%))	<i>Methanosarcina mazei</i> (mma:MM0121:628/653 10-627 (48%))
carbon monoxide dehydrogenase/acetyl CoA synthetase, nickel insertion protein	kustd1547	<i>Methanosarcina acetivorans</i> (MA1013:232/257 20-250 (30%))	<i>Methanobacterium thermoautotrophicum</i> (mth:MTH1120:273/257 1-229 (51%))
large subunit corrinoid/iron-sulfur protein	kuste3001	<i>Moorella thermoacetica</i> (L07099:446/257 2-43 (52%))	<i>Dehalococcoides CBDB1</i> (deh:cbdb_A651:448/257 2-68 (42%))
carbon monoxide dehydrogenase/acetyl CoA synthetase, beta subunit	kuste4610	<i>Methanosarcina mazei</i> (MM0121:628/658 7-658 (37%))	<i>Thermoanaerobacter tengcongensis</i> (tte:TTE1708:642/658 14-658 (41%))
formate dehydrogenase / nuoG-like	kustd1550	<i>Moorella thermoacetica</i> (AAB18330:893/896 1-887 (47%))	<i>Enterococcus faecalis</i> _V583 (efa:EF1390:906/896 3-894 (46%))
formate dehydrogenase / nuoF-like	kustd1551	<i>Ralstonia eutropha</i> (AJ223295:520/552 40-550 (40%))	<i>Thermoanaerobacter tengcongensis</i> (tte:TTE0893:596/552 31-549 (60%))
	kustd1552	<i>Escherichia coli</i> (b2285:166/162 27-144 (38%))	<i>Thermococcus kodakaraensis_KOD1</i> (tko:TK1614:154/162 31-160 (49%))
formate dehydrogenase, alpha subunit	kuste2423	<i>Moorella thermoacetica</i> (AAB18330:893/896 1-887 (48%))	<i>Enterococcus faecalis</i> _V583 (efa:EF1390:906/896 3-894 (46%))
formate dehydrogenase, cytochrome b556	kuste2856	<i>Escherichia coli</i> (b3892:211/295 15-208 (21%))	<i>Desulfotalea psychrophila</i> _LSv54 (dps:DP1985:567/295 16-290 (35%))
formate:quinone oxidoreductase (complex 1)	kustc0838	<i>Escherichia coli</i> (b2278:613/642 2-636 (38%))	<i>Geobacter sulfurreducens</i> (gsu:GSU0349:666/642 1-634 (57%))
	kustc0837	<i>Escherichia coli</i> (b2279:100/100 1-99 (38%))	<i>Geobacter sulfurreducens</i> (gsu:GSU0348:100/100 1-99 (63%))
	kustc0836	<i>Escherichia coli</i> (b2280:184/169 4-169 (26%))	<i>Geobacter sulfurreducens</i> (gsu:GSU0347:167/169 1-168 (42%))
	kustc0835	<i>Escherichia coli</i> (b2281:180/139 24-133 (46%))	<i>Geobacter sulfurreducens</i> (gsu:GSU0346:132/139 1-132 (48%))
	kustc0834	<i>Salmonella typhimurium</i> (L42521:325/332 6-328 (47%))	<i>Geobacter sulfurreducens</i> (gsu:GSU0345:348/332 6-330 (56%))
	kustc0833	no validated blast hit	<i>Methanosarcina acetivorans</i> (mac:MA4664:41/95 1-37 (51%))
	kustc0828	<i>Moorella thermoacetica</i> (AAB18330:893/890 3-874 (35%))	<i>Desulfotalea psychrophila</i> _LSv54 (dps:DP0682:887/890 1-874 (32%))
	kustc0827	<i>Ralstonia eutropha</i> (AJ223295:520/616 21-543 (38%))	<i>Thermococcus kodakaraensis_KOD1</i> (tko:TK1613:600/616 21-616 (57%))
	kustc0826	<i>Escherichia coli</i> (b2285:166/164 6-163 (34%))	<i>Geobacter sulfurreducens</i> (gsu:GSU0342:173/164 4-161 (47%))
	kustc0825	<i>Paracoccus denitrificans</i> (M93015:412/396 1-396 (45%))	<i>Geobacter sulfurreducens</i> (gsu:GSU0341:390/396 9-396 (60%))
	kustc0824	<i>Escherichia coli</i> (b2286:600/166 3-148 (39%))	<i>Sinorhizobium meliloti</i> (sme:SMa1531:182/166 7-151 (46%))
	kustc0823	<i>Escherichia coli</i> (b2287:220/167 15-164 (57%))	<i>Geobacter sulfurreducens</i> (gsu:GSU0339:170/167 13-164 (67%))
	kustc0822	<i>Escherichia coli</i> (b2288:147/117 9-116 (37%))	<i>Geobacter sulfurreducens</i> (gsu:GSU0338:118/117 4-117 (62%))
formate dehydrogenase, alpha subunit	kustc0484	<i>Moorella thermoacetica</i> (AAB18330:893/769 74-757 (34%))	<i>Symbiobacterium thermophilum</i> _IAM14863 (sth:STH2056:734/769 69-765 (39%))
formate dehydrogenase, alpha subunit	kustc0546	<i>Moorella thermoacetica</i> (AAB18330:893/733 35-706 (29%))	<i>Archaeoglobus fulgidus</i> (afu:AF1203:741/733 34-728 (40%))
formate dehydrogenase, beta subunit	kuste4570	<i>Moorella thermoacetica</i> (AAB18329:707/581 26-495 (41%))	<i>Thermococcus kodakaraensis_KOD1</i> (tko:TK1612:952/581 26-556 (42%))
formyltetrahydrofolate synthetase	kustb0169	<i>Clostridium cylindrosporium</i> (L12465:556/587 10-586 (44%))	<i>Desulfotalea psychrophila</i> _LSv54 (dps:DP2227:557/587 31-587 (73%))
methyltetrahydrofolate cyclohydrolase	kuste4247	<i>Methylobacterium capsulatus</i> (MCA0507:207/215 2-200 (22%))	<i>Treponema denticola</i> _ATCC_35405 (tde:TDE0046:213/215 1-208 (34%))
bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase and 5,10-methylene-tetrahydrofolate cyclohydrolase	kuste2296	<i>Escherichia coli</i> (b0529:288/303 1-295 (47%))	<i>Desulfotalea psychrophila</i> _LSv54 (dps:DP1901:313/303 1-295 (73%))
methylenetetrahydrofolate reductase	kustc0552	<i>Methanosarcina mazei</i> (MM0438:292/313 10-307 (40%))	<i>Sinorhizobium meliloti</i> (sme:SMc04340:363/313 7-307 (45%))

tca¹ tricarboxylic acid cycle*

enzyme	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database
pyruvate carboxylase	kustd1409	<i>Methanosarcina acetivorans</i> (MA0675:493/1149 6-456 (45%))	<i>Rhodopirellula baltica</i> (rba:RB10592:1166/1149 3-1147 (56%))
oxaloacetate decarboxylase	kustd2060	<i>Methanosarcina acetivorans</i> (MA0674:572/610 9-609 (28%))	<i>Campylobacter jejuni</i> (cjc:Cj0933c:599/610 6-607 (55%))
phosphoenolpyruvate carboxykinase	kuste4342	<i>Sinorhizobium meliloti</i> (U15199:536/516 106-469 (25%))	<i>Aeropyrum pernix</i> (ape:APE0033:493/516 1-506 (31%))
citrate synthase			
citrate lyase			
aconitate hydratase	kuste2878	<i>Escherichia coli</i> (b1276:891/641 13-605 (26%))	<i>Gloeobacter violaceus</i> (gvi:glr4087:645/641 4-635 (64%))
isocitrate dehydrogenase	kuste3602	<i>Escherichia coli</i> (b1136:416/423 20-422 (61%))	<i>Symbiobacterium thermophilum</i> _IAM14863 (sth:STH2544:421/423 14-422 (63%))
	kusta0017	<i>Leptospira borgpetersenii</i> (M59431:358/380 3-367 (56%))	<i>Leptospira interrogans serovar Copenhageni</i> (lic:LIC11768:358/380 3-367 (56%))
2-oxoacid dehydrogenase	kuste2314	<i>Clostridium magnum</i> (L31844:326/325 1-319 (35%))	<i>Thermoanaerobacter tengcongensis</i> (tte:TTE0186:333/325 1-323 (44%))
	kuste2317	<i>Clostridium magnum</i> (L31844:333/344 21-338 (47%))	<i>Oceanobacillus iheyensis</i> (oih:OB1865:327/344 21-344 (55%))
	kuste2318	<i>Escherichia coli</i> (b0727:405/416 2-394 (35%))	<i>Bacillus halodurans</i> (bha:BH2761:426/416 1-394 (41%))
	kuste3610	<i>Zymomonas mobilis</i> (X82291:466/474 8-460 (40%))	<i>Bacillus thuringiensis konkukian</i> (btk:BT9727_3906:473/474 8-469 (43%))
2-oxoacid - ferredoxin oxidoreductase**	kustc0357	<i>Desulfovibrio vulgaris</i> (DVU1569:577/363 2-328 (27%))	<i>Thermoanaerobacter tengcongensis</i> (tte:TTE198:355/363 2-346 (60%))
	kustc0358	<i>Chlorobium tepidum</i> (CT0162:342/245 18-216 (30%))	<i>Geobacter sulfurreducens</i> (gsu:GSU1860:247/245 1-243 (56%))
	kustc0356		<i>Geobacter sulfurreducens</i> (gsu:GSU1862:67/67 1-66 (43%))
succinyl-CoA synthetase	kustc0453	<i>Escherichia coli</i> (b0729:289/293 1-289 (58%))	<i>Bacillus thuringiensis konkukian</i> (btk:BT9727_3576:300/293 1-292 (65%))
	kustc0452	<i>Escherichia coli</i> (b0728:388/390 1-386 (46%))	<i>Geobacillus kaustophilus_HTA426</i> (gka:GK1208:386/390 1-381 (53%))
succinate dehydrogenase (complex2)	kustc0681	<i>Thermoplasma acidophilum</i> (X70908:137/126 19-95 (31%))	<i>Symbiobacterium thermophilum</i> _IAM14863 (sth:STH2637:140/126 22-126 (33%))
	kustc0682	<i>Escherichia coli</i> (b0722:115/124 7-113 (23%))	<i>Archaeoglobus fulgidus</i> (afu:AF0684:117/124 9-111 (31%))
	kustc0680	<i>Escherichia coli</i> (b0723:588/580 36-580 (42%))	<i>Symbiobacterium thermophilum</i> _IAM14863 (sth:STH2639:573/580 9-580 (56%))
	kustc0278	<i>Escherichia coli</i> (b0724:238/240 6-235 (42%))	<i>Symbiobacterium thermophilum</i> _IAM14863 (sth:STH2640:243/240 10-238 (48%))
fumarate hydratase	kustd2184	<i>Escherichia coli</i> (b4139:493/464 8-463 (47%))	<i>Geobacter sulfurreducens</i> (gsu:GSU0479:463/464 7-464 (55%))
malate dehydrogenase	kuste2399	<i>Lactobacillus sakei</i> (AF054624:325/313 4-306 (32%))	<i>Chlorobium tepidum</i> _TLS (cte:CT1507:310/313 5-312 (59%))

* the glyoxylate shunt was completely absent
 ** catalyses (de)carboxylation in both directions

pfor¹ pyruvate::ferredoxin oxidoreductase and related activities

enzyme	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database
pyruvate (2-oxoacid) ferredoxin oxidoreductase	kuste2339	Desulfovibrio vulgaris (DVU1569:577/570 6-566 (40%))	Methanosarcina_mazei (mma:MM0420:579/570 4-566 (50%))
pyruvate (2-oxoacid) ferredoxin oxidoreductase	kuste2338	Desulfovibrio vulgaris (DVU1570:284/287 12-282 (50%))	Methanosarcina_barkeri (mba:Mbar_A2215:283/287 14-278 (59%))
pyruvate (2-oxoacid) ferredoxin oxidoreductase	kustc1110	Hydrogenobacter thermophilus (AB054643:389/305 4-79 (25%))	Desulfotalea_psychrophila_LSV54 (dps:DP1200:409/305 1-301 (52%))
pyruvate (2-oxoacid) ferredoxin oxidoreductase	kustc1109	Hydrogenobacter thermophilus (AB054643:288/218 21-216 (30%))	Desulfotalea_psychrophila_LSV54 (dps:DP1201:308/218 5-216 (57%))
pyruvate (2-oxoacid) ferredoxin oxidoreductase	kuste4370	Hydrogenobacter thermophilus (AB054643:288/1192 1005-1110 (33%))	Desulfotalea_psychrophila_LSV54 (dps:DP2886:1180/1192 1-1188 (62%))

acs¹ acetyl CoA synthetase and related activities

enzyme	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database
acetyl-CoA synthetase	kustc1128	Bacillus subtilis (L17309:572/589 28-589 (58%))	Geobacillus_kaustophilus_HTA426 (gka:GK2806:571/589 27-589 (60%))
long chain acyl coa synthetase	kustb0215	Escherichia coli (b0037:522/528 47-523 (30%))	Thermoanaerobacter_tengcongensis (tte:TTE1960:495/528 50-523 (36%))
acetate CoA ligase (ADP forming)	kuste3169	Nostoc sp. PCC 6720 (Z48005:262/706 630-698 (33%))	Archaeoglobus_fulgidus (afu:AF1211:685/706 4-685 (43%))
phosphotransacetylase (truncated)	kuste3170	Escherichia coli (b0778:225/356 5-142 (22%))	Desulfovibrio_vulgaris_Hildenborough (dvv:DVU1438:354/356 4-354 (35%))
acetate CoA ligase (ADP forming) alpha subunit	kustc0502	Escherichia coli (b0729:289/462 62-222 (23%))	Methanosarcina_mazei (mma:MM0358:468/462 7-453 (45%))
acetate CoA ligase (ADP forming) beta subunit	kusta0048	Nostoc sp. PCC 6720 (Z48005:262/242 173-238 (28%))	Thermococcus_kodakaraensis_KOD1 (tko:TK0465:232/242 12-238 (47%))

gly¹ glycolysis/gluconeogenesis and related activities

enzyme	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database (e-value)
pyruvate kinase	kuste4167	Escherichia coli (b1676:470/472 5-472 (41%))	Synechocystis_sp_PCC6803 (syn:sl1275:591/472 5-471 (50%))
phosphoenolpyruvate synthase	kuste3000	Escherichia coli (b2416:575/922 646-574 (23%))	Rhodopseudomonas_palustris_CGA009 (rpa:RPA1051:913/922 2-918 (55%))
enolase	kustd1490	Enterococcus faecalis (AJ401152:432/430 1-421 (64%))	Geobacter_sulfurreducens (gsu:GSU2286:428/430 4-422 (68%))
phosphoglycerate mutase	kuste4326	Escherichia coli (b0755:250/231 3-228 (62%))	Thermoanaerobacter_tengcongensis (tte:TTE2487:249/231 1-228 (71%))
phosphoglycerate kinase	kustd1645	Xanthobacter flavus (U08462:397/397 14-392 (44%))	Geobacter_sulfurreducens (gsu:GSU1628:654/397 11-387 (60%))
glyceraldehyde-3-phosphate dehydrogenase	kustd1643	Streptomyces aureofaciens (U21191:332/333 20-331 (50%))	Chlorobium_tepidum_TLS (cte:CT1480:334/333 3-332 (63%))
triosephosphate isomerase	kuste4253	Lactococcus lactis (U07640:252/261 8-255 (42%))	Thermotoga_maritima (tma:TM0689:654/261 8-259 (49%))
fructose-bisphosphate aldolase	kustd1479	Escherichia coli (b2096:286/462 239-358 (23%))	Geobacter_sulfurreducens (gsu:GSU1245:364/462 118-383 (25%))
6-phosphofructokinase	kustc0560	Escherichia coli (b3916:320/367 5-331 (37%))	Geobacter_sulfurreducens (gsu:GSU1703:363/367 6-366 (53%))
fructose-1,6-bisphosphatase	kustd1478	Escherichia coli (b4232:332/338 8-336 (50%))	Desulfovibrio_vulgaris_Hildenborough (dvv:DVU1841:337/338 7-332 (58%))
glucosephosphate isomerase	kuste2903	Escherichia coli (b4025:549/549 2-549 (69%))	Vibrio_vulnificus_CMCP6 (vvu:VV11396:550/549 1-549 (71%))
phosphoglycerate mutase	kuste4326	Escherichia coli (b0755:250/231 3-228 (62%))	Thermoanaerobacter_tengcongensis (tte:TTE2487:249/231 1-228 (71%))
glucokinase	kuste3751	Bacillus megaterium (AJ000005:324/322 6-311 (30%))	Thermoanaerobacter_tengcongensis (tte:TTE0090:315/322 6-315 (40%))

1) abbreviations correspond to Figure 3
 Blast hits are indicated for each gene. Genes were blasted against a database of proteins with experimentally validated functions (www.cmbi.kun.nl/exprot) and against the KEGG genes database (www.genome.jp). The best Blast hits of each orf are summarized in the following notation: organism name (id of database entry: length of protein in the database/length of orf in Kuenenia stuttgartiensis start of Blast hit in K. stuttgartiensis - end of Blast hit in K. stuttgartiensis (percentage of amino acids identical)).