

SOM Table 2. Genes with known homologues involved in respiration

atp¹ ATP synthase and pyrophosphatase					
	enzyme	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database	
atpB	ATP synthase, F0F1-type	kuste3789	<i>Escherichia coli</i> (b3738:271/257 66-256 (27%))	<i>Parachlamydia_sp_UWE25</i> (pcu:pc1674:271/257 15-255 (39%))	
atpE		kuste3790	<i>Streptococcus pneumoniae</i> (Z26850:66/108 14-71 (34%))	<i>Parachlamydia_sp_UWE25</i> (pcu:pc1673:98/108 1-75 (40%))	
atpE		kuste3791	<i>Streptococcus pneumoniae</i> (Z26851:66/90 20-71 (40%))	<i>Geobacter_sulfurreducens</i> (gsu:GSU0333:91/90 3-90 (42%))	
atpA		kuste3793	<i>Synechococcus sp.</i> (X70431:503/504 7-500 (61%))	<i>Clostridium_perfringens</i> (cpe:CPE2189:502/504 1-500 (67%))	
atpG		kuste3794	<i>Escherichia coli</i> (b3733:287/290 1-289 (31%))	<i>Legionella_pneumophila_Paris</i> (lpp:ipp3054:288/290 1-289 (35%))	
atpD		kuste3795	<i>Synechococcus sp.</i> (X70432:482/471 24-469 (66%))	<i>Thermoanaerobacter_tengcongensis</i> (tte:TTE0637:461/471 10-469 (74%))	
atpC		kuste3796	<i>Escherichia coli</i> (b3731:139/134 1-126 (27%))	<i>Thermoanaerobacter_tengcongensis</i> (tte:TTE0638:138/134 1-134 (35%))	
atpD	ATP synthase, F0F1-type	kuste4592	<i>Synechococcus sp.</i> (X70432:482/462 8-460 (47%))	<i>Methanosarcina_acetivorans</i> (mac:MA2441:484/462 8-459 (68%))	
atpE		kuste4593	<i>Escherichia coli</i> (b3731:139/130 17-100 (30%))	<i>Chlorobium_tepidum_TLS</i> (cte:CT1032:129/130 1-124 (46%))	
	hypothetical protein hypothetical protein	kuste4594		<i>Chlorobium_tepidum</i> (cte:CT1031 111/107 27-110 (54%))	
		kuste4595		<i>Methanosarcina_barkeri</i> (mba:Mbar_A3103:101/104 2-97 (39%))	
atpB		kuste4596	<i>Streptococcus pneumoniae</i> (Z26851:238/236 10-223 (26%))	<i>Rhodopirellula_baltica</i> (rba:RB4911:228/236 1-220 (59%))	
atpE		kuste4597		<i>Rhodopirellula_baltica</i> (rba:RB4913: 93/109 1-84 (72%))	
atpF		kuste4598	<i>Proteus vulgaris</i> (AJ002737:917/255 41-113 (27%))	<i>Methanosarcina_acetivorans</i> (mac:MA2435:329/255 1-252 (32%))	
atpA		kuste4599	<i>Synechococcus sp.</i> (X70431:503/513 23-512 (45%))	<i>Methanosarcina_acetivorans</i> (mac:MA2434:533/513 15-506 (61%))	
atpG		kuste4600	<i>Escherichia coli</i> (b3733:287/299 1-292 (27%))	<i>Rhodopirellula_baltica</i> (rba:RB4917:306/299 1-295 (45%))	
atpG	ATP synthase, F0F1-type	kustc0579	<i>Escherichia coli</i> (b3733:287/279 1-272 (21%))	<i>Methylococcus_capsulatus_Bath</i> (mca:MCA2708:275/279 17-272 (26%))	
atpA		kustc0578	<i>Synechococcus sp.</i> (X70431:503/498 12-455 (48%))	<i>Thermoanaerobacter_tengcongensis</i> (tte:TTE0635:506/498 12-497 (50%))	
atpH		kustc0577	<i>Escherichia coli</i> (b3735:177/246 171-243 (31%))	<i>Methylococcus_capsulatus_Bath</i> (mca:MCA2701:253/246 1-239 (25%))	
atpC		kustc0576	<i>Escherichia coli</i> (b3737:79/88 13-79 (31%))	<i>Legionella_pneumophila_Paris</i> (lpp:ipp2332:91/88 11-87 (57%))	
atpB		kustc0575	<i>Escherichia coli</i> (b3738:271/221 29-214 (27%))	<i>Legionella_pneumophila_Philadelphia_1</i> (lpn:lpg1051:230/221 12-218 (49%))	
"atpI"		kustc0574		<i>Legionella_pneumophila_Philadelphia_1</i> (lpn:lpg1052: 92/92 3-85 (39%))	
atpE		kustc0573	<i>Escherichia coli</i> (b3731:139/134 5-92 (24%))	<i>Gluconobacter_oxydans_621H</i> (gox:GOX2168:138/134 7-105 (32%))	
atpD		kustc0572	<i>Synechococcus sp.</i> (X70432:482/454 3-454 (47%))	<i>Thermotoga_maritima</i> (tma:TM1610:468/454 2-454 (56%))	
VatpE		Vacuolar ATPase (proton pumping) hypothetical protein	kuste3864	<i>Borrelia_burgdorferi</i> (BB0096:200/210 1-199 (27%))	<i>Treponema_denticola_ATCC_35405</i> (tde:TDE1381:205/210 1-206 (29%))
			kuste3865		<i>Treponema_denticola_ATCC_35405</i> (tde:TDE1380:180/183 2-163 (31%))
VatpA			kuste3866	<i>Borrelia_burgdorferi</i> (BB0094:551/589 37-580 (56%))	<i>Treponema_denticola_ATCC_35405</i> (tde:TDE1683:589/589 16-578 (63%))
VatpB			kuste3867	<i>Borrelia_burgdorferi</i> (BB0093:434/437 1-429 (72%))	<i>Treponema_denticola_ATCC_35405</i> (tde:TDE1682:431/437 1-430 (71%))
VatpD			kuste3869	<i>Borrelia_burgdorferi</i> (BB0092:204/202 1-182 (48%))	<i>Borrelia_burgdorferi</i> (bbu:BB0092:204/202 1-192 (50%))
VatpI			kuste3870	<i>Borrelia_burgdorferi</i> (BB0091:608/583 1-582 (28%))	<i>Treponema_pallidum</i> (tpa:TP0429:622/583 1-580 (29%))
VatpK			kuste3871	<i>Borrelia_burgdorferi</i> (BB0090:144/152 9-147 (43%))	<i>Borrelia_garini</i> (bga:BG0091:144/152 9-147 (55%))
	pyrophosphate-energized vacuolar membrane proton pump; ppmp	kustd1836	<i>Methanosarcina_mazei</i> (M0700:676/800 80-783 (45%))	<i>Bacteroides_thetaiotaomicron_VPI-5482</i> (bth:BT3411:734/800 80-790 (61%))	
Ni-Fe Hydrogen evolving hydrogenase					
	enzyme	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database	
	hydrogenase 4, subunit D	kustd1773	<i>Escherichia coli</i> (b2482:672/678 2-676 (32%))	<i>Thermoanaerobacter_tengcongensis</i> (tte:TTE1706:673/678 3-677 (40%))	
	hydrogenase 4, subunit C	kustd1775	<i>Escherichia coli</i> (b2722:307/312 18-307 (33%))	<i>Methylococcus_capsulatus_Bath</i> (mca:MCA1141:312/312 6-311 (48%))	
	hydrogenase 4, subunit E	kustd1776	<i>Escherichia coli</i> (b2485:216/221 6-220 (19%))	<i>Azoarcus_sp_EbN1</i> (eba:ebA4191:219/221 9-221 (34%))	
	hydrogenase 4, subunit D	kustd1777	<i>Escherichia coli</i> (b2486:526/491 10-488 (39%))	<i>Thermoanaerobacter_tengcongensis</i> (tte:TTE1702:494/491 1-488 (42%))	
	hydrogenase 4, subunit G	kustd1778	<i>Escherichia coli</i> (b2721:569/531 7-530 (35%))	<i>Thermoanaerobacter_tengcongensis</i> (tte:TTE1700:576/531 56-530 (42%))	
	hydrogenase 4, subunit I	kustd1779	<i>Escherichia coli</i> (b2719:255/262 123-257 (50%))	<i>Desulfotalea_psychrophila_LSV54</i> (dps:DP1042:248/262 1-254 (38%))	
nuo¹ Complex I (proton and sodium pumping NADH::quinon oxidoreductase)					
	enzyme	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database	
nuoA	NADH::quinone oxidoreductase (complex I)*	kuste2660	<i>Escherichia coli</i> (b2288:147/138 32-124 (46%))	<i>Methylococcus_capsulatus_Bath</i> (mca:MCA1359:139/138 10-132 (54%))	
nuoB		kuste2661	<i>Escherichia coli</i> (b2287:220/212 18-212 (61%))	<i>Methylococcus_capsulatus_Bath</i> (mca:MCA1358:213/212 1-209 (61%))	
nuoCD		kuste2662	<i>Escherichia coli</i> (b2286:600/581 3-581 (59%))	<i>Methylococcus_capsulatus_Bath</i> (mca:MCA1357:587/581 6-581 (65%))	
nuoE		kuste2663	<i>Escherichia coli</i> (b2285:166/154 2-153 (49%))	<i>Pseudomonas_aeruginosa</i> (pae:PA2640:166/154 1-153 (50%))	
nuoF		kuste2664	<i>Escherichia coli</i> (b2284:445/427 7-421 (55%))	<i>Methylococcus_capsulatus_Bath</i> (mca:MCA1355:427/427 4-419 (67%))	
nuoG		kuste2665	<i>Escherichia coli</i> (b2283:910/904 1-888 (45%))	<i>Pseudomonas_aeruginosa</i> (pae:PA2642:905/904 1-888 (50%))	
nuoH		kuste2666	<i>Escherichia coli</i> (b2282:325/318 4-316 (59%))	<i>Methylococcus_capsulatus_Bath</i> (mca:MCA1353:316/318 11-317 (69%))	
nuoL		kuste2667	<i>Escherichia coli</i> (b2281:180/171 3-171 (68%))	<i>Methylococcus_capsulatus_Bath</i> (mca:MCA1352:171/171 1-171 (68%))	
nuoJ		kuste2668	<i>Escherichia coli</i> (b2280:184/189 6-168 (38%))	<i>Shigella_flexneri_2a</i> (sf:S2491:184/189 6-168 (53%))	
nuoK		kuste2669	<i>Escherichia coli</i> (b2279:100/102 26-102 (48%))	<i>Methylococcus_capsulatus_Bath</i> (mca:MCA1350:102/102 1-102 (64%))	
nuoL		kuste2670	<i>Escherichia coli</i> (b2278:613/626 32-626 (44%))	<i>Methylococcus_capsulatus_Bath</i> (mca:MCA1349:613/626 1-624 (53%))	

nuoM		kuste2671	Escherichia coli (b2277:509/545 60-498 (49%))	Methylococcus_capsulatus_Bath (mca:MCA1348:489/545 1-487 (57%))
nuoN		kuste2672	Escherichia coli (b2276:425/485 61-474 (44%))	Pseudomonas_aeruginosa (pae:PA2649:486/485 6-474 (44%))
nqrA	Na+ translocating NADH::quinone oxidoreductase	kuste3325	Methanothermobacter wolfeii (AJ009688:349/348 278-328 (33%))	Hemophilus influenzae (hin:HI1685:819/348 46-342 (25%))
nqrB		kuste3326	Vibrio alginolyticus (AB008030:414/367 113-353 (30%))	Thermotoga_maritima (tma:TM0245:318/367 55-352 (36%))
nqrC		kuste3327	Vibrio alginolyticus (AB008030:256/227 123-219 (33%))	Clostridium_tetani_E88 (ctc:CTC00675:339/227 51-221 (24%))
nqrD		kuste3328	Vibrio alginolyticus (AB008030:198/472 271-195 (24%))	Shewanella_oneidensis (son:SO0906:202/472 271-195 (26%))
nqrE		kuste3329	Vibrio alginolyticus (AB008030:407/545 38-464 (24%))	Hemophilus influenzae (hin:HI0171:411/545 1-464 (26%))
nqrE	Na+ translocating NADH::quinone oxidoreductase	kustc0732	Vibrio alginolyticus (AB008030:198/212 20-210 (42%))	Fusobacterium_nucleatum (fnu:FN1592:194/212 8-210 (55%))
nqrD		kustc0731	Vibrio alginolyticus (AB008030:210/210 17-188 (43%))	Clostridium_tetani_E88 (ctc:CTC01022:200/210 12-202 (55%))

* see also the putative formate::quinone oxidoreductase listed in the acetyl CoA pathway

Q¹ ubiquinone biosynthesis*

enzyme	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database
ubiA	4-hydroxybenzoate-octaprenyltransferase	kustd1781 Escherichia coli (b4040:290/288 1-283 (22%))	Geobacter_sulfurreducens (gsu:GSU0439:298/288 7-288 (42%))
ubiB	2-octaprenylphenol hydroxylase of ubiquinone biosynthetic pathway	kuste4161 Escherichia coli (b3835:546/562 65-479 (31%))	Geobacter_sulfurreducens (gsu:GSU1088:561/562 1-562 (38%))
ubiC	chorismate lyase		
ubiD	3-octaprenyl-4-hydroxybenzoate decarboxylase	kuste3161 Escherichia coli (b3843:497/589 1-585 (33%))	Archaeoglobus_fulgidus (afu:AF0209:481/589 1-585 (25%))
ubiE	ubiquinone/menaquinone biosynthesis methyltransferase	kuste3889 Escherichia coli (b3833:251/242 10-241 (33%))	Rhodopirellula_baltica (rba:RB2752:317/242 5-242 (44%))
ubiF	2-octoprenyl-3-methyl-6-methoxy-1,4-benzoquinone hydroxylase		
ubiG	3-demethylubiquinone-9 3-methyltransferase and 2-octaprenyl-6-hydroxy phenol methylase	kuste3239 Escherichia coli (b2232:240/264 54-152 (28%))	Bacillus cereus (bce:BC2100:226/264 2-202 (24%))
ubiG	3-demethylubiquinone-9 3-methyltransferase and 2-octaprenyl-6-methoxyphenol hydroxylase, FAD/NAD-binding	kuste3338 Escherichia coli (b2232:240/282 89-176 (35%))	Leptospira_interrogans_serovar_Copenhageni (lic:LIC10073:283/282 8-225 (28%))
ubiH			

* menaquinone biosynthesis was absent

bc1¹ complex III (bc1, quinol::cytochrome c oxidoreductase)

enzyme	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database
rieske iron-sulfur [2Fe-2S] protein	kuste4569	Bacillus subtilis (L47709:167/173 23-148 (34%))	Symbiobacterium_thermophilum_IAM14863 (sth:STH3146: 34%)
hypothetical iron sulfur protein	kuste4570	Moorella thermoacetica (AAB18329:707/581 26-495 (41%))	Thermococcus_kodakaraensis_KOD1 (tko:TK1612: 42%)
cytochrome b6 of bc1 complex	kuste4571	Bacillus subtilis (L47709:224/256 37-256 (34%))	Symbiobacterium_thermophilum_IAM14863 (sth:STH3148:258/256 16-256 (52%))
cytochrome b	kuste4572	Bacillus subtilis (L47709:255/240 21-78 (31%))	Symbiobacterium_thermophilum_IAM14863 (sth:STH3147: 39%)
hypothetical (hexaheme) cytochrome c hydroxylamine oxidoreductase	kuste4573		Desulfovibrio_vulgaris_Hildenborough (dvo:DVU0922: 32%)
rieske iron-sulfur [2Fe-2S] protein	kuste4574	Nitrosomonas europaea (U04053:570/584 6-508 (29%))	Silicibacter_pomeroyi_DSS-3 (sil:SPOA0201: 30%)
cytochrome b6 of bc1 complex	kustd1480	Bacillus subtilis (L47709:167/168 12-140 (26%))	Symbiobacterium_thermophilum_IAM14863 (sth:STH3146:178/168 71-147 (41%))
hypothetical protein	kustd1481	Synechococcus sp. PCC 7002 (X63049:222/275 73-275 (35%))	Symbiobacterium_thermophilum_IAM14863 (sth:STH3148:258/275 35-275 (54%))
hypothetical iron sulfur protein	kustd1482		Mycobacterium_avium_paratuberculosis (mpa:MAP2250c:731/51 5-47 (29%))
cytochrome b6 of bc1 complex	kustd1483	Moorella thermoacetica (AAB18329:707/566 19-482 (40%))	Thermococcus_kodakaraensis_KOD1 (tko:TK1612:952/566 19-549 (40%))
hypothetical (octa heme) cytochrome c	kustd1484	Bacillus subtilis (L47709:255/277 13-123 (28%))	Symbiobacterium_thermophilum_IAM14863 (sth:STH3147:253/277 35-179 (25%))
rieske iron-sulfur [2Fe-2S] protein	kustd1485	Bacillus firmus (M94110:342/948 331-407 (33%))	Rhodopirellula_baltica (rba:RB3953:857/948 435-393 (33%))
extended cytochrome bc of bc1 complex	kuste3096	Bacillus subtilis (L47709:167/162 4-139 (28%))	Oceanobacillus_ihayensis (oih:OB1776:170/162 4-156 (32%))
	kuste3097	Bacillus subtilis (L47709:224/630 1-213 (37%))	Chlorobium_tepidum_TLS (cte:CT0303:428/630 26-359 (36%))

cbb3 type terminal oxidase

enzyme	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database
cytochrome c oxidase, cbb3 type, maturation protein	kustc0430	Pseudomonas putida (PP4262:71/50 1-45 (55%))	Pseudomonas_aeruginosa (pae:PA1548:69/50 1-49 (51%))
cytochrome c oxidase, cbb3-type, subunit I	kustc0429	Rhodobacter capsulatus (X80134:532/710 15-470 (49%))	Bdellovibrio_bacteriovorus (bba:Bd2611:706/710 13-708 (66%))
hypothetical protein	kustc0428		Bdellovibrio_bacteriovorus (bba:Bd2612:54/56 1-54 (42%))
cytochrome c oxidase, cbb3-type, subunit ccoP	kustc0427	Rhodobacter capsulatus (X80134:297/193 3-177 (36%))	Bdellovibrio_bacteriovorus (bba:Bd2613:185/193 16-192 (38%))
hypothetical ferredoxin	kustc0426	Rhizobium leguminosarum (AJ001522:522/466 8-304 (35%))	Bdellovibrio_bacteriovorus (bba:Bd2614:468/466 18-464 (43%))
hypothetical protein	kustc0425		Bdellovibrio_bacteriovorus (bba:Bd2615:213/235 15-222 (34%))

nir¹ nitrite reductase (NirS)*

enzyme	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database
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cytochrome cd1 nitrite reductase; nirS	kuste4136	Paracoccus pantotrophus (AJ401462:596/621 69-621 (49%))	Dechloromonas aromatica (dar:Daro_3323:576/621 73-621 (50%))
hypothetical protein	kuste4137	Pseudomonas aeruginosa (PA1983:145/160 23-148 (22%))	Xanthomonas campestris_8004 (xcb:XC_2295:683/160 42-154 (29%))
heme d1 biosynthesis protein NirN; nirN	kuste4138	Azoarcus sp. (ebA876:534/569 40-480 (33%))	Silicibacter pomeroyi_DSS-3 (sil:SPOA0228:503/569 28-477 (33%))
heme d1 biosynthesis protein NirJ; nirJ	kuste4139	Pseudomonas aeruginosa (PA0511:387/362 1-362 (40%))	Azoarcus_sp_EbN1 (eba:ebA877:401/362 1-362 (43%))
heme d1 biosynthesis protein NirF; nirF	kuste4140	Pseudomonas aeruginosa (PA0516:392/387 75-381 (30%))	Pseudomonas aeruginosa (pae:PA0516:392/387 75-381 (30%))

* additional maturation proteins (NirD, NirE) present outside operon

hao¹ hydroxylamine oxidoreductase*

enzyme	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database
hao	hydroxylamine oxidoreductase	kuste2435 Nitrosomonas europaea (U04053:570/499 32-309 (25%))	Nitrosomonas_europaea (neu:NE2339:570/499 32-309 (25%))
hao		kuste2457 Nitrosomonas europaea (U04053:570/433 81-426 (22%))	Silicibacter_pomeroyi_DSS-3 (sil:SPOA0201:528/433 25-429 (22%))
hao		kustd1340 Nitrosomonas europaea (U04053:570/577 71-493 (26%))	Methylococcus_capsulatus_Bath (mca:MCA0956:559/577 54-465 (30%))
hao		kustd2021 Nitrosomonas europaea (U04053:570/554 57-333 (25%))	Nitrosomonas_europaea (neu:NE2044:570/554 57-333 (25%))
hao		kusta0043 Nitrosomonas europaea (U04053:570/591 159-547 (27%))	Methylococcus_capsulatus_Bath (mca:MCA0956:559/591 158-519 (30%))
hao		kustc1061 Nitrosomonas europaea (U04053:570/536 21-483 (29%))	Nitrosomonas_europaea (neu:NE2339:570/536 21-483 (29%))
hao		kustc0694 Nitrosomonas europaea (U04053:570/656 145-567 (26%))	Methylococcus_capsulatus_Bath (mca:MCA0956:559/656 128-539 (30%))
hao		kustc0458 Nitrosomonas europaea (U04053:570/554 52-554 (29%))	Methylococcus_capsulatus_Bath (mca:MCA0956:559/554 74-547 (31%))

* Two additional copies part of bc1 complex and unknown complex 2 (see SOM Figure 2)

nar/ret¹ nitrate reductase (NarG)

enzyme	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database
hypothetical protein	kustd1699		Xanthomonas_axonopodis (xac:XAC2712:227/263 117-239 (38%))
nitrate reductase, subunit alpha; narG	kustd1700	Escherichia coli (b1468:1246/1148 44-879 (33%))	Archaeoglobus_fulgidus (afu:AF0176:896/1148 61-859 (26%))
hypothetical protein	kustd1701	Mycoplasma_pulmonis (AL445564:314/322 153-224 (26%))	Acinetobacter_sp_AD1 (aci:ACIAD3534:185/322 220-300 (30%))
nitrate reductase chaperone narJ	kustd1702	Halobacterium_marismortui (rrnAC1204:226/269 26-237 (24%))	Chlorobium_tepidum_TLS (cte:CT0493:187/269 25-223 (26%))
nitrate reductase, FeS subunit; narH	kustd1703	Escherichia coli (b1467:514/410 23-343 (30%))	Haloarcula_marismortui_ATCC_43049 (hma:rrnAC1200:358/410 24-329 (43%))
nitrate reductase subunit; narM	kustd1704	Pyrobaculum_aerophilum (PAE3613:307/322 42-318 (25%))	Azoarcus_sp_EbN1 (eba:c1A62:214/322 45-308 (24%))
hypothetical monoheme cytochrome c	kustd1705		Plasmodium_falciparum (pfa:PF14_0770:344/182 29-163 (24%))
universal stress protein UspA	kustd1706	Plectonema_boryanum (D78208:508/434 376-422 (34%))	Methanosarcina_mazei (mma:MM1452:323/434 3-160 (29%))
conserved hypothetical (monoheme) protein	kustd1707		Nitrosomonas_europaea (neu:NE0925:131/188 44-129 (34%))
hypothetical (tetraheme) protein	kustd1708	Pseudomonas_stutzeri (Z28384:146/500 303-490 (26%))	Bdellovibrio_bacteriovorus (bba:Bd2601:215/500 328-490 (28%))
hypothetical (diheme) protein	kustd1709	Pyrobaculum_aerophilum (PAE3613:307/535 284-500 (30%))	Pyrobaculum_aerophilum (pai:PAE3613:307/535 271-500 (31%))
hypothetical (monoheme) protein	kustd1710		Leptospira_interrogans_serovar_Copenhageni (lic:LIC10684:119/256 144-238 (33%))
hypothetical (diheme) protein	kustd1711	Bacillus_firmus (M94110:342/316 171-224 (33%))	Rhodopirellula_baltica (rba:RB4621:1497/316 124-316 (33%))
hypothetical quinol oxidase	kustd1712		Staphylococcus_epidermidis_RP62A (ser:SERP0672:451/699 97-308 (27%))
conserved hypothetical protein	kustd1713		Pseudomonas_syringia (psb:Psyr_3943:224/252 110-245 (36%))

homologous to other known enzymes

enzyme	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database
hypothetical thioredoxin	kustd2197	Escherichia coli (b3781:127/108 1-108 (48%))	Photobacterium_profundum_SS9 (ppr:PBPRA3541:112/108 1-108 (55%))
hypothetical thioredoxin	kustc0967	Bradyrhizobium_japonicum (Z23140:221/166 48-141 (30%))	Geobacter_sulfurreducens (gsu:GSU3280:171/166 48-166 (39%))
hypothetical thioredoxin	kustc0860	Bradyrhizobium_japonicum (Z23140:221/161 43-136 (31%))	Geobacter_sulfurreducens (gsu:GSU3280:171/161 43-144 (48%))
hypothetical thioredoxin	kustc0978	Escherichia coli (b3801:551/758 90-225 (25%))	Methanosarcina_barkeri (mba:Mbar_A0261:711/758 51-756 (57%))
cytochrome c peroxidase	kustd1904	Pseudomonas_aeruginosa (PA4587:346/350 39-347 (45%))	Pseudomonas_fluorescens (pfl:PFL_5183:330/350 34-347 (57%))
cytochrome c peroxidase	kuste2905	Pseudomonas_aeruginosa (PA4587:346/358 47-355 (48%))	Vibrio_parahaemolyticus (vpa:VP1718:344/358 45-356 (58%))
hypothetical flavoprotein	kuste3160	Methanothermobacter_thermautotrophicus (U17835:404/391 6-389 (37%))	Methanococcus_jannaschii (mja:MJ0732:393/391 4-385 (46%))

large hypothetical multiheme (catalytic?) cytochromes, multicopper and molybdopterin proteins

enzyme	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database
hypothetical (tetradecaheme) protein	kuste4025	Nitrosomonas_europaea (U04053:570/338 41-337 (22%))	Methylococcus_capsulatus_Bath (mca:MCA2189:600/338 26-337 (22%))
hypothetical (undecaheme) protein	kuste2877	Nitrosomonas_europaea (U04053:570/404 185-353 (25%))	Geobacter_sulfurreducens (gsu:GSU2887:884/404 46-386 (25%))
hypothetical (octaheme) protein	kuste4281	Shewanella_frigidimarina (AJ132010:561/617 476-579 (37%))	Rhodopirellula_baltica (rba:RB878:480/617 150-549 (24%))
hypothetical multicopper oxidase	kuste4301	Bacillus_subtilis (U51115:511/425 94-285 (27%))	Burkholderia_pseudomallei_K96243 (bps:BPSS0456:431/425 1-421 (59%))
hypothetical siroheme/iron sulfur protein	kuste4564	Archaeoglobus_fulgidus (M95624:366/296 13-295 (24%))	Geobacter_sulfurreducens (gsu:GSU1351:322/296 10-273 (56%))
hypothetical siroheme/iron sulfur protein	kustc1191	Methanothermobacter_wolfei (AJ009688:349/308 118-235 (36%))	Clostridium_tetani_E88 (ctc:CTC01213:295/308 90-308 (29%))
hypothetical molybdopterin oxidoreductase with cytochrome b	kuste2658	Thiobacillus sp. KCT001 (AJ314793:211/556 389-555 (24%))	Mycobacterium_avium_paratuberculosis (mpa:MAP1497c:661/556 27-550 (42%))
hypothetical molybdopterin oxidoreductase	kustc0484	fdhA (Moorella_thermoacetica:AAB18330)	

hypothetical molybdopterine oxidoreductase	kustc0546	fdhA (Moorella thermoacetica:AAB18330)	Archaeoglobus_fulgidus (AF1203; e-146)
hypothetical molybdopterine oxidoreductase (with associated proteins)	kustc0714 kustc0713 kustc0712	Escherichia coli (b2285:166/152 17-149 (33%)) Ralstonia eutropha (AJ223295:520/594 16-519 (38%)) Moorella thermoacetica (AAB18329:707/693 104-575 (38%))	Thermococcus_kodakaraensis_KOD1 (tko:TK1614:154/152 21-148 (57%)) Thermococcus_kodakaraensis_KOD1 (tko:TK1613:600/594 12-591 (61%)) Thermococcus_kodakaraensis_KOD1 (tko:TK1612:952/693 5-680 (39%))

small electron carrier cytochromes

protein	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database
hypothetical (tetra heme) protein	kuste2461	Shewanella frigidimarina (AJ236923:588/476 306-473 (23%))	Rhodopirellula_baltica (rba:RB6885:770/476 52-461 (26%))
hypothetical (mono heme) protein	kuste3440	Bradyrhizobium japonicum (L07487:290/154 73-123 (26%))	Geobacter_sulfurreducens (gsu:GSU2513:146/154 73-154 (34%))
hypothetical (tri heme) protein	kuste4356		Desulfotalea_psychrophila_LSV54 (dps:DP0200:157/566 91-389 (36%))
hypothetical (mono heme) protein	kustd1686		Clostridium_tetani_E88 (ctc:CTC01556:579/162 39-142 (28%))
similar to cytochrome c553	kusta0044	Gluconacetobacter europaeus (Y08696:444/120 36-115 (29%))	Rhodopirellula_baltica (rba:RB12673:510/120 38-101 (33%))
hypothetical (mono heme) protein	kusta0085		Cryptococcus_neoformans_JEC21 (cne:CNK00010:1047/172 34-140 (26%))
hypothetical (mono heme) protein	kusta0088		Bradyrhizobium_japonicum (bja:blr2766:290/126 52-122 (33%))
similar to cytochrome c like protein; ccpA	kustc1220		Desulfotalea_psychrophila_LSV54 (dps:DP0200:157/169 5-168 (35%))
hypothetical (tetra heme) protein	kustc1170		Geobacter_sulfurreducens (gsu:GSU2937:324/255 95-244 (22%))
hypothetical (penta heme) protein	kustc1045		Photobacterium_profundum_SS9 (ppr:PBPR1680:496/390 53-379 (25%))
cytochrome c-552*	kustc0563	Bradyrhizobium japonicum (L07487:290/115 35-110 (27%))	Bordetella_pertussis (bpe:BP2172:312/115 24-111 (28%))
similar to cytochrome c-553	kustc0562	Bradyrhizobium japonicum (L07487:290/121 36-117 (31%))	Chromobacterium_violaceum (cvi:CV1171:309/121 34-121 (33%))
hypothetical (di heme) protein	kustc0559		Desulfotalea_psychrophila_LSV54 (dps:DP0507:292/291 1-282 (28%))

* purified and characterized, one of the dominant cytochromes of *K. stuttgartiensis* (Cirpus et al. 2005)

ferredoxins and iron sulfur proteins

protein	orf	corresponding gene with validated product	best blast hit in KEGG "genes" database
hypothetical ferredoxin	kuste3290	Pyrococcus_furiosus (X79502:67/61 5-61 (37%))	Desulfotalea_psychrophila_LSV54 (dps:DP1865:63/61 1-59 (49%))
hypothetical ferredoxin	kuste3419	Escherichia coli (b1109:434/357 64-107 (34%))	Thermotoga_maritima (tma:TM0034:357/357 1-354 (44%))
hypothetical ferredoxin	orf1474	Methanothermobacter wolfeii (AJ009688:349/105 4-68 (27%))	Archaeoglobus_fulgidus (afu:AF1669:150/105 1-104 (36%))
hypothetical ferredoxin	kuste3675	Methanothermobacter wolfeii (AJ009688:349/105 4-68 (27%))	Archaeoglobus_fulgidus (afu:AF1669:150/105 1-104 (36%))
hypothetical ferredoxin	kuste4015	Thauera aromatica (AJ224959:81/56 1-53 (42%))	Treponema_denticola_ATCC_35405 (tde:TDE1736:56/56 1-26 (65%))
hypothetical ferredoxin	kuste4141	Escherichia coli (b4379:287/132 15-63 (40%))	Chlorobium_tepidum_TLS (cte:CT1701:292/132 3-101 (49%))
hypothetical iron sulfur protein	kuste4192	Pseudomonas_aeruginosa (PA3805:252/505 359-491 (25%))	Methanococcus_jannaschii (mja:MJ0749:246/505 58-249 (29%))
hypothetical iron sulfur protein	kuste4657	Rhodobacter_capsulatus (Y10142:431/446 133-313 (25%))	Thermotoga_maritima (tma:TM0244:451/446 11-438 (43%))
hypothetical iron sulfur protein	kustd1272	Methanosarcina_barkeri (Y13763:259/396 262-367 (29%))	Methanosarcina_acetivorans (mac:MA1031:377/396 4-379 (40%))
hypothetical ferredoxin	kustd1690	Methanothermobacter wolfeii (AJ009688:349/274 139-254 (25%))	Bacteroides_fragilis_NCTC_9434 (bfs:BF2619:290/274 1-259 (48%))
hypothetical ferredoxin	kustd2018	Pyrococcus_furiosus (X79502:67/62 2-62 (50%))	Clostridium_perfringens (cpe:CPE2511:62/62 1-61 (58%))
hypothetical iron sulfur protein	kusta0002	Escherichia coli (b2978:761/265 1-216 (25%))	Geobacter_sulfurreducens (gsu:GSU3297:421/265 7-264 (37%))
hypothetical iron sulfur protein	kustc1224	Escherichia coli (b2204:287/456 316-382 (32%))	Geobacter_sulfurreducens (gsu:GSU0126:325/456 56-435 (32%))
hypothetical ferredoxin	kustc1054	Methanothermobacter wolfeii (AJ009688:349/70 1-38 (37%))	Thermoanaerobacter_tengcongensis (tte:TTE1605:69/70 3-67 (50%))
hypothetical ferredoxin	kustc0891	Escherichia coli (b2205:231/202 17-200 (32%))	Symbiobacterium_thermophilum_IAM14863 (sth:STH516:203/202 13-187 (42%))
hypothetical ferredoxin	kustc0775	Salmonella_typhimurium (AJ224978:250/141 10-139 (30%))	Archaeoglobus_fulgidus (afu:AF0950:157/141 11-141 (42%))
hypothetical ferredoxin	kustc0566	Escherichia coli (b0895:205/58 2-53 (31%))	Sulfolobus_solfataricus (sso:SSO11071:94/58 3-58 (37%))

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)).