

Gene	Product	EC no.	Nvie Locus	identity						Comment
<b>Candidate genes for 3-hydroxypropionate-4-hydroxybutyrate carbon fixation pathway including alcohol dehydrogenases</b>										
asd	aspartate-semialdehyde dehydrogenase	EC 1.2.1.11	NVIE_0243 40	85,75		358	Methanothermobacter thermautotrophicus , O26890,44.35 %	uncultured marine crenarchaeote, B3TA89, 64.5%	2	functions in amino acid biosynthesis; serves as candidate for malonyl-CoA reductase (EC 1.2.1.75) and succinyl-CoA reductase (EC 1.2.1.76)
hadh	hydroxyacyl-CoA dehydrogenase	EC 1.1.1.35	NVIE_0109 20	84,86		382	Rattus norvegicus, Q9VWK7, 40.8%	Candidatus Nitrosoarchaeum limnia, F3KJQ0, 64.72 %	2	candidate for malonate semialdehyde reductase/ hydroxypropionyl-CoA synthetase (EC 1.1.1.298) and (S)-3- hydroxybutyryl-CoA dehydrogenase (EC 1.1.2.1.157)
acsA-1	acetyl-CoA synthetase (AMP-forming)	EC 6.2.1.1	NVIE_0101 20	81,46		652	Pyrobaculum arsenaticum, A4WJG1, 58.53%	Nitrosopumilus maritimus, A9A4A8, 64%	2	
acsA-2	acetyl-CoA synthetase (AMP-forming)	EC 6.2.1.1	NVIE_0183 80	72,9	39,06	646	Methanotherx soehngeni, P27095, 41.7%	Nitrosopumilus maritimus, A9A1C7, 46.9%	2	
gabD (SSADH)	succinate-semialdehyde dehydrogenase	EC 1.2.1.16	NVIE_0162 40	85,68		464	Synechocystis sp., Q55585, 47%	Nitrosopumilus maritimus, A9A626, 52.42 %	2	candidate for succinyl-CoA reductase (EC 1.2.1.76)
phaA	acetoacetyl-CoA thiolase or ketoacyl-CoA thiolase	EC 2.3.1.- (9/16)	NVIE_0203 30	95,08		388	Methanobacterium thermoautotrophicum, O26884, 45.55%	uncultured crenarchaeote, Q702B1, 84.42%	3	candidate for acetoacetyl-CoA $\beta$ -ketothiolase (EC 2.3.1.9.)
	acetoacetyl-CoA thiolase or ketoacyl-CoA thiolase	EC 2.3.1.- (9/16)	NVIE_0049 40	71		365	Methanobacterium thermoautotrophicum, O26884, 35.6%	uncultured marine crenarchaeote , B3T732, 49.38%	3	candidate for acetoacetyl-CoA $\beta$ -ketothiolase (EC 2.3.1.9.)
hbcs	acetyl-CoA synthetase (ADP-forming)/ 4-hydroxybutyryl-CoA synthetase	EC (6.2.1.13)? 6.2.1.36	NVIE_0246 50	91,56		701	Methanocaldococcus jannaschii, Q58010, 40.65%	uncultured marine crenarchaeote, B3T7M0, 63.7%	2	Homologous gene in Nmar (Nmar_0206) experimentally proven to have 4-hydroxybutyryl-CoA synthetase activity
hpcs	3-hydroxypropionyl-CoA synthetase	EC 6.2.1.36	NVIE_0031 20	84,88		707	Methanocaldococcus jannaschii, Q58010, 34.87%	uncultured crenarchaeote 76h13, D4N757, 74.29%	3	Homologous gene in N.maritimus (Nmar_1309) experimentally demonstrated 3-hydroxypropionyl-CoA synthetase activity.
	putative protein with CoA-binding domain		NVIE_0062 60	72,79		139	Escherichia coli , P75874, 44.54 %	uncultured crenarchaeote, Q701V7, 57.45%	4	
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<b>Alcohol dehydrogenase, EC 1.1.1.-</b>										
	putative NAD-dependent alcohol dehydrogenase	(EC 1.1.1.1)	NVIE_01898	88,83		366	Geobacillus stearothermophilus, P12311, 30.4%	uncultured marine crenarchaeote, B3T4Z1, 58.54%	3	
adh	NAD-dependent alcohol dehydrogenase	EC 1.1.1.1	NVIE_01626	78,86		353	Sulfolobus tokodaii, Q96XE0, 49%	Candidatus Nitrosoarchaeum limnia, F3KHV4, 60.29%	2	
	putative NAD-dependent alcohol dehydrogenase	(EC 1.1.1.1)	NVIE_02442	90,62		352	Geobacillus stearothermophilus , P12311, 33.24%	Candidatus Nitrosoarchaeum limnia, F3KLL1, 60.22 %	3	highly abundant in proteome, putative acryloyl-coenzyme A reductase EC 1.3.1.84
adh	NAD-dependent alcohol dehydrogenase	EC 1.1.1.1	NVIE_02608	72,22		362	Geobacillus stearothermophilus , P42327, 41.45 %	uncultured marine crenarchaeote, B3T7D0, 54.68%	2	
	putative NAD-dependent alcohol dehydrogenase	(EC 1.1.1.1)	NVIE_02340	71,84		351	Sulfolobus acidocaldarius ,Q4J781, 31.28 %	uncultured crenarchaeote 57a5, D4N742, 48.55%	3	
	putative sugar alcohol dehydrogenase	EC 1.1.1.1	NVIE_00853	75,56		348	Bacillus subtilis, Q06004, 32.59%	Nitrosopumilus maritimus, A9A4J7, 53.53%	3	
adh	NAD-dependent alcohol dehydrogenase	EC 1.1.1.1	NVIE_00407	68,47		353	Sulfolobus tokodaii, Q96XE0, 38.48%	Mycobacterium vanbaalenii, A1TGC0, 43.9%	2	
	putative iron-containing alcohol dehydrogenase	(EC 1.1.1.1)	NVIE_02758	94,6		316	Clostridium kluyveri, P38945, 29.5%	uncultured marine crenarchaeote, B3TCN0, 63%	3	
	putative NAD-dependent alcohol dehydrogenase	(EC 1.1.1.1)	NVIE_016410			311	Mus musculus , Q924D0, 32.76 %	Pedospaera parvula, B9XBP9, 44.01 %	3	
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<b>Tricarboxylic acid cycle (oxidative)</b>										
glfA	citrate synthase	EC 2.3.3.1	NVIE_01504	87,95		392	Pyrococcus furiosus, Q53554, 42.82 %	Nitrosopumilus maritimus, A9A4L7, 62.47%	2	PF00285 (7.9e-132 )
aco	aconitate hydratase	EC 4.2.1.3	NVIE_0294 50	35,21		759	Dictyostelium discoideum, Q54XS2, 57.6 %	Nitrosopumilus maritimus , A9A454, 72.19 %	2	HGT; homologous gene replacement PF00330 (6.8e-153 )
(icd)	putative isocitrate/isopropylmalate dehydrogenase	EC 1.1.1.- (EC 1.1.1.41)	NVIE_0285 00	83,92		342	Methanocaldococcus jannaschii, Q58130, 38%	Cenarchaeum symbiosum, A0RUT8, 70.7%	3	PF00180 (6e-78 )
(o)orAC	2:oxoacid-ferredoxin oxidoreductase, fused alpha and gamma subunit	EC 1.2.7.-	NVIE_0294 80	75,77		648	Methanothermobacter thermautotrophicus , O27112, 31.11 %	uncultured crenarchaeote, Q701V2, 60%	3	candidate for pyruvate synthase and 2-oxoglutarate dehydrogenase PF01558 (6.1e-36 ) , PF01855 (1.5e-64 )
(o)orB	2:oxoacid-ferredoxin oxidoreductase, beta subunit	EC 1.2.7.-	NVIE_0294 90	84,16		325	Archaeoglobus fulgidus, O29782, 38.46%	uncultured crenarchaeote, Q701V1, 72.33 %	3	IPR011896 (2.7e-180 )
sucD	succinyl-CoA ligase, subunit alpha	EC 6.2.1.5	NVIE_0067 20	87,78		311	Bacillus subtilis, P80865, 48.04 %	Cenarchaeum symbiosum, A0RTT7, 68.23 %	2	SSF52210 (9.3e-41 )
sucC	succinyl-CoA ligase, subunit beta	EC 6.2.1.5	NVIE_0067 30	83,33			Thermus thermophilus, P25126, 40.85 %	uncultured marine crenarchaeote , B3T8N6, 58.7%	2	SSF52210 (5.5e-37 )
sdhA	succinate dehydrogenase flavoprotein subunit/fumarate reductase	EC 1.3.99.1	NVIE_0027 60	87,5		570	Mycobacterium bovis, P64175, 44%	Candidatus Nitrosoarchaeum limnia, F3KXK5, 73.03 %	2	TIGR01812 (4.9e-287)

Cellular Component: cytoplasm (GO:0005737), Biological  
Process: cellular amino acid biosynthetic process  
(GO:0008652), Molecular Function: oxidoreductase  
activity, acting on the aldehyde or oxo group of donors,  
NAD or NADP as acceptor (GO:0016620), Molecular  
Function: protein dimerization activity (GO:0046983)  
Biological Process: fatty acid metabolic process  
(GO:0006631), Molecular Function: oxidoreductase  
activity (GO:0016491)

Biological Process: metabolic process (GO:0008152),  
Molecular Function: transferase activity, transferring acyl  
groups other than amino-acyl groups (GO:0016747)  
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Molecular Function: transferase activity, transferring acyl  
groups other than amino-acyl groups (GO:0016747)

(sdhC)	putative succinate dehydrogenase/fumarate reductase	(EC 1.3.99.1)	NVIE_002750	90,91			Halobacterium salinarum, Q9HQ63, 27 %	Nitrosopumilus maritimus, A9A327, 63.5%	3	cytochrome subunit complex II
(sdhD)	putative succinate dehydrogenase/fumarate reductase	(EC 1.3.99.1)	NVIE_002740	80,36	119		Archaeoglobus fulgidus, Q29573, 30.77%	Nitrosopumilus maritimus, A9A328, 56.36%	3	cytochrome subunit complex II
sdhB	FeS-center protein of succinate dehydrogenase/fumarate reductase	EC 1.3.99.1	NVIE_002730	77,86	280		Haemophilus influenzae, P44893, 42%	Cenarchaeum symbiosum, A0R9Y9, 59.49%	2	cytochrome subunit complex II
(fumC)	putative fumarate hydratase	(EC 4.2.1.2)	NVIE_016290	83,91	461		Bacillus subtilis, P26899, 46.3%	Candidatus Nitrosoarchaeum koreensis, F9CZ25, 68.15 %	3	might also function as aspartate-ammonia lyase
mdh	malate dehydrogenase	EC 1.1.1.37	NVIE_013940	87,54	304	24,04 to NVIE_016290	Nitrosopumilus maritimus, A9A450, 61.7%	Cenarchaeum symbiosum, A0RX88, 66.7%	2	
	putative Succinyl-CoA ligase		NVIE_015940	547			Escherichia coli , P77187, 34.9 %	Clostridium ljungdahlii, D8GL66, 40.38 %	3	
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<b>Other genes putatively involved in pyruvate and glyoxylate metabolism</b>										
ytsJ	NAD(P)-dependent malic enzyme	EC 1.1.1.40/EC 1.1.1.38	NVIE_001830	52,55	409		Bacillus subtilis, O34962, 48.36%	Oceanobacillus iheyensis , Q8CXA9, 50%	2	not in Thaumarchaeota of the Nitrosopumilus cluster
	glyoxylate reductase	1.1.1.26	NVIE_007610	70,95	330		Korarchaeum cryptofilum, B1L765, 52.13%	uncultured crenarchaeote 57a5, D4N715, 53%	2	
	2-hydroxyacid dehydrogenase		NVIE_016370	88,1	312		Methanobacterium thermoautotrophicum, O27051, 53.47%, partial	uncultured Candidatus Nitrosocaldus sp, Q4LEF9, 60.59%	3	
(citE)	putative citrate/ citryl-CoA lyase	(EC 4.1.3.6 / 4.1.3.34)	NVIE_024430	77,51	289		Klebsiella pneumoniae, P17725 ,35.31 %	Candidatus Nitrosoarchaeum koreensis MY1, F9CZA1, 55.75 %	3	
(pox)	putative pyruvate dehydrogenase/ pyruvate oxidase	1.2.3.3	NVIE_000900	76,91	592		Bacillus subtilis, P96591, 41.9%	Solibacter usitatus, Q01Q35, 57.47%	3	not in Thaumarchaeota of the Nitrosopumilus cluster
acyP	acylphosphatase	EC 3.6.1.7	NVIE_023500	67,42	91		Thermofilum pendens, A1RZ22, 59.3%	Methanothermus fervidus, E3GYF7, 60.23%	2	
garR	putative Isocitrate lyase family enzyme	(EC 4.1.3.1)	NVIE_004460	90,07	293		Eubacterium barkeri , Q0QLE4, 45.3 %	uncultured marine crenarchaeote, B3T7Q9, 61.7%	3	candidate enzyme for 1. step of glyoxylate bypass
	phosphoglycolate phosphatase	EC 3.1.3.18	NVIE_025560	83,26	269		Nitrosopumilus maritimus, A9A492, 49.1 %	uncultured marine crenarchaeote , B3T7W6, 49.34 %	2	
	putative 2-hydroxy-3-oxopropionate reductase	1.1.1.60	NVIE_012350	74,91	306		Escherichia coli O6:H1 , P0ABQ3, 31.16 %	Nitrosopumilus maritimus , A9A3A2, 43.06 %	3	
	Carbonate dehydratase (Carbonic anhy	4.2.1.1	NVIE_017960		293		Methanosarcina thermophila, P40881, 46.9%	Archaeoglobus veneficus, F2KNT3, , 43.38%	2	gamma class. MetaCyc pathway: CO2 fixation into oxaloacetate (anapleurotic). This anapleurotic pathway replenishes the intermediates of the TCA cycle. Second enzyme: Phosphoenolpyruvate carboxylase (4.1.1.31, family IPR007566) missing. Proteins with domain IPR015813 though include: NVIE_004460, NVIE_011910, NVIE_014450, NVIE_024430. also pyruvate carboxylase and phosphoenolpyruvate (PEP) carboxylase utilize HCO3
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<b>Gluconeogenesis</b>										
pckA	ATP-dependent phosphoenolpyruvate carboxykinase	EC 4.1.1.49	NVIE_030210	84,84	523		Moorella thermoacetica, Q2RKS7, 62.25%	uncultured marine crenarchaeote, B3T8F8, 63.78 %	2	reversibel
ppdk	pyruvate, phosphate dikinase	EC 2.7.9.1/2	NVIE_014450	79,82	892		Entamoeba histolytica, P37213, 52.6%	Candidatus Nitrosoarchaeum limnia, F3KJ960, 60.16%	2	reversibel
eno	enolase	EC 4.2.1.11	NVIE_011810	83,29	417		Methanosphaera stadtmanae, Q2NG02, 44.58%	Candidatus Nitrosoarchaeum koreensis, F9CU46, 59.61 %	2	reversibel
apgM	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	EC 5.4.2.1	NVIE_006920	72,27	434		Aeropyrum pernix, Q9YBI2, 39.48%	Nitrosopumilus maritimus, A9A220, 56.98%	2	
gpmB	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	(EC 5.4.2.1)	NVIE_027510	71,5	207		Thermoplasma acidophilum, Q9HIJ2, 36.41%	uncultured marine crenarchaeote, B3T477, 45.54%	2	
pgk	phosphoglycerate kinase	EC 2.7.2.3	NVIE_003520	81,3	402		Symbiobacterium thermophilum , Q67SW6, 48.26%	Thermosediminibacter oceani, D9RZ29, 48.51 %	2	acquired horizontally
(gap)	putative glyceraldehyde-3-phosphate dehydrogenase, phosphorylating	(EC 1.2.1.59)	NVIE_005380	83	379		Pyrobaculum calidifontis, A3MTU1, 31.7 %	Cenarchaeum symbiosum, A0RW87, 52.17%	3	might be NAD(P)-dependent

PF01127 (0.00000000000014)

PF01127 (0.000000004 )

TIGR00384 (8.89e-75)

Biological Process: tricarboxylic acid cycle (GO:0006099),  
Molecular Function: lyase activity (GO:0016829)

PF00056 (1.300000000000001e-33)

Molecular Function: oxidoreductase activity, acting on the  
CH-OH group of donors, NAD or NADP as acceptor  
(GO:0016616), Molecular Function: cofactor binding  
(GO:0048037)Cellular Component: phosphopyruvate hydratase complex  
(GO:0000015), Molecular Function: magnesium ion  
binding (GO:0000287), Molecular Function:  
phosphopyruvate hydratase activity (GO:0004634),  
Biological Process: glycolysis (GO:0006096)

tpiA	triosephosphate isomerase	EC 5.3.1.1	NVIE_0144 20	72,73	227	Cenarchaeum symbiosum, O74044, 52%	Candidatus Nitrosoarchaeum limnia, F3KJ15, 51.15 %	2	
fbp	bifunctional fructose-1,6-bisphosphatase	EC 3.1.3.11	NVIE_0144 10	90,08	374	Methanocaldococcus jannaschii, Q57747, 43.41%	uncultured crenarchaeote 74A4, Q977K9, 67.91 %	2	
pgl	phosphoglucose isomerase	EC 5.3.1.9							present in Thaumarchaeota of Nitrosopumilus cluster
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<b>Embden-Meyerhoff pathway</b>									
	pfkB family carbohydrate kinase	EC 2.7.1.-	NVIE_0172 70	79	300	Methanocaldococcus jannaschii, Q57849, 27.87 %	Candidatus Nitrosoarchaeum limnia, F3KLT5, 52%	3	
	pfkB family carbohydrate kinase	EC 2.7.1.-	NVIE_0055 40	68,83	305	Klebsiella pneumoniae, P26420, 22.43%	uncultured crenarchaeote, Q6W3A2, 40.33%	3	
	pfkB family carbohydrate kinase	EC 2.7.1.-	NVIE_0242 30	69,97	344	Bacillus subtilis, P36945, 24.34%	uncultured crenarchaeote, Q701Z3, 49.71%	3	
(aroGFH) DAH7PS	putative 3-deoxy-7-phosphoheptulonate synthase	(EC 2.5.1.54)	NVIE_0058 50	88,03	260	Methanocaldococcus jannaschii, Q57843, 51.9%	uncultured crenarchaeote, Q702D4, 72.9%	3	(=phospho-2-dehydro-3-deoxyheptonate aldolase); Priam: EC 4.1.2.13, Fructose-bisphosphate aldolase (homologous protein of M. jannaschii MJ0400 is a bifunctional enzyme that also has fructose 1.6 bisphosphate aldolase activity); Tigr: phospho-2-dehydro-3-deoxyheptonate aldolase
	uncharacterized aldolase lsrF	(4.1.2.13)	NVIE_0085 40	80	281	Pasteurella multocida, Q9CLF7, 53.85 %	Nitrosopumilus maritimus, A9AAJ6, 67.75 %	3	
	pyruvate kinase	EC 2.7.1.40							not present in Thaumarchaeota of the Nitrosopumilus cluster
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<b>Other genes putatively involved in sugar/carbon metabolism</b>									
	F420-dependent oxidoreductase, G6PDH family		NVIE_0131 50	38%					
fabG	3-oxoacyl-[acyl-carrier-protein] reductase	EC 1.1.1.100	NVIE_0145 90	78,97					
sdr	glucose/ribitol dehydrogenase family protein	EC 1.1.1.-	NVIE_0185 00	76,21	248	Staphylococcus saprophyticus, Q49WS9, 46.77%	uncultured marine crenarchaeote, B3T3P6, 74.39%	3	47% similar to characterized clavaldehyde dehydrogenase of Streptomyces clavuligerus
sdr	glucose/ribitol dehydrogenase family protein	EC 1.1.1.-	NVIE_0117 50	72,05	232	Bacillus subtilis, P14802, 41.41%	Methanosarcina acetivorans, Q8TMH4, 43.51 %	3	
fabG	3-oxoacyl-[acyl-carrier-protein] reductase	EC 1.1.1.100	NVIE_0043 20	63,18	265	Thermotoga maritima, Q9X248, 38.13%	Candidatus Caldichaeum subterraneum, E6NAE7, 39.31 %	2	
sdr	glucose/ribitol dehydrogenase family protein	EC 1.1.1.-	NVIE_0202 60	65,03	297	Homo sapiens , Q9HBH5, 46.6 %	Oscillochloris trichoides DG-6, E1IGB7, 53.55%	3	similar to NADP retinol dehydrogenase, EC 1.1.1.300
sdr	glucose/ribitol dehydrogenase family protein	EC 1.1.1.-	NVIE_0052 40	77,14	598	Bacillus subtilis , P80869, 30.97 % partial	uncultured crenarchaeote 74A4, Q977K3, 47.69%	3	Nvie EC: 1.1.1.47 (glucose 1-dehydrogenase). Similar to B. megaterium and B.subtilis glucose dehydrogenase (31%) and E. coli gluconate 5-dehydrogenase
sdr	putative oxidoreductase, short chain dehydrogenase/reductase family	EC 1.1.1.-	NVIE_0123 20		268	Escherichia coli, P0AFP5, 37.11 %	Prevotella sp. oral taxon 299, D3IB72, 42.29 %	3	
sdr	putative oxidoreductase, short chain dehydrogenase/reductase family	EC 1.1.1.-	NVIE_0156 30		204	Bacillus subtilis, P37959, 39.77 %	uncultured marine crenarchaeote, B3T4F0, 55.03 %	3	
	putative PQQ dependent glucose 1-dehydrogenase	(EC 1.1.5.2)	NVIE_0236 30	68,53	375	Synechocystis sp. (strain PCC 6803), P73001, 32.65%	Candidatus Nitrosoarchaeum koreensis, F9CYN4, 43.85 %	3	371AA; candidate gene for a broad substrate specificity aldose sugar dehydrogenase (31.27% similar to yllI gene of E. coli K12 which has been demonstrated to be a PQQ dependent Glucose 1-dehydrogenase able to convert Glucose to Gluconate)(Nvie gene 32.26% similar to E.coli yllI)
	putative quinoprotein glucose/ sorbosone dehydrogenase		NVIE_0056 00	57,28	425	Escherichia coli (strain K12), P75804, 26.7%	Candidatus Nitrosoarchaeum koreensis, F9CYA4, 39.71 %	3	
	putative quinoprotein glucose/ sorbosone dehydrogenase		NVIE_0117 30	57,24	445	Escherichia coli (strain K12), P75804, 26.93%	Candidatus Nitrosoarchaeum koreensis, F9CYA4%	3	
	putative inositol-1-monophosphatase	EC 3.1.3.25	NVIE_0220 20	60,54	267	Methanothermobacter thermautotrophicus , O26957, 39.92 %	Cenarchaeum symbiosum , ADRY53, 48.24 %	2	
	putative inositol-1-monophosphatase	EC 3.1.3.25	NVIE_0252 60		264	Rhizobium loti, Q98F59, 34.23 %	Bartonella rochalimae, E6YNC5, 35.55 %	3	COG:Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family
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<b>Nonoxidative pentose-phosphate pathway</b>									
rpiA	ribose-5-phosphate isomerase	EC 5.3.3.16	NVIE_0016 20	71,56	228	Methanosarcina acetivorans, Q8TQ69, 39.82%	uncultured marine crenarchaeote , B3T7M8, 53.6%	2	
rpiA	ribose-5-phosphate isomerase	EC 5.3.3.16	-						
tktA+rpe	ribulose-phosphate 3-epimerase protein with N-terminal transketolase domain	EC 5.1.3.1. and EC 2.2.1.1	NVIE_0176 70	82,97	570	Methanocaldococcus jannaschii, Q58094, 46%	uncultured marine crenarchaeote, B3T607, 47.5%	2	blast results of ribulose-phosphate 3-epimerase only
tktA+rpe	ribulose-phosphate 3-epimerase protein with N-terminal transketolase domain	EC 5.1.3.1. and EC 2.2.1.1	-						blast results of NTD of transketolase only

IPR010210, Predicted phospho-2-dehydro-3-deoxyheptonate aldolase, 1.9e-120; PFI01791 (4.6e-47)

Molecular Function: ribose-5-phosphate isomerase activity (GO:0004751), Biological Process: pentose-phosphate shunt, non-oxidative branch (GO:0009052)

tkb	transketolase C-terminal subunit	EC 2.2.1.1	NVIE_017680	80		326	Methanocaldococcus jannaschii, Q58092, 44.3%	Candidatus Nitrosoarchaeum koreensis, F9CU25, 59.43%	2	
tal	transaldolase	EC 2.2.1.2	NVIE_017690	83,71		221	Nitrosopumilus maritimus, A9A413, 69.37%	Candidatus Nitrosoarchaeum koreensis, F9CU26, 66.37%	2	
prs	ribose-phosphate pyrophosphokinase	EC 2.7.6.1	NVIE_000630	70,34		295	Sulfolobus tokodaii, Q973F3, 33.1%	Candidatus Nitrosoarchaeum koreensis, F9CUJ0, 48.08%	2	converts ribose 5-phosphate into phosphoribosyl pyrophosphate (PRPP). The enzyme is involved in the synthesis of nucleotides (purines and pyrimidines), cofactors NAD and NADP, and amino acids histidine and tryptophan, linking these biosynthetic processes to the pentose phosphate pathway, from which the substrate ribose 5-phosphate is derived. The product phosphoribosyl pyrophosphate acts as an essential component of the purine salvage pathway and the de novo synthesis of purines.
	putative thiamine biosynthesis Thi4 protein / ribose 1,5-bisphosphate isomerase	5.3.1.29	NVIE_008130	92,19		273	Aeropyrum pernix , Q9Y9Z0, 56.86% (Putative ribose 1,5-bisphosphate isomerase)	Candidatus Nitrosoarchaeum koreensis MY1, F9CVY3, 72.97%	2	annotated as putative ribose 1,5-bisphosphate isomerase in all other thaumies
<b>Gene</b>	<b>Product</b>	<b>EC no.</b>	<b>Nvie Locus</b>	<b>identity</b>	<b>length</b>	<b>length</b>	<b>length</b>	<b>length</b>	<b>length</b>	<b>Comment</b>
<b>Sugar isomerases</b>										
	mannose-6-phosphate isomerase, type II, C-terminal domain protein	EC 5.3.1.8	NVIE_011080	53,12		125	Pseudomonas aeruginosa, P07874, 42%	Nitratiruptor sp. , A6Q1F0, 46.38%	3	
	mannose-6-phosphate isomerase, type II, C-terminal domain protein	EC 5.3.1.8	NVIE_021670	75,89		112	Salmonella typhimurium , P26340, 38.46%	Kytococcus sedentarius, C7NJR9, 50%	3	
	cupin domain-containing protein		NVIE_010800	58,82		107	Streptomyces coelicolor, Q53867, 39%	uncultured marine crenarchaeote , B3T8P4, 46.39%	3	COG0662: Mannose-6-phosphate isomerase
	cupin-domain containing protein		NVIE_004850			155	-	Nocardioopsis dassonvillei, D7B201, 44%	3	COG0662: Mannose-6-phosphate isomerase
pgm	alpha-D-phosphohexomutase	EC 5.4.2-	NVIE_015310	70,78		441	Pyrococcus horikoshii, O58973, 31.84%	Nitrosopumilus maritimus, A9A3T1, 49.2%	3	candidate for phosphoglucomutase (EC 5.4.2.10)/ phosphoglucomutase (EC 5.4.2.2) / phosphomannomutase (EC 5.4.2.8)/
gmM	alpha-D-phosphohexomutase (phosphoglucomutase)	EC 5.4.2-	NVIE_029320							candidate for phosphoglucomutase (EC 5.4.2.10)/ phosphoglucomutase (EC 5.4.2.2) / phosphomannomutase (EC 5.4.2.8)/
	putative phosphosugar isomerase		NVIE_007750	47,9		304	Pyrobaculum aerophilum, Q8ZT20, 30.22%	uncultured marine crenarchaeote KM3-34-D9_B3V515_37.59%	3	bitfunctional phosphoglucomutase/phosphomannose isomerase in A. pernix and T. acidophilum PMID: 14551194
<b>Gene</b>	<b>Product</b>	<b>EC no.</b>	<b>Nvie Locus</b>	<b>identity</b>	<b>length</b>	<b>length</b>	<b>length</b>	<b>length</b>	<b>length</b>	<b>Comment</b>
<b>Mannosylglycerate synthase and HAD-like dehalogenases</b>										
(ttuD)	putative hydroxypyruvate reductase	(EC 1.1.1.81)	NVIE_006140	55,63		450	Pyrococcus horikoshii, O58231, 40.77%	Candidatus Caldithrix subterraneum, F6P950, 42.6%	3	lysine, serine and threonine metabolism Glyoxylate and dicarboxylate metabolism
mngA	mannosyl-3-phosphoglycerate synthase	EC 2.4.1.217	NVIE_006110	75,38		401	Pyrococcus abyssi, Q9UZC1, 44.97%	uncultured crenarchaeote, Q8NKM8, 61%	2	see below
	phosphatase of the haloacid dehalogenase (HAD)-like hydrolase family		NVIE_015570	62,56		219	Mycobacterium avium , A0QJ11, 31.41% partial	uncultured crenarchaeote, Q8NKM9, 49%	3	candidate for a novel mannosyl-3-phosphoglycerate phosphatase; no close homolog in Thaumarchaeota of the Nitrosopumilus cluster but on soil fosmid 2914
(serB)	putative phosphoserine phosphatase, HAD-like hydrolase family	(EC 3.1.3.3)	NVIE_008210	77,93		224	Archaeoglobus fulgidus, O28142, 36%, partial	uncultured crenarchaeote, Q2V9E2, 70.6%	3	also involved in serine biosynthesis
	putative phosphoserine phosphatase, HAD-like hydrolase family		NVIE_014610	62,8		218	Haemophilus influenzae , P44004, 27.72%	Methanohalophilus mahii, D5EAS8, 41.3%	3	might function as beta-phosphoglucomutase (EC 5.4.2.6)
	phosphatase of the haloacid dehalogenase (HAD)-like hydrolase family	(3.6.1.1)	NVIE_012520 NVIE_012220	66,81		238	Methanopyrus kandleri, Q8TWR2, 33.33%	uncultured crenarchaeote, Q702F4, 46.7%	3	Biological Process: metabolic process (GO:0008152), Molecular Function: phosphoglycerate phosphatase activity (GO:0008967)
<b>Gene</b>	<b>Product</b>	<b>EC no.</b>	<b>Nvie Locus</b>	<b>identity</b>	<b>length</b>	<b>length</b>	<b>length</b>	<b>length</b>	<b>length</b>	<b>Comment</b>
<b>Acetamido sugar biosynthesis</b>										
glmS	glutamine-fructose-6-phosphate transaminase	EC 2.6.1.16	NVIE_008270	77,25		588	Pyrococcus abyssi, Q9V249, 43.58%	Nitrosopumilus maritimus, A9A435, 54.85%	2	UDP-N-acetyl-D-glucosamine biosynthesis
glmS	glutamine-fructose-6-phosphate transaminase	EC 2.6.1.16	NVIE_010410	53,99	60,78	586	Pyrococcus furiosus, Q8U4D1, 46%	Nitrosopumilus maritimus, A9A435, 53.48%	2	UDP-N-acetyl-D-glucosamine biosynthesis
(galT)	putative UDP-glucose-hexose-1-phosphate uridylyltransferase	(EC 2.7.7.12)	NVIE_006900	87,21		347	Arabidopsis thaliana, Q9FK51, 27.27%	uncultured marine crenarchaeote, B3T776, 61.85%	3	Biological Process: galactose metabolic process (GO:0006012), Molecular Function: UDP-glucose:hexose-1-phosphate uridylyltransferase activity (GO:0008108), Molecular Function: zinc ion binding (GO:0008270)
(wecB)	putative UDP-N-acetylglucosamine 2-epimerase	(EC 5.1.3.14)	NVIE_006890	80,42		486	Methanocaldococcus jannaschii, Q58899, 25.5%	Halorhabdus tiamatea, F7PK61, 45.18%	3	Biological Process: UDP-N-acetylglucosamine metabolic process (GO:0006047), Molecular Function: UDP-N-acetylglucosamine 2-epimerase activity (GO:0008761), Biological Process: lipopolysaccharide biosynthetic process (GO:0009103)

TIGR00292 (1.8e-62 ) TIGR00292: thiazole biosynthesis enzyme

Biological Process: thiamine biosynthetic process (GO:0009228)

PF07883 (0.000000000054)

PF07883 (0.0000000000031)

PTHR10937: GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (P01380) Similar

lysine, serine and threonine metabolism  
Glyoxylate and dicarboxylate metabolism  
Cellular Component: cytoplasm (GO:0005737), Molecular Function: mannosyl-3-phosphoglycerate synthase activity (GO:0050504), Biological Process: mannosylglycerate biosynthetic process (GO:0051479)

Biological Process: metabolic process (GO:0008152),  
Molecular Function: phosphoglycerate phosphatase activity (GO:0008967)

Molecular Function: glutamine-fructose-6-phosphate transaminase (isomerizing) activity (GO:0004360), Cellular Component: cytoplasm (GO:0005737), Biological Process: carbohydrate biosynthetic process (GO:0016051)

Biological Process: galactose metabolic process (GO:0006012), Molecular Function: UDP-glucose:hexose-1-phosphate uridylyltransferase activity (GO:0008108),  
Molecular Function: zinc ion binding (GO:0008270)

Biological Process: UDP-N-acetylglucosamine metabolic process (GO:0006047), Molecular Function: UDP-N-acetylglucosamine 2-epimerase activity (GO:0008761),  
Biological Process: lipopolysaccharide biosynthetic process (GO:0009103)

	putative glucosamine-1-phosphate N-acetyltransferase	(EC 2.3.1.157)	NVIE_006810	64,62	418	Methanococcus maripaludis, A6VG23, 27.68 %	Korarchaeum cryptofilum, B1L6K9, 34.38%	3	UDP-N-acetyl-D-glucosamine biosynthesis. Bifunctional protein GimU [Includes: UDP-N-acetylglucosamine pyrophosphorylase ; Glucosamine-1-phosphate N-acetyltransferase]
gmpp	nucleotidyl-transferase		NVIE_006800	83,47	235	Haemophilus ducreyi, Q9F664, 36.36 %	Cenarchaeum symbiosum, A0RUQ3, 50%	3	putative mannose-1-phosphate guanyltransferase (EC 2.7.7.13)
(thiD)	putative phosphomethylpyrimidine kinase	(EC 2.7.4.7)	NVIE_006780	70,05	476	Geobacter sulfurreducens , P61422, 44.79 %	Pyrococcus furiosus , Q8U193, 46.8 %	3	probably involved in thiamin metabolism
wecB	UDP-N-acetylglucosamine 2-epimerase	5.1.3.14	NVIE_008910	43	368	Methanococcus maripaludis, Q6M0B4, 50.68 %	Pyrococcus furiosus, Q8U2N9, 52.51 %	2	
(wecC)	UDP-glucose/GDP-mannose family dehydrogenase	1.1.1.22	NVIE_027330	74,22	457	Ralstonia solanacearum, P58591, 32.25%	Candidatus Nitrosoarchaeum koreensis, F9CY82, 50.11 %	3	might also use UDP-N-acetyl-D-mannosamine, candidate gene for wecC
	putative UDP-glucose/GDP-mannose dehydrogenase	1.1.1.22	NVIE_010320		295	Methanococcus maripaludis, A6VK13, 26.62 %	Desulfosporosinus sp. OT, G2G2L6, 33.21%	3	UDP-glucose/GDP-mannose dehydrogenase family, central domain protein
	putative UDP-glucose/GDP-mannose dehydrogenase	1.1.1.22	NVIE_023900		303	Methanococcus maripaludis , A4FY94, 25.48 %	Bacillus tusciae , D5WXX5, 40 %	3	
	UDP-N-acetyl-D-mannosaminuronate dehydrogenase	1.1.1.22	NVIE_023860	67,52	286	Methanococcus maripaludis, Q6LZC3, 26.96 %	Desulfosporosinus orientis, G7W550, 34.39 %	3	
(galE)	NAD-dependent epimerase/dehydratase family, includes UDP-galactose 4-epimerase-like proteins	EC 5.1.3.2	NVIE_021680	56,21	344	Methanocaldococcus jannaschii, Q57664, 36.75%	Thermoanaerobacter wiegellii, G2MV48, 40.48 %	3	
glmM	phosphoglucosamine mutase	EC 5.4.2.10	NVIE_029320	76,11		Methanothermobacter thermautotrophicus, O27627, 35%	Nitrosopumilus maritimus, A9A2Z2, 51.12 %	2	UDP-N-acetyl-D-glucosamine biosynthesis
<b>Gene</b>	<b>Product</b>	<b>EC no.</b>	<b>Nvie Locus</b>	<b>identity</b>					<b>Comment</b>
<b>Polyhydroxyalkanoate biosynthesis/cleavage</b>		<b>Length</b>							
(phaE)	putative poly(3-hydroxyalkanoate) synthase component		NVIE_003020	68%	269	Thiocystis violacea, P45367, 32.1%, partial	Cenarchaeum symbiosum, A0RX86, 29.4%	3	
phaC	poly(R)-hydroxyalkanoic acid synthase, class III	2.3.1.-	NVIE_003010	76,64%	381	Allochromatium vinosum, P45370, 39.6%	uncultured crenarchaeote, Q8NKN4, 56.72%	2	
	PHB depolymerase	3.1.1.-	NVIE_003000 or an alpha/beta hydrolase fold protein						look at the PHA-depolymerase engineering database. Some alpha/beta hydrolase fold protein?
phaAa	β-ketothiolase alpha subunit (Acetyl-CoA C-acetyltransferase)	EC 2.3.1.9	NVIE_020330	72,66	129	Methanocaldococcus jannaschii , Q58947, 29%	uncultured crenarchaeote, Q702B2, 60.9%	3	38% and 33% id with the H.mediterranei PhaA respectively 28% id with PhaAb (2nd subunit) of β-ketothiolase from H. mediterranei (HFX_1023 and HFX_1022). Contains OB-fold
(phaAb)	β-ketothiolase beta subunit	EC 2.3.1.9	NVIE_020320						
phaB	NADPH-dependent acetoacetyl-CoA reductase/dehydrogenase	EC:1.1.1.10	one of the sdr/fabG homologues						(3R)-3-hydroxyacyl-[acyl-carrier-protein]:NADP+ oxidoreductase
phaP	phasins								
<b>Gene</b>	<b>Product</b>	<b>EC no.</b>	<b>Nvie Locus</b>	<b>identity</b>					<b>Comment</b>
<b>Hydrolases</b>									
	alpha/beta hydrolase fold protein	(EC 3.-)	NVIE_002500	71,48	276	Pseudomonas putida , Q59695, 29.37 %	Nitrosopumilus maritimus, A9A3F8, 44.9%	3	candidate for enzyme involved in depolymerisation of polyhydroxyalkanoates in Thaumis (EC 3.1.1.75)
	alpha/beta hydrolase fold protein	(EC 3.-)	NVIE_018400	59,4	281	Pseudomonas sp., P19076, 31.8%	uncultured marine crenarchaeote, B3T6Z1, 37.8%	3	
	alpha/beta hydrolase fold protein		NVIE_008190		282	Bacillus subtilis, Q06734, 48.7%	Candidatus Kuenenia stuttgartiensis, Q1PY93, 50.92 %	2	similarity to non-heme chloroperoxidases
	putative Alpha/beta hydrolase fold protein		NVIE_007160		292	Staphylococcus aureus, Q99R57, 23.08 %	Roseiflexus sp. , A5UUA0, 37.67 %	3	
	putative Alpha/beta hydrolase fold protein, putative lipase		NVIE_017170		265	Moraxella sp. , P24640, 28.11 %	uncultured marine crenarchaeote HF4000_APKG2O16, B3T6Z1, 41.67 %	3	
	putative alpha/beta hydrolase fold protein		NVIE_026450	59,79	335	Dictyostelium discoideum , Q55EQ3, 25%	Thermotoga neapolitana , B9K8Y4, 26.7 %	3	
<b>Gene</b>	<b>Product</b>	<b>EC no.</b>	<b>Nvie Locus</b>	<b>identity</b>					<b>Comment</b>
<b>Glyoxalase/bleomycin resistance protein/dioxygenase</b>									
	glyoxalase/bleomycin resistance domain protein		NVIE_004470	60	136	Staphylococcus saprophyticus subsp. saprophyticus , Q49VY9, 31.86%	Oceanicola batsensis , A3U2S2, 39.84%	3	IPR004360
	glyoxalase/bleomycin resistance domain protein		NVIE_003830	70,34	161	Bacillus subtilis, O07918, 31.7%	Candidatus Nitrosoarchaeum limnia SFB1, F3KIZ9, 42.61 %	3	IPR004360
	glyoxalase/bleomycin resistance domain protein		NVIE_025150	62,5	163	Mycobacterium bovis , P64742, 39.13 %	Candidatus Nitrosoarchaeum koreensis MY1, F9CX83, 57.05 %	3	IPR004360

Molecular Function: phosphomethylpyrimidine kinase activity (GO:0008972). Biological Process: thiamin biosynthetic process (GO:0009228)

PF00984 (4e-18 )

PF09712, 3.5e-18

PF07167, 1.4e-12

PF12146 (0.00000000051 )

	putative glyoxalase/bleomycin resistance domain protein		NVIE_014480			135	-	uncultured archaeon, DJ1G14, 54.03%	3		
	putative glyoxalase/bleomycin resistance domain protein		NVIE_017150			122	-	Solibacter usitatus, Q01UG9, 57.85%	3		
	putative glyoxalase/bleomycin resistance domain protein		NVIE_018000			149	-	uncultured marine crenarchaeote, B3T443, 43.06%	3		
	putative glyoxalase/bleomycin resistance domain protein		NVIE_024660			166	-	Streptomyces sp. AA4, D9V2D7, 45.4%	3		
	Beta-lactamase-like protein	3.1.2.6	NVIE_002350	78,16	38,8	208	Bacillus amyloqueluefaciens, A7Z4X7, 33%	Candidatus Nitrosoarchaeum koreensis, F9CU50, 59.02%	3	put. Hydroxyacylglutathione hydrolase /Glyoxalase II (EC 3.1.2.6)	
	putative hydroxyacylglutathione hydrolase		NVIE_000090				Bacillus subtilis, P54435, 32.64%	Sphaerobacter thermophilus, D1C608, 40%	3		Beta-lactamase-like
	Putative metal-dependent RNase with beta-lactamase domain		NVIE_000450				Methanocaldococcus jannaschii, Q58633, 38.71%	Candidatus Nitrosoarchaeum koreensis MY1, F9CUD2, 50.78%	3		This family of proteins is universal in the archaea and consists of an N-terminal type-1 KH-domain, a central beta-lactamase domain, and a C-terminal motif associated with RNA metabolism. KH-domains are associated with RNA-binding, so this protein is a likely metal-dependent RNAase. This family was defined in [PMID: 18042280] as arCOG01782.
	Putative metal-dependent RNase with beta-lactamase domain		NVIE_006580				Methanocaldococcus jannaschii, Q58633, 40%	Nitrosopumilus maritimus, A9A2U6, 48.64%	3		
				75,63		701					
				87,13	39,24						
Gene	Product	EC no.	Nvie Locus	identity						Comment	
<b>11 subunit version of Complex I: type I NADH dehydrogenase</b>											
		1.6.99.5									
nuoA	NADH-quinone oxidoreductase, subunit A	EC 1.6.99.5	NVIE_011670	95,16		127	Nostoc punctiforme, B2J6S7, 38.46%	Candidatus Nitrosoarchaeum koreensis, F9CU02, 67.74%	2		
nuoB	NADH-quinone oxidoreductase, subunit B	EC 1.6.99.5	NVIE_011660	90,75		173	Streptomyces griseus subsp. Griseus, B1W4V9, 51.16%	Candidatus Nitrosoarchaeum limnia, F3KL58, 84.97%	2		
	NADH ubiquinone oxidoreductase 20 kDa subunit	EC 1.6.99.5	NVIE_007050		44,92	276	Escherichia coli, P16433, 54.61% partial	Candidatus Nitrosoarchaeum koreensis, F9CW32, 54.9%	2	Only in N.kor, Npum	
nuoC	NADH-quinone oxidoreductase, subunit C	EC 1.6.99.5	NVIE_1185	65,62		223	Chloroherpeton thalassium, B3QY46, 31.78%	Cenarchaeum symbiosum, A0RY67, 53.42%	2		
nuoD	NADH-quinone oxidoreductase, subunit D	EC 1.6.99.5	NVIE_011650	88,6		386	Desulfotomaculum reducens, A4J657, 39.34%	uncultured marine crenarchaeote, B3T914, 69.62%	2		
	putative NADH-quinone oxidoreductase, subunit D-related		NVIE_007060		23,96	559	Escherichia coli, P16431, 33.27%	Candidatus Nitrosoarchaeum koreensis, F9CW31, 52.08%	3		
nuoH	NADH-quinone oxidoreductase, subunit H	EC 1.6.99.5	NVIE_011640	83,85		421	Geobacillus sp., C5D984, 43.52%	Candidatus Nitrosoarchaeum koreensis, F9CU06, 64.4%	2	Thaumis have extendend NTD (ca.100AA)	
nuoI	NADH-quinone oxidoreductase, subunit I	EC 1.6.99.5	NVIE_011630	91,41		166	Thermobifida fusca, Q47LF2, 44.66%	uncultured marine crenarchaeote, B3T912, 79.88%	2		
nuoJ	NADH-quinone oxidoreductase, subunit J	EC 1.6.99.5	NVIE_011620	78,95		174	Plectonema boryanum, Q00243, 31.95%	Candidatus Nitrosoarchaeum koreensis, F9CU08, 56.73%	2		
nuoK	NADH-quinone oxidoreductase, subunit K	EC 1.6.99.5	NVIE_011610	84		100	Helicobacter pylori, C7C0H5, 48%	uncultured marine crenarchaeote, B3T3F4, 72.45%	2		
nuoM	NADH-quinone oxidoreductase, subunit M	EC 1.6.99.5	NVIE_011600	72,92		587	Nostoc sp., Q8YM86, 35.63%	uncultured marine crenarchaeote, B3T909, 58.32%	3		
nuoL	NADH-quinone oxidoreductase, subunit L	EC 1.6.99.5	NVIE_011590	79,53		687	Synechococcus sp., P31971, 35.51%	Cenarchaeum symbiosum, A0RY74, 66.32%	2		
nuoN	NADH-quinone oxidoreductase, subunit N	EC 1.6.99.5	NVIE_011580	85,49		503	Desulfitobacterium hafniense, B8FRJ7, 35.1%	Candidatus Nitrosoarchaeum koreensis, F9CU12, 60.57%	2		
Gene	Product	EC no.	Nvie Locus	identity						Comment	
<b>alternative NADH dehydrogenases, type-II NADH dehydrogenase, Coenzyme F420 dependent NADP dehydrogenase, nitroreductases, NADH-dependent FMN reductases, FAD dependent oxidoreductases</b>											
	putative FAD-dependent pyridine nucleotide-sulphide oxidoreductase (sulfide:quinone oxidoreductase-like)		NVIE_018490	62,81			Allochromatium vinosum, Q06530, 28.03%	Candidatus Nitrosoarchaeum koreensis, F9CUK0, 41.1%	3	NDH-II like, 23% identity to Acidianus ambivalens noxA, 12417325[uid], 25% similarity to SQR of Acidianus ambivalens (2 conserved cystein residues), EC: 1.6.99.3	
	NADH-dependent FMN reductase		NVIE_2290	68,42		197	Solanum tuberosum, Q8H9D2, 30.93% partial	Pedosphaera parvula Ellin514, B9XIB3, 43.15%	3	putative ferric-iron/chromate/azo dye reductase, related to Haloarchaeota	
	NADH-dependent FMN reductase		NVIE_027420	74,36		208	Bacillus subtilis, O07529, 32%	Pedosphaera parvula Ellin514, B9XIB3, 46%	3		
	NADH-dependent FMN reductase									putative ferric-iron/chromate/azo dye reductase, horizontally aquired	
	putative coenzyme F420-dependent NADP reductase		NVIE_027500	76,99		246				Nmar_0180, CENSya_1977	
	putative NADP oxidoreductase, coenzyme F420-dependent		NVIE_021174	65		213	Rattus norvegicus, Q4V8K1, 31.72%	Koribacter versatilis, Q1IVH0, 49%	3		
	nitroreductase-like protein		NVIE_000110	78,54		210	Archaeoglobus fulgidus, O30013, 31.5%	uncultured crenarchaeote, Q701Y9, 69.9%	3		
	nitroreductase-like protein		NVIE_006360	68		168	Archaeoglobus fulgidus, O28017, 34%	Candidatus Caldarchaeum subterraneum, E6N3D6, 51.52%	3		

PF07521, PF00753

Molecular Function: NADH dehydrogenase (ubiquinone) activity (GO:0008137), Biological Process: ATP synthesis coupled electron transport (GO:0042773), Biological Process: oxidation reduction (GO:0055114)

	Putative nitroreductase family protein		NVIE_016420			196	Mycobacterium smegmatis, P41401, 39.2%	Pelobacter propionicus, A1ANY8, 59.26%	3	
	Putative nitroreductase family protein		NVIE_000030			200	Mycobacterium smegmatis, P41401, 34.8%	Fischerella sp. JSC-11, G6FTP1, 54%	3	
	FAD/NAD(P)-binding oxidoreductase		NVIE_007970		90,36	280	Azotobacter vinelandii, Q44532, 29.51%	Candidatus Nitrosoarchaeum koreensis, F9CTX9, 67.02%	3	likely represents a ferredoxin-NADP reductase (EC 1.18.1.2); FAD-binding domain similar to Na(+)-translocating NADH-quinone reductase subunit F, but lacks 2Fe-2S ferredoxin-type domain
	FAD/NAD(P)-binding oxidoreductase		NVIE_017400		69,4	283	Shigella flexneri, P28901, 28.81%	Nitrosopumilus maritimus, A9A321, 45.96%	3	likely represents a ferredoxin-NADP reductase (EC 1.18.1.2); FAD-binding domain similar to Na(+)-translocating NADH-quinone reductase subunit F, but lacks 2Fe-2S ferredoxin-type domain
	Geranylgeranyl reductase family protein (putative digeranylgeranylglycerophospholipid reductase)		NVIE_011700		77,25	414	Methanothermobacter thermoautotrophicus, O27753, 31.76%	Candidatus Nitrosoarchaeum limnia, F3KI98, 51.89%	3	FAD-binding domain; candidate for electron-transferring NADH-dehydrogenase subunit nuoF
	Geranylgeranyl reductase family protein		NVIE_003360		72,19	388	Methanopyrus kandleri, Q8TUV8, 31.64%	Candidatus Nitrosoarchaeum koreensis, F9CYH9, 49.6%	3	FAD/NAD(P)-binding domain
<b>Gene</b>	<b>Product</b>	<b>EC no.</b>	<b>Nvie Locus</b>	<b>identity</b>						<b>Comment</b>
<b>F420/FMN/Flavin-dependent oxidoreductases</b>										
	luciferase-like monooxygenase family protein	(1.5.99.11)	NVIE_015060		87,5	360	Methanocaldococcus jannaschii, Q58929, 29.46%	uncultured marine crenarchaeote, B3TCN1, 59%	3	in other Thaumis this gene is in operon with zinc-dependent dehydrogenase, Nmar_1109, CENSYa_0548. abundant in Nvie proteome
	putative coenzyme F420-dependent glucose-6-phosphate dehydrogenase	(EC 1.1.98.2)	NVIE_013150		38,08	347	Nakamurella multipartita, C8XBB4, 37.86%	Methanofolius liminatans, O93735, 41.46%	3	not in other Thaumarchaeota; might substitute function of Glucose-6-phosphate dehydrogenase (EC 1.1.1.49)
	luciferase-like monooxygenase family protein	(1.5.99.11)	NVIE_004930		67,08	324	Mycobacterium tuberculosis, O53565, 28.24%	Candidatus Nitrosoarchaeum koreensis MY1, F9CWP6, 46.13%	3	
	luciferase-like monooxygenase family protein	(1.5.99.11)	NVIE_012810		37,97	249	Mycobacterium tuberculosis, P64769, 30.99%	Oscillochloris trichoides DG-6, E1ICT1, 46.8%	3	
	luciferase-like monooxygenase family protein	(1.5.99.11)	NVIE_023720			316	Mycobacterium tuberculosis, P64769, 33.88% %, partial	Kribbella flavida, D2PSK1, 40.55%	3	
	putative FMN-dependent luciferase-like monooxygenase family protein	(1.14.14.3)	NVIE_024070			349	Rhizobium sp., Q53218, 24.86%	Solibacter usitatus, Q01YC8, 76.11%	3	
<b>Gene</b>	<b>Product</b>	<b>EC no.</b>	<b>Nvie Locus</b>	<b>identity</b>						<b>Comment</b>
<b>Complex II</b>										
sdhA	succinate dehydrogenase flavoprotein subunit/fumarate reductase	EC 1.3.99.1	NVIE_002760		87,5	570				cytochrome subunit complex II
(sdhC)	putative succinate dehydrogenase/fumarate reductase	(EC 1.3.99.1)	NVIE_002750							cytochrome subunit complex II
(sdhD)	putative succinate dehydrogenase/fumarate reductase	(EC 1.3.99.1)	NVIE_002740							cytochrome subunit complex II
sdhB	FeS-center protein of succinate dehydrogenase/fumarate reductase	EC 1.3.99.1	NVIE_002730							cytochrome subunit complex II
<b>Gene</b>	<b>Product</b>	<b>EC no.</b>	<b>Nvie Locus</b>	<b>identity</b>						<b>Comment</b>
<b>Complex III: 1.10.2.2</b>										
(petB)	putative cytochrome b/b6 domain		NVIE_002610		84,27	543	Helicobacter mobilis, Q9ZGG0, 35.12%	Candidatus Nitrosoarchaeum koreensis, F9CYL5, 66.6%	3	
(petC)	rieske [2Fe-2S] iron-sulphur domain protein, cytochrome b6-f complex iron-sulfur subunit		NVIE_002620		74,29	206	Synechococcus sp., P26292, 28.32%	Cenarchaeum symbiosum, A0RTJ3, 68.04%	3	
<b>Gene</b>	<b>Product</b>	<b>EC no.</b>	<b>Nvie Locus</b>	<b>identity</b>						<b>Comment</b>
<b>Complex IV</b>										
	conserved hypothetical protein, putative Heme/copper-type cytochrome/quinol oxidase, subunit		NVIE_027520		64,71	89	Mus musculus, Q6ZQ89, 26.32% partial	Candidatus Nitrosoarchaeum limnia, F3KLE0, 46.58%		
(coxB)	putative heme-copper oxidase subunit II	(EC 1.9.3.1)	NVIE_027530		69,7	163	Bradyrhizobium japonicum, P98053, 32.53% partial	uncultured marine crenarchaeote, B3T479, 66.67%	3	
coxA1	heme-copper oxidase subunit I	EC 1.9.3.1	NVIE_027540		85,77	497	Rickettsia felis, Q4ULL5, 42.59%	Candidatus Nitrosoarchaeum limnia, F3KLD8, 69.68%	2	
coxA2	heme-copper oxidase subunit I		NVIE_001340		79,53	530	Bradyrhizobium japonicum, P31833, 41.24%	Candidatus Nitrosoarchaeum limnia, F3KLD8, 67.65%	2	
	blue (type 1) copper domain protein		NVIE_027550		52,4	284	Danio rerio, Q67FY3, 32.97% partial	Nitrosopumilus maritimus, A9A5W7, 34.98%	3	might be associated with Complex IV of electron transfer chain
(ctaA1)	putative cytochrome oxidase assembly protein		NVIE_027560		74,83	159	Bacillus licheniformis, Q65K14, 28.99% partial	Nitrosopumilus maritimus, A9A1W1, 48.53%	3	
(ctaA2)	putative cytochrome oxidase assembly protein		NVIE_020464		50,39	189	Haloarcula marismortui, Q5V556, 32.26% partial	uncultured marine crenarchaeote, B3T482, 40.	3	
<b>Gene</b>	<b>Product</b>	<b>EC no.</b>	<b>Nvie Locus</b>	<b>identity</b>						<b>Comment</b>
<b>Complex V: A1A0-type ATPse</b>										

PF00881, 2.4e-28

PF00881

FAD; Flavoprotein; Lipid biosynthesis; Lipid metabolism; NAD; Oxidoreductase; Phospholipid biosynthesis; Phospholipid metabolism

PF00296 (4.3e-62)

PF00296 (5.49e-53). The Nvie protein does not belong to the IPRO19945 F420\_G6P family. However, NCBI CD search identifies the TIGR03554 F420\_G6P\_DH family (2.66e-69)

PF00296 (2.3e-65)

PF00296 (4.1E-58)

PF00296 (6.9e-57)

PF00296 (2.4e-49)



atpE	archaeal A1A0-type ATP synthase, subunit E	EC 3.6.3.14	NVIE_0228 90	71,66	208	Cenarchaeum symbiosum, A0RXK2, 32.95%	Nitrosopumilus maritimus, A9A2R1, 38.98%	2	
atpA	archaeal A1A0-type ATP synthase, subunit A	EC 3.6.3.14	NVIE_0229 00	90,35	600	Nitrosopumilus maritimus, A9A2R0, 77.72%	Candidatus Nitrosoarchaeum koreensis, F9CZE0, 78.91%	2	
atpB	archaeal A1A0-type ATP synthase, subunit B	EC 3.6.3.14	NVIE_0229 10	95,02	463	Nitrosopumilus maritimus, A9A2Q9, 79.52%	Candidatus Nitrosoarchaeum koreensis, F9CZD9, 81.06 %	2	
atpD	archaeal A1A0-type ATP synthase, subunit D	EC 3.6.3.14	NVIE_0229 20	89,81	220	Methanopyrus kandleri, Q8TUS9, 34.62%	Candidatus Nitrosoarchaeum limnia, F3KLN2, 62.8 %	2	
atpK	archaeal A1A0-type ATP synthase, subunit K	EC 3.6.3.14	NVIE_0229 40	84,34	112	Arcobacter butzleri, A8EVM2, 35%	Nitrosopumilus maritimus, A9A2Q7, 61.7%	2	COG0636: F0F1-type ATP synthase, subunit c/Archaeal/vacuolar-type H+-ATPase, subunit K
atpI	archaeal A1A0-type ATP synthase, subunit I	EC 3.6.3.14	NVIE_0229 70	73,94	711	Archaeoglobus fulgidus, O29106, 24%	Cenarchaeum symbiosum A, A0RXK6, 45%	3	
atpC	archaeal A1A0-type ATP synthase, subunit C	EC 3.6.3.14	NVIE_0229 90	77,55	353	Methanocaldococcus jannaschii, Q57672, 24.19%	Candidatus Nitrosoarchaeum limnia, F3KLP0, 45.7%	2	
atpF	archaeal A1A0-type ATP synthase, subunit F	EC 3.6.3.14	NVIE_0056 20	85,71	98	Methanosphaera stadtmanae, Q2NF86, 31.11 %	Nitrosopumilus maritimus, A9A4J8, 56.12 %	2	
<b>Gene</b>	<b>Product</b>	<b>EC no.</b>	<b>Nvie Locus</b>	<b>identity</b>					<b>Comment</b>
<b>Pyrophosphatase</b>									
ppa	inorganic diphosphatase	EC 3.6.1.1	NVIE_0255 40	68,75		Aquifex aeolicus, O67501, 57.47 %	Staphylothermus marinus, A3DLS2, 61.27%	2	
<b>Gene</b>	<b>Product</b>	<b>EC no.</b>	<b>Nvie Locus</b>	<b>identity</b>					<b>Comment</b>
<b>Electron-transfer flavoproteins</b>									
(fixCX)	putative electron-transfer flavoprotein /FAD-dependent / fixCX-like		NVIE_0110 40	77,65	622	Escherichia coli, Q7AHT0, 34.9%	uncultured crenarchaeote, Q8NKM4, 65.76%	3	
etfA (fixB)	putative electron transfer flavoprotein, alpha subunit		NVIE_0110 50	79,74	391	Clostridium saccharobutylicum, P53578, 33.51 %	uncultured crenarchaeote, Q8NKM5, 66.7%	3	
etfB (fixA)	putative electron transfer flavoprotein, subunit beta		NVIE_0110 60	81,27	292	Clostridium acetobutylicum, P52040, 34.55 %	uncultured crenarchaeote, Q8NKM6, 72.28 %	3	
	putative guanosine polyphosphate pyrophosphohydrolase/synthetase		NVIE_0110 70	68,22	239		uncultured crenarchaeote 57a5, D4N720, 52.54%	3	Signal transduction
<b>Gene</b>	<b>Product</b>	<b>Length in AA</b>	<b>Nvie Locus</b>	<b>identity</b>					<b>Comment</b>
<b>rieske proteins (PF00355) and ferredoxins (PF00037, SSF54862)</b>									
	rieske [2Fe-2S] iron-sulphur domain protein	120	NVIE_0201 90	73,21	118	Homo sapiens, Q96NN9, 39%, partial	Sulfolobus islandicus ,C3NK88, 32.76%	3	adjacent to ferritin
	4Fe-4S ferredoxin iron-sulfur binding domain protein	97	NVIE_0206 10	97,94	97			3	
	4Fe-4S ferredoxin iron-sulfur binding domain protein	178	NVIE_0238 10	87,64	178			3	put. zinc-containing ferredoxin
	4Fe-4S ferredoxin iron-sulfur binding domain protein	207	NVIE_0008 90	75,71	226			3	Pyruvate/2-oxoglutarate dehydrogenase complex (COG0508), adjacent to pox gene
	protein with 4Fe-4S ferredoxin iron-sulfur binding domain	340	NVIE_0003 60	80	323			3	
	4Fe-4S ferredoxin iron-sulfur binding domain protein	97	NVIE_0130 10	87,37	105			3	put. zinc-containing ferredoxin
	4Fe-4S ferredoxin iron-sulfur binding domain protein		NVIE_0193 10		186			3	
	Rieske (2Fe-2S) domain-containing protein		NVIE_0224 10						
	putative Rieske 2Fe-2S domain protein		NVIE_0200 10						
	Rieske (2Fe-2S) domain-containing protein		NVIE_0281 40						
	Rieske (2Fe-2S) domain-containing protein		NVIE_0288 40						
	putative Rieske 2Fe-2S domain protein		NVIE_0301 40						
<b>Gene</b>	<b>Product</b>	<b>Length in AA</b>	<b>Nvie Locus</b>	<b>identity</b>					<b>Comment</b>
<b>Electron carriers, plastocyanines</b>									
	blue (type 1) copper domain protein	411	NVIE_00343 80	65,27	429	Paracoccus versutus, P22365, 33%	Candidatus Nitrosoarchaeum limnia , F3KKD7, 42.42 %	3	contains 2 cupredoxin domains and five transmembrane domains, Walker and co-workers (2011) suggest that the homologous enzyme of N. maritimus is a likely cM552 analog
	cupredoxin domain protein	154	NVIE_0295 80	58,23	170	Paracoccus versutus , P22365, 32.86 % partial	Nitrosopumilus maritimus , A9ASW7, 32.42 % partial	3	

Biological Process: ATP synthesis coupled proton transport (GO:0015986), Cellular Component: proton-transporting two-sector ATPase complex, catalytic domain (GO:0033178), Molecular Function: proton-transporting ATPase activity, rotational mechanism (GO:0046961)

Molecular Function: magnesium ion binding (GO:0000287), Molecular Function: inorganic diphosphatase activity (GO:0004427), Cellular Component: cytoplasm (GO:0005737), Biological Process: phosphate metabolic process (GO:0006796)

PF00355

PF00127



	blue (type 1) copper domain protein	157	NVIE_002600	55,48%		153	Paracoccus denitrificans, P22364, 27.7%	Nitrosopumilus maritimus, A9A4R0, 36%	3	
	blue (type 1) copper domain protein	135	NVIE_011200	35,76		191	Paracoccus denitrificans, P22364, 33.7%	Nitrosopumilus maritimus, A9A4R0, 38.41%	3	
	blue (type 1) copper domain protein	118	NVIE_011230	64,49		229	Paracoccus versutus, P22365, 32%	Frankia sp., E3J582, 41.86 %	3	
	unknown protein with C-terminal blue (type 1) copper domain	334	NVIE_024190	44,26		283	Synechococcus elongatus, P55020, 38.1 % partial	Microcystis aeruginosa, A8YB36, 39.5% partial	3	
	Putative copper-binding protein, plastocyanin/azurin family protein	274	NVIE_014374	48,56		275	Oryza sativa subsp. Indica, A2Y886, 29.32%	stus Nitrosoarchaeum koreensis, F9CWD5,	3	
	Putative copper-binding , plastocyanin/azurin family protein		NVIE_005340	44		132	Scenedesmus obliquus, P26956, 33.6%	Candidatus Nitrosoarchaeum koreensis , F9CWD5, 37.6%	3	
	blue (type 1) copper domain protein		NVIE_023620			141	Methylobacterium extorquens , P04172, 33.8%	Candidatus Nitrosoarchaeum limnia SFB1, F3KKH2, 39.5%	3	
	exported protein of unknown function with Blue (type 1) copper domain		NVIE_029900			370	Synechococcus sp, Q5N4W8, 39.58 % partial	Candidatus Nitrosoarchaeum koreensis MY1, F9CYK8, 28% partial	4	
	putative cupredoxin		NVIE_003680	60,63		134	Paracoccus versutus , P22365, 28.91 %	Methanocella paludicola, D1Z2J0, 37.29 % partial	3	SSF49503 (0.0000000022 )
	putative cupredoxin		NVIE_003910			278	Paracoccus versutus , P22365, 29.1 % partial	uncultured marine crenarchaeote , B3TBPO, 35.43 % partial	3	SSF49503 (8.2e-16 )
	putative cupredoxin		NVIE_002250		NVIE_023260 (43.48)	226			3	SSF49503 (0.00000000000011 )
	putative cupredoxin		NVIE_004200			153			3	SSF49503 (0.0000029)
	putative exported protein of unknown function with cupredoxin domain		NVIE_007310			546			5	SSF49503
	exported or membrane protein of unknown function with cupredoxin domain		NVIE_012040			274			5	SSF49503 (0.000000003)
	protein of unknown function with cupredoxin domain		NVIE_018590			584			5	SSF49503 (0.00000000000036)
	exported protein of unknown function with cupredoxin domain		NVIE_020060			300			5	SSF49503 (2e-16 )
	putative cupredoxin		NVIE_023260		NVIE_002250 (43.48 )	214			3	SSF49503 (0.00000000000014)
	exported protein of unknown function with cupredoxin domain		NVIE_025630			489			5	SSF49503 (0.000000000000035 )
Gene	Product	EC no. (Nvie)	Nvie Locus	identity						Comment
<b>Multicopper oxygenases</b>										
	multicopper oxidase		NVIE_000600	72,43		343	Neisseria meningitidis, Q9JTB8, 29.22%, partial	Nitrosopumilus maritimus, A9A1P4, 64.6%	3	Cu-oxidase type 3 and type 2
	multicopper oxidase		NVIE_026950	71,43	82,3	340	Neisseria meningitidis, Q9JTB8, 30.61%, partial	Nitrosopumilus maritimus, A9A1P4, 63.5%	3	Cu-oxidase type 3 and type 3
	multicopper oxidase		NVIE_019250	57,92		468	Neisseria meningitidis, Q9JTB8, 31.43 %	Candidatus Nitrosoarchaeum koreensis, F9CZ86, 58.11 %	3	Cu-oxidase type 3 and C-terminal blue copper domain
aniA	multicopper oxidase type 3		NVIE_017730	62,98	43,34	458	Neisseria gonorrhoeae, Q02219, 30.84%, partial	Candidatus Nitrosoarchaeum limnia, F3KKF0, 48.43 %	3	Cu-oxidase type 3 and type 2 and C-terminal blue copper domain
(nirK)	putative copper-containig nitrite reductase	1.7.2.1	NVIE_000530	72,49		380	Neisseria meningitidis, Q9JYE1, 28.66%, partial	uncultured crenarchaeote, D4N705, 59.95%	3	
Gene	Product	EC no. (Nvie)	Nvie Locus	identity						Comment
<b>Ammonia-monoxygenase</b>										
(amoA)	putative ammonia monoxygenase subunit A	1.14.99.39	NVIE_027270	95,63		216	Nitrosomonas europaea, Q04507, 25.99%, partial	uncultured crenarchaeote, G3KDG6, 99.54%	3	
(amoX)	conserved hypothetical protein/ putative ammonia monoxygenase-associated protein		NVIE_027280	89,04		102	Rattus norvegicus, Q6RI88, 32.29%	uncultured crenarchaeote, Q701V4, 76.53%	4	2 transmembrane domains, Glycine rich
(amoB)	putative ammonia monoxygenase subunit B	1.14.99.39	NVIE_028430	84,32		185	Nitrosomonas europaea, Q04508, 32.61%, partial	uncultured crenarchaeote, Q701V5, 67.96%	3	
(amoC6)	putative ammonia monoxygenase subunit C		NVIE_028544	97,28		187	Scenedesmus obliquus, Q1KVS7, 29%, partial	Cenarchaeum symbiosum, A0RUL8, 89.3%		
(amoC1)	putative ammonia monoxygenase subunit C		NVIE_000540	88,59		187	Scenedesmus obliquus, Q1KVS7, 30.65%, partial	Cenarchaeum symbiosum, A0RUL8, 83.42%	3	
(amoC2)	putative ammonia monoxygenase subunit C		NVIE_002330	89,13		187	Scenedesmus obliquus, Q1KVS7, 30.65%, partial	uncultured crenarchaeote, A4GIX5, 79.9%	3	
(amoC3)	putative ammonia monoxygenase subunit C		NVIE_011560	95,11		187	Scenedesmus obliquus, Q1KVS7, 302.26%, partial	Nitrosopumilus maritimus, A9A4U4, 91.49%	3	
(amoC4)	putative ammonia monoxygenase subunit C		NVIE_019080	95,11		184	Arabidopsis thaliana, Q9FMD7, 30.77%	Cenarchaeum symbiosum, A0RUL8, 88.04%	3	

Gene	Product	Nvie Locus	identity						Comment
(amoC5)	putative ammonia monooxygenase subunit C	NVIE_024080	75		187	Candida albicans, Q59X11, 28.3%	Cenarchaeum symbiosum, AORUL8, 72.734%	3	
Others									
	putative NorQ like ATPase	NVIE_017710	86,79		276	Staphylococcus epidermidis , Q8CP85, 35.52 %	Candidatus Nitrosoarchaeum koreensis, F9CY22, 68.56 %	3	homologous to RNAR_02017
	von willebrand factor type A domain protein	NVIE_017700	81,14		534	Acidianus ambivalens , P32985, 24.39 %partial	uncultured marine crenarchaeote , B3T7J8, 50.38%	3	homologous to RNAR_02018
	Kelch repeat-containing protein	NVIE_021960	59,17		165	adyrhizobium japonicum , Q89XJ6, 35.14 % partial	Candidatus Nitrosoarchaeum limnia, F3KL72, 42	3	(to convergence) results indicate significant similarities to nitrous oxide reductases
Gene	Product	Nvie Locus	identity						Comment
Urease									
ureD	urease accessory protein ureD	NVIE_014680	68,59		318	Cenarchaeum symbiosum, AORUR7, 41.11%	uncultured marine crenarchaeote HF4000_APKG7F11, 48%	2	UreD is involved in activation of the urease enzyme via the UreD-UreF-UreG-urease complex [PMID: 9209019] and is required for urease nickel metallocentre assembly [PMID: 7909161].
ureG	urease accessory protein ureG	NVIE_014690	83,81		219	Cenarchaeum symbiosum, AORUR8, 70%	uncultured marine crenarchaeote, B3T4E6, 75.94%	2	The activation of urease requires GTP hydrolysis and the formation of a preactivation complex consisting of apo-urease and urease accessory proteins Uref, UreH, and UreG. UreG is a SIMBI class GTPase that can be recruited by Uref-UreH complex
(ureF)	putative urease accessory protein ureF	NVIE_014700	63,31		244	Cyanothecce sp. (strain PCC 7424), B7K911, 31%	uncultured marine crenarchaeote, B3T9K1, 51.94%	3	UreF is proposed to modulate the activation process of urease by eliminating the binding of nickel irons to noncarbamylated protein. TMHMM software predicts a false TM. Overall structure helical.
(ureE)	putative urease accessory protein ureE	NVIE_014710	63,58		167	Natronomonas pharaonis, Q3IRZ1, 32.82%	uncultured marine crenarchaeote, B3T9K2, 37.65%	3	Members of this group are nickel-binding proteins required for urease metallocentre assembly. They are believed to function as metallochaperones to deliver nickel to urease apoprotein. It has been shown by yeast two-hybrid analysis that UreE forms a dimeric complex with UreG in Helicobacter pylori 26695 [PMID: 12388207]. The UreDFG-apoenzyme complex has also been shown to exist [PMID: 11157956, PMID: 7721685] and is believed to be, with the addition of UreE, the assembly system for active urease [PMID: 7721685]. The complexes, rather than the individual proteins, presumably bind to UreB via UreE/H recognition sites.
ureC1	urea amidohydrolase (urease), subunit alpha	EC 3.5.1.5	NVIE_014740	94,61	575	Bacillus halodurans, Q9KG59, 64.57%	uncultured marine crenarchaeote, B3T4E1, 70.18%	2	
ureC2		EC 3.5.1.5	NVIE_015020	69,28	69,63	571	Clostridium thermocellum, A3DGF8, 68.24%	uncultured marine crenarchaeote, B3T4E1, 77.5%	
ureB1	urea amidohydrolase (urease), subunit beta	EC 3.5.1.5	NVIE_014750	87,7		148	Bacillus sp., Q07398, 63.37%	Cenarchaeum symbiosum, AORUS2, 58.2%	2
ureB2		EC 3.5.1.5	NVIE_015010	60,98	60,16	121	Pseudomonas syringae pv. Tomato, Q883F3, 53.72%	Cenarchaeum symbiosum, AORUS2, 64.46%	2
ureA1	urea amidohydrolase (urease), subunit gamma	EC 3.5.1.5	NVIE_014760	90		100	Alcanivorax borkumensis, Q0VKX9, 68.69%	Synechococcus sp. PCC 7335, B4WPG2, 64.65%	2
ureA2		EC 3.5.1.5	NVIE_015000	64,65	58,59	100	Streptomyces avermitilis, Q826S1, 70%	Cenarchaeum symbiosum, AORUS1, 74.75%	2
Gene	Product	Nvie Locus	identity						Comment
Gene	Product	Nvie Locus	identity						Comment
<b>Creatine degradation</b>									
	creatinine amidohydrolase/ formamide hydrolase	EC 3.5.2.10	NVIE_0897						
	putative creatinase	EC 3.5.3.3	NVIE_011930	79,89		359	Pyrococcus furiosus, P81535, 33.97 %	Nitrosopumilus maritimus, A9A2U3, 51.27%	3
Gene	Product	Nvie Locus	identity						Comment
<b>Iron-sulfur cluster assembly</b>									
sufB	FeS cluster assembly protein sufB		NVIE_012430	94		466	Bacillus subtilis, O32162, 64.18%	Nitrosopumilus maritimus, A9A1A5, 80.69%	2
(sufD)	putative FeS cluster assembly protein sufD		NVIE_012440	75,37		473	Staphylococcus haemolyticus , Q4L4T1,24.01 %	Candidatus Nitrosoarchaeum limnia, F3KHU3, 49.05 %	3
	rieske [2Fe-2S] iron-sulphur domain protein		NVIE_012450	65,71		107	Pseudomonas aeruginosa, Q51493, 31%	uncultured gamma proteobacterium, E7C7I0, 47.06 %	3
sufS	cysteine desulfurase/selenocysteine lyase	EC 2.8.1.7/4.4.1.16	NVIE_012460	87,2		415	Bacillus halodurans, Q9K7A0, 55%	uncultured crenarchaeote 76h13, D4N762, 71.26%	2
nifU	SUF system FeS cluster assembly protein		NVIE_012470	90,14			Bacillus subtilis, O32163, 41.9%	uncultured crenarchaeote 29d5, D4NGY3, 79.8%	2

Molecular Function: iron ion binding (GO:0005506),  
Molecular Function: protein binding (GO:0005515),  
Biological Process: iron-sulfur cluster assembly  
(GO:0016226), Molecular Function: iron-sulfur cluster  
binding (GO:0051536)

sufC	FeS assembly ATPase SufC		NVIE_029610	87,95		259	Bacillus subtilis, P80866, 51.38%	Cenarchaeum symbiosum, AORXG9, 65.57%	3	
sufA	Fe-S cluster assembly protein sufA		NVIE_012090	87,07		116	Methylococcus capsulatus, Q60AU6, 55.14%	uncultured crenarchaeote 29d5, D4N6X8, 80%	2	
<b>Gene</b>	<b>Product</b>	<b>EC number</b>	<b>Nvie Locus</b>	<b>identity</b>						<b>Comment</b>
<b>Oxygen species detoxification</b>										
(cld)	putative chlorite dismutase		NVIE_029620	82,12		244	Mycobacterium smegmatis, A0QW25, 36.78%	Candidatus Nitrosoarchaeum koreensis, F9CVE8, 57.78%	3	42% id to N. defluviu chlorite dismutase homologue [NIDE3081]; N.gargensis has a Leucine residue at ARG173
sod	superoxide dismutase	EC 1.15.1.1	NVIE_030260	89,37		215	Geobacillus stearothermophilus, P00449, 56.65%	Candidatus Nitrosoarchaeum limnia, F3KMF7, 68.93 %	2	
	alkyl hydroperoxide reductase/ Thiol specific antioxidant family protein	(1.11.1.15)	NVIE_005140	75,11		219	Mycobacterium bovis, P59960, 29.9%, partial	Candidatus Nitrosoarchaeum koreensis, F9CZ14, 57.27 %	3	
	alkyl hydroperoxide reductase/ Thiol specific antioxidant family protein	(1.11.1.15)	NVIE_013750	77,16		178	Populus jackii, Q6QP16, 40.9%, partial	Cenarchaeum symbiosum, ADRY64, 60.65 %	3	
	alkyl hydroperoxide reductase/ Thiol specific antioxidant family protein	(1.11.1.15)	NVIE_011770	73,15		157	Bacillus subtilis, Q796Y8, 43.15%	Candidatus Nitrosoarchaeum koreensis, F9CVL3, 65.33 %	3	
	alkyl hydroperoxide reductase/ Thiol specific antioxidant family protein	(1.11.1.15)	NVIE_012680	79,89		189	Bacillus subtilis, O31820, 25.6%	Geobacillus sp. , C5D214, 27.04 %	3	
trxB	thioredoxin reductase	1.8.1.9	NVIE_008160	87,62		318	Streptomyces clavuligerus , Q05741, 57.28 %	Candidatus Nitrosoarchaeum limnia SF81, F3KID5, 63.46 %	2	Thioredoxin reductase in conjunction with thioredoxin is a ubiquitous oxidoreductase system with antioxidant and redox regulatory roles. Thioredoxin reductase (EC:1.8.1.9) reduces oxidised thioredoxin in the presence of NADPH. Reduced thioredoxin serves as an electron donor for thioredoxin peroxidase which consequently reduces H2O2 to H2O.
<b>Gene</b>	<b>Product</b>	<b>EC number</b>	<b>Nvie Locus</b>	<b>identity</b>						<b>Comment</b>
<b>Detoxification</b>										
arsC	arsenate reductase	EC 1.20.4.1	NVIE_020750	80,77		143	Brevibacillus brevis, C0ZEV2, 41.41%	Candidatus Nitrosoarchaeum koreensis, F9CV96, 55.73 %	2	different from the respiratory arsenate reductase (Arr) (PMID: 9738904) which belongs to the DMSO reductase protein family, contains molybdenum cofactor, zinc, two subunits and acts as the terminal electron acceptor for growth on acetate. This one belongs to the tyrosine phosphatase superfamily and the mechanism involves two conserved C residues
	put. arsenite methyltransferase	(EC 2.1.1.137)	NVIE_020760	59,85		253	Mus musculus, Q91WU5, 34%	Candidatus Nitrosoarchaeum koreensis, F9CV95, 56.52 %	3	only in <i>N. koreensis</i>
merA	mercuric reductase	EC 1.16.1.1	NVIE_012710	88,21		476	Staphylococcus aureus, P0A0E5, 42.92%	Candidatus Parvarchaeum acidiphilum, D2EFM6, 47.6%	2	closely related to mercury reductase of characterized <i>S. solfataricus</i> but not in Thaumarchaeota of the Nitrosopumilus cluster
<b>Gene</b>	<b>Product</b>	<b>EC number</b>	<b>Nvie Locus</b>	<b>identity</b>						<b>Comment</b>
<b>Alanine</b>										
ald	putative alanine dehydrogenase	(EC 1.4.1.1)	NVIE_011180	68,11		398	Oceanobacillus iheyensis, Q8CX61, 31.58%	Bacillus tusciae , D5WXY6, 34.41 %	3	not in other Thaumarchaeota
csd	putative cysteine desulfurase		NVIE_029160			393	Methanothermobacter thermautotrophicus , O27442, 33.25%	Candidatus Nitrosoarchaeum limnia, F3KLV8, 47.79%	3	This group represents a cysteine desulfurase, NifS type. NifS-like proteins are homodimeric and belong to the alpha-family of pyridoxal-5'-phosphate dependent enzymes [PMID: 10715213] which catalyse the reaction: L-cysteine + (enzyme)-cysteine = L-alanine + (enzyme)-S-sulphanyl cysteine
iscS	cysteine desulfurase	2.8.1.7	NVIE_013760	78,63		395	Dictyoglomus turgidum, B8DZS1, 51.41%	Candidatus Nitrosoarchaeum koreensis MY1, F9CUM8, 60%	2	
<b>Aspartate</b>										
aspC	aspartate aminotransferase	EC 2.6.1.1	NVIE_005740	69,01		464	Thermotoga maritima, Q9X0Y2, 36%	Nitrosopumilus maritimus, A9A229, 43%	2	
<b>Asparagine</b>										
asn	putative asparagine synthase	(EC 6.3.5.4)	NVIE_011110	65,2		546	Methanocaldococcus jannaschii, Q58516, 33.57%	uncultured crenarchaeote, Q8NKN0, 54.32%	3	not in other Thaumarchaeota, glutamine-hydrolyzing
asnB	putative asparagine synthase	(EC 6.3.5.4)	NVIE_008710	50,98			Mycobacterium tuberculosis, P64247, 28.65 %	enarchaeum symbiosum, AORWB9, 43.64 %	3	glutamine-hydrolyzing
	putative asparagine synthase	(EC 6.3.5.4)	NVIE_028600	65,2		318	Escherichia coli , P22106, 31.5%	didatus Nitrosoarchaeum limnia , F3KJF4, 3	3	glutamine-hydrolyzing
			NVIE_026410	63,01		252	Methanocaldococcus jannaschii, Q58516, 26.2 %	uncultured crenarchaeote, Q701W8, 49.78 %	3	
<b>Glutamate</b>										

PF06778, chlorite dismutase (2e-53)

Molecular Function: asparagine synthase (glutamine-hydrolyzing) activity (GO:0004066), Biological Process: asparagine biosynthetic process (GO:0006529)

gdhA	glutamate dehydrogenase [NAD(P)+]	EC 1.4.1.3	NVIE_0122 30	89,83	417	Thermococcus litoralis, Q56304, 54.85 %	cultured crenarchaeote 76h13, D4N759, 78.	2	
	putative glutamate racemase	EC 5.1.1.3	NVIE_0188 00	87,22	271				
<b>Glutamine</b>									
glnA 1	glutamate—ammonia ligase / glutamine synthetase	EC 6.3.1.2	NVIE_0121 60	71,92	495	Sulfolobus solfataricus, P23794, 46.34%	atus Caldiiarchaeum subterraneum, E6N9Q4	2	
glnA2	glutamate—ammonia ligase / glutamine synthetase		NVIE_0185 50		488	Sulfolobus solfataricus, P23794, 53.3%	ltured marine crenarchaeote , B3T3Q0, 60	2	
<b>Serine</b>									
	threonine ammonia-lyase	EC 4.3.1.19	NVIE_0000 60						
<b>Glycine</b>									
glyA	serine/glycine hydroxymethyltransferase	EC 2.1.2.1	NVIE_0218 60	88,15	462	Nitrosopumilus maritimus , A9A3Y9, 67.67 %	atus Nitrosoarchaeum limnia SFB1, F3KLZ	2	
<b>Threonine</b>									
thrA	aspartate kinase	EC 2.7.2.4	NVIE_0270 70	86,27	469	Methanocaldococcus jannaschii, Q57991, 45%	atus Nitrosoarchaeum limnia , F3KLU7, 53	2	
	putative aspartate kinase	(EC 2.7.2.4)	NVIE_0211 10	79,66	481	Methanocaldococcus jannaschii, Q57991, 28%	uncultured crenarchaeote, Q702C1, 67.9%	3	
asd	aspartate-semialdehyde dehydrogenase	EC 1.2.1.11	NVIE_0243 40						functions in amino acid biosynthesis; serves as candidate for malonyl-CoA reductase (EC 1.2.1.75) and succinyl-CoA reductase (EC 1.2.1.76)
hom	homoserine dehydrogenase	EC 1.1.1.3	NVIE_0052 70	85,07	337	Methanocaldococcus jannaschii, Q58997, 44.3%	cultured marine crenarchaeote, B3T9N5, 59	2	
thrB	homoserine kinase	EC 2.7.1.39	NVIE_0083 30	72,1	332	Thermoplasma volcanium, Q979X5, 38%	Nitrosopumilus maritimus, A9A532, 56%	2	
thrC	threonine synthase	EC 4.2.3.1	NVIE_0047 80	87,67	450	Methanocaldococcus jannaschii, Q58860, 36.8%	cultured marine crenarchaeote, B3T727, 6	2	
<b>Isoleucine</b>									
ilvA	threonine ammonia-lyase	4.3.1.19	NVIE_0000 60	78,47	417	Shigella flexneri, P0AGF9, 46.79 %	ltured marine crenarchaeote , B3T6W7, 61	2	
ilvB	acetolactate synthase, large unit	EC 2.2.1.6	NVIE_0085 60	90,55	562	Methanocaldococcus jannaschii, Q57725, 49%	atus Nitrosoarchaeum koreensis , F9CXJ9, 1	2	
ilvH	acetolactate synthase, small unit	EC 2.2.1.6	NVIE_0085 70	92,36	165	Methanocaldococcus jannaschii, Q57625, 51.5%	ethanothermus fervidus, E3GWW8, 55.13	2	
ilvC	ketol-acid reductoisomerase	EC 1.1.1.86	NVIE_0286 50	87,88	333	Nitrosopumilus maritimus, A9A2E4, 67%	atus Nitrosoarchaeum koreensis , F9CX93,	2	
ilvD	dihydroxy-acid dehydratase	EC 4.2.1.9	NVIE_0047 60	86,36	559	Sulfolobus tokodaii, Q96YK0, 59%	atus Nitrosoarchaeum koreensis, F9CWX2,	2	
ilvE	branched-chain-amino-acid transaminase	EC 2.6.1.42	NVIE_0076 50	78,1	305	Salmonella typhi, P0A1A6, 49.03 %	Nitrosopumilus maritimus, A9A316, 50.16 %	2	
<b>Valine</b>									
ilvB	acetolactate synthase, large unit	EC 2.2.1.6	NVIE_0085 60						
ilvH	acetolactate synthase, small unit	EC 2.2.1.6	NVIE_0085 70						
ilvC	ketol-acid reductoisomerase	EC 1.1.1.86	NVIE_0286 50						
ilvD	dihydroxy-acid dehydratase	EC 4.2.1.9	NVIE_0047 60						
ilvE	branched-chain-amino-acid transaminase	EC 2.6.1.42	NVIE_0076 50						
<b>Leucine</b>									
ilvB	acetolactate synthase, large unit	EC 2.2.1.6	NVIE_0085 60						
ilvH	acetolactate synthase, small unit	EC 2.2.1.6	NVIE_0085 70						
ilvC	ketol-acid reductoisomerase	EC 1.1.1.86	NVIE_0286 50						
ilvD	dihydroxy-acid dehydratase	EC 4.2.1.9	NVIE_0047 60						
	(R)-citramalate synthase / (2-isopropylmalate synthase , leuA)	EC 2.3.1.182/ EC 2.2.1.121	NVIE_0085 80	84,34	502	Methanopyrus kandleri, Q8TYB1, 54%	idatus Nitrosoarchaeum limnia, F3KJ1V, 65	2	EC 2.3.1.182: Involved in a novel pyruvate pathway for isoleucine biosynthesis that is found mainly in archaea.
leuC	3-isopropylmalate dehydratase large subunit	EC 4.2.1.33	NVIE_0074 70	86,14	473	Symbiobacterium thermophilum, Q67MJ2, 68%	us Nitrosoarchaeum koreensis MY1, F9CV3	2	

Molecular Function: glutamate-ammonia ligase activity (GO:0004356), Biological Process: glutamine biosynthetic process (GO:0006542), Biological Process: nitrogen compound metabolic process (GO:0006807)

			NVIE_0297 20	32,15						
leuD	3-isopropylmalate dehydratase small subunit	EC 4.2.1.33	NVIE_0074 60	81,31	196	Serratia proteamaculans , A8G9Q8, 60.1 %	Paenibacillus lactis 154, G4HFG0, 58.03 %	2		
leuD	3-isopropylmalate dehydratase small subunit		NVIE_0297 10		30,19					
leuB	3-isopropylmalate dehydrogenase	EC 1.1.1.85	NVIE_0085 90	85,38	341	Sulfolobus solfataricus, Q9UXB2, 50%	atus Nitrosoarchaeum koreensis, F9CXJ6, 6	2		
leuA	putative 2-isopropylmalate synthase	(2.3.1.182)	NVIE_0026 80	87,87	408	Methanopyrus kandleri, Q8TYB1, 38.99 %	cultured marine crenarchaeote , B3T4B1, 6	3	Methanogenic archaea contain three closely related homologues of the 2-isopropylmalate synthases (LeuA) represented by IPRO05671. Two of these in Methanococcus janaschii (MJ1392 - CimA [PMID: 9864346]; MJ0503 - AksA [PMID: 9665716]) have been characterised as catalyzing alternative reactions leaving the third (MJ1195) as the presumptive LeuA enzyme. CimA is citramalate (2-methylmalate) synthase, which condenses acetyl-CoA with pyruvate. This enzyme is believed to be involved in the biosynthesis of isoleucine in methanogens and possibly other	
ilvE	branched-chain-amino-acid transaminase	EC 2.6.1.42	NVIE_0211 20	44,73	311	sothermobacter thermautotrophicus , O27481,	uncultured crenarchaeote, Q702C0, 57.74 %	2		
<b>Lysine</b>										
AAA Pathway										
	(R)-citramalate synthase / (2-isopropylmalate synthase , leuA)	2.3.1.182/EC 2.3.1.181	NVIE_0085 80							EC 2.3.1.182: Involved in a novel pyruvate pathway for isoleucine biosynthesis that is found mainly in archaea.
leuC	3-isopropylmalate dehydratase large subunit	EC 4.2.1.33	NVIE_0074 70							
leuD	3-isopropylmalate dehydratase small subunit	EC 4.2.1.33	NVIE_0074 60							
leuB	3-isopropylmalate dehydrogenase	EC 1.1.1.85	NVIE_0085 90							
ilvE	branched-chain-amino-acid transaminase	EC 2.6.1.42	NVIE_0076 50							
lysX	alpha-aminoadipate--lysW ligase lysX		NVIE_0026 60	77,74	292	Thermus thermophilus, Q5SH23, 44.33 %	Cenarchaeum symbiosum, A0RTV2, 64.7%	2		
	alpha-aminoadipate--lysW ligase lysX		NVIE_0165 00		50					
lysW	alpha-aminoadipate carrier protein lysW		NVIE_0026 70	87,27	55	Sulfolobus solfataricus, Q980W8, 42.11 %	Nitrosopumilus maritimus, A9A1L1, 70.91 %	2		
argB (lysZ)	acetylglutamate/acetylaminoadipate kinase	EC 2.7.2.8	NVIE_1688	92,13	267	Nitrosopumilus maritimus, A9A1K7, 65.9%	cultured marine crenarchaeote, B3T3A9, 67	2		
argC (lysY)	N-acetyl-gamma-aminoadipyl-phosphate reductase	EC 1.2.1.38	NVIE_0164 90	95,43	350	Nitrosopumilus maritimus, A9A1K6, 76%	cultured marine crenarchaeote, B3T3B0, 7	2		
argD (lysJ)	acetylornithine and succinylornithine aminotransferase	EC 2.6.1.11	NVIE_0164 80	84,95		Methanopyrus kandleri, Q8TUZ5, 43.04 %	Nitrosopumilus maritimus, A9A1K8 , 60.93 %	2		
argE (lysK)	acetyl-lysine deacetylase	EC 3.5.1.-	NVIE_0026 50	84,21	381	Pyrococcus kodakaraensis , Q5JFW4, 35.11 %	atus Nitrosoarchaeum koreensis , F9CZ48,	2		
lysA	diaminopimelate decarboxylase LysA		NVIE_0234 90							
<b>Arginine</b>										
argG	argininosuccinate synthase	EC 6.3.4.5	NVIE_0165 20	85,89	410	Pyrococcus furiosus, Q8U484, 57%	ultured marine crenarchaeote, B3T3B3, 60	2		
argH	argininosuccinate lyase	EC 4.3.2.1	NVIE_0026 90	67,75	492	Nitrosopumilus maritimus, A9A331, 48%	ured Candidatus Nitrosocaldus sp., Q1ER98	2		
argB (lysZ)	acetylglutamylkinase	EC 2.7.2.8	NVIE_1688							
argC (lysY)	N-acetyl-gamma-aminoadipyl-phosphate reductase	EC 1.2.1.38	NVIE_0164 90							
argD (lysJ)	Acetylornithine transaminase	EC 2.6.1.11	NVIE_0164 80							
	Acetylornithine transaminase		NVIE_0020 50							
argE (lysK)	acetyl-lysine deacetylase	EC 3.5.1.-	NVIE_0026 50							
argA	N-acetylglutamate synthase	EC 2.3.1.1								The variant arginine biosynthesis IV (archaeobacteria), which has been described in the archaeobacterium Sulfolobus acidocaldarius, involves early intermediates that are protected not by acetylation but by a carrier protein (the LysW [LysW L-2-aminoadipate carrier protein]), which participates in the biosynthesis of both L-arginine and L-leucine in these organisms [Ouchi13].

PF00682 (4.7e-64 ), Pyruvate carboxyltransferase

carA	carbamoyl-phosphate synthase small chain (glutamine-hydrolyzing)	6.3.5.5	NVIE_0086 20	78,61	408	Pyrococcus furiosus, Q8U086, 49.18 %	atus Nitrosoarchaeum limnia SFB1, F3KJW2,	2	The product carbamoyl phosphate is an intermediate in the biosynthesis of arginine and the pyrimidine nucleotides. The amidotransferase domain within the small subunit of the enzyme hydrolyzes glutamine to ammonia via a thioester intermediate.
carB	carbamoyl-phosphate synthase large chain	6.3.5.5	NVIE_0086 30	84,72	1022	Lithobates catesbeiana, Q91293, 48.74 %	us Nitrosoarchaeum koreensis MY1, F9CXX	2	
argF	ornithine carbamoyltransferase	2.1.3.3	NVIE_0301 10	80,07	320	Pyrococcus abyssii, O93656, 56.52 %	Nitrosopumilus maritimus, A9A594, 59%	2	
	putative carbamate kinase with BmpA-like periplasmic binding domain	2.7.2.2	NVIE_0159 70		636				
<b>Histidine</b>									
hisG	ATP phosphoribosyltransferase	EC 2.4.2.17	NVIE_0235 80	88,62	329	Solibacter usitatus, Q01ZU0, 35.92 %	atus Nitrosoarchaeum koreensis, F9CYN1,	2	
hisE	phosphoribosyl-ATP diphosphatase	EC 3.6.1.31							
hisI	phosphoribosyl-AMP cyclohydrolase	EC 3.5.4.19	NVIE_0205 80	80,73	159	Nitrosopumilus maritimus, A9A5W9, 64.15%	uncultured crenarchaeote, Q702A1, 72%	2	
hisA	1-(5-phosphoribosyl)-5-[[5-phosphoribosylamino]methylideneamino]imidazole-4-carboxamide isomerase	EC 5.3.1.16	NVIE_2407	69,49	235	Nitrosopumilus maritimus, A9A5X1, 50.64%	ultured marine crenarchaeote, B3T633, 47.	2	
hisH	imidazole glycerol phosphate synthase subunit hisH	EC 2.4.2.-	NVIE_0235 30	75,12	210	ermoanaerobacter tengcongensis, Q8R883, 48.	ultured marine crenarchaeote, B3T634, 59	2	
hisF	imidazole glycerol phosphate synthase subunit hisF	EC 5.3.1.16	NVIE_0235 20	84,87	271	Nitrosopumilus maritimus, A9A5X0, 65%	atus Nitrosoarchaeum koreensis, F9CYM4,	2	
hisB	imidazoleglycerol-phosphate dehydratase	EC 4.2.1.19	NVIE_0235 40	81,54		Cenarchaeum symbiosum, A0RZ75, 59.9%	Nitrosopumilus maritimus, A9A5X3, 56.77%	2	
hisC	histidinol-phosphate transaminase	EC 2.6.1.9	NVIE_0235 60	63,51	364	Pyrococcus furiosus, Q8TH25, 35.52%	nitrosopumilus maritimus, A9A5X5, 37.82%	2	
hisN	histidinol-phosphatase	EC 3.1.3.15							putative candidate: RNAR_03150
hisD	histidinol dehydrogenase	EC 1.1.1.23	NVIE_0235 70	73,46	440	Methanopyrus kandleri, Q8TXG3, 42%	atus Nitrosoarchaeum koreensis, F9CYN0,	2	
	putative haloacid dehalogenase domain protein hydrolase		NVIE_0235 50	68,83	317	Bacillus halodurans, Q9K6Y7, 35.05 % partial, Pyrophosphatase ppaX	Candidatus Nitrosoarchaeum koreensis, F9CYM8, 40.91 %	3	in operon. Putative candidate for hisN or hisE?
<b>Tryptophan</b>									
(aroGFH)	putative 3-deoxy-7-phosphoheptulonate synthase	(EC 2.5.1.54)	NVIE_0058 50						(=phospho-2-dehydro-3-deoxyheptonate aldolase); Priam: EC 4.1.2.13, Fructose-bisphosphate aldolase (homologous protein of M. jannaschii is a bifunctional enzyme that also has fructose 1.6 bisphosphate aldolase activity); Tigr: phospho-2-dehydro-3-deoxyheptonate aldolase (duplication: RNAR_01196 32% to RNAR_00186)
aroB	3-dehydroquinate synthase	EC 4.2.3.4	NVIE_0058 40	82,67	367	Nitrosopumilus maritimus, A9A235, 56.9%	uncultured crenarchaeote, Q702D3, 64.88%	2	
aroD	putative 3-dehydroquinate dehydratase	(EC 4.2.1.10)	NVIE_0057 80	61,78	226	Dehalococcoides ethenogenes, Q3Z989, 36.87%	idatus Nitrosoarchaeum limnia, F3KI40, 41	2	
aroE	shikimate dehydrogenase	EC 1.1.1.25	NVIE_0587	76,45	284	Nitrosopumilus maritimus, A9A233, 50.18%	cultured marine crenarchaeote, B3T788, 5	2	
aroK	shikimate kinase	EC 2.7.1.71	NVIE_0057 70	77,94	286	Methanocaldococcus jannaschii, Q58835, 42.12%	idatus Nitrosoarchaeum koreensis, F9CVK2	2	
aroA	3-phosphoshikimate 1-carboxyvinyltransferase	EC 2.5.1.19	NVIE_0057 60	77,96	432	Nitrosopumilus maritimus, A9A231, 46%	idatus Nitrosoarchaeum limnia, F3KI37, 45	2	
aroC	chorismate synthase	EC 4.2.3.5	NVIE_0057 50	83,24	371	Dehalococcoides sp., Q3Z2I6, 54.4 %	atus Caldriarchaeum subterraneum, E6N894,	2	
trpE	anthranilate synthase component I	EC 4.1.3.27	NVIE_0047 70	75,81	462	othermobacter thermautotrophicus, O27692,	idatus Nitrosoarchaeum limnia, F3KJB6, 54	2	
trpG	anthranilate synthase component II	EC 4.1.3.27	NVIE_0053 90	81,12	202	Thermotoga maritima, Q08654, 55.1 %	idatus Nitrosoarchaeum limnia, F3KJB7, 67	2	
trpD	anthranilate phosphoribosyltransferase	EC 2.4.2.18	NVIE_0054 00	70,59	361	Clostridium thermocellum, A3DD58, 46.2%	lostridium thermocellum, E6UQF5, 46.27	2	
trpF	phosphoribosylanthranilate isomerase	EC 5.3.1.24							Nmar und Csym auch nicht
trpC	indole-3-glycerol-phosphate synthase	EC 4.1.1.48	NVIE_0054 80	64,79	267	methanocaldococcus jannaschii, Q58328, 44.05	idatus Nitrosoarchaeum limnia, F3KJB9, 46	2	
trpB	tryptophan synthase beta chain	EC 4.2.1.20	NVIE_0054 70	81,25	416	rmoanaerobacter tengcongensis, Q8R9M9, 66	Nitrosopumilus maritimus, A9A2A0, 71.03 %	2	
trpA	tryptophan synthase alpha chain	EC 4.2.1.20	NVIE_0054 60	66,92	278	methanocaldococcus jannaschii, Q60180, 42.22	Nitrosopumilus maritimus, A9A2A1, 47.35%	2	
<b>Phenylalanine</b>									

PF01959 (2.0000000000000001e-112)

(aroGFH)	putative 3-deoxy-7-phosphoheptulonate synthase	(EC 2.5.1.54)	NVIE_005850							(=phospho-2-dehydro-3-deoxyheptonate aldolase); Priam: EC 4.1.2.13, Fructose-bisphosphate aldolase (homologous protein of M. jannaschii is a bifunctional enzyme that also has fructose 1.6 bisphosphate aldolase activity); Tigr: phospho-2-dehydro-3-deoxyheptonate aldolase (duplication: RNAR_01196 32% to RNAR_00186)
aroB	3-dehydroquinase synthase	EC 4.2.3.4	NVIE_005840							
aroD	putative 3-dehydroquinase dehydratase	(EC 4.2.1.10)	NVIE_005780							
aroE	shikimate dehydrogenase	EC 1.1.1.25	NVIE_0587							
aroK	shikimate kinase	EC 2.7.1.71	NVIE_005770							
aroA	3-phosphoshikimate 1-carboxyvinyltransferase	EC 2.5.1.19	NVIE_005760							
aroC	chorismate synthase	EC 4.2.3.5	NVIE_005750							
	chorismate mutase	EC 5.4.99.5								Nmar und Csym auch nicht, Eurys ja, Crens nein
	putative prephenate dehydrogenase	(EC 1.3.1.12)	NVIE_0582	50,88		285	Methanocaldococcus jannaschii, Q58029, 26%	Cenarchaeum symbiosum, A0RU40, 37.5%	3	not full length to M. jannaschii
pheA	prephenate dehydratase	EC 4.2.1.51	NVIE_023460	70,57		282	Arabidopsis thaliana, Q9SSE7, 43.93 %	tus CaldIarchaeum subterraneum, E6P7T3,	3	
aspC	aspartate aminotransferase	EC 2.6.1.1	NVIE_005740							alternative: RNAR_03149 putative histidinol-phosphate transaminase (EC 2.6.1.9)
<b>Tyrosine</b>										
(aroGFH)	putative 3-deoxy-7-phosphoheptulonate synthase	(EC 2.5.1.54)	NVIE_005850							(=phospho-2-dehydro-3-deoxyheptonate aldolase); Priam: EC 4.1.2.13, Fructose-bisphosphate aldolase (homologous protein of M. jannaschii is a bifunctional enzyme that also has fructose 1.6 bisphosphate aldolase activity); Tigr: phospho-2-dehydro-3-deoxyheptonate aldolase (duplication: RNAR_01196 32% to RNAR_00186)
aroB	3-dehydroquinase synthase	EC 4.2.3.4	NVIE_005840							
aroD	putative 3-dehydroquinase dehydratase	(EC 4.2.1.10)	NVIE_005780							
aroE	shikimate dehydrogenase	EC 1.1.1.25	NVIE_0587							
aroK	shikimate kinase	EC 2.7.1.71	NVIE_005770							
aroA	3-phosphoshikimate 1-carboxyvinyltransferase	EC 2.5.1.19	NVIE_005760							
aroC	chorismate synthase	EC 4.2.3.5	NVIE_005750							
	chorismate mutase	EC 5.4.99.5								
	putative prephenate dehydrogenase	(EC 1.3.1.12)	NVIE_0582							not full length to M. jannaschii
pheA	prephenate dehydratase	EC 4.2.1.51	NVIE_023460							
aspC	aspartate aminotransferase	EC 2.6.1.1	NVIE_005740							alternative: RNAR_03149 putative histidinol-phosphate transaminase (EC 2.6.1.9)
<b>Methionine</b>										
metH1	putative methionine synthase	(EC 2.1.1.13)	NVIE_025960	81,61		315	Mycobacterium tuberculosis, O33259, 42.38 %	Nitrosopumilus maritimus, A9A115, 75%	3	Thaumarchaeota-specific
metH	putative methionine synthase	(EC 2.1.1.13)	NVIE_025920	80,91		843	Synechocystis sp., Q55786, 34 %	Nitrosopumilus maritimus, A9A114, 67%	3	Thaumarchaeota-specific
	putative 5,10-methylenetetrahydrofolate reductase-like protein		NVIE_025880	59,61		255				5-Methyltetrahydrofolate is used to convert homocysteine (a potentially toxic amino acid) to methionine by the enzyme methionine synthase.
	<i>remaining steps unclear</i>									
<b>Cysteine</b>										
cysM1	putative cysteine synthase	(EC 2.5.1.47)	NVIE_017430	79,38		529	Schizosaccharomyces pombe, O59701, 23.7%	tus Nitrosoarchaeum limnia SFB1, F3KND1,	3	not full length to C. jejuni; duplication: RNAR_01257 25% to RNAR_02735
cysM2	<i>remaining steps unclear</i>		NVIE_008170	87,69	26,56	334	Aquifex aeolicus, O67507, 39.38 %	us Nitrosoarchaeum koreensis MY1, F9CVX	3	
ahcY	<i>adenosylhomocysteinase</i>		NVIE_022390							
<b>Proline catabolism (biosynthesis unclear)</b>										
	putative proline dehydrogenase	(EC 1.5.99.8)	NVIE_021980	72,43		296	Bacillus subtilis, O32179, 31%	tus Nitrosoarchaeum limnia SFB1, F3KKF9,	3	
rocA	1-pyrroline-5-carboxylate dehydrogenase	EC 1.5.1.12	NVIE_021970							



Aminopeptidases										
Gene	Product	EC number	Nvie Locus	identity					Comment	
map	methionyl aminopeptidase	EC 3.4.11.18	NVIE_007810	79,32		298	Pyrococcus horikoshii, O58362, 46.46 %	Nitrosopumilus maritimus, A9A368, 60.27%	2	
	putative membrane alanyl aminopeptidase	(EC 3.4.11.2)	NVIE_018390	72,99		824	Homo sapiens (Human), P55786, 25.87 %	Myxococcus fulvus , F8CQZ4, 38.43%	3	not full length to S. tokodaii
pepA	leucyl aminopeptidase	EC 3.4.11.1	NVIE_017650	50,1		517	Cenarchaeum symbiosum, A0RUAS, 49%	atus Nitrosoarchaeum limnia SFB1, F3KL37	2	
<b>Archaean Lipid biosynthesis: Mevalonate pathway -&gt; Acetyl-CoA -&gt; Mevalonate -&gt; IPP: candidate for isopentenyl phosphate kinase</b>										
hcs	putative hydroxymethylglutaryl-CoA synthase	(EC 2.3.3.10)	NVIE_000050	86,7		470	Saccharomyces cerevisiae, P54839, 30.12%	uncultured marine crenarchaeote , B3T723, 64.72 %	3	
mvaA	hydroxymethylglutaryl-CoA reductase	EC 1.1.1.188	NVIE_023590	74,74		418	Archaeoglobus fulgidus, O28538, 54.46%	Candidatus Nitrosoarchaeum limnia, F3KNI4, 55.1 %	2	
mvk	mevalonate kinase	EC 2.7.1.36	NVIE_011870	57,76		331	Pyrococcus kodakaraensis, Q5JJC6, 39.82 %	Candidatus Nitrosoarchaeum limnia, F3KL19, 44.03%	2	
	phosphomevalonate kinase									
	diphosphomevalonate decarboxylase									
	aspartate/glutamate/uridylylate kinase family protein		NVIE_008070	69,08		260	Methanocaldococcus jannaschii, Q60352, 25.28%	Candidatus Nitrosoarchaeum limnia, F3KL20, 48.05%	3	candidate for isopentenyl phosphate kinase
<b>Archaean Lipid biosynthesis: Conversion of IPP to DMAPP</b>										
fni	isopentenyl-diphosphate Delta-isomerase	EC 5.3.3.2	NVIE_008060	87,32		362	Nostoc sp., Q8YNH4, 48.68 %	Candidatus Micrarchaeum acidiphilum, C7DIS0, 53.8%	2	
<b>Archaean Lipid biosynthesis: Elongation of side chains</b>										
gds	Geranylgeranyl pyrophosphate synthase	EC 2.5.1.1	NVIE_0823	71,43		335	Sulfolobus acidocaldarius, P39464, 39%	Nitrosopumilus maritimus, A9A424, 52.9%	2	includes: dimethylallyltransferase, geranyltransferase ; farnesyltransferase; duplication: RNAR_01109 30% to RNAR_01273
			NVIE_01157	77,9	28,57	287	Escherichia coli , P0AD57, 38.98 %	Nitrosopumilus maritimus, A9A329, 52.57 %	2	
<b>Archaean Lipid biosynthesis: Synthesis of glycerol phosphate backbone</b>										
egsA	sn-glycerol-1-phosphate dehydrogenase	EC 1.1.1.261	NVIE_000470	77,23		357	Nitrosopumilus maritimus , A9A2U8, 55.33 %	Candidatus Nitrosoarchaeum koreensis, F9CUD4, 55.33 %	2	
<b>Archaean Lipid biosynthesis: Linking backbone and side chains</b>										
	geranylgeranylgeranyl phosphate synthase	EC 2.5.1.41	NVIE_020530	86,94		254	Nitrosopumilus maritimus, A9A3Z1, 61.45%	Candidatus Nitrosoarchaeum koreensis, F9CUU0, 61.38 %	2	
	putative digeranylgeranylgeranyl phosphate synthase	(EC 2.5.1.42)	NVIE_026430	49,35		321	Methanoculleus marisnigri, A3CW74, 26.51%	Methanothermobacter feravidus, E3GYQ7, 28.26%	3	
<b>Archaean Lipid biosynthesis: Addition of polar head groups</b>										
pgsA	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	EC 2.7.8.5	NVIE_005560	73,08		202	Pyrococcus horikoshii, O58215, 33.17 %	Nitrosopumilus maritimus, A9A2A9, 55.94%	2	
<b>Archaean Lipid biosynthesis: reduction/ hydrogenation?</b>										
	Geranylgeranyl reductase family protein	EC 1.3.1.	NVIE_003360							FAD/NAD(P)-binding domain
	putative digeranylgeranylgeranylphospholipid reductase		NVIE_012510	83,99		484	Methanococcoides burtonii , Q12YW2, 26.24 %	Candidatus Nitrosoarchaeum limnia SFB1, F3KNCS, 60.8 %	3	
<b>Archaean Lipid metabolism?</b>										
	putative acyl transferase/acyl hydrolase/lysophospholipase domain containing protein		NVIE_013450	44,77		356	Meyerozyma guilliermondii, A5DHA3, 37.66% partial	uncultured crenarchaeote, Q8NKM7, 41.33%		
<b>Archaean Lipid biosynthesis:myo-inositol biosynthesis</b>										
	putative myo-inositol-1-phosphate synthase	5.5.1.4	NVIE_008100	72,35		340	Mycobacterium tuberculosis, P71703, 30.29 %	Korarchaeum cryptofilum , B1L4M2, 41.45%	3	
	putative myo-inositol-1-phosphate synthase	5.5.1.4	NVIE_003260	88,12	32,57%	367	Mycobacterium bovis , P59967, 49.72 %	Thermobaculum terrenum , D1CEG0, 52.21 %	3	1.1a's have only this one
	putative inositol-1-monophosphatase	EC 3.1.3.25	NVIE_022020	60,54		267	Methanothermobacter thermoautotrophicus , O26957, 39.92 %	Cenarchaeum symbiosum , A0RY53, 48.24 %	2	
	putative inositol-1-monophosphatase	EC 3.1.3.25	NVIE_025260			264	Rhizobium loti, Q98F59, 34.23 %	Bartonella rochalimae, E6YNC5, 35.55 %	3	COG:Archaean fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family
<b>Flavin biosynthesis</b>										
gch3	GTP cyclohydrolase III	EC 3.5.4.29	NVIE_021890	77,6		250	Methanobrevibacter smithii, ASULV0, 36.1 %	uncultured marine crenarchaeote , B3T7T2, 47.39%	2	

Molecular Function: hydroxymethylglutaryl-CoA reductase (NADPH) activity (GO:0004420), Biological Process: coenzyme A metabolic process (GO:0015936), Molecular Function: coenzyme binding (GO:0050662), Biological Process: oxidation reduction (GO:0055114)

Molecular Function: glutamate 5-kinase activity (GO:0004349), Biological Process: proline biosynthetic process (GO:0006561)



Gene	Product	Length in AA	Nvie Locus	identity	Best BLAST hit in TrEMBL database (Nvie)	Functional domains (Nvie)			
(flaK)	putative archaeal preflagellin peptidase FlaK	249	NVIE_009600	75,81	247	Methanocaldococcus jannaschii, Q58312, 25.31 %	Candidatus Nitrosoarchaeum limnia, F3KJ59, 34.76 %	3	
(flaK)	putative archaeal preflagellin peptidase FlaK	299	NVIE_010080	42,15	246	Methanocaldococcus jannaschii, Q58312, 24.69 %	Candidatus Nitrosoarchaeum limnia, F3KJ59, 30.36 %	3	
(trmB)	putative transcriptional regulator, TrmB	281	NVIE_009920	39,85	335	-	Candidatus Nitrosoarchaeum koreensis, F9CX53, 26.83 %	3	
	putative transcriptional regulator, TrmB		NVIE_010060	39,16	283		Nitrosopumilus maritimus, A9A4B2, 28.85%	3	
	putative transcriptional regulator, TrmB		NVIE_009780		583		Candidatus Nitrosoarchaeum limnia, F3KJ39, 22.39 %	3	
flaB3	archaeal flagellin	228	NVIE_009950		55,16	230	Aeropyrum pernix, Q9YAN8, 38.18 %	idatus Nitrosoarchaeum limnia, F3KJ34, 56	3
flaB1			NVIE_009770	50,45	224	Aeropyrum pernix, Q9YAN8, 37.14 %	idatus Nitrosoarchaeum limnia, F3KJ38, 51	3	
flaB2			NVIE_009930	47,89	218	Aeropyrum pernix, Q9YAN8, 37.8 %	idatus Nitrosoarchaeum limnia, F3KJ38, 46	3	
	hypothetical protein	512	NVIE_009960	31,67	486				
(flaG)	putative flagellar protein FlaG	164	NVIE_009970	42,95	156	Archaeoglobus fulgidus, O29210, 24.38 %	idatus Nitrosoarchaeum limnia, F3KJ31, 39	3	
(flaF)	putative flagellar protein FlaF	179	NVIE_009980	41,57	178	Dictyostelium discoideum, Q54UI3, 26.42 %	idatus Nitrosoarchaeum limnia, F3KJ30, 36	3	
flaH	flagella protein FlaH	235	NVIE_009990	68,24	234		Ignisphaera aggregans, E05RR3, 44.21 %	2	
(flaJ)	putative flagella assembly protein FlaJ	526	NVIE_010000	47,65	500	Methanocaldococcus jannaschii, Q58311, 22.61 %	Candidatus Nitrosoarchaeum limnia, F3KJ27, 41.51 %	3	Type II secretion system protein F family enzyme
flaI	archaeal flagella protein FlaI	564	NVIE_009910	69,77	563	Methanocaldococcus jannaschii, Q58310, 44.06 %	idatus Nitrosoarchaeum limnia, F3KJ28, 60	2	Type II secretion system protein E family enzyme
	putative KaiC family protein kinase		NVIE_010030		254	Synechocystis sp., P74503, 31.87% partial	Methanocella paludicola, D121M4, 42.29%	3	KaiC, encoded in the kaiABC operon that controls circadian rhythms in Cyanobacteria, performs autophosphorylation and acts as its own transcriptional repressor.
(cheR)	putative chemotaxis MCP methyltransferase CheR	271	NVIE_009900	37,83	275	Borrelia burgdorferi, O51069, 34.14 %	ed methanogenic archaeon RC-1, Q0W7Y2	3	
cheD	chemoreceptor glutamine deamidase CheD	171	NVIE_009890	47,59	173	Archaeoglobus fulgidus, O29224, 43.45%	Roseburia inulinivorans, C0FQH3, 44.23%	2	
(cheC)	putative chemotaxis protein CheC	211	NVIE_009880	44,62	204	Bacillus subtilis, P40403, 27.82 %	idatus Nitrosoarchaeum limnia, F3KJ20, 33	3	
cheA	chemotactic sensor histidine kinase CheA	574	NVIE_009870	56,79	542	Bacillus subtilis, P29072, 40.53 %	cultured archaeon GZfos23H9, Q64CE2, 39.4	2	
cheB	chemotaxis response regulator methylesterase CheB	360	NVIE_009860	47,03	368	Pyrococcus abyssi, Q9UYF3, 45.53 %	Thermincola potens, D5X906, 46.42 %	2	
cheY	chemotaxis response regulator CheY	126	NVIE_009850	68,25	126	Bacillus subtilis, P45709, 52.14 %	idatus Nitrosoarchaeum limnia, F3KJ18, 60	2	
cheW	chemotaxis protein CheW (Positive regulator of CheA protein activity)	192	NVIE_009840	52,03	166	Escherichia coli, P0A964, 31.94 %	esulfovibrio africanus str., F3Z0W4, 43.97	2	
(MCP)	putative methyl-accepting chemotaxis protein	395	NVIE_009790	39,52	761	Bacillus subtilis, P39215, 26.46 %	alanaerobium praevalens, E3DMK4, 30.04	3	
(MCP)	putative methyl-accepting chemotaxis protein	396	NVIE_009820 NVIE_001950 NVIE_001930	64,2	360	Myxococcus xanthus, P43500, 42.68% partial	Pirellula staleyi, D2R1M1, 51.14 %	3	

PF06745, Circadian clock protein KaiC/DNA repair protein RadA (1.4e-53)

Biological Process: chemotaxis (GO:0006935), Molecular Function: protein-glutamine glutaminase activity (GO:0050568)

Molecular Function: two-component response regulator activity (GO:0000156), Biological Process: two-component signal transduction system (phosphorelay) (GO:0000160), Cellular Component: cytoplasm (GO:0005737), Biological Process: chemotaxis (GO:0006935), Molecular Function: protein-glutamate methylesterase activity (GO:0008984)

Molecular Function: signal transducer activity (GO:0004871), Biological Process: chemotaxis (GO:0006935), Biological Process: signal transduction (GO:0007165), Cellular Component: membrane (GO:0016020)

COG0840 (Methyl-accepting chemotaxis protein)

	putative signal transduction response regulator, receiver domain	123	NVIE_020450	68,03		122	Gemella haemolysans , C5NUG6, 33.62 %	PF00072 (0.000000000000029)	3
	putative signal transduction response regulator, receiver domain	136	NVIE_026340	37%		128	Candidatus Nitrosoarchaeum koreensis, F9CWU2, 40.78 %	PF00072 (6e-21 )	3
	putative signal transduction response regulator, receiver domain		NVIE_0132			267	delta proteobacterium NaphS2, D8EYU4, 34% partial	PF00072(1.4000000000000002e-22 )	3
	putative signal transduction response regulator, receiver domain		NVIE_007410			132	Desulfatibacillum alkenivorans , B8FG89, 35.48 %	PF00072 (6.2e-23)	3
	putative signal transduction response regulator, receiver domain		NVIE_030040			253	Lactococcus lactis subsp. cremoris , Q030CS, 33.61 %	PF00072 (3.6000000000000003e-22)	3
	putative Polar-differentiation response regulator divK		NVIE_021320			127	Candidatus Nitrosoarchaeum koreensis, F9CW22, 33.33 %	PF00072 (1e-21 )	3
	putative signal transduction response regulator, receiver domain		NVIE_021330			132	Uncultured methanogenic archaeon RC-I, Q0W6W7, 35.59 %	PF00072 (1.7e-18)	3
Gene	Product	EC no.	Nvie Locus	identity					
<b>Histidine kinases (25)</b>									
	hypothetical protein with ATP-binding domain		NVIE_005330	78		565			
	putative signal transduction histidine kinase, with PAS, phosphoacceptor and ATP binding domain		NVIE_015250	45,86		382	Methanohalophilus mahii , D5E6V5, 31.69 %		3
	putative membrane associated signal transduction histidine kinase, with phosphoacceptor and ATP binding domain	2.7.13.3	NVIE_005590	44,1		566	Candidatus Nitrosoarchaeum limnia, F3KJ14, 31.96 %		3
	putative signal transduction histidine kinase, with phosphoacceptor and ATP binding domain	2.7.13.3	NVIE_030060	42,83		727	uncultured crenarchaeote, Q8NKM3, 33%		3
	putative membrane associated signal transduction histidine kinase, with phosphoacceptor and ATP binding domain	2.7.13.3	NVIE_001040			590	uncultured archaeon, D1JAG2, 32.67 %		3
	putative membrane associated signal transduction histidine kinase, with extracellular ligand binding and ATP binding domain	2.7.13.3	NVIE_001570			635	Pseudomonas stutzeri , F2N6L1, 28.69 %		3
	putative membrane associated signal transduction histidine kinase, with phosphoacceptor and ATP binding domain	2.7.13.3	NVIE_007400			606	Desulfomicrobium baculatum, C7LNV3, 38.43 %		3
	putative membrane associated signal transduction histidine kinase, with HAMP linker, ATP binding domain	2.7.13.3	NVIE_021340			674	Methanococcus vannielii, A6JUPU7, 24%		3
	putative membrane associated signal transduction histidine kinase, with PAS fold, HAMP linker, phosphoacceptor, ATP binding domain	2.7.13.3	NVIE_026350			786	Sulfurimonas gotlandica, B6BIE4, 33% partial		3
	putative membrane associated signal transduction histidine kinase, with phosphoacceptor and ATP binding domain	2.7.13.3	NVIE_021310			633	Candidatus Nitrosoarchaeum koreensis, F9CW21, 33.45 %		3

COG0323:DNA mismatch repair enzyme (predicted ATPase)

IPR003594: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase (0.00000017 )

PF00512

adjacent to CheY-like response regulator receiver domain

PF00512, Signal transduction histidine kinase, subgroup 1, dimerisation/phosphoacceptor domain; IPR009082, Signal transduction histidine kinase, homodimeric; IPR005467, Signal transduction histidine kinase, core; IPR004358, Signal transduction histidine kinase-related protein, C-terminal

PF00512 (0.0000000000089 )

PF00512; PF03924, CHASE domain

PF00512

PF00672

PF00989, PF00512, PF00672