Table S1 Complete list of proteins identified in the metaproteome analyses. Proteins only in summer (red), only in winter (blue), and in both seasons (green). The number of unique peptides and assigned spectra are shown for each protein, using both the NR database and AntComb, in summer (S) or winter (W). At least two unique peptides were required to validate a protein assignment.

Annotation & function	**Best match of protein**	**Phylogenetic grouping of best match**	**Unique peptides**				**Assigned spectra**			
			NR		**AntComb**		**NR**		**AntComb**	
			S	**W**	**S**	**W**	**S**	**W**	**S**	**W**
BACTERIA & ARCHAEA										
TRANSPORT										
Transport – Cell Membrane										
ABC transport system, general amino acids										
ABC transport system, general amino acids, periplasmic binding protein	88% identity to General amino acid ABC transport system, periplasmic binding protein [YhdW] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**30**	**25**	**0**	**0**	**161**	**229**
ABC transport system, general amino acids, periplasmic binding protein	82% identity to General amino acid ABC transport system, periplasmic binding protein [YhdW] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**7**	**10**	**0**	**0**	**15**	**63**
ABC transport system, general amino acids, periplasmic binding protein	91% identity to General amino acid ABC transport system, periplasmic binding protein [YhdW] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**4**	**3**	**0**	**0**	**14**	**44**
ABC transport system, general amino acids, periplasmic binding protein	92% identity to General amino acid ABC transport system, periplasmic binding protein [YhdW] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**5**	**0**	**0**	**15**	**50**
ABC transport system, general amino acids, periplasmic binding protein	92% identity to General amino acid ABC transport system, periplasmic binding protein [YhdW] [*Candidatus* Pelagibacter ubique	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**2**	**0**	**0**	**12**	**40**

	HTCC1002]									
ABC transport system, general amino acids, periplasmic binding protein	88% identity to General amino acid ABC transport system, periplasmic binding protein [YhdW] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**2**	**0**	**0**	**16**	**49**
ABC transport system, general amino acids, periplasmic binding protein	83% identity to General amino acid ABC transport system, periplasmic binding protein [YhdW] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**3**	**0**	**0**	**4**	**19**
ABC transport system, general amino acids, periplasmic binding protein	86% identity to General amino acid ABC transport system, periplasmic binding protein [YhdW] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**20**
ABC transport system, general amino acids, ATP-binding protein	94% identity to General amino acid transport, ATP-binding protein [YhdZ] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**2**	**2**	**0**	**0**	**4**	**3**	**0**	**0**
ABC transport system, general amino acids, periplasmic binding protein	77% identity to General amino acid ABC transport system, periplasmic binding protein [YhdW] [Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**6**	**14**	**0**	**0**	**10**	**96**
ABC transport system, general amino acids, periplasmic binding protein	100% identity to General amino acid ABC transport system, periplasmic binding protein [YhdW] [Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**0**	**0**	**0**	**7**	**0**
ABC transport system, general amino acids, periplasmic binding protein	64% identity to General amino acid ABC transport system, periplasmic binding protein [YhdW] [*Candidatus* Puniceispirillum marinum (strain IMCC1322)]	Alphaproteobacteria (SAR116 cluster)	**0**	**0**	**2**	**5**	**0**	**0**	**2**	**10**
ABC transport system, general amino acids, periplasmic binding protein	61% identity to General amino acid ABC transport system, periplasmic binding protein [YhdW] [*Hoeflea phototrophica* DFL-43]	Alphaproteobacteria (Rhizobiales)	**0**	**0**	**10**	**12**	**0**	**0**	**30**	**192**
ABC transport system, general amino acids, periplasmic binding protein	100% identity to General amino acid ABC transport system, periplasmic binding protein [YhdW] [*Psychromonas ingrahamii* 37]	Gammaproteobacteria (Alteromonadales)	**2**	**1**	**0**	**0**	**2**	**1**	**0**	**0**
ABC transport system, general amino acids, periplasmic binding protein	100% identity to General amino acid ABC transport system, periplasmic binding protein [YhdW] [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	**3**	**0**	**0**	**0**	**7**	**0**	**0**	**0**
ABC transport system, glycine betaine										
ABC transport system, glycine betaine, periplasmic binding protein	95% identity to Glycine betaine ABC transport system, periplasmic binding protein [OpuAC] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**10**	**15**	**0**	**0**	**37**	**143**
ABC transport system, glycine betaine, periplasmic binding protein	64% identity to Glycine betaine ABC transport system, periplasmic binding protein [OpuAC] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**7**	**0**	**0**	**9**	**86**

ABC transport system, glycine betaine, periplasmic binding protein	87% identity to Glycine betaine ABC transport system, periplasmic binding protein [OpuAC] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**5**	**0**	**0**	**4**	**29**
ABC transport system, glycine betaine, periplasmic binding protein	86% identity to Glycine betaine ABC transport system, periplasmic binding protein [OpuAC] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**3**	**0**	**0**	**2**	**26**
ABC transport system, glycine betaine, periplasmic binding protein	100% identity to Glycine betaine ABC transport system, periplasmic binding protein [OpuAC] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**3**	**0**	**0**	**5**	**10**
ABC transport system, glycine betaine, periplasmic binding protein	75% identity to Glycine betaine ABC transport system, periplasmic binding protein [OpuAC] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**19**
ABC transport system, glycine betaine, periplasmic binding protein	68% identity to Glycine betaine ABC transport system, periplasmic binding protein [OpuAC] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**3**	**0**	**0**	**4**	**18**
ABC transport system, glycine betaine, periplasmic binding protein	67% identity to Glycine betaine ABC transport system, periplasmic binding protein [OpuAC] [*Candidatus* Pelagibacter ubique]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**4**	**3**	**0**	**0**	**10**	**11**
ABC transport system, proline/glycine betaine, periplasmic binding protein	94% identity to Proline/glycine betaine ABC transport system, periplasmic binding protein [ProX] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**3**	**0**	**0**	**4**	**8**
ABC transport system, proline/glycine betaine, periplasmic binding protein	96% identity to Proline/glycine betaine ABC transport system, periplasmic binding protein [ProX] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**7**	**0**	**0**	**7**	**16**
ABC transport system, proline/glycine betaine, periplasmic binding protein	78% identity to Proline/glycine betaine ABC transport system, periplasmic binding protein [ProX] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**5**
ABC transport system, proline/glycine betaine, periplasmic binding protein	60% identity to Proline/glycine betaine ABC transport system, periplasmic binding protein [ProX] [Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**3**	**0**	**0**	**18**	**27**
ABC transport system, proline/glycine betaine, periplasmic binding protein	35% identity to Proline/glycine betaine ABC transport system, periplasmic binding protein [ProX] [*Pseudovibrio* sp. JE062]	Alphaproteobacteria (Rhodobacterales)	**0**	**0**	**2**	**6**	**0**	**0**	**5**	**35**
ABC transport system, proline/glycine betaine, periplasmic binding protein	83% identity Proline/glycine betaine ABC transport system, periplasmic binding protein [ProX] [Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**1**	**2**	**0**	**0**	**5**	**18**
ABC transport system, proline/glycine betaine, periplasmic binding protein	54% identity to Proline/glycine betaine ABC transport system, periplasmic binding protein [ProX] [Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**17**
ABC transport system, proline/glycine betaine, periplasmic binding protein	34% identity to Proline/glycine betaine ABC transport system, periplasmic binding protein [ProX] [*Pseudovibrio* sp. JE062]	Alphaproteobacteria (Rhodobacterales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**13**
ABC transport system, proline/glycine betaine, periplasmic binding protein	48% identity to Proline/glycine betaine ABC transport system, periplasmic binding protein [ProX] [*Shewanella frigidimarina* (strain NCIMB 400)]	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**

ABC transport system, proline/glycine betaine, periplasmic binding protein	45% identity to Proline/glycine betaine ABC transport system, periplasmic binding protein [ProX] [*Desulfovibrio aespoeensis* Aspo-2]	Deltaproteobacteria (Desulfovibrionales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**5**
ABC transport system, branched chain amino acids										
ABC transport system, branched-chain amino acids, periplasmic binding protein	96% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [LivJ] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**14**	**18**	**0**	**0**	**34**	**81**
ABC transport system, branched-chain amino acids, periplasmic binding protein	87% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [LivJ] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**5**	**0**	**0**	**2**	**19**
ABC transport system, branched-chain amino acids, periplasmic binding protein	97% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [LivJ] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
ABC transport system, branched-chain amino acids, periplasmic binding protein	96% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [BraC] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**1**	**3**	**0**	**0**	**1**	**3**	**0**	**0**
ABC transport system, branched-chain amino acids, periplasmic binding protein	82% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [LivJ] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**4**	**0**	**0**	**1**	**5**
ABC transport system, branched-chain amino acids, periplasmic binding protein	68% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [LivJ] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**4**	**0**	**0**	**1**	**6**
ABC transport system, branched-chain amino acids, periplasmic binding protein	84% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [LivJ] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**7**	**10**	**0**	**0**	**21**	**42**
ABC transport system, branched-chain amino acids, periplasmic binding protein	69% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [LivJ] [*Pseudovibrio* sp. JE062]	Alphaproteobacteria (Rhodobacterales)	**0**	**0**	**4**	**10**	**0**	**0**	**8**	**38**
ABC transport system, branched-chain amino acids, periplasmic binding protein	62% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [LivJ] [uncultured *Roseobacter* sp]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**1**	**7**	**0**	**0**	**2**	**18**
ABC transport system, branched-chain amino acids, periplasmic binding protein	100% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [LivJ] [*Sulfitobacter* sp. EE-36]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**2**	**2**	**2**	**5**	**3**	**2**	**8**
ABC transport system, branched-chain amino acids, periplasmic binding protein	78% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [LivJ] [uncultured *Roseobacter* sp]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**4**	**4**	**0**	**0**	**9**	**6**
ABC transport system, branched-chain amino acids, periplasmic binding protein	70% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [LivJ] [uncultured *Roseobacter* sp]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**1**	**4**	**0**	**0**	**1**	**10**
ABC transport system, branche-chain amino acids, periplasmic binding protein	64% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [LivJ] [Rhodobacterales bacterium HTCC2150]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**6**	**6**	**0**	**0**	**33**	**37**
ABC transport system, branched-chain amino acids, periplasmic binding protein	48% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [LivJ]	Alphaproteobacteria (Rhodobacterales,	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**37**

	[*Roseobacter* sp. AzwK-3b]	*Roseobacter* clade)								
ABC transport system, branched-chain amino acids, periplasmic binding protein	72% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [LivK] [*Candidatus* Puniceispirillum marinum (strain IMCC1322)]	Alphaproteobacteria (SAR116 cluster)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**4**
ABC transport system, branched-chain amino acids, periplasmic binding protein	100% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [LivK] [*Minibacterium massiliensis*]	Betaproteobacteria (Burkholderiales)	**0**	**3**	**0**	**0**	**0**	**34**	**0**	**0**
ABC transport system, branched-chain amino acids, periplasmic binding protein	50% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [*Rhizobium etli* (strain CFN 42 / ATCC 51251)]	Alphaproteobacteria (Rhizobiales)	**0**	**0**	**1**	**5**	**0**	**0**	**1**	**13**
ABC transport system, branched-chain amino acids, periplasmic binding protein	61% identity to Leu/Ile/Val ABC transport system, periplasmic binding protein [*Azospirillum* sp. B510]	Alphaproteobacteria (Rhizobiales)	**0**	**0**	**2**	**7**	**0**	**0**	**2**	**22**
ABC transport system, glutamate/glutamine/aspartate/asparagine										
ABC transport system, glutamate/glutamine/aspartate/asparagine, periplasmic binding protein	100% identity to Glutamate/glutamine/aspartate/asparagine ABC transport system, periplasmic binding protein [BztA] [alpha proteobacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**3**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
ABC transport system, glutamate/glutamine/aspartate/asparagine, periplasmic binding protein	56% identity to Glutamate/glutamine/aspartate/asparagine ABC transport system, periplasmic binding protein [BztA] [*Rhodopseudomonas capsulata*]	Alphaproteobacteria (Rhodobacterales)	**0**	**0**	**1**	**2**	**0**	**0**	**7**	**10**
ABC transport system, glutamate/glutamine/aspartate/asparagine, periplasmic binding protein	71% identity to Glutamate/glutamine/aspartate/asparagine ABC transport system, periplasmic binding protein [BztA] [*Ruegeria pomeroyi*]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**2**	**0**	**0**	**9**	**3**
ABC transport system, glutamate/glutamine/aspartate/asparagine, periplasmic binding protein	64% identity to Glutamate/glutamine/aspartate/asparagine ABC transport system, periplasmic binding protein [BztA] [*Ruegeria pomeroyi* DSS-3]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**0**	**0**	**0**	**4**	**0**
ABC transport system, glutamate/glutamine/aspartate/asparagine, periplasmic binding protein	90% identity to Glutamate/glutamine/aspartate/asparagine-binding protein [BztA] [uncultured marine bacterium Ant4D3]	Gammaproteobacteria (unclassified)	**66**	**75**	**68**	**129**	**66**	**75**	**68**	**129**
ABC transport system, histidine										
ABC transport sytem, histidine, periplasmic binding protein	47% identity to Histidine ABC transport system, periplasmic histidine-binding protein [HisJ] [*Desulfobacterium autotrophicum* HRM2]	Deltaproteobacteria (Desulfobacterales)	**0**	**0**	**5**	**0**	**0**	**0**	**8**	**0**
ABC transport system, octopine										

ABC transport sytem, octopine, periplasmic binding protein	90% identity to Octopine ABC transport system, periplasmic binding protein [OccT] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**5**	**1**	**0**	**0**	**15**	**3**	**0**	**0**
ABC transport system, taurine										
ABC transport system, taurine, periplasmic binding protein	92% identity to Taurine ABC transport system, periplasmic binding protein [TauA] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**17**	**16**	**0**	**0**	**85**	**78**
ABC transport system, taurine, periplasmic binding protein	62% identity to Taurine ABC transport system, periplasmic binding protein [TauA] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**6**	**10**	**0**	**0**	**25**	**48**
ABC transport system, taurine, periplasmic binding protein	58% identity to Taurine ABC transport system, periplasmic binding protein [TauA] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**8**	**0**	**0**	**1**	**25**
ABC transport system, taurine, periplasmic binding protein	61% identity to Taurine ABC transport system, periplasmic binding protein [TauA] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**2**	**0**	**0**	**4**	**10**
ABC transport system, taurine, periplasmic binding protein	70% identity to Taurine ABC transport system, periplasmic binding protein [TauA] [*Ruegeria pomeroyi*]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**1**	**5**	**0**	**0**	**2**	**52**
ABC transport system, sulfonate/nitrate/bicarbonate										
ABC transport system, sulfonate/nitrate/bicarbonate, periplasmic binding protein	73% identity to Sulfonate/nitrate/bicarbonate transport system, periplasmic binding protein [TauA] [*Phaeobacter gallaeciensis* BS107]	Alphaproteobacteria (Rhodobacterales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
ABC transport system, sulfonate/nitrate/bicarbonate, periplasmic binding protein	74% identity to Sulfonate/nitrate/bicarbonate transport system periplasmic binding protein [TauA] [*Methylibium petroleiphilum* (strain PM1)]	Betaproteobacteria (Burkholderiales)	**0**	**0**	**3**	**0**	**0**	**0**	**9**	**0**
ABC transport system, sulfonate/nitrate/bicarbonate, periplasmic binding protein	47% identity to Sulfonate/nitrate/bicarbonate transport system periplasmic binding protein [TauA] [*Methylibium petroleiphilum* (strain PM1)]	Betaproteobacteria (Burkholderiales)	**0**	**0**	**2**	**4**	**0**	**0**	**3**	**17**
ABC transport system, sulfonate/nitrate/bicarbonate, periplasmic binding protein	64% identity to Sulfonate/nitrate/bicarbonate transport system, periplasmic binding protein [TauA] [*Methylibium petroleiphilum* (strain PM1)]	Betaproteobacteria (Burkholderiales)	**0**	**0**	**3**	**3**	**0**	**0**	**5**	**6**
ABC transport system, sulfonate/nitrate/bicarbonate, periplasmic binding protein	31% identity to Putative sulfonate/nitrate/bicarbonate transport system, periplasmic binding protein [TauA] [*Verminephrobacter eiseniae* EF01-2]	Betaproteobacteria (Burkholderiales)	**0**	**0**	**4**	**2**	**0**	**0**	**8**	**2**
ABC transport system, sulfonate/nitrate/bicarbonate, ATP-binding protein	74% identity to Sulfonate/nitrate/bicarbonate transport system, ATPase protein [TauB] [*Methylibium petroleiphilum* PM1]	Betaproteobacteria (Burkholderiales)	**0**	**0**	**4**	**5**	**0**	**0**	**8**	**25**

ABC transport system, spermidine/putrescine										
ABC transport system, spermidine/putrescine, periplasmic binding protein	90% identity to Spermidine/putrescine ABC transport system, periplasmic binding protein [PotD] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**16**
ABC transport system, spermidine/putrescine, periplasmic binding protein	65% identity to Spermidine/putrescine ABC transport system, periplasmic binding protein [PotD] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**5**	**6**	**0**	**0**	**10**	**36**
ABC transport system, spermidine/putrescine, periplasmic binding protein	72% identity to Spermidine/putrescine ABC transport system, periplasmic binding protein [PotD] [*Candidatus* Pelagibacter ubique]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**5**	**0**	**0**	**8**	**24**
ABC transport system, spermidine/putrescine, periplasmic binding protein	96% identity to Spermidine/putrescine ABC transport system, periplasmic binding protein [PotD] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**9**
ABC transport system, spermidine/putrescine, periplasmic binding protein	80% identity to Spermidine/putrescine ABC transport system, periplasmic binding protein [PotD] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**2**	**0**	**0**	**7**	**12**
ABC transport system, spermidine/putrescine, periplasmic binding protein	78% identity to Spermidine/putrescine ABC transport system, periplasmic binding protein [PotD] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**3**	**0**	**0**	**3**	**21**
ABC transport system, spermidine/putrescine, periplasmic binding protein	100% identity to Spermidine/putrescine ABC transport system, periplasmic binding protein [PotD] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**2**	**3**	**0**	**0**	**10**	**18**	**0**	**0**
ABC transport system, spermidine/putrescine, periplasmic binding protein	50% identity to Spermidine/putrescine ABC transport system, periplasmic binding protein [PotD] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**
ABC transport system, spermidine/putrescine, periplasmic binding protein	84% identity to Spermidine/putrescine ABC transport system, periplasmic binding protein [PotD] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**2**	**0**	**0**	**5**	**10**
ABC transport system, spermidine/putrescine, ATP-binding protein	88% identity to Spermidine/putrescine ABC transport system, ATPase subunit [PotA] [*Roseovarius* sp. 217]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
ABC transport system, spermidine/putrescine, periplasmic binding protein	75% identity to Spermidine/putrescine ABC transport system, periplasmic binding protein [PotD] [*Roseobacter* sp. SK209-2-6]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**3**	**5**	**0**	**0**	**17**	**18**
ABC transport system, spermidine/putrescine, periplasmic binding protein	50% identity to Spermidine/putrescine ABC transport system, periplasmic binding protein [PotD] [*Roseobacter* sp. MED193]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**1**	**3**	**0**	**0**	**2**	**13**

ABC transport system, spermidine/putrescine, periplasmic binding protein	58% identity to Spermidine/putrescine ABC transport system, periplasmic binding protein [PotF] [*Ruegeria* sp. R11]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**5**	**0**	**0**	**4**	**17**
ABC transport system, spermidine/putrescine, periplasmic binding protein	49% identity to Spermidine/putrescine ABC transport system, periplasmic binding protein [PotD] [Rhodobacterales bacterium HTCC2150]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**3**	**0**	**0**	**8**	**32**
ABC transport system, spermidine/putrescine, periplasmic binding protein	64% identity to Spermidine/putrescine ABC transport system, periplasmic binding protein [PotD] [*Octadecabacter antarcticus* 238]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**
ABC transport system, spermidine/putrescine, periplasmic binding protein	49% identity to Spermidine/putrescine ABC transport system, periplasmic binding protein [PotD] [*Silicibacter lacuscaerulensis* ITI-1157]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**4**	**3**	**0**	**0**	**10**	**10**
ABC transport system, spermidine/putrescine, periplasmic binding protein	85% identity to Spermidine/putrescine ABC transport system, periplasmic binding protein [PotD] [*Candidatus* Puniceispirillum marinum (strain IMCC1322)]	Alphaproteobacteria (SAR116 cluster)	**0**	**0**	**1**	**2**	**0**	**0**	**1**	**5**
ABC transport system, spermidine/putrescine, ATP-binding protein	70% identity to Spermidine/putrescine ABC transport system, ATPase subunit [PotA] [Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
ABC transport system, sorbitol/mannitol										
ABC transport system, sorbitol/mannitol, ATP-binding protein	61% identity to Sorbitol/mannitol ABC transport system, ATP-binding subunit [MltK] [*Pseudovibrio* sp. JE062]	Alphaproteobacteria (Rhodobacterales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
ABC transport system, sorbitol/mannitol, periplasmic binding protein	78% identity to Sorbitol/mannitol ABC transport system, periplasmic binding protein [*Hoeflea phototrophica* DFL-43]	Alphaproteobacteria (Rhizobiales)	**0**	**0**	**5**	**5**	**0**	**0**	**7**	**15**
ABC transport system, sorbitol/mannitol, periplasmic binding protein	50% identity to Sorbitol/mannitol ABC transport system, periplasmic binding protein [*Marinomonas* sp. MED121]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**14**
ABC transport system, sugar										
ABC transport system, sugar, periplasmic binding protein	89% identity to Probable sugar ABC transport system, periplasmic binding protein [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**9**	**15**	**0**	**0**	**16**	**52**
ABC transport system, sugar, periplasmic binding protein	100% identity to Probable sugar ABC transport system, periplasmic binding protein [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**5**	**2**	**0**	**0**	**9**	**3**	**0**	**0**
ABC transport system, sugar, periplasmic binding protein	100% identity to Probable sugar ABC transport system, periplasmic binding protein [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**2**	**0**	**0**	**0**	**3**	**0**	**0**
ABC transport system, sugar, periplasmic binding protein	100% identity to Probable sugar ABC transport system, periplasmic binding protein [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**1**	**2**	**0**	**0**	**3**	**5**	**0**	**0**

ABC transport system, sugar, periplasmic binding protein	100% identity to Probable sugar ABC transport system, periplasmic binding protein *Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**1**	**0**	**0**	**5**	**4**
ABC transport system, sugar, periplasmic binding protein	97% identity to Probable sugar ABC transport system, periplasmic binding protein [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**1**	**0**	**0**	**5**	**3**
ABC transport system, sugar, periplasmic binding protein	63% identity to Probable sugar ABC transport system, periplasmic binding protein [*Octadecabacter antarcticus* 307]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**3**	**8**	**0**	**0**	**5**	**123**
ABC transport system, sugar, periplasmic binding protein	74% identity to Probable sugar ABC transport system, periplasmic binding protein [Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**3**	**11**	**0**	**0**	**3**	**35**
ABC transport system, sugar, periplasmic binding protein	63% identity to Probable sugar ABC transport system, periplasmic binding protein [*Jannaschia* sp. (strain CCS1)]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**12**
ABC transport system, sugar, periplasmic binding protein	48% identity to Probable sugar ABC transport system, periplasmic binding protein [Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**
ABC transport system, sugar, periplasmic binding protein	100% identity to Sugar ABC transport system, periplasmic binding protein [MalK] [Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**0**	**0**	**0**	**6**	**0**	**0**	**0**
ABC transport system, sugar, periplasmic binding protein	100% identity to Sugar ABC transport system, periplasmic binding protein [MalK] [*Labrenzia aggregata* IAM 12614]	Alphaproteobacteria (Rhodobacterales)	**0**	**3**	**0**	**0**	**0**	**8**	**0**	**0**
ABC transport system, sugar, periplasmic binding protein	100% identity to Probable sugar ABC transport system, periplasmic binding protein [alpha proteobacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**1**	**1**	**2**	**1**	**1**	**3**	**3**	**4**
ABC transport system, sugar, periplasmic binding protein	83% identity to Probable sugar ABC transport system, periplasmic binding protein [*Roseobacter denitrificans* (strain ATCC 33942 / OCh 114)	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**3**	**1**	**0**	**0**	**10**	**1**
ABC transport system, sugar, periplasmic binding protein	88% identity to Sugar ABC transport system, periplasmic binding protein [MalK] [*Ruegeria pomeroyi* DSS-3]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**5**
ABC transport system, sugar, periplasmic binding protein	65% identity to Probable sugar ABC transport system, periplasmic binding protein [*Phaeobacter gallaeciensis* 2.10]	Alphaproteobacteria (Rhodobacterales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**17**
ABC transport system, sugar, periplasmic binding protein	48% identity to Sugar ABC transport system, periplasmic binding protein [MalK] [*Roseobacter* sp. SK209-2-6]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**13**
ABC transport system, sugar, periplasmic binding protein	79% identity to Sugar ABC transport system, periplasmic binding protein [MalK] [*Stappia aggregata* IAM 12614]	Alphaproteobacteria (Rhodobacterales)	**0**	**0**	**2**	**5**	**0**	**0**	**3**	**26**
ABC transport system, sugar, periplasmic binding protein	76% identity to Sugar ABC transport system periplasmic sugar-binding protein [MalK] [*Candidatus Candidatus* Puniceispirillum marinum IMCC1322]	Alphaproteobacteria (SAR116 cluster)	**0**	**0**	**3**	**3**	**0**	**0**	**12**	**8**

ABC transport system, sugar, periplasmic binding protein	50% identity to Probable sugar ABC transport system, peripalsmic binding protein [*Rhizobium etli* (strain CFN 42 / ATCC 51251)]	Alphaproteobacteria (Rhizobiales)	**0**	**0**	**0**	**12**	**0**	**0**	**0**	**52**
ABC transport system, sugar, periplasmic binding protein	67% identity to Probable sugar ABC transport system, periplasmic binding protein [*Hoeflea phototrophica* DFL-43]	Alphaproteobacteria (Rhizobiales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**9**
ABC transport system, sugar, periplasmic binding protein	68% identity to Probable sugar ABC transport system, periplasmic binding protein [HCH_02309] [*Hahella chejuensis* (strain KCTC 2396)]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**3**	**3**	**0**	**0**	**6**	**8**
ABC transport system, sugar, periplasmic binding protein	65% identity to Probable sugar ABC transport system, periplasmic binding protein [*Hahella chejuensis* (strain KCTC 2396)]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**9**
ABC transport system, sugar, periplasmic binding protein	61% identity to Probable sugar ABC transport system, periplasmic binding protein [*Hahella chejuensis* (strain KCTC 2396)]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**
ABC transport system, sugar, periplasmic binding protein	64% identity to Probable sugar ABC transport system, periplasmic binding protein [*Marinomonas* sp. (strain MWYL1)]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
ABC transport system, sugar, periplasmic binding protein	49% identity to Probable sugar ABC transport system, periplasmic binding protein [*Acidothermus cellulolyticus* (strain ATCC 43068 / 11B)]	Actinobacteria	**0**	**0**	**4**	**3**	**0**	**0**	**10**	**6**
ABC transport system, ribose										
ABC transport system, ribose, periplasmic binding protein	50% identity to Ribose ABC transport system, periplasmic binding protein [RbsB] [*Rhizobium etli* (strain CFN 42 / ATCC 51251)]	Alphaproteobacteria (Rhizobiales)	**0**	**0**	**4**	**5**	**0**	**0**	**4**	**22**
ABC transport system, ribose, periplasmic binding protein	45% identity to Ribose ABC transport system, periplasmic binding protein [RbsB] [*Rhizobium* sp. (strain NGR234)]	Alphaproteobacteria (Rhizobiales)	**0**	**0**	**3**	**3**	**0**	**0**	**5**	**13**
ABC transport system, ribose, periplasmic binding protein	59% identity to Ribose ABC transport system, periplasmic binding protein [RbsB] [*Rhizobium etli* (strain CFN 42 / ATCC 51251)]	Alphaproteobacteria (Rhizobiales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**6**
ABC transport system, ribose, periplasmic binding protein	90% identity to Ribose ABC transport system, periplasmic binding protein [RbsB] [*Escherichia coli* O6] (*likely contaminant*)	Gammaproteobacteria (Enterobacteriales)	**0**	**2**	**0**	**0**	**0**	**4**	**0**	**0**
ABC transport system, oligopeptide										
ABC transport system, oligopeptide, periplasmic binding protein	57% identity to Probable oligopeptide ABC transport system, periplasmic binding protein [OppA] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**16**	**0**	**0**	**0**	**44**
ABC transport system, oligopeptide, periplasmic binding protein	67% identity to Oligopeptide ABC transport system, periplasmic binding protein [OppA]	Alphaproteobacteria (Rhodobacterales,	**0**	**0**	**10**	**9**	**0**	**0**	**38**	**27**

	[*Roseobacter* sp. GAI101]	*Roseobacter* clade)								
ABC transport system, oligopeptide, periplasmic binding protein	67% identity to Oligopeptide ABC transport system, periplasmic binding protein [OppA] [*Pseudovibrio* sp. JE062]	Alphaproteobacteria (Rhodobacterales)	**0**	**0**	**4**	**10**	**0**	**0**	**4**	**36**
ABC transport system, oligopeptide, periplasmic binding protein	68% identity to Oligopeptide ABC transport system, periplasmic binding protein [OppA] [*Roseovarius nubinhibens* ISM]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**15**
ABC transport system, oligopeptide, periplasmic binding protein	66% identity to Oligopeptide ABC transport system, periplasmic binding protein [OppA] [*Roseobacter* sp. GAI101]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**4**	**0**	**0**	**3**	**22**
ABC transport system, oligopeptide, periplasmic binding protein	100% identity to Oligopeptide ABC transport system, periplasmic binding protein [OppA] [Rhodobacterales bacterium HTCC2083]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**1**	**0**	**0**	**4**	**8**	**0**	**0**
ABC transport system, oligopeptide, periplasmic binding protein	78% identity to Oligopeptide ABC transport system, periplasmic binding protein [OppA] [Rhodobacterales bacterium HTCC2083]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**5**	**2**	**0**	**0**	**7**	**5**
ABC transport system, oligopeptide, periplasmic binding protein	60% identity to Oligopeptide ABC transport system, periplasmic binding protein [OppA] [Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**2**	**0**	**0**	**2**	**2**
ABC transport system, oligopeptide, periplasmic binding protein	67% identity to Oligopeptide ABC transport system, periplasmic binding protein [OppA] [*Roseobacter denitrificans* (strain ATCC 33942 / OCh 114)	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**5**
ABC transport system, oligopeptide, periplasmic binding protein	63% identity to Oligopeptide ABC transport system, periplasmic binding protein [OppA] [*Oceanicola granulosus* HTCC2516]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
ABC transport system, oligopeptide, periplasmic binding protein	68% identity to Oligopeptide ABC transport system, periplasmic binding protein [OppA] [*Reinekea blandensis* MED297]	Gammaproteobacteria (unclassified)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**15**
ABC transport system, ectoine/hydroxyectoine										
ABC transport system, ectoine/hydroxyectoine, periplasmic binding protein	88% identity to Ectoine/hydroxyectoine ABC transport system, periplasmic binding protein [EhuB] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**2**	**0**	**0**	**2**	**3**
ABC transport system, glycerol-3-phosphate										
ABC transport system, glycerol-3-phosphate, periplasmic binding protein	68% identity to Glycerol-3-phosphate ABC transport system, periplasmic binding protein [UgpB] [*Roseobacter* sp. AzwK-3b]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**5**	**8**	**0**	**0**	**5**	**38**
ABC transport system, glycerol-3-phosphate, periplasmic binding protein	66% identity to Glycerol-3-phosphate ABC transport system, periplasmic binding protein [UgpB] [Rhodobacterales bacterium HTCC2083]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**

ABC transport system, glycerol-3-phosphate, periplasmic binding protein	69% identity to Glycerol-3-phosphate ABC transport system, periplasmic binding protein [Rhodobacterales bacterium HTCC2150]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**1**	**4**	**0**	**0**	**1**	**9**
ABC transport system, glycerol-3-phosphate, periplasmic binding protein	100% identity to Glycerol-3-phosphate ABC transport system, periplasmic binding protein [Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
ABC transport system, glycerol-3-phosphate, periplasmic binding protein	66% identity to Glycerol-3-phosphate ABC transport system, periplasmic binding protein [UgpB] [*Hoeflea phototrophica* DFL-43]	Alphaproteobacteria (Rhizobiales)	**0**	**0**	**3**	**10**	**0**	**0**	**4**	**25**
ABC transport system, phosphonate										
ABC transport system, phosphonate, periplasmic binding protein	85% identity to Phosphonate ABC transport system, periplasmic binding protein [PhnD] [*Marinomonas* sp. MED121]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**11**
ABC transport system, phosphonate, periplasmic binding protein	100% identity to Phosphonate ABC transport system, periplasmic binding protein [PhnD] [*Roseobacter denitrificans* (strain ATCC 33942 / OCh 114)	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**5**
ABC transport system, iron										
ABC transport system, iron, periplasmic binding protein	88% identity to Iron ABC transport system, periplasmic binding protein [SfuC] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**4**	**3**	**0**	**0**	**4**	**9**
ABC transport system, iron, periplasmic binding protein	100% identity to Iron ABC transport system, periplasmic binding protein [SfuC] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**2**	**1**	**0**	**0**	**3**	**1**	**0**	**0**
ABC transport system, unknown solute										
ABC transport system, periplasmic binding protein	41% identity to Putative ABC transport periplasmic binding protein [*Burkholderia glumae* (strain BGR1)]	Betaproteobacteria (Burkholderiales)	**0**	**0**	**4**	**0**	**0**	**0**	**7**	**0**
ABC transport system, periplasmic binding protein	35% identity to Putative ABC transport periplasmic binding protein [*Frankia alni* (strain ACN14a)]	Actinobacteria	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**9**
ABC transport system, permease										
ABC transport system, permease	69% identity to Putative permease of ABC transport system [Nmar_1712] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**4**
ABC transport system, permease	93% identity to Putative permease of ABC transport system [Nmar_1714] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**

TRAP transporter										
TRAP dicarboxylate transporter, periplasmic binding protein DctP	86% identity to TRAP dicarboxylate transporter, periplasmic binding subunit DctP [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**6**	**13**	**0**	**0**	**45**	**155**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	93% identity to TRAP dicarboxylate transporter, periplasmic binding subunit DctP [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**10**	**13**	**0**	**0**	**25**	**118**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	98% identity to TRAP dicarboxylate transporter, periplasmic binding subunit DctP [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**15**	**15**	**0**	**0**	**63**	**82**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	98% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**4**	**8**	**0**	**0**	**12**	**94**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	93% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**5**	**7**	**0**	**0**	**13**	**33**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	93% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**4**	**0**	**0**	**1**	**27**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	93% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**5**	**0**	**0**	**2**	**11**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	94% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**2**	**0**	**0**	**1**	**16**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	95% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Candidatus* Pelagibacter sp. IMCC9063]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**4**	**0**	**0**	**2**	**12**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	87% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**11**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	94% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**2**	**0**	**0**	**1**	**13**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	97% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**3**	**3**	**0**	**0**	**3**	**8**	**0**	**0**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	83% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**2**	**0**	**0**	**4**	**9**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	88% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**2**	**0**	**0**	**1**	**10**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	86% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Candidatus*	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**7**	**0**	**0**	**2**	**23**

	Pelagibacter sp. HTCC7211]									
TRAP dicarboxylate transporter, periplasmic binding protein DctP	97% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**3**	**0**	**0**	**1**	**10**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	51% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Octadecabacter antarcticus* 307]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**6**	**8**	**0**	**0**	**25**	**61**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	54% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [Rhodobacterales bacterium HTCC2083]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**23**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	87% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [Rhodobacterales bacterium HTCC2083]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**4**	**3**	**0**	**0**	**14**	**10**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	54% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Ruegeria pomeroyi* DSS-3]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**3**	**0**	**0**	**2**	**14**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	59% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Roseovarius nubinhibens* ISM]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**4**	**1**	**0**	**0**	**7**	**1**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	83% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [Rhodobacterales bacterium HTCC2150]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**0**	**0**	**0**	**6**	**0**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	83% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Candidatus Candidatus* Puniceispirillum marinum IMCC1322]	Alphaproteobacteria (SAR116 cluster)	**0**	**0**	**3**	**3**	**0**	**0**	**10**	**12**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	69% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Candidatus Candidatus* Puniceispirillum marinum IMCC1322]	Alphaproteobacteria (SAR116 cluster)	**0**	**0**	**3**	**11**	**0**	**0**	**8**	**97**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	100% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [alpha proteobacterium BAL199]	Alphaproteobacteria (unclassified)	**2**	**2**	**0**	**0**	**4**	**7**	**0**	**0**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	38% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Marinomonas* mediterranea MMB-1]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**4**	**6**	**0**	**0**	**7**	**16**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	60% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Grimontia hollisae* CIP 101886]	Gammaproteobacteria (Vibrionales)	**0**	**0**	**1**	**5**	**0**	**0**	**1**	**23**
TRAP dicarboxylate transporter, periplasmic binding protein DctP	76% identity to TRAP dicarboxylate transporter, periplasmic binding protein DctP [*Reinekea* sp. MED297]	Gammaproteobacteria (unclassified)	**0**	**0**	**2**	**9**	**0**	**0**	**4**	**21**
TRAP-associated extracytoplasmic immunity (TAXI) system										

TRAP-associated extracytoplasmic immunity (TAXI) protein	82% identity to TRAP-associated extracytoplasmic immunity (TAXI) protein [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	0	0	5	11	0	0	18	77
TRAP-associated extracytoplasmic immunity (TAXI) protein	98% identity to TRAP-associated extracytoplasmic immunity (TAXI) protein [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	0	0	3	7	0	0	13	28
TRAP-associated extracytoplasmic immunity (TAXI) protein	81% identity to TRAP-associated extracytoplasmic immunity (TAXI) protein [Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	0	0	3	3	0	0	12	18
TRAP-associated extracytoplasmic immunity (TAXI) protein	100% identity to TRAP-associated extracytoplasmic immunity (TAXI) protein [*Ruegeria pomeroyi* DSS-3]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	0	1	1	2	0	2	1	5
Tripartite tricarboxylate transporter (TTT)										
Tripartite tricarboxylate transporter (TTT), periplamic binding protein TctC	100% identity to Tripartite tricarboxylate transporter (TTT), periplamic binding protein TctC [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	5	4	0	0	12	22	0	0
Tripartite tricarboxylate transporter (TTT), periplamic binding protein TctC	81% identity to Tripartite tricarboxylate transporter (TTT), periplamic binding protein TctC [*Candidatus* Pelagibacter sp. IMCC9063]	Alphaproteobacteria (SAR11 cluster)	0	0	6	6	0	0	16	27
Tripartite tricarboxylate transporter (TTT), periplamic binding protein TctC	96% identity to Tripartite tricarboxylate transporter (TTT), periplamic binding protein TctC [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	0	0	4	3	0	0	10	13
Tripartite tricarboxylate transporter (TTT), periplamic binding protein TctC	63% identity to Tripartite tricarboxylate transporter (TTT), periplamic binding protein TctC [*Silicibacter lacuscaerulensis* ITI-1157]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	0	0	2	3	0	0	3	11
Tripartite tricarboxylate transporter (TTT) family, periplamic binding protein TctC	66% identity to Tripartite tricarboxylate transporter (TTT), periplamic binding protein TctC [*Silicibacter lacuscaerulensis* ITI-1157]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	0	0	1	3	0	0	2	10
Permease for cytosine/purines, uracil, thiamine, allantoin										
Permease for cytosine/purines, uracil, thiamine, allantoin	98% identity to Permease for cytosine/purines, uracil, thiamine, allantoin [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	0	0	0	3	0	0	0	8
Ammonium transporter										
Ammonium transporter	68% identity to Ammonium transporter [Amt] [*Octadecabacter antarcticus* 238]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	0	0	0	3	0	0	0	22
Ammonium transporter	52% identity to Ammonium transporter [Amt] [*Roseovarius nubinhibens* ISM]	Alphaproteobacteria (Rhodobacterales,	0	0	1	2	0	0	6	2

		Roseobacter clade)								
Ammonium transporter	100% identity to Ammonium transporter [Amt] [Nmar_1698] [*Nitrosopumilus maritimus* (strainSCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**1**	**0**	**3**	**0**	**3**	**0**	**12**
Methanesulfonate transporter										
Methanesulfonate transporter	92% identity to Methanesulfonate transporter [MsmE] [uncultured bacterium Sargasso-2222818]	Bacteria (unclassified)	**0**	**3**	**0**	**0**	**0**	**4**	**0**	**0**
Na+/solute symporter										
Na+/solute symporter	85% identity to Na+/solute symporter, Ssf family [YjcG] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**7**	**6**	**0**	**0**	**52**	**71**
Na+/solute symporter	71% identity to Na+/solute symporter, Ssf family [YjcG] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**4**	**5**	**0**	**0**	**14**	**43**
Na+/solute symporter	85% identity to Na+/solute symporter, Ssf family [YjcG] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**2**	**0**	**0**	**12**	**22**
Na+/solute symporter	73% identity to Probable Na+/solute symporter [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**2**	**0**	**0**	**4**	**3**
Bmp family protein										
Bmp basic membrane lipoprotein family protein	62% identity to Bmp basic membrane lipoprotein family protein [Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**0**	**12**	**0**	**0**	**0**	**30**
Bmp basic membrane lipoprotein family protein	66% identity to Bmp basic membrane lipoprotein family protein [*Pseudovibrio* sp. JE062]	Alphaproteobacteria (Rhodobacterales)	**0**	**0**	**2**	**2**	**0**	**0**	**4**	**7**
Cellulose-binding protein										
Cellulose-binding protein	33% identity to Putative cellulose-binding protein [CttA] [*Ruminococcus flavefaciens*]	Firmicutes (Clostridia)	**0**	**0**	**4**	**3**	**0**	**0**	**9**	**5**
Efflux protein										
Efflux protein, AcrB family	51% identity to Acriflavin resistance protein precursor / Efflux protein TolC family [Rmag_0369] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**3**
E fflux protein TolC family	37% identity to Efflux protein TolC family [*Pseudomonas stutzeri* (strain A1501)]	Gammaproteobacteria (Pseudomonadales)	**0**	**0**	**2**	**0**	**0**	**0**	**4**	**0**

Preprotein translocase										
Preprotein translocase, YajC subunit	82% identity to Preprotein translocase, YajC subunit [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**3**	**0**	**0**	**0**	**8**	**0**	**0**	**0**
Preprotein translocase, YajC subunit	80% identity to Preprotein translocase, YajC subunit [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**
SecD protein	62% identity to Protein-export membrane protein SecD precursor [Rmag_1006] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**3**
Preprotein translocase, SecY subunit	93% identity to Preprotein translocase subunit SecY [Nmar_0402] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**7**
Outer Membrane – Transport, Attachment, Motility										
TonB-dependent receptor (TBDR)										
TonB-dependent receptor	52% identity to TonB-dependent receptor [*Maricaulis maris* MCS10]	Alphaproteobacteria (Rhodobacterales)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
TonB-dependent receptor	100% identity to TonB-dependent receptor [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**8**	**0**	**0**	**0**	**10**	**0**	**0**	**0**
TonB-dependent receptor	100% identity to TonB-dependent receptor] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**4**	**0**	**0**	**0**	**4**	**0**	**0**	**0**
TonB-dependent receptor	33% identity to TonB-dependent receptor [*Erythrobacter litoralis* (strain HTCC2594)]	Alphaproteobacteria (Sphingomonadales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**15**
TonB-dependent receptor	60% identity to TonB-dependent receptor] [*Caulobacter segnis* ATCC 21756]	Alphaproteobacteria (Caulobacterales)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**
TonB-dependent receptor	40% identity to TonB-dependent receptor [*Caulobacter segnis* ATCC 21756]	Alphaproteobacteria (Caulobacterales)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
TonB-dependent receptor	43% identity to TonB-dependent receptor [*Shewanella denitrificans* OS217]	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**10**	**9**	**0**	**0**	**45**	**30**
TonB-dependent receptor	39% identity to TonB-dependent receptor [*Shewanella loihica* PV-4]	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**8**	**1**	**0**	**0**	**41**	**1**
TonB-dependent receptor	62% identity to TonB-dependent receptor [*Shewanella benthica* KT99]	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**2**	**0**	**0**	**0**	**13**	**0**
TonB-dependent receptor	100% identity to TonB-dependent receptor [*Pseudoalteromonas tunicata* D2]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**6**	**0**	**0**	**0**
TonB-dependent receptor	32% identity to TonB-dependent receptor [*Shewanella* sp. MR-4]	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**2**	**0**	**0**	**0**	**5**	**0**
TonB-dependent receptor	43% identity to TonB-dependent receptor [*Alteromonas macleodii* ATCC 27126]	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**3**	**0**	**0**	**0**	**4**	**0**

TonB-dependent receptor	48% identity to TonB-dependent receptor [Alteromonadales bacterium TW-7]	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**6**
TonB-dependent receptor	100% identity to TonB-dependent receptor [Alteromonadales bacterium TW-7]	Gammaproteobacteria (Alteromonadales)	**4**	**0**	**0**	**0**	**11**	**0**	**0**	**0**
TonB-dependent receptor	33% identity to TonB-dependent receptor [*Pseudomonas fluorescens* (strain SBW25)]	Gammaproteobacteria (Pseudomonadales)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**
TonB-dependent receptor	47% identity to TonB-dependent receptor [*Xanthomonas axonopodis* pv. citri (Citrus canker)]	Gammaproteobacteria (Xanthomonadales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**7**
TonB-dependent receptor	50% identity to TonB-dependent receptor [*Xanthomonas campestris* pv. *campestris*]	Gammaproteobacteria (Xanthomonadales)	**0**	**0**	**2**	**1**	**0**	**0**	**3**	**3**
TonB-dependent receptor	73% identity to TonB-dependent receptor [uncultured marine gamma proteobacterium EB000-45B06]	Gammaproteobacteria (unclassified)	**0**	**0**	**7**	**1**	**0**	**0**	**13**	**2**
TonB-dependent receptor	61% identity to TonB-dependent receptor [gamma proteobacterium IMCC3088]	Gammaproteobacteria (unclassified)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**
TonB-dependent receptor	50% identity to TonB-dependent receptor [gamma proteobacterium NOR5-3]	Gammaproteobacteria (OMG)	**0**	**0**	**3**	**0**	**0**	**0**	**15**	**0**
TonB-dependent receptor	100% identity to TonB-dependent receptor [gamma proteobacterium NOR51-B]	Gammaproteobacteria (OMG)	**2**	**0**	**0**	**0**	**5**	**0**	**0**	**0**
TonB-dependent receptor	47% identity to TonB-dependent receptor [gamma proteobacterium NOR5-3]	Gammaproteobacteria (OMG)	**0**	**0**	**1**	**3**	**0**	**0**	**1**	**5**
TonB-dependent receptor	61% identity to TonB-dependent receptor [gamma proteobacterium NOR5-3]	Gammaproteobacteria (OMG)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**
TonB-dependent receptor	37% identity to TonB-dependent receptor [gamma proteobacterium NOR5-3]	Gammaproteobacteria (OMG)	**0**	**0**	**2**	**1**	**0**	**0**	**6**	**1**
TonB-dependent receptor	100% identity to TonB-dependent receptor [marine gamma proteobacterium HTCC2207]	Gammaproteobacteria (OMG)	**3**	**1**	**0**	**0**	**11**	**1**	**0**	**0**
TonB-dependent receptor	52% identity to TonB-dependent receptor [marine gamma proteobacterium HTCC2148]	Gammaproteobacteria (OMG)	**0**	**0**	**5**	**1**	**0**	**0**	**6**	**5**
TonB-dependent receptor	43% identity to TonB-dependent receptor [marine gamma proteobacterium HTCC2148]	Gammaproteobacteria (OMG)	**0**	**0**	**3**	**1**	**0**	**0**	**11**	**5**
TonB-dependent receptor	76% identity to TonB-dependent receptor [marine gamma proteobacterium HTCC2148]	Gammaproteobacteria (OMG)	**0**	**0**	**5**	**2**	**0**	**0**	**12**	**3**
TonB-dependent receptor	50% identity to TonB-dependent receptor [marine gamma proteobacterium HTCC2148]	Gammaproteobacteria (OMG)	**0**	**0**	**1**	**2**	**0**	**0**	**1**	**5**
TonB-dependent receptor	67% identity to TonB-dependent receptor [*Congregibacter litoralis* KT71]	Gammaproteobacteria (OMG)	**0**	**0**	**3**	**0**	**0**	**0**	**9**	**0**
TonB-dependent receptor	65% identity to TonB-dependent receptor [marine gamma proteobacterium HTCC2207]	Gammaproteobacteria (OMG)	**0**	**0**	**2**	**0**	**0**	**0**	**6**	**0**
TonB-dependent receptor	30% identity to TonB-dependent receptor [marine gamma proteobacterium HTCC2148]	Gammaproteobacteria (OMG)	**0**	**0**	**1**	**2**	**0**	**0**	**1**	**6**

TonB-dependent receptor	73% identity to TonB-dependent receptor [marine gamma proteobacterium HTCC2143]	Gammaproteobacteria (OMG)	1	0	2	2	2	0	7	7
TonB-dependent receptor	56% identity to TonB-dependent receptor [marine gamma proteobacterium HTCC2207]	Gammaproteobacteria (OMG)	0	0	1	4	0	0	4	7
TonB-dependent receptor	100% identity to TonB-dependent receptor [uncultured marine bacterium EB0_49D07]	Bacteria (unclassified)	0	3	0	0	0	3	0	0
TonB-dependent receptor	75% identity to TonB-dependent receptor [*Polaribacter* sp. MED152]	Bacteroidetes (Flavobacteria)	0	0	5	0	0	0	6	0
TonB-dependent receptor	61% identity to TonB-dependent receptor [gamma proteobacterium HTCC2207]	Bacteroidetes (Flavobacteria)	0	0	2	0	0	0	2	0
TonB-dependent receptor (SusC/RagA)	42% identity to TonB-dependent receptor [SusC/RagA] [*Dyadobacter fermentans* (strain ATCC 700827 / DSM 18053 / NS114)]	Bacteroidetes (Flavobacteria)	0	0	2	0	0	0	2	0
TonB-dependent receptor (SusC/RagA)	55% identity to TonB-dependent receptor [SusC/RagA] [*Psychroflexus torquis* ATCC 700755]	Bacteroidetes (Flavobacteria)	0	0	10	0	0	0	20	0
TonB-dependent receptor (SusC/RagA)	51% identity to TonB-dependent receptor [SusC/RagA] [*Psychroflexus torquis* ATCC 700755]	Bacteroidetes (Flavobacteria)	0	0	7	0	0	0	18	0
TonB-dependent receptor (SusC/RagA)	64% identity to TonB-dependent receptor [SusC/RagA] [*Cellulophaga lytica* DSM 7489]	Bacteroidetes (Flavobacteria)	0	0	10	0	0	0	14	0
TonB-dependent receptor (SusC/RagA)	84% identity to TonB-dependent receptor plug [Flavobacteria bacterium MS024-2A]	Bacteroidetes (Flavobacteria)	0	0	3	1	0	0	12	2
TonB-dependent receptor (SusC/RagA)	73% identity to TonB-dependent receptor [SusC/RagA] [Flavobacteria bacterium MS024-2A]	Bacteroidetes (Flavobacteria)	0	0	6	0	0	0	12	0
TonB-dependent receptor (SusC/RagA)	82% identity to TonB-dependent receptor [SusC/RagA] [Flavobacteria bacterium MS024-2A]	Bacteroidetes (Flavobacteria)	0	0	4	1	0	0	12	1
TonB-dependent receptor (SusC/RagA)	84% identity to TonB-dependent receptor [SusC/RagA] [Flavobacteria bacterium MS024-2A]	Bacteroidetes (Flavobacteria)	0	0	3	1	0	0	15	1
TonB-dependent receptor (SusC/RagA)	76% identity to TonB-dependent receptor [SusC/RagA] [*Polaribacter* sp. MED152]	Bacteroidetes (Flavobacteria)	0	0	6	0	0	0	12	0
TonB-dependent receptor (SusC/RagA)	88% identity to TonB-dependent receptor [SusC/RagA] [Flavobacteria bacterium MS024-2A]	Bacteroidetes (Flavobacteria)	0	0	3	0	0	0	8	0
TonB-dependent receptor (SusC/RagA)	63% identity to TonB-dependent receptor [SusC/RagA] [*Cellulophaga lytica* DSM 7489]	Bacteroidetes (Flavobacteria)	0	0	6	0	0	0	6	0
TonB-dependent receptor (SusC/RagA)	55% identity to TonB-dependent receptor [SusC/RagA] [Flavobacteria bacterium MS024-2A]	Bacteroidetes (Flavobacteria)	0	0	2	0	0	0	7	0
TonB-dependent receptor (SusC/RagA)	69% identity to TonB-dependent receptor [SusC/RagA] [*Polaribacter* sp. MED152]	Bacteroidetes (Flavobacteria)	0	0	3	0	0	0	3	0

TonB-dependent receptor (SusC/RagA)	66% identity to TonB-dependent receptor [SusC/RagA] [*Polaribacter* sp. MED152]	Bacteroidetes (Flavobacteria)	**0**	**0**	**5**	**0**	**0**	**0**	**5**	**0**
TonB-dependent receptor (SusC/RagA)	59% identity to TonB-dependent receptor [SusC/RagA][*Zunongwangia profunda* SM-A87]	Bacteroidetes (Flavobacteria)	**0**	**0**	**3**	**0**	**0**	**0**	**3**	**0**
TonB-dependent receptor (SusC/RagA)	46% identity to TonB-dependent receptor [SusC/RagA] [Flavobacteria bacterium MS024-2A]	Bacteroidetes (Flavobacteria)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
TonB-dependent receptor (SusC/RagA)	80% identity to TonB-dependent receptor [SusC/RagA] [*Polaribacter irgensii* 23-P]	Bacteroidetes (Flavobacteria)	**0**	**0**	**5**	**0**	**0**	**0**	**10**	**0**
TonB-dependent receptor (SusC/RagA)	72% identity to TonB-dependent receptor [SusC/RagA] [*Polaribacter irgensii* 23-P]	Bacteroidetes (Flavobacteria)	**0**	**0**	**14**	**0**	**0**	**0**	**27**	**0**
TonB-dependent receptor (SusC/RagA)	62% identity to TonB-dependent receptor [SusC/RagA] [*Robiginitalea biformata* HTCC2501]	Bacteroidetes (Flavobacteria)	**0**	**0**	**7**	**0**	**0**	**0**	**12**	**0**
TonB-dependent receptor (SusC/RagA)	40% identity to TonB-dependent receptor [SusC/RagA] [*Capnocytophaga ochracea* (strain ATCC 27872 / DSM 7271 / JCM 12966 / VPI 2845)	Bacteroidetes (Flavobacteria)	**0**	**0**	**1**	**4**	**0**	**0**	**6**	**6**
TonB-dependent receptor (SusC/RagA)	46% identity to TonB-dependent receptor [SusC/RagA] [*Spirosoma linguale* DSM 74]	Bacteroidetes (Cytophagia)	**0**	**0**	**3**	**2**	**0**	**0**	**5**	**3**
TonB-dependent receptor (SusC/RagA)	52% identity to TonB-dependent receptor [SusC/RagA] [*Zunongwangia profunda* SM-A87]	Bacteroidetes (Flavobacteria)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
TonB-dependent receptor (SusC/RagA)	42% identity to TonB-dependent receptor [SusC/RagA] [*Leadbetterella byssophila* (strain DSM 17132 / KACC 11308 / 4M15)]	Bacteroidetes (Cytophagia)	**0**	**0**	**3**	**0**	**0**	**0**	**3**	**0**
TonB-dependent receptor (SusC/RagA)	46% identity to TonB-dependent receptor [SusC/RagA] [*Zunongwangia profunda* (strain DSM 18752 / CCTCC AB 206139 / SM-A87)]	Bacteroidetes (Flavobacteria)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
TonB-dependent receptor (SusC/RagA)	53% identity to TonB-dependent receptor [SusC/RagA] [*Polaribacter* sp. MED152]	Bacteroidetes (Flavobacteria)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**
TonB-dependent receptor (SusC/RagA)	90% identity to TonB-dependent receptor [SusC/RagA] [*Polaribacter irgensii* 23-P]	Bacteroidetes (Flavobacteria)	**0**	**0**	**9**	**0**	**0**	**0**	**20**	**0**
TonB-dependent receptor (SusC/RagA)	48% identity to TonB-dependent receptor [SusC/RagA] [Flavobacteriales bacterium ALC-1]	Bacteroidetes (Flavobacteria)	**0**	**0**	**3**	**0**	**0**	**0**	**4**	**0**
TonB-dependent receptor (SusC/RagA)	61% identity to TonB-dependent receptor [SusC/RagA] [*Polaribacter irgensii* 23-P]	Bacteroidetes (Flavobacteria)	**0**	**0**	**7**	**0**	**0**	**0**	**10**	**0**
TonB-dependent receptor (SusC/RagA)	37% identity to TonB-dependent receptor [SusC/RagA] [*Capnocytophaga ochracea* (strain ATCC 27872 / DSM 7271 / JCM 12966 / VPI 2845)	Bacteroidetes (Flavobacteria)	**0**	**0**	**3**	**1**	**0**	**0**	**8**	**1**
TonB-dependent receptor (SusC/RagA)	56% identity to TonB-dependent receptor [SusC/RagA] [*Robiginitalea biformata* (strain ATCC BAA-864 / HTCC2501 / KCTC 12146)]	Bacteroidetes (Flavobacteria)	**0**	**0**	**3**	**0**	**0**	**0**	**7**	**0**

TonB-dependent receptor (SusC/RagA)	45% identity to TonB-dependent receptor [SusC/RagA] [*Cellulophaga algicola* (strain DSM 14237 / IC166 / ACAM 630)]	Bacteroidetes (Flavobacteria)	0	0	4	0	0	0	6	0
TonB-dependent receptor (SusC/RagA)	100% identity to TonB-dependent receptor [SusC/RagA] [*Capnocytophaga sputigena* Capno]	Bacteroidetes (Flavobacteria)	2	0	0	0	5	0	0	0
TonB-dependent receptor (SusC/RagA)	44% identity to TonB-dependent receptor [SusC/RagA] [*Marivirga tractuosa* (strain ATCC 23168 / DSM 4126 / NBRC 15989 / NCIMB 1408 / VKM B-1430 / H-43)]	Bacteroidetes (Flavobacteria)	0	0	2	1	0	0	3	2
TonB-dependent receptor (SusC/RagA)	61% identity to TonB-dependent receptor [SusC/RagA] [*Dokdonia donghaensis* MED134]	Bacteroidetes (Flavobacteria)	0	0	4	0	0	0	6	0
TonB-dependent receptor (SusC/RagA)	47% identity to TonB-dependent receptor [SusC/RagA] [*Cellulophaga algicola* (strain DSM 14237 / IC166 / ACAM 630)]	Bacteroidetes (Flavobacteria)	0	0	2	0	0	0	3	0
TonB-dependent receptor (SusC/RagA)	66% identity to TonB-dependent receptor [SusC/RagA] [*Croceibacter atlanticus* (strain ATCC BAA-628 / HTCC2559 / KCTC 12090)]	Bacteroidetes (Flavobacteria)	0	0	2	0	0	0	4	0
Outer membrane protein (SusD/RagB)	53% identity to SusD/RagB outer membrane protein [*Cellulophaga algicola* (strain DSM 14237 / IC166 / ACAM 630)]	Bacteroidetes (Flavobacteria)	0	0	2	0	0	0	2	0
Outer membrane protein (SusD/RagB)	63% identity to SusD/RagB outer membrane protein [Flavobacteriales bacterium ALC-1]	Bacteroidetes (Flavobacteria)	0	0	1	2	0	0	1	2
Gliding motility protein										
Gliding motility protein	100% identity to Gliding motility protein [GldL] [Flavobacteria bacterium MS024-2A]	Bacteroidetes (Flavobacteria)	0	0	2	0	0	0	2	0
Flagellin										
Flagellin	100% identity to Flagellin [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	5	0	0	0	7	0	0	0
Flagellin	100% identity to Flagellin (FliC-like) [*Pseudoalteromonas haloplanktis* TAC125]	Gammaproteobacteria (Alteromonadales)	5	0	0	0	16	0	0	0
Flagellin	100% identity to Flagellin [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	2	0	0	0	7	0	0	0
Flagellin	100% identity to Flagellin [*Escherichia coli* str. K-12 substr. MG1655] (*likely contaminant*)	Gammaproteobacteria (Enterobacteriales)	0	2	0	0	0	2	0	0
OmpA/MotB/Oar outer membrane protein										
OmpA/MotB	80% identity to OmpA/MotB family protein [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	0	0	2	0	0	0	7	0

Oar protein	31% identity to Oar-like outer membrane protein / OmpA/MotB family protein [*Maricaulis maris* (strain MCS10)]	Alphaproteobacteria (Rhodobacterales)	0	0	3	3	0	0	4	6
OmpA/MotB	100% identity to OmpA/MotB family protein [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	4	0	0	0	8	0	0	0
OmpA/MotB	96% identity to Outer membrane protein A [OmpA] [*Shigella dysenteriae*]	Gammaproteobacteria (Enterobacteriales)	0	2	0	0	0	3	0	0
Oar/OmpA protein	31% identity to OmpA family Oar-like protein [*Pseudoalteromonas* sp. SM9913]	Gammaproteobacteria (Alteromonadales)	0	0	8	0	0	0	18	0
OmpA	100% identity to OmpA family protein with TonB box [Alteromonadales strain TW-7]	Gammaproteobacteria (Alteromonadales)	3	0	0	0	6	0	0	0
OmpA/MotB	65% identity to OmpA/MotB family protein [Rmag_0516] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	0	0	0	3	0	0	0	7
OmpA/MotB	89% identityt to OmpA/MotB family protein [Flavobacteria bacterium MS024-2A]	Bacteroidetes (Flavobacteria)	0	0	4	0	0	0	6	0
OmpA/MotB	77% identity to OmpA/MotB family protein [Flavobacteria bacterium MS024-2A]	Bacteroidetes (Flavobacteria)	0	0	2	0	0	0	3	0
Peptidoglycan-associated lipoprotein										
Peptidoglycan-associated lipoprotein	43% identity to Peptidoglycan-associated lipoprotein [Pal] [*Marinomonas* sp. MED121]	Gammaproteobacteria (Oceanospirillales)	0	0	3	0	0	0	13	0
MotA/TolQ/ExbB proton channel protein										
MotA/TolQ/ExbB	100% identity to MotA/TolQ/ExbB proton channel family protein [*Pseudoalteromonas haloplanktis* TAC125]	Gammaproteobacteria (Alteromonadales)	5	0	0	0	9	0	0	0
MotA/TolQ/ExbB	77% identity to MotA/TolQ/ExbB proton channel family protein [gamma proteobacterium HTCC2207]	Gammaproteobacteria (OMG)	0	0	4	1	0	0	6	1
MotA/TolQ/ExbB	77% identity to MotA/TolQ/ExbB proton channel family protein [gamma proteobacterium HTCC2207]	Gammaproteobacteria (OMG)	0	0	3	0	0	0	7	0
MotA/TolQ/ExbB	47% identity to MotA/TolQ/ExbB proton channel family protein [marine gamma proteobacterium HTCC2143]	Gammaproteobacteria (OMG)	0	0	2	0	0	0	2	0
OmpF porin										
OmpF	99% identity to Outer membrane protein F [OmpF] [*Escherichia coli* (strain K12)] (*likely contaminant*)	Gammaproteobacteria (Enterobacteriales)	2	1	0	0	2	1	0	0

OmpF-like	70% identity to Putative uncharacterized protein [KB13_263] [beta proteobacterium KB13]	Betaproteobacteria (unclassified)	**0**	**0**	**2**	**3**	**0**	**0**	**11**	**13**
OmpH										
OmpH (outer membrane chaperone Skp)	100% identity to outer membrane OmpH (chaperone Skp) [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**2**	**0**	**0**	**0**	**4**	**0**	**0**	**0**
Maltoporin										
Maltoporin	100% identity to Maltoporin [*Escherichia coli* 536] (*likely contaminant*)	Gammaproteobacteria (Enterobacteriales)	**0**	**3**	**0**	**0**	**0**	**3**	**0**	**0**
PorA										
PorA outer membrane protein porin	100% identity to Major outer membrane protein [*Campylobacter jejuni* subsp. jejuni 84-25] (*likely contaminant*)	Epsilonproteobacteria (Campylobacterales)	**5**	**0**	**0**	**0**	**7**	**0**	**0**	**0**
Outer membrane protein assembly										
Outer membrane protein assembly complex, YaeT protein	46% identity to Outer membrane protein assembly complex, YaeT protein [*Bermanella marisrubri*]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**4**	**0**	**0**	**0**	**9**	**0**
Outer membrane protein assembly complex, YaeT protein	41% identity to probable Outer membrane protein, YaeT [*Oceanospirillum* sp. MED92]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
Outer membrane protein assembly, AsmA protein	100% identity to AsmA protein [*Pseudoalteromonas haloplanktis* TAC125]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
GENERAL METABOLISM										
Carbon fixation: 3-Hydroxypropionate/4-hydroxybutyrate cycle (archaeal)										
Acetyl-CoA/propionyl-CoA carboxylase - Steps (1)& (7)										
Acetyl-CoA/propionyl-CoA carboxylase (ATP-binding subunit)	86% identity to Carbamoyl-phosphate synthase L chain ATP-binding [Nmar_0273] [*Nitrosopumilus maritimus* (strain SCM1)] *Nmar_0273 is the homolog of Msed_0147, the protein identified as the ATP-binding subunit of Acetyl-CoA/propionyl-CoA carboxylase in Metallosphaera sedula (Berg et al., 2007).*	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**

Acetyl-CoA/propionyl-CoA carboxylase (ATP-binding subunit)	74% identity to Carbamoyl-phosphate synthase L chain ATP-binding [Nmar_0273] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**7**
Acetyl-CoA/propionyl-CoA carboxylase (carboxylase subunit)	84% identity to Carboxyl transferase [Nmar_0272] [*Nitrosopumilus maritimus* (strain SCM1)] *Nmar_0272 is the homolog of Msed_0147, the protein identified as the carboxylase subunit of Acetyl-CoA/propionyl-CoA carboxylase in Metallosphaera sedula (Berg et al., 2007).*	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Malonic semilaldehyde reductase - Step (3)										
Malonic semialdehyde reductase	77% identity to Short-chain dehydrogenase/reductase [Nmar_1043] [*Nitrosopumilus maritimus* (strain SCM1)] *In M. sedula, the enzyme responsible for this step is Msed_1993 (Kockelkorn & Fuchs, 2009), but no obvious homolog exists in N. maritimus. Hallam et al. (2006) proposed a homolog of malonyl-CoA reductase from the bacterium Chloroflexus aurantiacus as responsible for the second and third steps in the archaeon Cenarchaeum symbiosum. Nmar_1043 is the homologous protein in N. maritimus.*	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**11**	**0**	**0**	**0**	**32**	**0**	**0**
Malonic semialdehyde reductase	77% identity to Short-chain dehydrogenase/reductase [Nmar_1043] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**8**
3-Hydroxypropionyl-CoA synthetase - Step (4)										
3-Hydroxypropionyl-CoA synthetase	84% identity to CoA-binding domain protein [Nmar_1309] [*Nitrosopumilus maritimus* (strain SCM1)] *In M. sedula, this step is catalyzed by Msed_1496, an AMP-forming 3-hydroxypropionyl-CoA synthetase (Alber et al., 2008). The N. maritimus genome lacks an obvious homolog, although it does encode a putative ADP-forming hydroxypropionyl-CoA synthetase (Nmar_1309) that might catalyze this step (Walker et al., 2010).*	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**25**
Acryloyl-CoA reductase - Step (6)										

Acryloyl-CoA reductase	81% identity to Alcohol dehydrogenase zinc-binding domain protein [Nmar_1622] [*Nitrosopumilus maritimus* (strain SCM1)] *Nmar_1622 is a homolog of Msed_1426, the protein identified as acryloyl-CoA reductase in M. sedula (Berg et al., 2007).*	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**9**
Acryloyl-CoA reductase	80% identity to Alcohol dehydrogenase zinc-binding domain protein [Nmar_1622] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**11**	**0**	**0**	**0**	**45**
Acryloyl-CoA reductase?	82% identity to Alcohol dehydrogenase GroES domain protein [Nmar_0523] [*Nitrosopumilus maritimus* (strain SCM1)] *Nmar_0523 is a homolog of Msed_1426, the protein identified as acryloyl-CoA reductase in M. sedula (Berg et al., 2007).*	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**11**
Methylmalonyl-CoA mutase - Step (9)										
Methylmalonyl-CoA mutase, large subunit	87% identity to Methylmalonyl-CoA mutase, large subunit [Nmar_0954] [*Nitrosopumilus maritimus* (strain SCM1)] *Nmar_0954 is the homolog of Msed_0638, the protein identified as the large subunit of methymalonyl-CoA mutase in M. sedula (Berg et al., 2007).*	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Succinic semialdehyde reductase - Step (11)										
Succinic semialdehyde reductase	90% identity to Iron-containing alcohol dehydrogenase [Nmar_1110] [*Nitrosopumilus maritimus* (strain SCM1)] *In M. sedula, the enzyme responsible for this step is Msed_1424 (Berg et al., 2007; Kockelkorn & Fuchs, 2009), but no obvious homolog exists in N. maritimus. Walker et al. (2010) proposed that Nmar_1110 is succinic semialdehyde reductase in N. maritimus.*	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**16**
3-Hydroxybutyryl-CoA synthetase - Step (12)										
4-Hydroxybutyryl-CoA synthetase (AMP-forming)	90% identity to CoA-binding domain protein [Nmar_0206] [*Nitrosopumilus maritimus* (strain SCM1)] *In M. sedula, the enzyme responsible for this step is Msed_1422 (Berg et al., 2007), but no obvious homolog exists in N. maritimus. Walker et al. (2010) proposed that Nmar_0206 is the 4-hydroxybutyryl-CoAsynthetase (AMP-forming) in N. maritimus.*	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**9**

4-Hydroxybutyryl-CoA dehydratase - Step (13)										
4-Hydroxybutyryl-CoA dehydratase	97% identity to Vinylacetyl-CoA delta-isomerase [Nmar_0207] [*Nitrosopumilus maritimus* (strain SCM1)] *Nmar_0207 is the homolog of Msed_1321, the protein identified as 4-hydroxybutyryl-CoA dehydratase in M. sedula (Berg et al., 2007; Ramos-Vera et al., 2011).*	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**2**	**0**	**0**	**0**	**4**	**0**	**0**
4-Hydroxybutyryl-CoA dehydratase	91% identity to Vinylacetyl-CoA delta-isomerase [Nmar_0207] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**6**
Crotonyl-CoA hydratase - Step (14)										
Crotonyl-CoA hydratase	100% identity to Enoyl-CoA hydratase/isomerase [Nmar_1308] [*Nitrosopumilus maritimus* (strain SCM1)] *In M. sedula, this step and the next step are catalyzed by a single bifunctional enzyme (Msed_0399), but in N. maritimus they are catalyzed by two separate steps (Ramos-Vera et al., 2011). Nmar_1308 is the homolog of the C-terminal of Msed_0399, identified as crotonyl-CoA hydratase in M. sedula (Ramos-Vera et al., 2011).*	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**2**	**0**	**0**	**0**	**3**	**0**	**0**
3-Hydroxybutyryl-CoA dehydrogenase (NAD+) - Step (15)										
3-Hydroxybutyryl-CoA dehydrogenase (NAD+)	87% identity to 3-Hydroxybutyryl-CoA dehydrogenase [Nmar_1028] [*Nitrosopumilus maritimus* (strain SCM1)] *In M. sedula, this step and the previous step are catalyzed by a single bifunctional enzyme (Msed_0399), but in N. maritimus they are catalyzed by two separate steps (Ramos-Vera et al., 2011). Nmar_1028 is the homolog of the N-terminal of Msed_0399, identified as 3-hydroxybutyryl-CoA dehydrogenase (NAD+) in M. sedula (Ramos-Vera et al., 2011).*	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**8**
Acetoacetyl-CoA beta-ketothiolase - Step (16)										
Acetoacetyl-CoA beta-ketothiolase	88% identity to Propanoyl-CoA C-acyltransferase [Nmar_1631] [*Nitrosopumilus maritimus* (strain SCM1)] *Nmar_1631 is the homolog of Msed_0656, the protein identified as*	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**9**

	a possible candidate for acetoacetyl-CoA beta-ketothiolase in M. sedula (Berg et al., 2007).									
Carbon fixation: Reverse tricarboxylic acid cycle										
Pyruvate:ferredoxin oxidoreductase (EC 1.2.7.1)										
Pyruvate:ferredoxin oxidoreductase, gamma subunit	100% identity to Pyruvate:ferredoxin oxidoreductase gamma subunit [PorG] [*Candidatus* Leptospirillum rubarum]	Nitrospirae	**0**	**2**	**0**	**0**	**0**	**3**	**0**	**0**
Krebs cycle										
Aconitate hydratase (EC 4.2.1.3)										
Aconitate hydratase	100% identity to Aconitate hydratase [AcnA] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**2**	**0**	**0**	**0**	**2**	**0**	**0**
Aconitate hydratase	100% identity to aconitate hydratase 1 [AcnA] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Aconitate hydratase	100% identity to Aconitate hydratase 2 [AcnB] [*Pseudoalteromonas haloplanktis* (strain TAC 125)]	Gammaproteobacteria (Alteromonadales)	**4**	**1**	**0**	**0**	**6**	**1**	**0**	**0**
Aconitate hydratase	100% identity to Aconitate hydratase [AcnA] [*Moritella* sp. PE36],	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**5**	**0**	**0**	**0**
Aconitate hydratase	74% identity to Aconitate hydratase 2 [AcnB] [*Pseudomonas mendocina* (strain ymp)]	Gammaproteobacteria (Pseudomonadales)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**
Aconitate hydratase	85% identity to Aconitate hydratase [AcnA] [Nmar_1482] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**6**	**0**	**0**	**0**	**13**
Isocitrate dehydrogenase (EC 1.1.1.41)										
Isocitrate dehydrogenase	93% identity to Isocitrate dehydrogenase (NAD(+)) [Icd] [Nmar_1379] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Succinyl-CoA synthetase (EC 6.2.1.5)										
Succinyl-CoA synthetase, beta subunit	100% identity to Succinyl-CoA synthetase, beta subunit [SucC] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**5**	**0**	**0**	**0**	**6**	**0**	**0**	**0**
Succinyl-CoA synthetase, beta subunit	100% identity to Succinyl-CoA synthetase, beta subunit [SucC] [*Pseudoalteromonas haloplanktis* TAC125]	Gammaproteobacteria (Alteromonadales)	**3**	**0**	**0**	**0**	**9**	**0**	**0**	**0**

Succinyl-CoA synthetase, beta subunit	79% identity to Succinyl-CoA synthetase, beta subunit [SucC] [*Neptuniibacter caesariensis*]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**3**	**0**	**0**	**0**	**3**	**0**
Succinyl-CoA synthetase, alpha subunit	91% identity to Succinyl-CoA synthetase, alpha subunit [SucD] [Nmar_1124] [*Nitrosopumilus maritimus* (strain SCM1]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**18**
Succinyl-CoA synthetase, beta subunit	92% identity to Succinyl-CoA synthetase, beta subunit [SucC] [Nmar_1123] [*Nitrosopumilus maritimus* (strain SCM1]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**6**	**0**	**0**	**0**	**15**
Succinate dehydrogenase (EC 1.3.99.1)										
Succinate dehydrogenase/fumarate reductase, flavoprotein subunit	97% identity to Succinate dehydrogenase or fumarate reductase, flavoprotein subunit [SdhA] [Nmar_0258] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**2**	**0**	**0**	**0**	**5**	**0**	**0**
Malate dehydrogenase (EC 1.1.1.37)										
Malate dehydrogenase	97% identity to Malate dehydrogenase [Mdh] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**4**	**0**	**0**	**6**	**10**
Malate dehydrogenase	100% identity to malate dehydrogenase [Mdh] [Alteromonadales bacterium TW-7]	Gammaproteobacteria (Alteromonadales)	**3**	**0**	**0**	**0**	**5**	**0**	**0**	**0**
Malate dehydrogenase	52% identity to Malate dehydrogenase [Mdh] [gamma proteobacterium NOR51-B]	Gammaproteobacteria (OMG)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
Malate dehydrogenase	71% identity to Malate dehydrogenase [Mdh] [*Proteus mirabilis* (strain HI4320)]	Gammaproteobacteria (Enterobacteriales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**7**
Malate dehydrogenase	100% identity to Malate dehydrogenase [Mdh] [*Vibrio* sp.]	Gammaproteobacteria (Vibrionales)	**4**	**0**	**0**	**0**	**7**	**0**	**0**	**0**
Malate dehydrogenase	85% identity to Malate dehydrogenase [Mdh] [Nmar_0338] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**28**
Glyoxylate bypass										
Isocitrate lyase (EC 4.1.3.1)										
Isocitrate lyase	100% identity to isocitrate lyase [AceA] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**2**	**1**	**0**	**0**	**6**	**1**	**0**	**0**
Isocitrate lyase	100% identity to Isocitrate lyase [AceA] [Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**0**	**0**	**0**	**4**	**0**	**0**	**0**
Isocitrate lyase	83% identity to Isocitrate lyase [AceA] [*Colwellia psychrerythraea* (strain 34H /ATCC BAA-681)	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**

Isocitrate lyase	100% identity to Isocitrate lyase [AceA] [*Pseudomonas stutzeri* A1501]	Gammaproteobacteria (Pseudomonadales)	2	0	0	0	3	0	0	0
Isocitrate lyase	82% identity to Isocitrate lyase [AceA] [Rmag_0538] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	0	0	0	2	0	0	0	5
Isocitrate lyase	83% identity to Isocitrate lyase [AceA] [*Neptuniibacter caesariensis*]	Gammaproteobacteria (Oceanospirillales)	0	0	2	2	0	0	9	2
Malate synthase (EC 2.3.3.9)										
Malate synthase	58% identity to Malate synthase [AceB] [*Hahella chejuensis* (strain KCTC 2396)]	Gammaproteobacteria (Oceanospirillales)	0	0	4	2	0	0	10	4
Glycolysis/Gluconeogenesis										
Phosphoenolpyruvate synthase (EC 2.7.9.2)										
Phosphoenolpyruvate synthase	71% identity to Phosphoenolpyruvate synthase [PpsA] [*Pseudomonas fluorescens* (strain Pf-5 / ATCC BAA-477)]	Gammaproteobacteria (Pseudomonadales)	0	0	0	2	0	0	0	2
Phosphoenolpyruvate carboxykinase (EC 4.1.1.49)										
Phosphoenolpyruvate carboxykinase	73% identity to Phosphoenolpyruvate carboxykinase (ATP) [PckA] [*Hahella chejuensis* (strain KCTC 2396)]	Gammaproteobacteria (Oceanospirillales)	0	0	2	0	0	0	3	0
Phosphoenolpyruvate carboxykinase	100% identity to Phosphoenolpyruvate carboxykinase (ATP) [PckA] [*Moritella* sp. PE36],	Gammaproteobacteria (Alteromonadales)	2	0	0	0	2	0	0	0
Phosphoenolpyruvate carboxykinase	94% identity to Phosphoenolpyruvate carboxykinase (ATP) [PckA] [Nmar_0392] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	2	0	0	0	3
Enolase (EC 4.2.1.11)										
Enolase	100% identity to Enolase [Eno] [*Psychromonas ingrahamii* 37]	Gammaproteobacteria (Alteromonadales)	3	1	0	0	8	2	0	0
Enolase	84% identity to Enolase [Eno] [Nmar_0317] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	4	0	0	0	7
Phosphoglycerate mutase (EC 5.4.2.1)										
Phosphoglycerate mutase	75% identity to Phosphoglycerate mutase [ApgM] [Nmar_0537] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	3	0	0	0	6

Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)										
Glyceraldehyde-3-phosphate dehydrogenase	81% identity to Glyceraldehyde-3-phosphate dehydrogenase [GapA] [Rmag_0063] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**7**
Glyceraldehyde-3-phosphate dehydrogenase	100% identity to Gyceraldehyde-3-phosphate dehydrogenase, type I [GapA] [Vibrio harveyi HY01],	Gammaproteobacteria (Vibrionales)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Glyceraldehyde 3-phosphate dehydrogenase	100% identity to Glyceraldehyde 3- phosphate dehydrogenase [GapA] [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Fructose-1,6-bisphosphate aldolase (EC 4.1.2.13)										
Fructose-1,6-bisphosphate aldolase	74% identity to Fructose-bisphosphate aldolase [Fda] [*Prochlorococcus marinus* str. MIT 9202]	Cyanobacteria	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**7**
Fructose-1,6-bisphosphatase (EC 3.1.3.11)										
Fructose 1,6-bisphosphatase type II	100% identity to Fructose 1,6-bisphosphatase II [GlpX] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**3**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Fructose-1,6-bisphosphatase type V (archaeal)	88% identity to Fructose-1,6-bisphosphatase type V [Nmar_1035] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**3**	**0**	**0**	**0**	**6**	**0**	**0**
Glycerol kinase (EC 2..7.1.30)										
Glycerol kinase	100% identity to Glycerol kinase (GlpK) [*Shigella flexneri* 5 str. 8401]	Gammaproteobacteria (Enterobacteriales)	**0**	**2**	**0**	**0**	**0**	**2**	**0**	**0**
Transketolase (EC 2.2.1.1.)										
Transketolase	76% identity to Transketolase [TktA] [Rmag_0062] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**4**
NITROGEN & AMINO ACID METABOLISM										
Ammonia monooxygenase (EC 1.14.99.39)										
Ammonia monooxygenase, subunit B	100% identity to Ammonia monooxygenase subunit B [AmoB] [*Nitrosospira* sp. NpAV]	Betaproteobacteria (Nitrosomonadales)	**0**	**2**	**0**	**0**	**0**	**13**	**0**	**0**
Ammonia monooxygenase subunit B	100% identity to Ammonia monooxygenase subunit B [AmoB] [Nmar_1503] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**1**	**0**	**2**	**0**	**8**	**0**	**6**

Ammonia monooxygenase subunit B	100% identity to Ammonia monooxygenase subunit B [AmoB] [*Cenarchaeum symbiosum* A]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**7**
Nitrite oxidoreductase (EC 1.7.99.4)										
Nitrite oxidoreductase, alpha subunit	68% identity to Nitrite oxidoreductase alpha subunit [NxrA] ([*Candidatus* Nitrospira defluvii]	Nitrospirae	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Nitrite oxidoreductase, alpha subunit	78% identity to Nitrite oxidoreductase, alpha subunit [NarG] ([*Candidatus* Kuenenia stuttgartiensis]	Planctomycetes	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Glutamate dehydrogenase (EC 1.4.1.3)										
Glutamate dehydrogenase	89% identity to Glutamate dehydrogenase [GdhA] [Nmar_1312] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**8**	**0**	**0**	**0**	**20**
Glutamate dehydrogenase	91% identity to Glutamate dehydrogenase [GdhA] [Nmar_1312] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**14**
Glutamate synthase (EC 6.3.1.2)										
Glutamate synthase, large subunit	62% identity to Glutamate synthase large subunit [GltA] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**6**
Glutamate synthase, small subunit	70% identity to Glutamine amidotransferase [GltB] [*Candidatus* Pelagibacter ubique HTTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**2**	**0**	**0**	**2**	**14**
Glutamate synthase, small subunit	100% identity to to Glutamine amidotransferase [GltB] [*Candidatus* Pelagibacter ubique HTTCC1002]	Alphaproteobacteria (SAR11 cluster)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Glutamate synthase, small subunit	59% identity to Glutamine amidotransferase [GltB] (GXGXG motif-containing protein) [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**7**	**0**	**0**	**3**	**45**
Glutamate synthase, small subunit	71% identity to Glutamine amidotransferase [GltB] (GXGXG motif-containing protein) [*Roseovarius nubinhibens* ISM]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**1**	**0**	**0**	**4**	**1**
Glutamate synthase, large subunit	100% identity to Glutamate synthase large subunit [GltA] [*Roseobacter* sp. AzwK-3b],	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**3**	**2**	**0**	**0**	**7**	**13**	**0**	**0**
Glutamine synthetase (EC 6.3.1.2)										
Glutamine synthetase	72% identity to GlnT-like protein [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**9**	**0**	**0**	**0**	**38**

Glutamine synthetase	74% identity to GlnT-like protein [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**3**	**0**	**0**	**7**	**5**
Glutamine synthetase	90% identity to Glutamine synthetase [GlnA] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**2**	**0**	**0**	**5**	**4**
Glutamine synthetase	100% identity to Glutamine synthetase, type I [GlnA] [*Thalassobium* sp. R2A62]	Alphaproteobacteria (Rhodobacterales)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Glutamine synthetase	63% identity to Glutamine synthetase, type III [Snov_0455] [*Starkeya novella* DSM 506]	Alphaproteobacteria (Rhizobiales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Glutamine synthetase	80% identity to Glutamine synthetase [MED121_09298] [*Marinomonas* sp. MED121]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**8**	**0**	**0**	**0**	**25**	**0**
Glutamine synthetase	81% identity to Glutamine synthetase [Rmag_0498] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Carbamoyl phosphate synthase (EC 6.3.5.5)										
Carbamoyl phosphate synthase, large subunit	100% identity to Carbamoyl phosphate synthase large subunit [CarB] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**3**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Nitrogen regulatory protein P-II										
Nitrogen regulatory protein P-II	100% identity to Nitrogen regulatory protein P-II 2 [*Pseudomonas aeruginosa* PAO1]	Gammaproteobacteria (Pseudomonadales)	**2**	**0**	**2**	**0**	**6**	**0**	**8**	**0**
Aspartate aminotransferase (EC 2.6.1.1)										
Aspartate aminotransferase	93% identity to Aspartate transaminase [AspC] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**2**	**0**	**0**	**1**	**3**
Aspartate aminotransferase	72% identity to Aminotransferase: putative aspartate aminotransferase [AspC] [Rmag_0425] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**3**
Serine-pyruvate aminotransferase (EC 2.6.1.51)										
Serine-pyruvate aminotransferase	70% identity to Serine--pyruvate transaminase [Agxt] [Nmar_1731] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**9**	**0**	**0**	**0**	**37**
Taurine –pyruvate aminotransferase (EC 2.6.1.77)										
Taurine-pyruvate aminotransferase	88% identity to Class III aminotransferase: possibly taurine-pyruvate aminotransferase [Tpa] *Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**2**	**0**	**0**	**3**	**6**

Taurine-pyruvate aminotransferase	74% identity to Taurine-pyruvate aminotransferase [Tpa] [*Octadecabacter antarcticus* 238]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**1**	**0**	**0**	**5**	**2**
Aspartokinase (EC 2.7.2.4)										
Aspartate kinase	100% identity to Aspartokinase [YclM] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Aspartate kinase	79% identity to Aspartokinase [Nmar_1754] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**5**
Fumarate hydratase (E.C. 4.2.1.2)										
Fumarate hydratase	85% identity to Fumarate hydratase [FumC] [*Kordia algicida* OT-1]	Bacteroidetes (Flavobacteria)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
Phosphoglycerate dehydrogenase (EC 1.1.1.95)										
Phosphoglycerate dehydrogenase	100% identity to Phosphoglycerate dehydrogenase [SerA] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**4**	**0**	**0**	**0**	**4**	**0**	**0**	**0**
Phosphoglycerate dehydrogenase	90% identity to Phosphoglycerate dehydrogenase [SerA] [Nmar_1258] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**20**
Phosphoglycerate dehydrogenase	89% identity to Phosphoglycerate dehydrogenase [SerA] [Nmar_1258] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**15**
Serine hydroxymethyltransferase (EC 2.1.2.1)										
Serine hydroxymethyltransferase	100% identity to Serine hydroxymethyltransferase [GlyA] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Glycine cleavage system, T-protein (EC 2.1.2.10)										
Glycine cleavage system, T-protein	90% identity to Glycine cleavage T-protein family [GcvT] [uncultured marine bacterium 578]	Bacteria (unclassified)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**14**
Glycine cleavage system, L-protein (Dihydrolipoyl dehydrogenase) (EC 1.8.1.4)										

Glycine cleavage system, L-protein	68% identity to Dihydrolipoyl dehydrogenase [Lpd] [*Neptuniibacter caesariensis*]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**
Ketol-acid reductoisomerase (EC 1.1.1.86)										
Ketol-acid reductoisomerase	93% identity to Ketol-acid reductoisomerase [IlvC] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**1**	**1**	**1**	**2**	**1**	**2**	**1**	**4**
Ketol-acid reductoisomerase	100% identity to Ketol-acid reductoisomerase [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Ketol-acid reductoisomerase	93% identity to Ketol-acid reductoisomerase [IlvC] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**10**
Ketol-acid reductoisomerase	90% identity to Ketol-acid reductoisomerase [IlvC] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**21**
Dihydroxy-acid dehydrogenase (EC 4.2.1.9)										
Dihydroxy-acid dehydratase	97% identity to Dihydroxy-acid dehydratase [IlvD] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**1**	**2**	**0**	**0**	**1**	**2**	**0**	**0**
Acetolactate synthase (EC 2.2.1.6)										
Acetolactate synthase	79% identity to Acetolactate synthase, large subunit [IlvI] [Rmag_0445] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Acetolactate synthase	86% identity to Acetolactate synthase [IlvI] [Nmar_1072] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**2**	**0**	**0**	**0**	**2**	**0**	**0**
3-Isopropylmalate dehydrogenase (EC 1.1.1.85)										
3-Isopropylmalate dehydrogenase	86% identity to 3-Isopropylmalate dehydrogenase [LeuB] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**1**	**0**	**0**	**2**	**1**
Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27)										
Methylmalonate-semialdehyde dehydrogenase	74% identity to Methylmalonate-semialdehyde dehydrogenase [MmsA] [*Colwellia psychrerythraea* (strain 34H / ATCC BAA-681)	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**3**	**0**	**0**	**0**	**13**	**0**
Methylmalonate-semialdehyde dehydrogenase	72% identity to Methylmalonate-semialdehyde dehydrogenase [MmsA] [*Colwellia psychrerythraea* 34H]	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**

3-Hydroxyisobutyrate dehydrogenase (EC 1.1.1.31)										
3-Hydroxyisobutyrate dehydrogenase	100% identity to 3-Hydroxyisobutyrate dehydrogenase [MmsB] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
Dihydrodipicolinate synthase (EC 4.2.1.52)										
Dihydrodipicolinate synthase	51% identity to Dihydrodipicolinate synthase (DHDPS) [DapA] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
LysX biosynthesis enzyme										
Lysine biosynthesis enzyme LysX	86% identity to Lysine biosynthesis enzyme LysX [Nmar_1295] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Lysine biosynthesis enzyme LysX	93% identity to Lysine biosynthesis enzyme LysX [Nmar_1295] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Methionine synthase (EC 2.1.1.13)										
Methionine synthase	74% identity to Methionine synthase (Dihydropteroate synthase / 5-methyltetrahydrofolate S-homocysteine methyltransferase (Pterin binding enzyme domain protein)) [MetH] [marine gamma proteobacterium HTCC2148]	Gammaproteobacteria (OMG)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Methionine synthase, cobalamin-dependent	85% identity to Methionine synthase [MetH] [Nmar_1267] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**6**
Methionine synthase, cobalamin-dependent	74% identity to Methionine synthase [MetH] [Nmar_1267] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Methionine adenosyltransferase (EC 2.5.1.6)										
Methionine adenosyltransferase	83% identity to Methionine adenosyltransferase [MetK] [Nmar_0085] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**9**
O-Acetylhomoserine (thiol)-lyase (EC 2.5.1.49)										

O-acetylhomoserine (thiol)-lyase	81% identity to O-acetylhomoserine (thiol)-lyase [MetY] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**14**	**0**	**0**	**1**	**74**
O-acetylhomoserine (thiol)-lyase	87% identity to O-acetylhomoserine (thiol)-lyase [MetY] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**4**
O-acetylhomoserine (thiol)-lyase	71% identity to O-acetylhomoserine (thiol)-lyase [MetY] [*Candidatus* Pelagibacter ubique].	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**22**
N-Acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)										
N-Acetyl-gamma-glutamyl-phosphate reductase	100% identity to N-acetyl-gamma-glutamyl-phosphate/N-acetyl-gamma-aminoadipyl-phosphate reductase [ArgC] [Nmar_1289] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**2**	**0**	**3**	**0**	**8**	**0**	**16**
N-Acetyl-gamma-glutamyl-phosphate reductase	90% identity to N-acetyl-gamma-glutamyl-phosphate/N-acetyl-gamma-aminoadipyl-phosphate reductase [ArgC] [Nmar_1289] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**
Chorismate mutase (EC 5.4.99.5)										
Chorismate mutase	68% identity to Chorismate mutase [TyrA] [Rmag_0626] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Prephenate dehydrogenase (EC 1.3.1.12)										
Prephenate dehydrogenase	79% identity to Prephenate dehydrogenase [TyrA] [Nmar_0545] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**24**
Cyclohexadienyl dehydratase (EC 4.2.1.51)(EC 4.2.1.91)										
Cyclohexadienyl dehydratase	94% identity to Cyclohexadienyl dehydratase [PheC] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
Cyclohexadienyl dehydratase	91% identity to Cyclohexadienyl dehydratase [PheC] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**1**	**0**	**0**	**5**	**2**
Cyclohexadienyl dehydratase	83% identity to Cyclohexadienyl dehydratase [PheC] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**4**	**4**	**0**	**0**	**4**	**5**
Tryptophanase (EC 4.1.99.1)										

Tryptophanase	100% identity to tryptophanase [TnaA] [*Escherichia fergusonii*] (*likely contaminant*)	Gammaproteobacteria (Enterobacteriales)	0	9	0	0	0	11	0	0
SULFUR METABOLISM										
Sulfoacetylaldehyde acetyltransferase (EC 2.3.3.15)										
Sulfoacetaldehyde acetyltransferase	100% identity to Sulfoacetaldehyde acetyltransferase [Xsc] [*Candidatus* Pelagibacter ubique HTCC1062	Alphaproteobacteria (SAR11 cluster)	2	2	0	0	3	5	0	0
Sulfoacetaldehyde acetyltransferase	75% identity to Sulfoacetaldehyde acetyltransferase [Xsc] [Rhodobacterales bacterium KLH11]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	0	0	5	1	0	0	19	1
Sulfoacetaldehyde acetyltransferase	76% identity to Sulfoacetaldehyde acetyltransferase [Xsc] [*Silicibacter lacuscaerulensis* ITI-1157]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	0	0	2	1	0	0	4	1
Sulfoacetaldehyde acetyltransferase	82% identity to Sulfoacetaldehyde acetyltransferase [VIBC2010_19930] [*Vibrio caribbenthicus* ATCC BAA-2122]	Gammaproteobacteria (Vibrionales)	0	0	1	6	0	0	2	17
Adenylylsulfate (APS) reductase (EC 1.8.99.2)										
Adenylylsulfate reductase, alpha subunit	82% identity to Adenylylsulfate reductase, alpha subunit [AprA] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	0	0	0	3	0	0	0	6
Adenylylsulfate reductase, alpha subunit	79% identity to Adenylylsulfate reductase, alpha subunit [Rmag_0088] [AprA] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	0	0	5	2	0	0	16	4
Adenylylsulfate reductase, membrane anchor	56% identity to Adenylylsulfate reductase membrane anchor [AprM] [uncultured alpha proteobacterium EBAC2C11]	Alphaproteobacteria (SAR116 cluster)	0	0	2	1	0	0	6	1
Cysteine desulfurase (EC 2.8.1.7)										
Cysteine desulfurase	86% identity to Cysteine desulfurase [IscS] [Nmar_0497] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	3	0	0	0	5
Sulfite reductase (EC 1.8.7.1)										
Sulfite reductase, beta subunit	76% identity to Sulfite reductase, beta subunit (ferredoxin) [CysI] [Nmar_0679] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	2	0	0	0	2

Iron-sulfur assembly protein										
FeS assembly protein	82% identity to FeS assembly protein SufD [Nmar_0496] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**6**	**0**	**0**	**0**	**12**
FeS assembly protein	90% identity to FeS assembly protein SufB [Nmar_0495] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**6**	**0**	**0**	**0**	**14**
FeS assembly protein	88% identity to FeS assembly ATPase SufC [Nmar_0516] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**6**	**0**	**0**	**0**	**12**
Methanesulfonate monooxygenase, hydroxylase										
Methanesulfonate monooxygenase, hydroxylase alpha subunit	67% identity to Methanesulfonate monooxygenase, hydroxylase alpha subunit [MsmA] [Rieske (2Fe-2S) domain protein] [*Methylobacterium nodulans* (strain ORS2060 / LMG 21967)]	Alphaproteobacteria (Rhizobiales)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**
OTHER CARBON METABOLISM										
One-carbon metabolism										
Sarcosine oxidase (EC 1.5.3.1)										
Sarcosine oxidase	59% identity to Putative monomeric sarcosine oxidase [SoxA] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**
Sarcosine oxidase, alpha subunit	43% identity to Sarcosine oxidase subunit alpha [SoxA] [*Rhodobacter capsulatus* SB 1003]	Alphaproteobacteria (Rhodobacterales)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**
Sarcosine oxidase	69% identity to Putative monomeric sarcosine oxidase [SoxA] [marine gamma proteobacterium HTCC2148]	Gammaproteobacteria (OMG)	**0**	**0**	**2**	**1**	**0**	**0**	**6**	**2**
Dimethylglycine dehydrogenase (EC 1.5.99.2)										
Dimethylglycine dehydrogenase	93% identity to Dimethylglycine dehydrogenase [Dmg] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**2**	**0**	**0**	**3**	**4**
Methanol dehydrogenase (EC. 1.1.99.8)										
Methanol dehydrogenase, large subunit	100% identity to Methanol dehydrogenase large subunit [MxaF] [Methylophilales bacterium	Betaproteobacteria (Methylophilales,	**8**	**8**	**0**	**0**	**25**	**38**	**0**	**0**

	HTCC2181]	OM43 clade)								
Methanol dehydrogenase, large subunit	96% identity to Methanol dehydrogenase large subunit [MxaF] [Methylophilales bacterium HTCC2181]	Betaproteobacteria (Methylophilales, OM43 clade)	**0**	**0**	**2**	**4**	**0**	**0**	**14**	**15**
Formate dehydrogenase (EC 1.2.1.2)										
Formate dehydrogenase, beta subunit	84% identity to Formate dehydrogenase, beta subunit [FdhB] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**2**	**0**	**0**	**1**	**3**
Formate dehydrogenase, beta subunit	56% identity to Formate dehydrogenase, beta subunit [FdhB] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Formate dehydrogenase, alpha subunit	100% identity to Formate dehydrogenase, alpha subunit [FdhA] [*Ruegeria pomeroyi* DSS-3]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**1**	**2**	**0**	**0**	**1**	**6**
Formate dehydrogenase, alpha subunit	100% identity to Formate dehydrogenase, alpha subunit [FdhA] [Rhodobacterales bacterium HTCC2083]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**3**	**3**	**0**	**0**	**5**	**8**	**0**	**0**
Formate tetrahydrofolate ligase (EC 6.3.4.3)										
Formate--tetrahydrofolate ligase	97% identity to Formate--tetrahydrofolate ligase [Fhs] [*Candidatus* Pelagibacter ubique TCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**4**	**4**	**0**	**0**	**7**	**8**
Formate--tetrahydrofolate ligase	67% identity to Formate--tetrahydrofolate ligase [Fhs] [*Roseobacter* sp. SK209-2-6]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**12**	**0**	**0**	**2**	**29**
Formate--tetrahydrofolate ligase	63% identity to Formate--tetrahydrofolate ligase [Fhs] [*Methylocella silvestris* (strain BL2 / DSM 15510 / NCIMB 13906)]	Alphaproteobacteria (Rhizobiales)	**0**	**0**	**6**	**4**	**0**	**0**	**22**	**8**
Formate--tetrahydrofolate ligase	60% identity to Formate--tetrahydrofolate ligase [Fhs] [*Methylocella silvestris* (strain BL2 / DSM 15510 / NCIMB 13906)]	Alphaproteobacteria (Rhizobiales)	**0**	**0**	**2**	**0**	**0**	**0**	**4**	**0**
Formamidase (EC 3.5.1.49)										
Formamidase	61% identity to Formamidase [FmdA] [*Synechococcus* sp. PCC 7335]	Cyanobacteria	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Dimethylformamidase (EC 3.5.1.56)										
N,N-dimethylformamidase, large subunit	40% identity to Large subunit of N,N-dimethylformamidase [*Methylobacterium chloromethanicum* (strain CM4 / NCIMB 13688)]	Alphaproteobacteria (Rhizobiales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**9**

3-Methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)										
3-Methyl-2-oxobutanoate hydroxymethyltransferase	76% identity to 3-Methyl-2-oxobutanoate hydroxymethyltransferase [*Candidatus* Puniceispirillum marinum (strain IMCC1322)]	Alphaproteobacteria (SAR116 cluster)	**0**	**0**	**5**	**1**	**0**	**0**	**10**	**2**
Dimethylsulfoniopropionate (DMSP) degradation										
DMSP demethylase										
DMSP demethylase	99% identity to DMSP demethylase (aminomethyltransferase) [DmdA] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**2**	**3**	**0**	**0**	**4**	**5**	**0**	**0**
DMSP demethylase	60% identity to DMSP demethylase (aminomethyltransferase) [DmdA] [marine gamma proteobacterium HTCC2148]	Gammaproteobacteria (OMG)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
3-Methylmercaptopropionyl-CoA ligase										
3-Methylmercaptopropionyl-CoA ligase	56% identity to Acyl-CoA dehydrogenase [FadE] [*Neptuniibacter caesariensis*] *Regarded here as 3-methylmercaptopropionyl-CoA ligase [DmdC]*	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
3-Methylmercaptopropionyl-CoA ligase	67% identity to Probable acyl-CoA dehydrogenase [FadE] [marine gamma proteobacterium HTCC2143] *Regarded here as 3-methylmercaptopropionyl-CoA ligase [DmdC]*	Gammaproteobacteria (OMG)	**0**	**0**	**4**	**1**	**0**	**0**	**7**	**1**
Fatty acid & lipid metabolism										
Acyl carrier protein (ACP)										
Acyl carrier protein (ACP)	100% identity to Acyl carrier protein (ACP) [AcpP] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**2**	**0**	**0**	**0**	**10**	**0**	**0**	**0**
3-Hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)										
3-Hydroxyacyl-CoA dehydrogenase	49% identity to 3-hydroxyacyl-CoA dehydrogenas,NAD-binding [FadB] [*Stenotrophomonas maltophilia* (strain R551-3)]	Gammaproteobacteria (Xanthomonadales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Fatty oxidation complex										

Fatty oxidation complex, alpha subunit	100% identity to Fatty oxidation complex, alpha subunit [FadB] [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	**3**	**0**	**0**	**0**	**5**	**0**	**0**	**0**
Long chain fatty acid-coA ligase										
Long-chain-fatty-acid--CoA ligase	48% identity to Long-chain-fatty-acid--CoA ligase [FadD] [*Shewanella violacea* (strain JCM 10179 / CIP 106290 / LMG 19151 / DSS12)]	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**14**
3-Oxoacyl-[acyl-carrier-protein] synthase										
3-oxoacyl-[acyl-carrier-protein] synthase	100% identity to 3-oxoacyl-[acyl-carrier-protein] synthase [FabB] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**2**	**1**	**0**	**0**	**4**	**5**	**0**	**0**
Enoyl-[acyl-carrier-protein] reductase										
Enoyl-[acyl-carrier-protein] reductase	96% identity to Enoyl-[acyl-carrier-protein] reductase (NADH2) [FabI] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**4**	**3**	**0**	**0**	**5**	**6**
Acetyl-CoA C-acetyltransferase										
Acetyl-CoA C-acetyltransferase	100% identity to Acetyl-CoA C-acetyltransferase [AtoB] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**3**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Trans-hexaprenyltrantransferase (EC 2.5.1.30)										
Trans-hexaprenyltranstransferase	100% identity to Trans-hexaprenyltranstransferase [HepT] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**3**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10)										
Hydroxymethylglutaryl-CoA synthase	100% identity to Hydroxymethylglutaryl-CoA synthase [HmgS] [Nmar_0828] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**
Nucleotide metabolism										
Adenosylhomocysteinase (EC 3.3.1.1)										
Adenosylhomocysteinase	100% identity to Adenosylhomocysteinase [AhcY] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**2**	**2**	**0**	**0**	**2**	**5**	**0**	**0**

Adenosylhomocysteinase	100% identity to Adenosylhomocysteinase [AhcY] [*Saccharophagus degradans* 2-40]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Adenosylhomocysteinase	75% identity to Adenosylhomocysteinase [AhcY] [Rmag_0739] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**2**	**4**	**0**	**0**	**2**	**8**
Adenosylhomocysteinase	100% identity to Adenosylhomocysteinase [AhcY] [*Candidatus* Vesicomyosocius okutanii HA]	Gammaproteobacteria (GSO-EOSA-1)	**1**	**2**	**0**	**0**	**1**	**2**	**0**	**0**
Adenosylhomocysteinase	75% identity to Adenosylhomocysteinase [AhcY] [Rmag_0739] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**1**	**2**	**0**	**0**	**1**	**4**
Adenosylhomocysteinase	100% identity to Adenosylhomocysteinase [AhcY] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Adenosylhomocysteinase	100% identity to Adenosylhomocysteinase [AhcY] [*Erythrobacter* sp. SD-21]	Alphaproteobacteria (Sphingomonadales)	**2**	**1**	**0**	**0**	**2**	**4**	**0**	**0**
Adenosylhomocysteinase	86% identity to Adenosylhomocysteinase [AhcY] [Nmar_0964] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**10**	**0**	**0**	**0**	**42**
Adenosylhomocysteinase	89% identity to Adenosylhomocysteinase [AhcY] [Nmar_0964] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**14**
Adenylosuccinate synthetase (EC 6.3.4.4)										
Adenylosuccinate synthetase	100% to Adenylosuccinate synthetase [PurA] [Nmar_1420] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**2**	**0**	**2**	**0**	**7**	**0**	**10**
Adenylosuccinate lyase (EC 4.3.2.2)										
Adenylosuccinate lyase	100% identity to Adenylosuccinate lyase [PurB] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**2**	**0**	**0**	**0**	**5**	**0**	**0**
Adenylosuccinate lyase	100% identity to adenylosuccinate lyase [PurB] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**3**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Adenylosuccinate lyase	87% identity to Adenylosuccinate lyase [PurB] [Nmar_1455] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)										
Inosine-5'-monophosphate dehydrogenase	100% identity to Inosine-5'-monophosphate dehydrogenase [GuaB] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Inosine-5'-monophosphate dehydrogenase	81% identity to Inosine-5'-monophosphate dehydrogenase [GuaB] [Nmar_1569]	Marine Group I Crenarchaeota	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**5**

	[*Nitrosopumilus maritimus* (strain SCM1)]	(Nitrosopumilales)								
Myo-inositol-1-phosphate synthase (EC 5.5.1.4)										
Myo-inositol-1-phosphate synthase	85% identity to Myo-inositol-1-phosphate synthase [Ino1] [Nmar_0649] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**16**
Pseudouridylate synthase (EC 4.2.1.70)										
Pseudouridylate synthase	87% identity to Pseudouridylate synthase [TruB] [Nmar_0406] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**4**
Ribonucleoside-diphosphate reductase (EC 1.17.4.1)										
Ribonucleoside-diphosphate reductase	87% identity to Ribonucleoside-diphosphate reductase [Rnr] [Nmar_1627] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**8**	**0**	**0**	**0**	**24**
Nucleoside diphosphate kinase (EC 2.7.4.6)										
Nucleoside diphosphate kinase	82% identity to Nucleoside diphosphate kinase [NdK] [*Pseudomonas fluorescens* Pf-5]	Gammaproteobacteria (Pseudomonadales)	**0**	**0**	**2**	**0**	**0**	**0**	**5**	**0**
5-Nucleotidase (EC 3.1.3.5)										
5-Nucleotidase	62% identity to 5-Nucleotidase (5'-ribonucleotide phosphohydrolase) [UshA] [*Ruegeria pomeroyi*]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**10**
Alcohol & Aldehyde metabolism										
Acetaldehyde dehydrogenase (EC 1.2.1.3)										
Acetaldehyde dehydrogenase	93% identity to Acetaldehyde dehydrogenase II (ACDH-II) [AldA] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**5**	**6**	**0**	**0**	**24**	**54**
Lactaldehyde dehydrogenase (EC 1.2.1.22)										
Lactaldehyde dehydrogenase	97% identity to Lactaldehyde dehydrogenase [AldA] [*Escherichia coli* (strain K12)] (*likely contaminant*)	Gammaproteobacteria (Enterobacteriales)	**0**	**2**	**0**	**0**	**0**	**2**	**0**	**0**

Aldehyde dehydrogenase (EC 1.2.1.3)										
Aldehyde dehydrogenase	100% identity to Aldehyde dehydrogenase (NAD) [AldH] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**2**	**0**	**0**	**0**	**5**	**0**	**0**
Aldehyde dehydrogenase	100% identity to Aldehyde dehydrogenase [AldH] [Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**1**	**0**	**0**	**2**	**1**	**0**	**0**
Alcohol dehydrogenase (EC 1.1.1.1)										
Alcohol dehydrogenase	97% identity to Zinc-binding alcohol dehydrogenase [YhdH] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**6**	**0**	**0**	**1**	**13**
Short chain dehydrogenase										
Short chain dehydrogenase	79% identity to Short chain dehydrogenase [YdfG] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
Short-chain dehydrogenase/reductase SDR	80% identity to Short-chain dehydrogenase/reductase SDR [YdfG] [Nmar_1786] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Aromatic compound degradation										
Mandelate dehydrogenase (EC 1.1.99.31)										
L(+)-mandelate dehydrogenase	53% identity to L(+)-mandelate dehydrogenase [MdlB] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
Phenylhydantoinase (EC 3.5.2.-)										
Phenylhydantoinase	72% identity to Phenylhydantoinase [HyuA] [*Colwellia psychrerythraea* 34H]	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**
Lipopolysaccharide synthesis										
2-Dehydro-3-deoxyphosphooctonate aldolase (EC 2.5.1.55)										
2-Dehydro-3-deoxyphosphooctonate aldolase	89% identity to 2-Dehydro-3-deoxyphosphooctonate aldolase [KdsA] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**1**	**0**	**0**	**4**	**1**

Coenzyme & cofactor metabolism										
Delta-aminolevulinic acid dehydratase (EC 4.2.1.24)										
Delta-aminolevulinic acid dehydratase	72% identity to Delta-aminolevulinic acid dehydratase [HemB] [Rmag_0409] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Delta-aminolevulinic acid dehydratase	82% identity to Delta-aminolevulinic acid dehydratase [HemB] [Nmar_0509] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
2-Phospho-L-lactate transferase (EC 2.7.8.28)										
2-Phospho-L-lactate transferase	89% identity to 2-Phospho-L-lactate transferase (CofD) (LPPG domain containing protein) [Nmar_0626] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**9**	**0**	**0**	**0**	**57**
Precorrin-3B C17-methyltransferase (EC 2.1.1.131)										
Precorrin-3B C17-methyltransferase	79% identity to Precorrin-3B C17-methyltransferase (Cobalamin biosynthesis CbiG protein) [CbiG] [Nmar_0082] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**
Precorrin-2 C20-methyltransferase (EC 2.1.1.130)										
Precorrin-2 C20-methyltransferase	85% identity to Precorrin-2 C20-methyltransferase [CobI] [Nmar_0058] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**
Pyridoxal biosynthesis lyase										
Pyridoxal biosynthesis lyase	89% identity to Pyridoxal biosynthesis lyase PdxS (Vitamin B6 biosynthesis protein) [Nmar_1479] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**5**
Phosphomethylpyrimidine synthase (EC 4.-.-.-)										
Phosphomethylpyrimidine synthase	82% identity to Phosphomethylpyrimidine synthase / Thiamine biosynthesis protein ThiC [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**4**

Ribulose-1,5-biphosphate synthetase (EC 5.3.1.n2)										
Ribulose-1,5-biphosphate synthetase	83% identity to Ribulose-1,5-biphosphate synthetase [Nmar_0678] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**53**
Sorbosone dehydrogenase (EC:1.1.1.-)										
L-sorbosone dehydrogenase	90% identity to L-sorbosone dehydrogenase [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**15**
Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)										
Ribose-phosphate pyrophosphokinase	75% identity to Ribose-phosphate pyrophosphokinase [Prs] [Rmag_0109] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**5**
PHOSPHATE METABOLISM										
Phosphonoacetate hydrolase (EC 3.11.1.2)										
Phosphonoacetate hydrolase	62% identity to Phosphonoacetate hydrolase [PhnA] [*Alicycliphilus denitrificans* BC]	Betaproteobacteria (Burkholderiales)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
ENERGY CONSERVATION										
Proteorhodopsin										
Proteorhodopsin	73% identity to Bacteriorhodopsin [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**7**
Proteorhodopsin	76% identity to Bacteriorhodopsin [*Candidatus* Pelagibacter ubique 1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**2**	**0**	**0**	**10**	**9**
Proteorhodopsin	73% identity to Bacteriorhodopsin [gamma proteobacterium HTCC2207]	Gammaproteobacteria (OMG)	**0**	**0**	**2**	**2**	**0**	**0**	**10**	**3**
ATP synthase (EC 3.6.3.14)										
F_0F_1 ATP synthase, subunit alpha	100% identity to F_0F_1-type ATP synthase subunit alpha [AtpA] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**4**	**3**	**0**	**0**	**8**	**12**	**0**	**0**

F_0F_1 ATP synthase, subunit beta	100% identity to F_0F_1-type ATP synthase subunit beta [AtpD] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	12	11	0	0	75	62	0	0
F_0F_1 ATP synthase, subunit gamma	100% identity to F_0F_1-type ATP synthase subunit gamma [AtpG] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	2	2	0	0	2	7	0	0
F_0F_1 ATP synthase, subunit beta	100% identity to F_0F_1-type ATP synthase subunit beta [AtpD] [*Rhodobacter sphaeroides* (strain ATCC 17025 / ATH 2.4.3)]	Alphaproteobacteria (Rhodobacterales)	3	2	0	0	18	2	0	0
F_0F_1 ATP synthase, subunit alpha	100% identity to F_0F_1-type ATP synthase subunit alpha [AtpA] [*Loktanella vestfoldensis* SKA53]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	0	0	6	1	0	0	21	3
F_0F_1 ATP synthase, subunit alpha	92% identity to F_0F_1-type ATP synthase subunit alpha [AtpA] [*Loktanella vestfoldensis* SKA53]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	0	0	2	0	0	0	2	0
F_0F_1 ATP synthase, subunit alpha	100% identity to F_0F_1-type ATP synthase subunit alpha [AtpA] Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	0	0	2	0	0	0	2	0
F_0F_1 ATP synthase, subunit beta	100% identity to F_0F_1-type ATP synthase subunit beta [AtpD] [*Oceanibulbus indolifex* HEL-45]	Alphaproteobacteria (Rhodobacterales)	4	1	0	0	8	3	0	0
F_0F_1 ATP synthase, subunit beta	100% identity to F_0F_1-type ATP synthase subunit beta [AtpD] [*Sphingomonas wittichii* RW1]	Alphaproteobacteria (Sphingomonadales)	2	0	0	0	4	0	0	0
F_0F_1 ATP synthase, subunit alpha	100% identity F_0F_1-type to ATP synthase subunit alpha [AtpA] [*Pseudoalteromonas haloplanktis* TAC125]	Gammaproteobacteria (Alteromonadales)	4	0	0	0	13	0	0	0
F_0F_1 ATP synthase, subunit beta	100% identity to F_0F_1-type ATP synthase subunit beta [AtpD] [Alteromonadales bacterium TW-7	Gammaproteobacteria (Alteromonadales)	3	0	0	0	5	0	0	0
F_0F_1 ATP synthase, subunit alpha	100% identity to F_0F_1-type ATP synthase subunit alpha [AtpA] [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	2	0	0	0	2	0	0	0
F_0F_1 ATP synthase, subunit beta	100% identity to F_0F_1-type ATP synthase subunit beta [AtpD] [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	2	0	0	0	2	0	0	0
F_0F_1 ATP synthase, subunit beta	84% identity to F_0F_1-type ATP synthase subunit beta [AtpD] [*Neptuniibacter caesariensis*]	Gammaproteobacteria (Oceanospirillales)	0	0	21	11	0	0	68	27
F_0F_1 ATP synthase, subunit alpha	82% identity to F_0F_1-type ATP synthase subunit alpha [AtpA] [*Neptuniibacter caesariensis*]	Gammaproteobacteria (Oceanospirillales)	0	0	21	7	0	0	69	15
F_0F_1 ATP synthase, subunit gamma	68% identity to F_0F_1-type ATP synthase subunit gamma [AtpG] [*Neptuniibacter caesariensis*]	Gammaproteobacteria (Oceanospirillales)	0	0	4	1	0	0	9	4
F_0F_1 ATP synthase, subunit epsilon	74% identity to F_0F_1-type ATP synthase subunit epsilon [AtpC] [*Oceanospirillum* sp. MED92]	Gammaproteobacteria (Oceanospirillales)	0	0	2	0	0	0	4	0
F_0F_1 ATP synthase, subunit alpha	100% identity to F_0F_1-type ATP synthase subunit alpha [AtpA] [*Aeromonas hydrophila* subsp. *hydrophila* (strain ATCC 7966 / NCIB 9240)]	Gammaproteobacteria (Aeromonadales)	2	0	0	0	5	0	0	0
F_0F_1 ATP synthase, subunit alpha	100% identity to F_0F_1-type ATP synthase, subunit alpha [AtpA] [*Cellvibrio japonicus* Ueda107]	Gammaproteobacteria (Pseudomonadales)	3	1	0	0	5	1	0	0

F_0F_1 ATP synthase, subunit b (= subunit I)	59% identity to F_0F_1-type ATP synthase subunit b [AtpF] [*Pseudomonas putida* (strain KT2440)]	Gammaproteobacteria (Pseudomonadales)	**0**	**0**	**3**	**0**	**0**	**0**	**8**	**0**
F_0F_1 ATP synthase, subunit alpha	100% identity to F_0F_1-type ATP synthase subunit alpha [AtpA] [*Reinekea* sp. MED297]	Gammaproteobacteria (unclassified)	**2**	**0**	**0**	**0**	**6**	**0**	**0**	**0**
F_0F_1 ATP synthase, subunit alpha	82% identity to F_0F_1-type ATP synthase subunit alpha [AtpA] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**9**	**11**	**0**	**0**	**21**	**27**
F_0F_1 ATP synthase, subunit beta	83% identity to F_0F_1-type ATP synthase subunit beta [AtpD] [*Candidatus* Vesicomyosocius okutanii]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**6**	**10**	**0**	**0**	**21**	**19**
F_0F_1 ATP synthase, subunit gamma	72% identity to F_0F_1-type ATP synthase gamma chain [AtpG] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**3**
F_0F_1 ATP synthase, subunit alpha	100% identity to F_0F_1-type ATP synthase subunit alpha [AtpA] [gamma proteobacterium HTCC2207]	Gammaproteobacteria (OMG)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
F_0F_1 ATP synthase, subunit beta	96% identity to F_0F_1-type ATP synthase subunit beta [AtpD] [*Limnobacter* sp. MED105]	Betaproteobacteria (Burkholderiales)	**0**	**2**	**0**	**0**	**0**	**6**	**0**	**0**
V-type ATP synthase, subunit alpha	84% identity to V-type ATP synthase subunit alpha [AtpA] [Nmar_1691] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
V-type ATP synthase, subunit alpha	88% identity to V-type ATP synthase subunit alpha [AtpA] [Nmar_1691] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**9**	**0**	**0**	**0**	**32**
V-type ATP synthase, subunit alpha	88% identity to V-type ATP synthase subunit alpha [AtpA] [Nmar_1691] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**4**
V-type ATP synthase, subunit alpha	100% identity to V-type ATP synthase subunit alpha [AtpA] [Nmar_1691] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**13**
V-type ATP synthase, subunit beta	89% identity to V-type ATP synthase subunit beta [AtpB] [Nmar_1690] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**12**
V-type ATP synthase, subunit beta	93% identity to V-type ATP synthase subunit beta [AtpB] [Nmar_1690] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**9**	**0**	**0**	**0**	**25**
V-type ATP synthase, subunit C	78% identity to V-type ATP synthase subunit C [AtpC] [Nmar_1700] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**17**
V-type ATP synthase, subunit D	100% identity to V-type ATP synthase subunit D [Nmar_1689] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**2**	**0**	**0**	**0**	**3**	**0**	**0**
V-type ATP synthase, subunit I	72% identity to V-type ATP synthase, subunit I [AtpI] [Nmar_1693] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**8**	**0**	**0**	**0**	**31**
Pyrophosphatase (EC 3.6.1.1)										

Pyrophosphatase	100% identity to Membrane-bound proton-translocating pyrophosphatase [HppA] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**7**	**5**	**0**	**0**	**27**	**27**	**0**	**0**
Pyrophosphatase	100% identity to Membrane-bound proton-translocating pyrophosphatase [HppA] [*Nitrosococcus oceani* (strain ATCC 19707 / NCIMB 11848)]	Gammaproteobacteria (Chromatiales)	**2**	**2**	**1**	**2**	**4**	**8**	**6**	**6**
NAD(P) transhydrogenase (EC 1.6.1.1)										
NAD(P) transhydrogenase, alpha subunit	87% identity to NAD(P) transhydrogenase, alpha subunit [PntA] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
NAD(P) transhydrogenase, alpha subunit	96% identity to NAD(P) transhydrogenase, alpha subunit [PntA] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**2**	**0**	**0**	**0**	**5**	**0**	**0**	**0**
NAD(P) transhydrogenase, alpha subunit	71% identity to NAD(P) transhydrogenase, alpha subunit [PntA] [*Serratia proteamaculans* (strain 568)]	Gammaproteobacteria (Enterobacteriales)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
NADH dehydrogenase (quinone) (EC 1.6.99.5)										
NADH dehydrogenase (quinone)	88% identity to NADH dehydrogenase (Quinone) [NdhH] [Nmar_0279] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**5**
NADP reductase, ferredoxin-dependent (EC 1.18.1.2)										
NADP reductase, ferredoxin-dependent	85% identity to Oxidoreductase FAD/NAD(P)-binding domain protein [Nmar_0267] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**4**
NADP reductase, ferredoxin-dependent	85% identity to Oxidoreductase FAD/NAD(P)-binding domain protein [Nmar_0253] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
NADP reductase, ferredoxin-dependent	85% identity to Oxidoreductase FAD/NAD(P)-binding domain protein [Nmar_0253] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**10**
NADP reductase, F420-dependent (EC 1.6.99.-)										
NADP reductase, F420-dependent	89% identity to NADP oxidoreductase coenzyme F420-dependent [Nmar_0180] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Cytochrome c oxidase (EC 1.9.3.1)										

Cytochrome c oxidase subunit II	86% identity to Cytochrome c oxidase polypeptide II (Cytochrome aa3 subunit 2) (CoxB/CtaC) [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
Cytochrome c oxidase subunit II	63% identity to Cytochrome c oxidase subunit II [CoxB/CtaC] [Rmag_0034] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**
Electron transfer flavoprotein										
Electron transfer flavoprotein, alpha and beta subunits	47% identity to Electron transfer flavoprotein, alpha subunit [EftA] [*Oceanicaulis alexandrii* HTCC2633]	Alphaproteobacteria (Rhodobacterales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**6**
Electron transfer flavoprotein, beta subunit	66% identity to Electron transfer flavoprotein beta-subunit [EFtB] [alpha proteobacterium BAL199]	Alphaproteobacteria (unclassified)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**
Electron transfer flavoprotein, beta subunit	100% identity to Electron transfer flavoprotein, beta subunit [EftB] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**5**	**0**	**0**	**0**	**6**	**0**	**0**	**0**
Electron transfer flavoprotein, beta subunit	100% identity to Electron transfer flavoprotein, beta subunit [EftB] [*Roseobacter* sp. MED193]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Ferredoxin										
Ferredoxin	80% identity to 4Fe-4S ferredoxin iron-sulfur binding domain protein [Nmar_0443] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**
Ferredoxin	84% identity to 4Fe-4S ferredoxin iron-sulfur binding domain protein [Nmar_0238] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Ferredoxin	100% identity to 4Fe-4S ferredoxin iron-sulfur binding domain protein [Nmar_1537] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Multicopper oxidase										
Multicopper oxidase	87% identity to Multicopper oxidase NirK-like [Nmar_1667] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**31**
Multicopper oxidase	34% identity to Multicopper oxidase type 3 [*Ruminococcus* sp. 5_1_39BFAA]	Firmicutes (Clostridia)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**9**
Blue (Type 1) copper domain protein										

Blue (Type 1) copper domain protein	72% identity to Blue (Type 1) copper domain protein [Nmar_0185] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**5**
Plastocyanin-family protein										
Plastocyanin-family protein	63% identity to Putative copper-binding protein / plastocyanin/azurin family protein [Nmar_0343] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**9**
OXIDATIVE STRESS										
Alkyl hydroperoxide reductase (peroxiredoxin) (EC 1.11.1.15)										
Alkyl hydroperoxide reductase	80% identity to Putative alkyl hydroperoxide reductase [*Pseudomonas fluorescens* (strain SBW25)]	Gammaproteobacteria (Pseudomonadales)	**0**	**0**	**5**	**0**	**0**	**0**	**13**	**0**
Peroxiredoxin	100% identity to Peroxiredoxin [PrdX] [*Psychroflexus torquis* ATCC 700755]	Bacteroidetes (Flavobacteria)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**5**
Thioredoxin										
Thioredoxin	99% identity to Thioredoxin [TrxA] [*Shigella flexneri*]	Gammaproteobacteria (Enterobacteriales)	**0**	**3**	**0**	**0**	**0**	**24**	**0**	**0**
Thioredoxin	67% identity to Thioredoxin [TrxA] [*Neisseria meningitidis* serogroup B]	Betaproteobacteria (Neisseriales)	**0**	**0**	**2**	**0**	**0**	**0**	**7**	**0**
Glutathione S-transferase (EC 2.5.1.18)										
Glutathione S-transferase	100% identity to Glutathione S-transferase-like protein [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**3**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
REPLICATION & DNA-BINDING PROTEINS										
DNA gyrase (EC 5.99.1.3)										
DNA gyrase, subunit A	100% identity to DNA gyrase subunit A [GyrA] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
DNA gyrase, subunit A	89% identity to DNA gyrase subunit A [GyrA] [*Candidatus* Pelagibacter ubique]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**

DNA gyrase, subunit A	64% identity to DNA gyrase subunit A [GyrA] [*Hahella chejuensis* KCTC 2396]	Gammaproteobacteria (Oceanospirillales)	0	0	2	0	0	0	3	0
DNA gyrase, subunit A	80% identity to DNA gyrase subunit A [GyrA] [Rmag_0306] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	0	0	1	5	0	0	1	10
DNA gyrase, subunit B	68% identity to DNA gyrase subunit B [GyrB] [Rmag_0003] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	0	0	2	10	0	0	2	28
DNA topoisomerase (EC 5.99.1.2 / EC 5.99.1.3)										
DNA topoisomerase I	68% identity to DNA topoisomerase I [TopA] [Rmag_1034] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	0	0	0	7	0	0	0	16
DNA topoisomerase VI, A subunit	100% identity to DNA topoisomerase VI, A subunit [Top6A] [Nmar_1407] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	2	0	0	0	5
DNA topoisomerase VI, B subunit	100% identity to DNA topoisomerase VI, B subunit [Top6B] [Nmar_1408] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	5	0	0	0	13	0	0
MCM family protein (replication control)										
MCM family protein	87% identity to MCM family protein [Nmar_0242] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	4	0	0	0	9
DNA polymerase sliding clamp										
DNA polymerase sliding clamp	87% identity to DNA polymerase sliding clamp (Proliferating cell nuclear antigen homolog) [PcnA] [Nmar_1755] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	3	0	0	0	16
FtsZ cell division protein										
FtsZ cell division protein	87% identity to Cell division protein FtsZ [*Candidatus* Pelagibacter ubique HTT1062]	Alphaproteobacteria (SAR11 cluster)	1	2	0	0	1	4	0	0
Recombinase A										
Recombinase A	100% identity to Recombinase A [RecA] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	2	2	0	0	3	2	0	0
Recombinase A	100% identity to Recombinase A [RecA] [*Novosphingobium aromaticivorans* (strain DSM 12444)]	Alphaproteobacteria (Sphingomonadales)	2	0	0	0	2	0	0	0

Recombinase A	76% identity to Recombinase A [RecA] [*Thiomicrospira crunogena* (strain XCL-2)]	Gammaproteobacteria (Thiotrichales)	**0**	**0**	**1**	**5**	**0**	**0**	**1**	**10**
Excinuclease										
Excinuclease ABC chain A	100% identity to Excinuclease ABC chain A [UvrA] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**3**	**2**	**0**	**0**	**7**	**3**	**0**	**0**
Excinuclease ABC subunit A	100% identity to Excinuclease ABC subunit A [UvrA] [*Haemophilus somnus* 129PT] (*likely contaminant*)	Gammaproteobacteria (Pasteurellales)	**2**	**2**	**0**	**0**	**3**	**4**	**0**	**0**
Cold shock proteins										
CspL protein (RNA-binding)	100% identity to Cold shock domain protein [CspL] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**2**	**1**	**0**	**0**	**6**	**1**	**0**	**0**
Cold shock protein CspC	100% identity to Cold shock protein, transcription antiterminator [CspC] [*Pseudoalteromonas haloplanktis* TAC125]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Cold shock protein	93% identity to Cold-shock family protein [*Pseudoalteromonas atlantica* (strain T6c / BAA-1087)]	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**2**	**1**	**0**	**0**	**15**	**1**
Cold shock protein	100% identity to Cold-shock family protein [*Colwellia psychrerythraea* 34H]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**5**	**0**	**0**	**0**
Cold shock protein	100% identity to Cold shock family protein [Alteromonadales bacterium TW-7]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Cold shock protein	79% identity to Cold-shock family protein [*Thiomicrospira crunogena* (strain XCL-2)]	Gammaproteobacteria (Thiotrichales)	**0**	**0**	**4**	**1**	**0**	**0**	**21**	**1**
Cold shock protein	77% identity to Cold-shock family protein [uncultured SUP05 cluster bacterium]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
DNA-binding protein HU										
DNA-binding protein HU	100% identity to DNA-binding protein HU [Hup] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**3**	**2**	**0**	**0**	**9**	**4**	**0**	**0**
DNA-binding protein HU	93% identity to DNA-binding protein HU, form N [Hup] [Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**
DNA-binding protein HU	100% identity to DNA-binding protein HU [Hup] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**5**	**0**	**0**	**0**	**9**	**0**	**0**	**0**
DNA-binding protein HU	80% identity to DNA-binding protein HU [Hup] [*Colwellia psychrerythraea* 34H]	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**5**	**0**	**0**	**0**	**16**	**0**

DNA-binding protein HU	81% identity to DNA-binding protein HU [Hup] [marine gamma proteobacterium HTCC2143]	Gammaproteobacteria (OMG)	**0**	**0**	**6**	**0**	**0**	**0**	**12**	**0**
DNA-binding protein HU	86% identity to DNA-binding protein HU [Hup] [Rmag_0380] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**5**	**4**	**0**	**0**	**14**	**24**
DNA-binding protein HU	83% identity to DNA-binding protein HU [Hup] [uncultured SUP05 cluster bacterium]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
DNA-binding protein HU	100% identity to DNA-binding protein HU [Hup] [Flavobacteria bacterium MS024-2A],	Bacteroidetes (Flavobacteria)	**0**	**0**	**2**	**0**	**0**	**0**	**4**	**0**
DNA-binding protein HU	100% identity to DNA-binding protein HU [Hup] [Flavobacteria bacterium MS024-2A]	Bacteroidetes (Flavobacteria)	**4**	**0**	**0**	**0**	**6**	**0**	**0**	**0**
DNA-binding protein HU	81% identity to DNA-binding protein HU [Hup] [*Polaribacter irgensii* 23-P]	Bacteroidetes (Flavobacteria)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
DNA-binding protein HU	97% identity to DNA-binding protein HU [Hup] [*Polaribacter irgensii* 23-P]	Bacteroidetes (Flavobacteria)	**0**	**0**	**4**	**0**	**0**	**0**	**8**	**0**
TRANSCRIPTION & RNA-BINDING PROTEINS										
Transcription initiation factor TFIIB										
Transcription initiation factor TFIIB	73% identity to Transcription factor TFIIB cyclin-related [Nmar_0020] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**15**
Transcription initiation factor TFIIB	66% identity to Transcription factor TFIIB cyclin-related [Nmar_0979] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**5**
Transcription termination factor Rho (EC 3.6.4.-)										
Transcription termination factor Rho	100% identity to Transcription termination factor Rho [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**8**	**10**	**0**	**0**	**29**	**54**	**0**	**0**
Transcription termination factor Rho	100% identity to Transcription termination factor Rho [*Oceanibulbus indolifex* HEL-45]	Alphaproteobacteria (Rhodobacterales)	**2**	**1**	**0**	**0**	**2**	**3**	**0**	**0**
Transcription termination factor Rho	83% identity to Transcription termination factor Rho [Rmag_0477] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**1**	**4**	**0**	**0**	**1**	**6**
DNA-directed RNA polymerase (RNAP) (EC 2.7.7.6)										
DNA-directed RNA polymerase, alpha subunit	100% identity to DNA-directed RNA polymerase, alpha subunit [RpoA] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**9**	**6**	**0**	**0**	**24**	**23**

DNA-directed RNA polymerase, beta subunit	100% identity to DNA-directed RNA polymerase, beta subunit [RpoB] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	11	12	0	0	33	28	0	0
DNA-directed RNA polymerase, beta subunit	100% identity to DNA-directed RNA polymerase, beta subunit [RpoB] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	12	8	0	0	34	28	0	0
DNA-directed RNA polymerase, sigma factor	100% identity to DNA-directed RNA polymerase, sigma factor RpoD [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	0	2	0	0	0	5	0	0
DNA-directed RNA polymerase, beta subunit	94% identity to DNA-directed RNA polymerase, beta subunit [RpoB] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	0	0	3	1	0	0	4	1
DNA-directed RNA polymerase, omega subunit	77% identity to DNA-directed RNA polymerase, omega subunit [RpoZ] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	0	0	2	1	0	0	2	1
DNA-directed RNA polymerase,, alpha subunit	100% identity to DNA-directed RNA polymerase, alpha subunit [RpoA] [*Roseobacter* sp. SK209-2-6]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	5	2	0	0	11	2	0	0
DNA-directed RNA polymerase,alpha subunit	100% identity to DNA-directed RNA polymerase, alpha subunit [RpoA] [*Loktanella vestfoldensis* SKA53]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	2	0	0	0	4	0	0	0
DNA-directed RNA polymerase, beta subunit	100% identity to DNA-directed RNA polymerase, beta subunit [RpoB] [Rhodobacterales bacterium Y4I]	Alphaproteobacteria (Rhodobacterales)	4	1	0	0	7	1	0	0
DNA-directed RNA polymerase, beta' subunit	100% identity to DNA-directed RNA polymerase, beta' subunit [RpoC] [*Roseobacter denitrificans* OCh 114]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	2	1	0	0	5	2	0	0
DNA-directed RNA polymerase, beta' subunit	100% identity to DNA-directed RNA polymerase, beta' subunit [RpoC] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	5	0	0	0	12	0	0	0
DNA-directed RNA polymerase, beta subunit	100% identity to DNA-directed RNA polymerase, beta subunit [RpoB] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	5	0	0	0	6	0	0	0
DNA-directed RNA polymerase, alpha subunit	100% identity to DNA-directed RNA polymerase, alpha subunit [RpoA] [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	3	0	0	0	3	0	0	0
DNA-directed RNA polymerase, beta subunit	100% identity to DNA-directed DNA-directed RNA polymerase, beta subunit [RpoB] [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	2	0	0	0	2	0	0	0
DNA-directed RNA polymerase, beta' subunit	100% identity to DNA-directed RNA polymerase, beta' subunit [RpoC] [*Pseudoalteromonas haloplanktis* TAC125]	Gammaproteobacteria (Alteromonadales)	2	0	0	0	2	0	0	0
DNA-directed RNA polymerase, beta subunit	79% identity to DNA-directed RNA polymerase, beta subunit [RpoB] [*Neptuniibacter caesariensis*]	Gammaproteobacteria (Oceanospirillales)	0	0	22	4	0	0	55	7
DNA-directed RNA polymerase, alpha subunit	76% identity to DNA-directed RNA polymerase, alpha subunit [RpoA] [*Marinomonas* sp. (strain MWYL1)]	Gammaproteobacteria (Oceanospirillales)	0	0	12	2	0	0	27	6

DNA-directed RNA polymerase, alpha subunit	70% identity to DNA-directed RNA polymerase, alpha subunit [RpoA] (*Pseudomonas fluorescens* subsp. *cellulosa*)]	Gammaproteobacteria (Oceanospirillales)	0	0	3	2	0	0	5	2
DNA-directed RNA polymerase, beta' subunit	78% identity to DNA-directed RNA polymerase, beta' subunit [RpoC] [*Neptuniibacter caesariensis*]	Gammaproteobacteria (Oceanospirillales)	0	0	4	1	0	0	6	1
DNA-directed RNA polymerase, beta subunit	100% identity to DNA-directed RNA polymerase, beta subunit [RpoB] [*Hahella chejuensis* KCTC 2396],	Gammaproteobacteria (Oceanospirillales)	2	0	0	0	5	0	0	0
DNA-directed RNA polymerase, beta subunit	69% identity to DNA-directed RNA polymerase, beta subunit [RpoB] [*Marinomonas* sp. MED121]	Gammaproteobacteria (Oceanospirillales)	0	0	3	0	0	0	5	0
DNA-directed RNA polymerase, beta' subunit	100% identity to DNA-directed RNA polymerase, beta' subunit [RpoC] [*Pseudomonas mendocina* ymp]	Gammaproteobacteria (Pseudomonadales)	2	1	0	0	7	2	0	0
DNA-directed RNA polymerase, beta subunit	100% identity to DNA-directed RNA polymerase, beta subunit [RpoB] [*Candidatus* Ruthia magnifica]]	Gammaproteobacteria (GSO-EOSA-1)	0	0	4	11	0	0	16	36
DNA-directed RNA polymerase, alpha subunit	77% identity to DNA-directed RNA polymerase, alpha subunit [RpoA] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	0	0	3	3	0	0	3	7
DNA-directed RNA polymerase, sigma factor	53% identity to RNA polymerase sigma factor [RpoD] [Rmag_0108] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	0	0	0	2	0	0	0	3
DNA-directed RNA polymerase, beta subunit	83% identity to DNA-directed RNA polymerase, beta subunit [RpoB] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	0	0	1	2	0	0	1	2
DNA-directed RNA polymerase, beta' subunit	79% identity to DNA-directed RNA polymerase, beta' subunit [RpoC] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	0	0	1	8	0	0	1	14
DNA-directed RNA polymerase, alpha subunit	100% identity to DNA-directed RNA polymerase, alpha subunit [RpoA] [*Polaribacter* sp. MED152]	Bacteroidetes (Flavobacteria)	2	0	0	0	2	0	0	0
DNA-directed RNA polymerase, subunit A'	88% identity to DNA-directed RNA polymerase, subunit A' [Nmar_0348] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	5	0	0	0	15
DNA-directed RNA polymerase, subunit A'	100% identity to DNA-directed RNA polymerase, subunit A' [Nmar_0348] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	8	0	0	0	20	0	0
DNA-directed RNA polymerase, subunit beta	100% identity to DNA-directed RNA polymerase, subunit beta [Nmar_0347] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	9	0	0	0	40	0	0
DNA-directed RNA polymerase, subunit beta	93% identity to DNA-directed RNA polymerase, subunit beta [Nmar_0347] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	2	0	0	0	10
DNA-directed RNA polymerase, subunit beta'	88% identity to DNA-directed RNA polymerase, subunit beta' [Nmar_0348] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	2	0	0	0	8

DNA primase (EC 2.7.7.-)										
DNA primase	100% identity to Toprim sub domain protein [Nmar_1302] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**3**	**0**	**0**	**0**	**6**	**0**	**0**
Antitermination factor NusA										
Antitermination factor NusA	100% identity to Antitermination factor NusA [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**5**	**7**	**0**	**0**	**7**	**15**	**0**	**0**
Antitermination factor NusA	74% identity to Antitermination factor NusA [Rmag_0053] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**14**
Transcriptional regulators										
Transcriptional regulator, CarD	100% identity to Putative uncharacterized protein CarD [*Candidatus* Pelagibacter ubique HTTC1002]	Alphaproteobacteria (SAR11 cluster)	**2**	**1**	**0**	**0**	**4**	**1**	**0**	**0**
Transcriptional regulatory, AtoC	70% identity to C4-dicarboxylate transport transcriptional regulatory protein [*Roseovarius* sp. HTCC2601]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**1**	**3**	**0**	**0**	**1**	**5**
Transcriptional regulator, LacI	90% identity to Transcriptional regulator, LacI [uncultured marine microorganism HF4000_009A22]	Bacteria? (unclassified)	**0**	**0**	**2**	**1**	**0**	**0**	**5**	**3**
Transcriptional regulator, LacI	81% identity to Transcriptional regulator, LacI [uncultured marine microorganism HF4000_009A22]	Bacteria? (unclassified)	**0**	**0**	**7**	**7**	**0**	**0**	**17**	**28**
Transcriptional regulator, LacI	59% identity to Transcriptional regulator, LacI [uncultured marine microorganism HF4000_APKG2K17]	Bacteria? (unclassified)	**0**	**0**	**6**	**8**	**0**	**0**	**10**	**26**
Transcriptional regulator, LacI	65% identity to Transcriptional regulator, LacI [uncultured marine microorganism HF4000_APKG2K17]	Bacteria? (unclassified)	**0**	**0**	**5**	**6**	**0**	**0**	**9**	**11**
Transcriptional regulator, LysR	65% identity to Transcriptional regulator, LysR [uncultured marine bacterium HF10_25F10]	Bacteria? (unclassified)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**6**
Transcriptional regulator, ArsR	100% identity to ArsR family transcriptional regulator [*Methanococcoides burtonii* DSM 6242]	Euryarchaeota (Methanosarcinales)	**2**	**0**	**0**	**0**	**9**	**0**	**0**	**0**
Transcriptional regulator, ArsR	80% identity to ArsR family transcriptional regulator [Nmar_1628] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**11**
Transcriptional regulator, MerR	74% identity to MerR family transcriptional regulator [Nmar_0978] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**6**

Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8)										
Polyribonucleotide nucleotidyltransferase	100% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**6**	**9**	**0**	**0**	**16**	**18**	**0**	**0**
Polyribonucleotide nucleotidyltransferase	94% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**5**	**4**	**0**	**0**	**10**	**14**
Polyribonucleotide nucleotidyltransferase	91% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Polyribonucleotide nucleotidyltransferase	87% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [*Candidatus* Pelagibacter ubique]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**2**	**0**	**0**	**5**	**7**
Polyribonucleotide nucleotidyltransferase	100% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [*Octadecabacter antarcticus* 307]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**2**	**0**	**0**	**8**	**2**	**0**	**0**
Polyribonucleotide nucleotidyltransferase	100% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Polyribonucleotide nucleotidyltransferase	100% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [*Pseudoalteromonas haloplanktis* TAC125]	Gammaproteobacteria (Alteromonadales)	**7**	**1**	**0**	**0**	**11**	**1**	**0**	**0**
Polyribonucleotide nucleotidyltransferase	100% identity to Polyribonucleotide nucleotidyltransferase [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	**3**	**0**	**0**	**0**	**4**	**0**	**0**	**0**
Polyribonucleotide nucleotidyltransferase	70% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [*Chromohalobacter salexigens* (strain DSM 3043 / ATCC BAA-138 / NCIMB 13768)]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**1**	**2**	**0**	**0**	**1**	**3**
Polyribonucleotide nucleotidyltransferase	68% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [*Neptuniibacter caesariensis*]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**2**	**2**	**0**	**0**	**5**	**5**
Polyribonucleotide nucleotidyltransferase	90% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [*Marinomonas* sp. MED121]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
Polyribonucleotide nucleotidyltransferase	76% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [*Pseudomonas aeruginosa*]	Gammaproteobacteria (Pseudomonadales)	**0**	**0**	**9**	**4**	**0**	**0**	**39**	**25**
Polyribonucleotide nucleotidyltransferase	71% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [uncultured gamma proteobacterium HF0070_08D07]	Gammaproteobacteria (unclassified)	**0**	**0**	**2**	**1**	**0**	**0**	**4**	**5**
Polyribonucleotide nucleotidyltransferase	56% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [uncultured gamma proteobacterium HF0010_01E20]	Gammaproteobacteria (unclassified)	**0**	**0**	**6**	**0**	**0**	**0**	**7**	**0**

Polyribonucleotide nucleotidyltransferase	76% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**2**	**7**	**0**	**0**	**3**	**35**
Polyribonucleotide nucleotidyltransferase	63% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**1**	**8**	**0**	**0**	**1**	**38**
Polyribonucleotide nucleotidyltransferase	54% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**7**
Polyribonucleotide nucleotidyltransferase	92% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [marine gamma proteobacterium HTCC2207]	Gammaproteobacteria (OMG)	**0**	**0**	**2**	**1**	**0**	**0**	**5**	**2**
Polyribonucleotide nucleotidyltransferase	76% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [marine gamma proteobacterium HTCC2143]	Gammaproteobacteria (OMG)	**0**	**0**	**2**	**0**	**0**	**0**	**8**	**0**
Polyribonucleotide nucleotidyltransferase	67% identity to Polyribonucleotide nucleotidyltransferase [Pnp] [*Candidatus* Nitrospira defluvii]	Nitrospirae	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**12**
Exosome complex										
Exosome complex exoribonuclease Rrp42	84% identity to Exosome complex RNA-binding protein Rrp42 [3' exoribonuclease] [Nmar_0433] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**14**	**0**	**0**	**0**	**50**
Exosome complex exoribonuclease Rrp42	84% identity to Exosome complex RNA-binding protein Rrp42 [3' exoribonuclease] [Nmar_0433] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**12**
Exosome complex exoribonuclease Rrp42	77% identity to Exosome complex RNA-binding protein Rrp42 [3' exoribonuclease] [Nmar_0433] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**9**
Exosome complex exoribonuclease Rrp41	72% identity to Exosome complex exonuclease Rrp41 [Exosome complex exonuclease 1] [Nmar_0432] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**12**
Exosome complex exoribonuclease Rrp41	100% identity to Exosome complex exonuclease Rrp41 [Exosome complex exonuclease 1] [Nmar_0432] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Exosome complex exoribonuclease Rrp41	77% identity to Exosome complex exonuclease Rrp41 [Exosome complex exonuclease 1] [Nmar_0432] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**5**
Exosome complex RNA-binding protein Rrp4	81% identity to Exosome complex RNA-binding protein Rrp4 [*Nitrosopumilus maritimus* SCM1] [KH type 1 domain protein] [Nmar_0431] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**

RNA helicase, ATP-dependent (EC 2.3.1.129)										
RNA helicase, ATP-dependent	94% identity to Probable ATP-dependent RNA helicase [RhlE] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**2**	**0**	**0**	**1**	**2**
DEAD/DEAH box RNA helicase										
ATP-dependent RNA helicase DeaD	58% identity to ATP-dependent RNA helicase DeaD] [*Cellvibrio japonicus* (strain Ueda107)]	Gammaproteobacteria (Pseudomonadales)	**0**	**0**	**7**	**0**	**0**	**0**	**14**	**0**
DEAD/DEAH box helicase domain-containing protein	67% identity to DEAD/DEAH box helicase domain protein [Rmag_0942] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
DEAD/DEAH box helicase domain-containing protein	86% identity to DEAD/DEAH box helicase domain protein [Nmar_1182] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**24**
Nucleic acid OB-fold proteins										
Nucleic acid binding OB-fold tRNA/helicase	78% identity to nucleic acid binding OB-fold tRNA/helicase-type [Nmar_0089] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Nucleic acid binding OB-fold	74% identity to Putative uncharacterized protein with OB fold [Nmar_0505] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Ribonucleases (other)										
RNase E/G	91% identity to Ribonuclease E/G [Rne] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**2**	**2**	**0**	**0**	**4**	**3**	**0**	**0**
RNase E	100% identity to Ribonuclease E [Rne] [*Saccharophagus degradans* 2-40]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**8**	**0**	**0**	**0**
RNase	87% identity to RNase, metallo-beta-lactamase superfamily [Nmar_1727] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**5**
TRANSLATION & PROTEIN CHAPERONES										
Ribosomal subunits										
Ribosomal protein S1	100% identity to 30S ribosomal protein S1 [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**7**	**8**	**0**	**0**	**18**	**16**	**0**	**0**
Ribosomal protein S2	100% identity to 30S ribosomal protein [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**3**	**3**	**0**	**0**	**3**	**4**	**0**	**0**

Ribosomal protein L3	82% identity to 50S ribosomal protein L3 [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**4**	**2**	**0**	**0**	**6**	**2**
Ribosomal protein S4	95% identity to 30S ribosomal protein S4 [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**4**	**5**	**0**	**0**	**11**	**10**
Ribosomal protein S7	98% identity to 30S ribosomal protein S7 [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**1**	**0**	**0**	**5**	**1**
Ribosomal protein S8	88% identity to 30S ribosomal protein S8 [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**5**	**0**	**0**	**0**	**10**	**0**
Ribosomal protein S10	97% identity to 30S ribosomal protein S10 [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**1**	**0**	**2**	**0**	**1**	**0**	**6**	**0**
Ribosomal protein S12	94% identity to 30S ribosomal protein S12 [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**1**	**0**	**0**	**7**	**1**
Ribosomal protein S16	92% identity to 30S ribosomal protein S16 [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**4**	**0**	**0**	**9**	**17**
Ribosomal protein L1	91% identity to 50S ribosomal protein L1 [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**7**	**1**	**0**	**0**	**8**	**2**
Ribosomal protein L2	91% identity to 50S ribosomal protein L2 [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**2**	**0**	**0**	**4**	**3**
Ribosomal protein L4	85% identity to 50S ribosomal protein L4 [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**2**	**0**	**0**	**7**	**2**
Ribosomal protein L6	100% identity to 50S ribosomal protein L6 [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**2**	**0**	**0**	**0**	**6**	**0**	**0**	**0**
Ribosomal protein L7/L12	89% identity to 50S ribosomal protein L7/L12 [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**
Ribosomal protein L25	90% identity to 50S ribosomal protein L25 (General stress protein CTC) [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**3**	**0**	**0**	**1**	**7**
Ribosomal protein S1	92% identity to 30S ribosomal protein S1 [*Roseobacter* sp. MED193]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
Ribosomal protein S7	100% identity to 30S ribosomal protein S7 [*Roseobacter denitrificans* OCh 114]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Ribosomal protein S11	100% identity to 30S ribosomal protein S11 [*Roseobacter* sp. CCS2]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**3**	**0**	**0**	**0**	**7**	**0**	**0**	**0**
Ribosomal protein L7/L12	100% identity to 50S ribosomal protein L7/L12 [*Roseovarius nubinhibens* ISM]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**
Ribosomal protein L7/L12	100% identity to 50S ribosomal protein L7/L12 [*Roseovarius nubinhibens* ISM]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**3**	**1**	**0**	**0**	**9**	**1**	**0**	**0**
Ribosomal protein S10	100% identity to 30S ribosomal protein S10 [*Ruegeria pomeroyi* DSS-3]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**0**	**2**	**0**	**11**	**0**	**9**	**0**

Ribosomal protein L14	100% identity to 50S ribosomal protein L14 [*Paracoccus denitrificans* PD1222]	Alphaproteobacteria (Rhodobacterales)	**2**	**0**	**0**	**0**	**4**	**0**	**0**	**0**
Ribosomal protein L22	100% identity to 50S ribosomal protein L22 [*Octadecabacter antarcticus* 307]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**0**	**0**	**0**	**4**	**0**	**0**	**0**
Ribosomal protein S1	100% identity to 30S ribosomal protein S1 [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**3**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Ribosomal protein S2	100% identity to 30S ribosomal protein S2 [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	**3**	**0**	**0**	**0**	**9**	**0**	**0**	**0**
Ribosomal protein S3	100% identity to 30S ribosomal protein S3 [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Ribosomal protein S4	100% identity to 30S ribosomal protein S4 [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	**5**	**0**	**0**	**0**	**9**	**0**	**0**	**0**
Ribosomal protein S7	100% identity to 30S ribosomal protein S7 [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**7**	**0**	**0**	**0**
Ribosomal protein S8	100% identity to 30S ribosomal protein S8 [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	**3**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Ribosomal protein S11	100% identity to 30S ribosomal protein S11 [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	**3**	**0**	**0**	**0**	**4**	**0**	**0**	**0**
Ribosomal protein S16	100% identity to 30S ribosomal protein S16 [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Ribosomal protein L9	100% identity to 50S ribosomal protein L9 [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**8**	**0**	**0**	**0**
Ribosomal protein L2	100% identity to 50S ribosomal protein L2 [*Pseudoalteromonas haloplanktis* TAC125]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Ribosomal protein L4	100% identity to 50S ribosomal protein L4 [*Pseudoalteromonas haloplanktis* TAC125]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**4**	**0**	**0**	**0**
Ribosomal protein L1	100% identity to 50S ribosomal protein L1 [*Psychromonas ingrahamii* 37]	Gammaproteobacteria (Alteromonadales)	**3**	**0**	**0**	**0**	**10**	**0**	**0**	**0**
Ribosomal protein S9	82% identity to 30S ribosomal protein S9 [*Glaciecola* sp. HTCC2999]	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**4**	**0**	**0**	**0**	**12**	**0**
Ribosomal protein S1	100% identity to 30S ribosomal protein S1 [Alteromonadales bacterium TW-7]	Gammaproteobacteria (Alteromonadales)	**7**	**0**	**0**	**0**	**7**	**0**	**0**	**0**
Ribososomal protein L24	100% identity to 50S ribosomal protein S3 [Alteromonadales bacterium TW-7]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Ribosomal protein S5	100% identity to 30S ribosomal protein S5 [Alteromonadales bacterium TW-7]	Gammaproteobacteria (Alteromonadales)	**4**	**0**	**0**	**0**	**8**	**0**	**0**	**0**
Ribososomal protein S8	100% identity to 30S ribosomal protein S8 [Alteromonadales bacterium TW-7]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Ribosomal protein L1	100% identity to 50S ribosomal protein L1 [Alteromonadales bacterium TW-7]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Ribosomal protein L3	100% identity to 50S ribosomal protein L3 [Alteromonadales bacterium TW-7]	Gammaproteobacteria (Alteromonadales)	**3**	**0**	**0**	**0**	**11**	**0**	**0**	**0**

Ribososomal protein L15	100% identity to 50S ribosomal protein L15 [Alteromonadales bacterium TW-7]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**5**	**0**	**0**	**0**
Ribososomal protein L7/L12	100% identity to 50S ribosomal protein L7/L12 [Alteromonadales bacterium TW-7]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Ribosomal protein L9	100% identity to 50S ribosomal protein L9 [Alteromonadales bacterium TW-7]	Gammaproteobacteria (Alteromonadales)	**3**	**0**	**0**	**0**	**11**	**0**	**0**	**0**
Ribososomal protein L14	100% identity to 50S ribosomal protein L14 [Alteromonadales bacterium TW-7]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Ribososomal protein L24	100% identity to 50S ribosomal protein L24 [Alteromonadales bacterium TW-7]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Ribosomal protein L16	100% identity to 50S ribosomal protein L16 [*Teredinibacter turnerae* T7901]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Ribosomal protein L1	78% identity to 50S ribosomal protein L1 [*Thioalkalivibrio* sp. HL-EbGR7]	Gammaproteobacteria (Chromatiales)	**0**	**0**	**8**	**2**	**0**	**0**	**29**	**5**
Ribosomal protein S1	79% identity to 30S ribosomal protein S1 [*Oceanospirillum* sp. MED92]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**8**	**0**	**0**	**0**	**21**	**0**
Ribosomal protein S1	73% identity to 30S ribosomal protein S1 [*Oceanospirillum* sp. MED92]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**3**	**0**	**0**	**0**	**3**	**0**
Ribosomal protein S2	77% identity to 30S ribosomal protein S2 [*Oceanospirillum* sp. MED92]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**6**	**1**	**0**	**0**	**16**	**7**
Ribosomal protein S3	85% identity to 30S ribosomal protein S3 [*Oceanospirillum* sp. MED92]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**4**	**3**	**0**	**0**	**16**	**4**
Ribosomal protein S7	83% identity to 30S ribosomal protein S7 [*Oceanospirillum* sp. MED92]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**4**	**0**	**0**	**0**	**10**	**0**
Ribosomal protein L5	85% identity to 50S ribosomal protein L5 [*Oceanospirillum* sp. MED92]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
Ribosomal protein L14	93% identity to 50S ribosomal protein L14 [*Oceanospirillum* sp. MED92]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**4**	**0**	**0**	**0**	**7**	**0**
Ribosomal protein L15	81% identity to 50S ribosomal protein L15 [*Oceanospirillum* sp. MED92]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**4**	**0**	**0**	**0**	**7**	**0**
Ribosomal protein S19	89% identity to 30S ribosomal protein S19 [*Oceanospirillum* sp. MED92]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**3**	**0**	**0**	**0**	**4**	**0**
Ribosomal protein L22	83% identity to 50S ribosomal protein L22 [*Oceanospirillum* sp. MED92]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**2**	**0**	**0**	**0**	**4**	**0**
Ribosomal protein L3	78% identity to 50S ribosomal protein L3 [*Marinomonas mediterranea* MMB-1]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**5**	**2**	**0**	**0**	**20**	**2**
Ribosomal protein L10	80% identity to 50S ribosomal protein L10 [*Marinomonas* mediterranea MMB-1]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**3**	**0**	**0**	**0**	**4**	**0**
Ribosomal protein L20	87% identity to 50S ribosomal protein L20 [*Marinomonas* mediterranea MMB-1]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**4**	**0**	**0**	**0**	**6**	**0**
Ribosomal protein S10	92% identity to 30S ribosomal protein S10 [*Marinomonas* sp. MWYL1]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**4**	**0**	**0**	**0**	**9**	**0**

Ribosomal protein L19	85% identity to 50S ribosomal protein L19 [*Marinobacter aquaeolei* VT8]	Gammaproteobacteria (Alteromonadales)	0	0	2	0	0	0	4	0
Ribosomal protein L21	81% identity to 50S ribosomal protein L21 [*Marinobacter aquaeolei* (strain ATCC 700491 / DSM 11845 / VT8)	Gammaproteobacteria (Alteromonadales)	0	0	4	0	0	0	4	0
Ribosomal protein S4	77% identity to 30S ribosomal protein S4 [*Oceanobacter* sp. RED65]	Gammaproteobacteria (Oceanospirillales)	0	0	6	2	0	0	16	3
Ribosomal protein S6	75% identity to 30S ribosomal protein S6 [*Oceanobacter* sp. RED65]	Gammaproteobacteria (Oceanospirillales)	0	0	2	0	0	0	4	0
Ribosomal protein L23	76% identity to 50S ribosomal protein L23 [*Oceanobacter* sp. RED65]	Gammaproteobacteria (Oceanospirillales)	0	0	5	0	0	0	17	0
Ribosomal protein L13	86% identity to 50S ribosomal protein L13 [*Chromohalobacter salexigens* DSM 3043]	Gammaproteobacteria (Oceanospirillales)	0	0	2	0	0	0	2	0
Ribosomal protein S3	100% identity to 30S ribosomal protein S3 [*Escherichia coli* O157:H7 EDL933] (*likely contaminant*)	Gammaproteobacteria (Enterobacteriales)	0	4	0	0	0	5	0	0
Ribosomal protein L19	100% identity to 50S ribosomal protein L19 [*Chromohalobacter salexigens* DSM 3043]	Gammaproteobacteria (Oceanospirillales)	2	0	0	0	3	0	0	0
Ribosomal protein S1	100% identity to 30S ribosomal protein S1 [*Klebsiella pneumoniae* subsp. *pneumoniae* MGH]	Gammaproteobacteria (Enterobacteriales)	0	2	0	0	0	2	0	0
R ibosomal protein S4	100% identity to 30S ribosomal protein S4 [rpsD] [*Shigella sonnei* (strain Ss046)]	Gammaproteobacteria (Enterobacteriales)	1	2	0	0	1	3	0	0
Ribosomal protein L4	75% identity to 50S ribosomal protein L4/L1 [*Acinetobacter lwoffii* SH145]	Gammaproteobacteria (Pseudomonadales)	0	0	3	0	0	0	9	0
Ribosomal protein L4/L1 family	65% identity to 50S ribosomal protein L4 [*Acinetobacter johnsonii* SH046]	Gammaproteobacteria (Pseudomonadales)	0	0	2	0	0	0	7	0
Ribosomal protein L18	76% identity to 50S ribosomal protein L18 [*Acinetobacter baumannii* SDF]	Gammaproteobacteria (Pseudomonadales)	0	0	3	0	0	0	4	0
Ribosomal protein S7	100% identity to 30S ribosomal protein S7 [*Pseudomonas aeruginosa* PACS2]	Gammaproteobacteria (Pseudomonadales)	3	0	0	0	9	0	0	0
Ribosomal protein S5	86% identity 30S to ribosomal protein S5 [gamma proteobacterium NOR5-3]	Gammaproteobacteria (OMG)	0	0	7	0	0	0	17	0
Ribosomal protein L16	91% identity to 50S ribosomal protein L16 [gamma proteobacterium IMCC3088]	Gammaproteobacteria (unclassified)	0	0	2	0	0	0	3	0
Ribosomal protein L11	77% identity to 50S ribosomal protein L11 [*Reinekea blandensis* MED297]	Gammaproteobacteria (unclassified)	0	0	2	0	0	0	6	0
Ribosomal protein S1	85% identity to 30S ribosomal protein S1 [uncultured SUP05 cluster bacterium]	Gammaproteobacteria (GSO-EOSA-1)	0	0	0	2	0	0	0	4
Ribosomal protein S1	83% identity to 30S ribosomal protein S1 [uncultured SUP05 cluster bacterium]	Gammaproteobacteria (GSO-EOSA-1)	0	0	0	2	0	0	0	3
Ribosomal protein S1	89% identity to 30S ribosomal protein S1 [uncultured SUP05 cluster bacterium]	Gammaproteobacteria (GSO-EOSA-1)	0	0	3	4	0	0	4	10

Ribosomal protein L1P	81% identity to 50S ribosomal protein L1P [uncultured SUP05 cluster bacterium]	Gammaproteobacteria (GSO-EOSA-1)	0	0	3	4	0	0	5	18
Ribosomal protein L3	77% identity to 50S ribosomal protein L3 [uncultured SUP05 cluster bacterium]	Gammaproteobacteria (GSO-EOSA-1)	0	0	2	5	0	0	4	25
Ribosomal protein S2	87% identity to 30S ribosomal protein S2 [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	0	0	1	2	0	0	1	5
Ribosomal protein S3P	81% identity to 30S ribosomal protein S3 [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	0	0	0	2	0	0	0	3
Ribosomal protein L2	72% identity to 50S ribosomal protein L2 [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	0	0	1	2	0	0	1	9
Ribosomal protein L4	71% identity to 50S ribosomal protein L4 [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	0	0	0	3	0	0	0	6
Ribosomal protein S1	56% identity to 30S ribosomal protein S1 [marine gamma proteobacterium HTCC2143]	Gammaproteobacteria (OMG)	0	0	5	2	0	0	13	4
Ribosomal protein S7	92% identity to 30S ribosomal protein S7 [marine gamma proteobacterium HTCC2207]	Gammaproteobacteria (OMG)	0	0	2	0	0	0	4	0
Ribosomal protein S10	100% identity to 30S ribosomal protein S10 [marine gamma proteobacterium HTCC2207]	Gammaproteobacteria (OMG)	0	0	2	0	0	0	5	0
Ribosomal protein S17	75% identity to 30S ribosomal protein S17 [marine gamma proteobacterium HTCC2143]	Gammaproteobacteria (OMG)	0	0	3	0	0	0	5	0
Ribosomal protein S18	83% identity to 30S ribosomal protein S18 [marine gamma proteobacterium HTCC2148]	Gammaproteobacteria (OMG)	0	0	2	0	0	0	3	0
Ribosomal protein L2	85% identity to 50S ribosomal protein L2 [marine gamma proteobacterium HTCC2143]	Gammaproteobacteria (OMG)	0	0	3	2	0	0	19	3
Ribosomal protein L7/L12	75% identity to 50S ribosomal protein L7/L12 [*Flavobacterium psychrophilum* JIP02/86]	Bacteroidetes (Flavobacteria)	0	0	2	0	0	0	2	0
Ribosomal protein L9	66% identity to 50S ribosomal protein L9 [marine gamma proteobacterium HTCC2143]	Gammaproteobacteria (OMG)	0	0	3	0	0	0	5	0
Ribosomal protein S2P	79% identity to Ribosomal protein S2P [Nmar_0316] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	2	0	0	0	3
Ribosomal protein S3	87% identity to Ribosomal protein S3 [Nmar_0804] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	5	0	0	0	20
Ribosomal protein S4E	82% identity to Ribosomal protein S4E [Nmar_0798] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	3	0	0	0	13
Ribosomal protein S4P	78% identity to Ribosomal protein S4P [Nmar_0324] [*Nitrosopumilus maritimus* SCM1]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	3	0	0	0	31
Ribosomal protein S5P	91% identity to Ribosomal protein S5 [Nmar_0399] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	9	0	0	0	16

Ribosomal protein S7P	84% identity to Ribosomal protein S7P [Nmar_0355] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**4**
Ribosomal protein S8e	74% identity to Ribosomal protein S8e [Nmar_0520] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Ribosomal protein S13P	83% identity to Ribosomal protein S13P [Nmar_0325] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Ribosomal protein L1	80% identity to Ribosomal protein L1 [Nmar_0382] [*Nitrosopumilus maritimus* SCM1]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**14**
Ribosomal protein L2	87% identity to 30S ribosomal protein L2P [Nmar_0102] [*Nitrosopumilus maritimus* SCM1]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**18**
Ribosomal protein L3	87% identity to Ribosomal protein L3 [Nmar_0809] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**19**
Ribosomal protein L4P	72% identity to Ribosomal protein L4/L1e [Nmar_0808] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**6**	**0**	**0**	**0**	**43**
Ribosomal protein L6	77% identity to Ribosomal protein L6 [Nmar_0794] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Ribosomal protein L10	77% identity to Ribosomal protein L10 [Nmar_0381] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**31**
Ribosomal protein L12P	98% identity to Ribosomal protein L12P [Nmar_0374] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**3**
Ribosomal protein L14b/L23e	87% identity to Ribosomal protein L14P [Nmar_0800] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**3**
GTP-binding protein										
GTP-binding protein	100% identity to GTP-binding protein [TypA] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**2**	**3**	**0**	**0**	**10**	**15**	**0**	**0**
GTP-binding protein	67% identity to GTP-binding protein [TypA] [Rmag_0368] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Translation initation factor 2 (IF-2)										
Translation initiation factor 2	100% identity to Translation initiation factor 2 (IF-2) [InfB] [*Candidatus* Pelagibacter ubique HTCC1062],	Alphaproteobacteria (SAR11 cluster)	**2**	**2**	**0**	**0**	**5**	**2**	**0**	**0**

Translation initiation factor 2	93% identity to Translation initiation factor 2 (IF-2) [InfB] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
Translation initiation factor 2	100% identity to Translation initiation factor 2 (IF-2) [InfB] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**1**	**0**	**0**	**2**	**1**
Translation initiation factor 2	61% identity to Translation initiation factor 2 (IF-2) [InfB] [*Neptuniibacter caesariensis*]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**5**	**0**	**0**	**0**	**8**	**0**
Translation initiation factor 2	62% identity to Translation initiation factor 2 (IF-2) [InfB] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**1**	**3**	**0**	**0**	**2**	**7**
Translation initiation factor 2	91% identity to Translation initiation factor 2 (IF-2) [InfB] [*Oceanibulbus indolifex* HEL-45]	Alphaproteobacteria (Rhodobacterales)	**1**	**0**	**2**	**0**	**1**	**0**	**6**	**0**
Translation initiation factor 2	74% identity to Translation initiation factor 2 (IF-2) [InfB] [*Marinomonas* sp. MED121]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**3**	**0**	**0**	**0**	**4**	**0**
Translation initation factor 2 (a/eIF2)										
Translation initiation factor 2, alpha subunit	83% identity to Translation initiation factor IF-2, alpha subunit [Nmar_0077] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**
Translation initiation factor 2, gamma subunit	82% identity to Translation initiation factor 2, gamma subunit [Nmar_0072] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**
Translation elongation factor EF-1 alpha (EF-1A)										
Translation elongation factor EF-1 alpha	86% identity to Translation elongation factor 1-alpha (EF-1 alpha) [Nmar_1034] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**15**	**0**	**0**	**0**	**229**	**0**	**0**
Translation elongation factor EF-1 alpha	89% identity to Translation elongation factor 1-alpha (EF-1 alpha) [Nmar_1034] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**25**
Translation elongation factor EF-2 (EF-2)										
Translation elongation factor EF-2	100% identity to Translation elongation factor EF-2 [Nmar_0748] [*Nitrosopumilus maritimus* SCM1]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**4**	**0**	**0**	**0**	**30**	**0**	**0**
Translation elongation factor EF-2	96% identity to Translation elongation factor EF-2 [Nmar_0748] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**16**
Translation elongation factor G (EF-G)										

Translation elongation factor G	100% identity to Translation elongation factor G (EF-G) [FusA] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**7**	**4**	**0**	**0**	**23**	**33**	**0**	**0**
Translation elongation factor G	95% identity to Translation elongation factor G (EF-G) [FusA] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**4**	**5**	**0**	**0**	**6**	**17**
Translation elongation factor G	100% identity to Translation elongation factor G (EF-G) [FusA] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**2**	**1**	**0**	**0**	**2**	**1**	**0**	**0**
Translation elongation factor G	100% identity to Translation elongation factor G (EF-G) [FusA] [*Roseobacter* sp. SK209-2-6]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**5**	**2**	**0**	**0**	**11**	**5**	**0**	**0**
Translation elongation factor G	100% identity to Translation elongation factor G (EF-G) [FusA] [Rhodobacterales bacterium HTCC2083]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Translation elongation factor G	100% identity to Translation elongation factor G (EF-G) [FusA] [*Jannaschia* sp. CCS1]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Translation elongation factor G	100% identity to Translation elongation factor G (EF-G) [FusA] [*Roseobacter* sp. SK209-2-6]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**5**	**0**	**2**	**0**	**11**	**0**	**5**	**0**
Translation elongation factor G	100% identity to Translation elongation factor G (EF-G) [FusA] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**5**	**0**	**0**	**0**	**7**	**0**	**0**	**0**
Translation elongation factor G	85% identity to Translation elongation factor G (EF-G) [FusA] [*Glaciecola* sp. HTCC2999]	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**15**	**7**	**0**	**0**	**41**	**22**
Translation elongation factor G	100% identity to Translation elongation factor G (EF-G) [FusA] [*Shewanella denitrificans* OS217]	Gammaproteobacteria (Alteromonadales)	**3**	**0**	**0**	**0**	**5**	**0**	**0**	**0**
Translation elongation factor G	100% identity to Translation elongation factor G (EF-G) [FusA] [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**4**	**0**	**0**	**0**
Translation elongation factor G	86% identity to Translation elongation factor G (EF-G) [FusA] [uncultured SUP05 cluster bacterium]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**2**	**11**	**0**	**0**	**2**	**44**
Translation elongation factor G	87% identity to Translation elongation factor G (EF-G) [FusA] [uncultured SUP05 cluster bacterium]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**1**	**7**	**0**	**0**	**1**	**27**
Translation elongation factor Ts (EF-Ts)										
Translation elongation factor Ts	100% identity to Translation elongation factor Ts (EF-Ts) [Tsf] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**3**	**0**	**0**	**0**	**4**	**0**	**0**	**0**
Translation elongation factor Ts	67% identity to Translation elongation factor Ts (EF-Ts) [Tsf] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**10**
Translation elongation factor Tu (EF-Tu)										

Translation elongation factor Tu	88% identity to Translation elongation factor Tu (EF-Tu) [Tuf] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**20**	**20**	**0**	**0**	**55**	**89**
Translation elongation factor Tu	86% identity to Translation elongation factor Tu (EF-Tu) [Tuf] [*Candidatus* Pelagibacter sp. HTCC7211]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**3**	**0**	**0**	**1**	**9**
Translation elongation factor Tu	100% identity to Translation elongation factor Tu (EF-Tu) [Tuf] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**1**	**2**	**0**	**0**	**1**	**4**
Translation elongation factor Tu	82% identity to Translation elongation factor Tu (EF-Tu) [Tuf] [*Octadecabacter antarcticus* 307]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**2**	**0**	**0**	**3**	**2**
Translation elongation factor Tu	100% identity to Translation elongation factor Tu (EF-Tu) [Tuf] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**4**	**0**	**0**	**0**	**7**	**0**	**0**	**0**
Translation elongation factor Tu	100% identity to Translation elongation factor Tu (EF-Tu) [Tuf] [*Shewanella amazonensis* SB2B]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Translation elongation factor Tu	100% identity to Translation elongation factor Tu (EF-Tu) [Tuf] [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	**6**	**0**	**0**	**0**	**17**	**0**	**0**	**0**
Translation elongation factor Tu	100% identity to Translation elongation factor Tu (EF-Tu) [Tuf] [*Colwellia psychrerythraea* 34H]	Gammaproteobacteria (Alteromonadales)	**6**	**1**	**0**	**0**	**11**	**1**	**0**	**0**
Translation elongation factor Tu	100% identity to Translation elongation factor Tu (EF-Tu) [Tuf] [*Allochromatium vinosum* DSM 180]	Gammaproteobacteria (Chromatiales)	**2**	**0**	**0**	**0**	**5**	**0**	**0**	**0**
Translation elongation factor Tu	83% identity to Translation elongation factor Tu (EF-Tu) [Tuf] [*Neptuniibacter caesariensis*]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**2**	**1**	**0**	**0**	**12**	**4**
Translation elongation factor Tu	100% identity to Translation elongation factor Tu (EF-Tu) [Tuf] [*Alcanivorax borkumensis* SK2]	Gammaproteobacteria (Oceanospirillales)	**0**	**2**	**0**	**0**	**0**	**7**	**0**	**0**
Translation elongation factor Tu	100% identity to Translation elongation factor Tu (EF-Tu) [Tuf] [*Klebsiella pneumoniae* subsp. *pneumoniae* MGH 78578]	Gammaproteobacteria (Enterobacteriales)	**5**	**6**	**0**	**0**	**25**	**14**	**0**	**0**
Translation elongation factor Tu	100% identity to Translation elongation factor Tu (EF-Tu) [Tuf] [*Coxiella burnetii*]	Gammaproteobacteria (Legionellales)	**0**	**2**	**0**	**0**	**0**	**3**	**0**	**0**
Translation elongation factor Tu	90% identity to Translation elongation factor Tu (EF-Tu) [Tuf] [uncultured marine gamma proteobacterium EB000-45B06]	Gammaproteobacteria (unclassified)	**0**	**0**	**4**	**1**	**0**	**0**	**8**	**4**
Translation elongation factor Tu	92% identity to Translation elongation factor Tu (EF-Tu) [Tuf] [uncultured gamma proteobacterium HF0010_16J05]	Gammaproteobacteria (unclassified)	**0**	**0**	**3**	**1**	**0**	**0**	**10**	**2**
Translation elongation factor Tu	86% identity to Elongation factor Tu 2 (EF-Tu 2) [Tuf2] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**8**	**16**	**0**	**0**	**19**	**96**
Translation elongation factor Tu	89% identity to Translation elongation factor Tu (EF-Tu) [Tuf] [marine gamma proteobacterium HTCC2143]	Gammaproteobacteria (OMG)	**0**	**0**	**2**	**1**	**0**	**0**	**4**	**1**
Translation elongation factor Tu	100% identity to Translation elongation factor Tu (EF-Tu) [Tuf] [*Polaribacter* sp. MED152]	Bacteroidetes (Flavobacteria)	**2**	**1**	**0**	**0**	**3**	**1**	**0**	**0**

Aspartyl-tRNA synthetase (EC 6.1.1.12)										
Aspartyl-tRNA synthetase	71% identity to Aspartyl-tRNA synthetase [AspS] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**8**
Glutamyl-tRNA reductase (EC 1.2.1.70)										
Glutamyl-tRNA reductase	76% identity to Glutamyl-tRNA reductase [HemA] [Nmar_0265] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**10**
Lysyl-tRNA synthetase (EC 6.1.1.6)										
Lysyl-tRNA synthetase	100% identity to Lysyl-tRNA synthetase [LysS] [Nmar_0578] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**2**	**0**	**0**	**0**	**2**	**0**	**0**
Phenylalanyl-tRNA synthetase (EC 6.1.1.20)										
Phenylalanyl-tRNA synthetase, beta subunit	100% identity to Phenylalanyl-tRNA synthetase beta subunit [PheT] [Rmag_0642] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**13**
Phenylalanyl-tRNA synthetase, beta subunit	91% identity to Phenylalanyl-tRNA synthetase [PheT] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**1**	**0**	**0**	**3**	**3**
Prolyl-tRNA synthetase (EC:6.1.1.15)										
Prolyl-tRNA synthetase	100% identity to Prolyl-tRNA synthetase [ProS] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**2**	**0**	**0**	**0**	**2**	**0**	**0**
Seryl-tRNA synthetase (EC 6.1.1.11)										
Seryl-tRNA synthetase	75% identity to Seryl-tRNA synthetase [SerS] [Rmag_1008] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Valyl-tRNA synthetase (EC 6.1.1.9)										
Valyl-tRNA synthetase	75% identity to Valyl-tRNA synthetase [ValS] [Nmar_1477] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**

Trigger factor										
Trigger factor	100% identity to Trigger factor (TF) [Tig] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**1**	**2**	**0**	**0**	**1**	**5**	**0**	**0**
Trigger factor	92% identity to Trigger factor (TF) [Tig] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
Trigger factor	100% identity to Trigger factor (TF) [Tig] [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	**4**	**0**	**0**	**0**	**5**	**0**	**0**	**0**
Trigger factor	52% identity to Trigger factor (TF) [Tig] [*Marinomonas* sp. (strain MWYL1)]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**3**	**1**	**0**	**0**	**9**	**1**
Peptidylprolyl isomerase (PpiC-type)										
Peptidyl-prolyl cis-trans isomerase (PpiC-type)	100% identity to PpiC-type peptidyl-prolyl cis-trans isomerase [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Peptidyl-prolyl cis-trans isomerase (PpiC-type)	42% identity to PpiC-type peptidyl-prolyl cis-trans isomerase [Rmag_0656] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**7**
Peptidylprolyl isomerase (FKBP-type)										
Peptidylprolyl cis-trans isomerase (FKBP-type)	86% identity to Peptidylprolyl isomerase FKBP-type [Nmar_1730] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**16**	**0**	**0**	**0**	**65**
DnaK chaperonin										
DnaK	100% identity Chaperone protein DnaK [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**10**	**7**	**0**	**0**	**38**	**21**	**0**	**0**
DnaK	87% identity to Chaperone protein DnaK [*Octadecabacter antarcticus* 307]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**6**	**2**	**0**	**0**	**49**	**20**	**0**	**0**
DnaK	40% identity to Chaperone protein DnaK [*Oceanicola granulosus* HTCC2516]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**11**
DnaK	100% identity to Chaperone protein DnaK [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**2**	**0**	**0**	**0**	**5**	**0**	**0**	**0**
DnaK	86% identity to Chaperone protein DnaK [*Marinomonas* sp. (strain MWYL1)]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**4**	**2**	**0**	**0**	**6**	**2**
DnaK	80% identity to Chaperone protein DnaK [*Marinomonas* sp. (strain MWYL1)]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**3**	**0**	**0**	**0**	**5**	**0**
DnaK	80% identity to Chaperone protein DnaK [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**7**	**0**	**0**	**0**	**25**

DnaK	86% identity to Chaperone protein DnaK [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**13**	**0**	**0**	**0**	**62**
DnaK	89% identity to Chaperone protein DnaK [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**6**
GroEL chaperonin										
GroEL	92% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**23**	**21**	**0**	**0**	**93**	**69**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**2**	**3**	**0**	**0**	**7**	**5**	**0**	**0**
GroEL	85% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**1**	**0**	**0**	**5**	**1**
GroEL	58% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
GroEL	81% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**1**	**0**	**0**	**10**	**3**
GroEL	73% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**5**	**0**	**0**	**6**	**10**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Ruegeria pomeroyi* DSS-3]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**15**	**14**	**0**	**0**	**120**	**91**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [Rhodobacterales bacterium HTCC2150]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**3**	**4**	**0**	**0**	**14**	**20**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Rhodobacter sphaeroides* ATCC 17029]	Alphaproteobacteria (Rhodobacterales)	**0**	**3**	**0**	**0**	**0**	**17**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Roseovarius nubinhibens* ISM]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**1**	**2**	**0**	**0**	**17**	**16**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Oceanicola granulosus* HTCC2516]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**3**	**0**	**0**	**8**	**9**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Oceanicaulis alexandrii* HTCC2633]	Alphaproteobacteria (Rhodobacterales)	**2**	**2**	**0**	**0**	**5**	**13**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [Rhodobacterales	Alphaproteobacteria (Rhodobacterales,	**5**	**0**	**0**	**0**	**21**	**0**	**0**	**0**

	bacterium HTCC2255]	*Roseobacter* clade)								
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Ruegeria* sp. R11]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**3**	**0**	**0**	**11**	**6**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Loktanella vestfoldensis* SKA53]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**1**	**0**	**0**	**6**	**6**	**0**	**0**
GroEL	90% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Roseobacter litoralis* Och 149]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**1**	**2**	**0**	**0**	**5**	**6**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [Rhodobacterales bacterium HTCC2083]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**2**	**0**	**0**	**4**	**7**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**10**	**2**	**0**	**0**	**40**	**13**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Magnetococcus* sp. (strain MC-1)]	Alphaproteobacteria (unclassified)	**3**	**4**	**0**	**0**	**7**	**31**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Gluconacetobacter diazotrophicus* PAl 5]	Alphaproteobacteria (Rhodospirillales)	**0**	**2**	**0**	**0**	**0**	**7**	**0**	**0**
GroEL	88% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Magnetospirillum magneticum* (strain AMB-1 / ATCC 700264)]	Alphaproteobacteria (Rhodospirillales)	**1**	**3**	**0**	**0**	**4**	**7**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Parvularcula bermudensis* (strain ATCC BAA-594 / HTCC2503 / KCTC 12087)]	Alphaproteobacteria (Parvarculales)	**1**	**2**	**0**	**0**	**4**	**17**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Rhizobium loti* (*Mesorhizobium loti*)]	Alphaproteobacteria (Rhizobiales)	**1**	**2**	**0**	**0**	**4**	**28**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Azorhizobium caulinodans* ORS 571]	Alphaproteobacteria (Rhizobiales)	**2**	**1**	**0**	**0**	**5**	**24**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Mesorhizobium* sp. BNC1]	Alphaproteobacteria (Rhizobiales)	**2**	**1**	**0**	**0**	**10**	**1**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Aurantimonas manganoxydans* SI85-9A1]	Alphaproteobacteria (Rhizobiales)	**1**	**2**	**0**	**0**	**4**	**2**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Ochrobactrum thiophenivorans*]	Alphaproteobacteria (Rhizobiales)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Salmonella enterica* subsp. *enterica* serovar Newport str. SL254]	Gammaproteobacteria (Enterobacteriales)	**4**	**3**	**0**	**0**	**14**	**31**	**0**	**0**

GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Escherichia coli* 536] (*likely contaminant*)	Gammaproteobacteria (Enterobacteriales)	**2**	**4**	**0**	**0**	**6**	**5**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Pseudomonas aeruginosa*]	Gammaproteobacteria (Pseudomonadales)	**0**	**0**	**21**	**11**	**0**	**0**	**116**	**28**
GroEL	73% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Pseudomonas putida* (strain GB-1)]	Gammaproteobacteria (Pseudomonadales)	**0**	**0**	**4**	**2**	**0**	**0**	**16**	**7**
GroEL	70% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Cellvibrio japonicus* (strain Ueda107)	Gammaproteobacteria (Pseudomonadales)	**0**	**0**	**3**	**0**	**0**	**0**	**7**	**0**
GroEL	79% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**10**	**15**	**0**	**0**	**23**	**58**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [marine gamma proteobacterium HTCC2207]	Gammaproteobacteria (OMG)	**1**	**2**	**0**	**0**	**8**	**11**	**0**	**0**
GroEL	87% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [gamma proteobacterium HTCC2207]	Gammaproteobacteria (OMG)	**0**	**0**	**3**	**1**	**0**	**0**	**8**	**1**
GroEL	87% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL][*Helicobacter pullorum* MIT 98-5489]	Epsilonproteobacteria (Campylobacterales)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
GroEL	71% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Candidatus* Nitrospira defluvii]	Nitrospirae	**0**	**0**	**0**	**10**	**0**	**0**	**0**	**42**
GroEL	80% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Dokdonia donghaensis* MED134]	Bacteroidetes (Flavobacteria)	**0**	**0**	**10**	**1**	**0**	**0**	**31**	**5**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [*Cytophaga hutchinsonii* ATCC 33406]	Bacteroidetes (Flavobacteria)	**0**	**2**	**0**	**0**	**0**	**3**	**0**	**0**
GroEL	76% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Polaribacter* sp. MED152]	Bacteroidetes (Flavobacteria)	**0**	**0**	**2**	**0**	**0**	**0**	**4**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Nitrosospira multiformis* (strain ATCC 25196 / NCIMB 11849)]	Betaproteobacteria (Nitrosomonadales)	**3**	**3**	**0**	**0**	**6**	**26**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Aromatoleum aromaticum* EbN1]	Betaproteobacteria (Rhodocyclales)	**2**	**2**	**0**	**0**	**5**	**28**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Oxalobacter formigenes* HOxBLS]	Betaproteobacteria (Burkholderiales)	**2**	**1**	**0**	**0**	**14**	**24**	**0**	**0**

GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Haliangium ochraceum* DSM 14365]	Deltaproteobacteria (Myxococcales)	**1**	**3**	**0**	**0**	**4**	**67**	**0**	**0**
GroEL	100% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [*Campylobacter concisus* 13826]	Epsilonproteobacteria (Campylobacterales)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
GroEL	95% identity to GroEL protein (Chaperonin) (Protein Cpn60) [GroL] [uncultured marine microorganism HF4000_ANIW137I15]	Bacteria? (unclassified)	**1**	**3**	**0**	**0**	**1**	**5**	**0**	**0**
GroES chaperonin										
GroES	100% identity to GroES protein (Chaperonin) (Protein Cpn10) [GroS] [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**3**	**0**	**0**	**0**	**7**	**0**
GroES	74% identity to GroES protein (Chaperonin) (Protein Cpn10) [GroS] [*Oceanospirillum* sp. MED92]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**4**	**1**	**0**	**0**	**11**	**1**
Hsp90 / HtpG (Heat shock protein 90)										
Hsp90	71% identity to Chaperone protein HtpG / Heat shock protein Hsp90 [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**6**	**0**	**0**	**0**	**11**
Hsp90	100% identity to Chaperone protein HtpG / Heat shock protein Hsp90 [Rhodobacterales bacterium HTCC2255]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Hsp90	68% identity to Chaperone protein HtpG / Heat shock protein Hsp90 [*Saccharophagus degradans* (strain 2-40 / ATCC 43961 / DSM 17024)]	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**2**	**1**	**0**	**0**	**5**	**1**
Cpn60 (Thermosome)										
Cpn60	82% identity to Thermosome/Cpn60 [Nmar_1577] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**15**	**0**	**0**	**0**	**69**
Cpn60	86% identity to Thermosome/Cpn60 [Nmar_1792] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**16**
Cpn60	100% identity to Thermosome/Cpn60 [Nmar_1792] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**12**	**0**	**0**	**0**	**52**
Cpn60	100% identity to Thermosome/Cpn60 [Nmar_1577] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**8**

Cpn60	94% identity to Thermosome/Cpn60 [Nmar_1577] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**7**
AAA family ATPase										
AAA family ATPase	100% identity to AAA ATPase (MoxR-like) [marine gamma proteobacterium HTCC2080]	Gammaproteobacteria (unclassified)	**1**	**0**	**1**	**2**	**4**	**0**	**4**	**3**
AAA family ATPase	100% identity to ATPase AAA-2 / ClpB chaperone [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	**3**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
AAA family ATPase	89% identity to AAA family ATPase, CDC48 subfamily [Nmar_0101] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**26**	**0**	**0**	**0**	**117**
ATPase AAA-2	100% identity to ATPase AAA-2 [*Trichodesmium erythraeum* (strain IMS101)	Cyanobacteria	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
RubisCO, post-translational activation										
CbbQ/NirQ/NorQ family protein: ATPase chaperone	30% identity to CbbQ-1 protein [*Thiomicrospira crunogena* (strain XCL-2)]	Gammaproteobacteria (Thiotrichales)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**21**
PROTEOLYSIS										
Proteasome complex (EC 3.4.25.1)										
Proteasome, alpha subunit	100% identity to Proteasome endopeptidase complex, alpha subunit [PsmA] [Nmar_1314] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**6**
Proteasome, alpha subunit	82% identity to Proteasome endopeptidase complex, alpha subunit [PsmA] [Nmar_1314] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Proteasome, alpha subunit	83% identity to Proteasome endopeptidase complex, alpha subunit [PsmA] [Nmar_0811] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Proteasome, beta subunit	85% identity to Proteasome endopeptidase complex, beta 1 subunit [PsmB1] [Nmar_0694] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Leucyl aminopeptidase (EC 3.4.11.1)										
Leucyl aminopeptidase	100% identity to Leucyl aminopeptidase [PepA] [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**4**	**3**	**0**	**0**	**7**	**7**	**0**	**0**
Leucyl aminopeptidase	70% identity to Leucyl aminopeptidase [PepA] [*Neptuniibacter caesariensis*]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**

Leucyl aminopeptidase	59% identity to Leucyl aminopeptidase [PepA] [Rmag_0211] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Leucyl aminopeptidase	100% identity to Leucyl aminopeptidase [PepA] [Nmar_0296] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**2**	**0**	**0**	**0**	**10**	**0**	**0**
PepF/M3 family oligoendopeptidase										
PepF/M3 family oligoendopeptidase	100% identity to Oligoendopeptidase, pepF/M3 family [Nmar_1177] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**3**	**0**	**0**	**0**	**9**	**0**	**0**
Peptidase M1 membrane alanine aminopeptidase										
Peptidase M1 membrane alanine aminopeptidase	68% identity to Peptidase M1 membrane alanine aminopeptidase [Nmar_0957] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**5**
Peptidase M10										
Peptidase M10	66% identity to Peptidase M10 [*Cupriavidus taiwanensis* (strain R1 / LMG 19424)	Betaproteobacteria (Burkholderiales)	**0**	**0**	**2**	**1**	**0**	**0**	**10**	**2**
Clp protease										
ATP-binding protease component ClpA	76% identity to ATP-binding protease component ClpA [*Neptuniibacter caesariensis*]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
Carboxyl-terminal protease (EC 3.4.21.102)										
Carboxyl-terminal protease	57% identity to Periplasmic protease / Carboxyl-terminal protease [Rmag_0620] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**5**
FtsH metalloprotease (EC 3.4.24.-)										
FtsH metalloprotease	100% identity to Zinc-dependent metalloprotease FtsH [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**1**	**2**	**0**	**0**	**1**	**5**	**0**	**0**
FtsH metalloprotease	50% identity to Zinc-dependent metalloprotease FtsH [*Neptuniibacter caesariensis*]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
HflKC membrane complex/ SPFH domain / Band 7 family										

HflC	76% identity to Membrane proteinase HflC [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**11**	**12**	**0**	**0**	**24**	**30**
HflC	85% identity to Membrane proteinase HflC [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**8**	**9**	**0**	**0**	**17**	**29**
HflC	75% identity to Membrane proteinase HflC [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
HflC	75% identity to Membrane proteinase HflC [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**0**	**2**	**2**	**0**	**0**	**2**	**4**
HflC	79% identity to Membrane proteinase HflC [*Roseobacter* sp. GAI101]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**5**	**0**	**0**	**0**	**15**	**0**
HflC	61% identity to Membrane proteinase HflC [Rmag_0533] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**2**	**4**	**0**	**0**	**6**	**15**
HflC	75% identity to Membrane proteinase HflC [*Candidatus* Vesicomyosocius okutanii]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**2**	**2**	**0**	**0**	**3**	**14**
HflK	56% identity to Proteinase HflK [Rmag_0534] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**10**
HflK	58% identity to Proteinase HflK [Rmag_0534] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**8**	**0**	**0**	**0**	**18**
HflK	85% identity to Proteinase HflK [uncultured *Roseobacter* sp]	Alphaproteobacteria (Rhodobacterales, *Roseobacter* clade)	**0**	**0**	**2**	**1**	**0**	**0**	**6**	**3**
HflK	62% identity to Proteinase HflK [*Neptuniibacter caesariensis*]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**11**	**4**	**0**	**0**	**35**	**5**
SPFH domain / Band 7 family protein	82% identity to SPFH domain / Band 7 family protein [*Pseudoalteromonas tunicata* D2]	Gammaproteobacteria (Alteromonadales)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
SPFH domain / Band 7 family protein	38% identity to SPFH domain / Band 7 family protein [*Mesorhizobium opportunistum* WSM2075]	Alphaproteobacteria (Rhizobiales)	**0**	**0**	**0**	**8**	**0**	**0**	**0**	**21**
SPFH domain / Band 7 family protein	76% identity to SPFH domain / Band 7 family protein [Nmar_0825] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**16**
SPFH domain / Band 7 family protein	64% identity SPFH domain / Band 7 family protein [Nmar_0825] [*Nitrosopumilus maritimus*]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**31**
La protease										
La protease	100% identity to ATP-dependent protease La [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**0**	**2**	**0**	**0**	**0**	**2**	**0**	**0**
La protease	75% identity to ATP-dependent protease La [Rmag_0208] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**

Zn-dependent protease										
Zn-dependent protease	58% identity to Secreted Zn-dependent protease [Nmar_0467] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**7**
Zn-dependent protease	67% identity to Secreted Zn-dependent protease [Nmar_0467] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**4**	**0**	**0**	**0**	**12**
CELL STRUCTURE										
Rod shape-determining protein MreB										
Rod shape-determining protein MreB	100% identity to Rod shape-determining protein MreB [*Candidatus* Pelagibacter ubique HTCC1062]	Alphaproteobacteria (SAR11 cluster)	**2**	**2**	**0**	**0**	**4**	**5**	**0**	**0**
Rod shape-determining protein MreB	87% identity to Rod shape-determining protein MreB [*Oceanospirillum* sp. MED92]	Gammaproteobacteria (Oceanospirillales)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**
Rod shape-determining protein MreB	82% identity to Rod shape-determining protein MreB [Rmag_0794] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**
HYPOTHETICAL PROTEINS										
Epimerase/dehydratase, NAD-dependent										
Epimerase/dehydratase, NAD-dependent	67% identity to NAD-dependent epimerase/dehydratase [Nmar_0977] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**4**
Fumarylacetoacetate (FAA) hydrolase family protein										
Fumarylacetoacetate (FAA) hydrolase family protein	71% identity to Fumarylacetoacetate (FAA) hydrolase family protein [Nmar_0310] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**12**
Monooxygenase, flavin-dependent										
Luciferase-like monooxygenase/ Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase	100% identity to Luciferase family protein Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase [Nmar_1109] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**3**	**0**	**0**	**0**	**13**	**0**	**0**

PfkB family carbohydrate kinase										
PfkB family carbohydrate kinase	82% identity to PfkB domain protein [Nmar_1745] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	7	0	0	0	39
Trans-sialidase										
Trans-sialidase	47% identity to Trans-sialidase [Nmar_0559] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	5	0	0	0	29
Trans-sialidase	53% identity to Trans-sialidase [Nmar_0559] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	2	0	0	0	3
UbiD family decarboxylase										
UbiD family decarboxylase	87% identity to UbiD family decarboxylase [Nmar_1597] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	2	0	0	0	2
UbiD family decarboxylase	86% identity to UbiD family decarboxylase [Nmar_0555] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	2	0	0	0	2
TPR (tetratricopeptide) proteins										
TPR-repeat protein	100% identity to Tetratricopeptide TPR_2 potein [*Sphingopyxis alaskensis* RB2256]	Alphaproteobacteria (Sphingomonadales)	3	0	0	0	6	0	0	0
TPR-repeat protein	35% identity to Tetratricopeptide repeat protein [Acidobacteria bacterium (strain Ellin345)]	Actinobacteria	0	0	2	0	0	0	8	0
TPR-repeat protein	73% identity to Tetratricopeptide TPR_2 repeat protein [Nmar_0681] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	12	0	0	0	30
Radical SAM domain proteins										
Radical SAM domain protein	100% identity to Radical SAM domain protein [Nmar_0115] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	3	0	0	0	4	0	0
Radical SAM domain protein	90% identity to Radical SAM domain protein [Nmar_1388] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	2	0	0	0	5
Radical SAM domain protein	93% identity to Radical SAM domain protein [Nmar_0336] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	0	0	0	4	0	0	0	9

Other hypothetical proteins										
Hypothetical protein (no signal peptide)	88% identity to Putative uncharacterized protein [*Candidatus* Pelagibacter ubique HTCC1002]	Alphaproteobacteria (SAR11 cluster)	**2**	**1**	**0**	**0**	**3**	**1**	**0**	**0**
Hypothetical protein (signal peptide)	52% identity to Putative uncharacterized protein [Rmag_0260] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**6**
Hypothetical protein (signal peptide)	48% identity to Putative uncharacterized protein [Rmag_0260] [*Candidatus* Ruthia magnifica]	Gammaproteobacteria (GSO-EOSA-1)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**5**
Hypothetical protein (signal peptide)	42% identity to Putative uncharacterized protein [*Gluconacetobacter diazotrophicus* (strain ATCC 49037 / DSM 5601 / PAl5)]	Alphaproteobacteria (Rhodospirillales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**6**
Hypothetical protein (signal peptide)	100% identity to Putative uncharacterized protein [Alteromonadales bacterium TW-7]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Hypothetical protein (no signal peptide)	100% identity to Putative uncharacterized protein [*Moritella* sp. PE36]	Gammaproteobacteria (Alteromonadales)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Hypothetical protein (no signal peptide)	38% identity to Putative uncharacterized protein [*Prochlorococcus marinus* (strain NATL2A)]	Cyanobacteria	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
Hypothetical protein (signal peptide; protease?)	77% identity to Putative uncharacterized protein [Flavobacteria bacterium MS024-2A]	Bacteroidetes (Flavobacteria)	**0**	**0**	**2**	**0**	**0**	**0**	**2**	**0**
Hypothetical protein (signal peptide)	75% identity to Putative uncharacterized protein [uncultured marine bacterium EB0_35D03]	Bacteria (unclassified)	**0**	**0**	**1**	**2**	**0**	**0**	**1**	**3**
Hypothetical protein (signal peptide)	25% identity to Putative uncharacterized protein [*Candidatus* Puniceispirillum marinum (strain IMCC1322)]	Alphaproteobacteria (SAR116 cluster)	**0**	**0**	**3**	**0**	**0**	**0**	**7**	**0**
Hypothetical protein (signal peptide; adhesin?)	44% identity to Putative uncharacterized protein (collagen triple helix repeat) [Nmar_0682] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**5**
Hypothetical protein (signal peptide)	77% identity to Putative uncharacterized protein: possible protease [Nmar_1648] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Hypothetical protein (no signal peptide)	86% identity to Putative uncharacterized protein [Nmar_1538] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Hypothetical protein (no signal peptide)	90% identity to Putative uncharacterized protein [Nmar_1398] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Hypothetical protein (no signal peptide)	80% identity to Putative uncharacterized protein [Nmar_0700] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Hypothetical protein (signal peptide)	62% identity to Putative uncharacterized protein [Nmar_1199] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**5**
Hypothetical protein (signal peptide)	52% identity to Putative uncharacterized protein [Nmar_0627] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**

Hypothetical protein (signal peptide)	62% identity to Putative uncharacterized protein [Nmar_0627] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**8**
Hypothetical protein (no signal peptide)	91% identity to Putative uncharacterized protein [Nmar_1599] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Hypothetical protein (signal peptide)	37% identity to Putative uncharacterized protein [Nmar_1547] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**17**
Hypothetical protein (no signal peptide)	81% identity to Putative uncharacterized protein [Nmar_1469] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**2**
Hypothetical protein (no signal peptide)	66% identity to Putative uncharacterized protein [Nmar_0209] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**5**
Hypothetical protein (no signal peptide)	90% identity to Putative uncharacterized protein [Nmar_0269] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Hypothetical protein (no signal peptide)	66% identity to Putative uncharacterized protein [Nmar_1396] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Hypothetical protein (no signal peptide)	87% identity to Putative uncharacterized protein [Nmar_0067] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**0**	**0**	**3**	**0**	**0**	**0**	**5**
Hypothetical protein (no signal peptide; coiled-coil protein)	86% identity to Putative uncharacterized protein / coiled-coil protein [Nmar_1038] [*Nitrosopumilus maritimus* (strain SCM1)]	Marine Group I Crenarchaeota (Nitrosopumilales)	**0**	**5**	**0**	**0**	**0**	**8**	**0**	**0**
Hypothetical protein (signal peptide)	100% identity to S-layer-related protein [*Methanococcoides burtonii* DSM 6242]	Euryarchaeota (Methanosarcinales)	**0**	**5**	**0**	**0**	**0**	**18**	**0**	**0**
EUKARYOTE PROTEINS										
Photosystem proteins										
Photosystem II reaction center protein D1	100% identity to photosystem II reaction center protein D1 [*Flintiella sanguinaria*]	Rhodophyta (red alga)	**3**	**0**	**0**	**0**	**18**	**0**	**0**	**0**
Photosystem I subunit VII	100% identity to photosystem I subunit VII [*Guillardia theta*]	Cryptophyta	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Photosystem II 44 kDa protein	100% identity to photosystem II 44 kDa protein [*Emiliania huxleyi*]	Haptophyta (coccolithophore)	**4**	**1**	**0**	**0**	**31**	**1**	**0**	**0**
Photosystem II protein D2	100% identity to photosystem II protein D2 [*Emiliania huxleyi*]	Haptophyta (coccolithophore)	**2**	**1**	**0**	**0**	**18**	**1**	**0**	**0**
Photosystem II cytochrome c550	82% identity to Cytochrome c-550 [PsbV] [*Emiliania huxleyi*]	Haptophyta (coccolithophore)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**

Photosystem II 47 kDa protein	100% identity to photosystem II 47 kDa protein [*Odontella sinensis*]	Bacillariophyta (diatom)	**3**	**2**	**0**	**0**	**12**	**2**	**0**	**0**
Ribulose-1,5-bisphosphate carboxylase/oxygenase (RubisCO) (EC 4.1.1.39)										
Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	100% identity to Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Ostreococcus tauri*]	Chlorophyta (green alga / microalga)	**1**	**3**	**0**	**0**	**1**	**12**	**0**	**0**
Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	100% identity to Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Zellera tawallina*]	Rhodophyta (red alga)	**2**	**3**	**0**	**0**	**4**	**4**	**0**	**0**
ATP synthase										
ATP synthase, subunit A	100% identity to ATP synthase, alpha subunit, chloroplastic [AtpA] [*Ostreococcus tauri*]	Chlorophyta (green alga / microalga)	**3**	**1**	**4**	**0**	**3**	**3**	**10**	**0**
ATP synthase, CF1 alpha subunit	100% identity to CF1 alpha subunit of ATP synthase [*Pyramimonas parkeae*]	Chlorophyta (green alga)	**2**	**1**	**0**	**0**	**8**	**3**	**0**	**0**
ATP synthase, alpha subunit	100% identity to ATP synthase alpha subunit, chloroplastic [*Callithamnion collabens*]	Rhodophyta (red alga)	**2**	**1**	**0**	**0**	**19**	**5**	**0**	**0**
ATP synthase, beta 1 subunit	85% identity to ATP synthase subunit beta, chloroplastic [AtpB] [*Emiliania huxleyi*]	Haptophyta (coccolithophore)	**0**	**0**	**8**	**1**	**0**	**0**	**43**	**3**
ATP synthase, CF1 alpha subunit	87% identity to ATP synthase subunit alpha, chloroplastic [AtpA] [*Emiliania huxleyi*]	Haptophyta (coccolithophore)	**0**	**0**	**10**	**2**	**0**	**0**	**33**	**2**
ATP synthase, CF1 alpha subunit	100% identity to ATP synthase CF1 alpha subunit, chloroplastic [AtpA] [*Emiliania huxleyi*]	Haptophyta (coccolithophore)	**2**	**0**	**0**	**0**	**4**	**0**	**0**	**0**
ATP synthase, CF1 beta subunit	100% identity to ATP synthase CF1 beta subunit, chloroplastic [*Oltmannsiellopsis viridis*]	Chlorophyta (green alga)	**2**	**0**	**0**	**0**	**24**	**0**	**0**	**0**
Mitochondrial ATPase, inner membrane	100% identity to Mitochondrial ATPase, inner membrane [*Thalassiosira pseudonana* CCMP1335]	Haptophyta (diatom/coccolithophore)	**2**	**0**	**0**	**0**	**6**	**0**	**0**	**0**
ATP synthase, beta subunit	100% identity to F-ATPase beta subunit [*Glomus* sp. A1] (*likely contaminant*)	Fungi	**2**	**1**	**0**	**0**	**2**	**2**	**0**	**0**
Mitochondrial ATPase, beta subunit	100% identity to Mitochondrial F-ATPase beta subunit [*Candida haemulonii*] (*likely contaminant*)	Fungi	**2**	**1**	**0**	**0**	**2**	**2**	**0**	**0**
Phosphoglycerate kinase (EC 2.7.2.3)										
Phosphoglycerate kinase	100% identity to Phosphoglycerate kinase [*Isochrysis galbana*]	Haptophyta (microalga)	**2**	**0**	**0**	**0**	**2**	**0**	**0**	**0**
Methionine adenosyltransferase (EC 2.5.1.6)										

S-adenosylmethionine synthetase	100% identity to S-adenosylmethionine synthetase [MetK] [*Thalassiosira pseudonana* CCMP1335]	Haptophyta (diatom/coccolithophore)	**2**	**1**	**0**	**0**	**5**	**2**	**0**	**0**
Carbamate kinase										
Carbamate kinase	100% identity to Carbamate kinase [*Giardia lamblia* ATCC 50803] (*likely contaminant*)	Diplomonadida	**0**	**5**	**0**	**0**	**0**	**26**	**0**	**0**
Translation elongation factor EF-1										
Translation elongation factor EF-1 alpha	100% identity to EF-1 alpha-like protein (ISS) [*Ostreococcus tauri*]	Chlorophyta (green alga / microalga)	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Hsp70										
Hsp70	100% identity to 70kDa heat shock protein [*Gammarus locusta*]	Crustacea	**2**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
Hsp90										
Hsp90	100% identity to Hsp90 [*Chrysochromulina* sp. NIES-1333]	Haptophyta (golden alga)	**4**	**1**	**0**	**0**	**11**	**1**	**0**	**0**
Histone										
Histone H2A	100% identity to Histone H2A [*Ostreococcus tauri*]	Chlorophyta (green alga / microalga)	**0**	**0**	**2**	**0**	**0**	**0**	**3**	**0**
Histone H2A	100% identity to Histone H2A [*Thalassiosira pseudonana* CCMP1335]	Haptophyta (diatom/coccolithophore)	**2**	**0**	**0**	**0**	**7**	**0**	**0**	**0**
Tubulin										
Alpha-tubulin	100% identity to Alpha tubulin [*Chrysochromulina* sp. NIES-1333]	Haptophyta (golden alga)	**8**	**3**	**0**	**0**	**14**	**6**	**0**	**0**
Beta-tubulin	100% identity to Beta tubulin [*Chrysochromulina* sp. TKB79]	Haptophyta (golden alga)	**4**	**0**	**0**	**0**	**4**	**0**	**0**	**0**
Alpha-tubulin	100% identity to Alpha-tubulin [*Cyanophora paradoxa*]	Glaucophyta (alga)	**2**	**1**	**0**	**0**	**2**	**1**	**0**	**0**
Beta-tubulin	95% identity to Beta tubulin [*Euplotes crassus*]	Ciliophora (ciliate)	**6**	**3**	**0**	**0**	**38**	**13**	**0**	**0**

Rubber elongation factor										
Rubber elongation factor	100% identity to Elongation factor protein [*Hevea brasiliensis*] (*likely contaminant – latex gloves?*)	Tracheophyta	**2**	**2**	**0**	**0**	**2**	**7**	**0**	**0**
Hypothetical proteins										
TPR-repeat protein	50% identity to Tetratricopeptide repeat protein [*Ectocarpus siliculosus*]	Heterokontophyta (brown alga)	**0**	**0**	**3**	**0**	**0**	**0**	**8**	**0**
Hypothetical protein	100% identity to Hypothetical protein [*Vitis vinifera*] (*likely contaminant*)	Tracheophyta	**3**	**0**	**0**	**0**	**3**	**0**	**0**	**0**
PHAGE PROTEINS										
Capsid protein Gp23, major head subunit	65% identity to Capsid protein Gp23, major head subunit [*Synechococcus* phage S-SSM7]		**0**	**0**	**2**	**9**	**0**	**0**	**4**	**28**
Major capsid protein	100% identity to Major capsid protein (MCP) [*Phaeocystis pouchetii* virus (PpV01)]		**4**	**1**	**0**	**0**	**8**	**3**	**0**	**0**
Tail sheath monomer	40% identity to Tail sheath monomer [Gp18] [*Prochlorococcus* phage Syn33]		**0**	**0**	**0**	**7**	**0**	**0**	**0**	**17**
Capsid protein Gp23, major head subunit	66% identity to Capsid protein Gp23, major head subunit [*Synechococcus* phage S-SM2]		**0**	**0**	**1**	**4**	**0**	**0**	**1**	**11**
Capsid protein Gp23, major head subunit	67% identity to Capsid protein Gp23, major head subunit [uncultured Myoviridae]		**0**	**0**	**1**	**2**	**0**	**0**	**3**	**3**
Capsid protein Gp23, major head subunit	61% identity to Capsid protein Gp23, major head subunit [Gp23] [*Synechococcus* phage S-SSM7]		**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**
Capsid protein Gp27	39% identity to Capsid protein Gp27 [*Streptomyces* phage phiSASD1]		**0**	**0**	**0**	**2**	**0**	**0**	**0**	**3**

References

Alber BE, Kung JW, Fuchs G (2008). 3-Hydroxypropionyl-coenzyme A synthetase from *Metallosphaera sedula*, an enzyme involved in autotrophic CO_2 fixation. *J Bacteriol* **190:** 1383-1389.

Berg IA, Kockelkorn D, Buckel W, Fuchs G. (2007). A 3-hydroxypropionate/4-hydroxybutyrate autotrophic carbon dioxide assimilation pathway in Archaea. *Science* **318:** 1782-1786.

Hallam SJ, Konstantinidis KT, Putnam N, Schleper C, Watanabe Y, Sugahara J *et al.* (2006). Genomic analysis of the uncultivated marine crenarchaeote *Cenarchaeum symbiosum*. *Proc Natl Acad Sci U S A* **103:** 18296-18301.

Kockelkorn D, Fuchs G. (2009) Malonic semialdehyde reductase, succinic semialdehyde reductase, and succinyl-coenzyme A reductase from *Metallosphaera sedula*: enzymes of the autotrophic 3-hydroxypropionate/4-hydroxybutyrate cycle in Sulfolobales. *J Bacteriol* **191:** 6352-6362.

Ramos-Vera WH, Weiss M, Strittmatter E, Kockelkorn D, Fuchs G. (2011). Identification of missing genes and enzymes for autotrophic carbon fixation in crenarchaeota. *J Bacteriol* **193:** 1201-1211.

Walker CB, de la Torre JR, Klotz MG, Urakawa H, Pinel N, Arp DJ *et al*. (2010). *Nitrosopumilus maritimus* genome reveals unique mechanisms for nitrification and autotrophy in globally distributed marine crenarchaea. *Proc Natl Acad Sci U S A* **107:** 8818-8823.