Kalmar, Sweden 2014-12-04

Project:	BLUEPRINT
Deliverable:	3.1
Work package:	3

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Compilation of signature genes indicative of GES/sub-GES conditions from literature on model microorganisms and natural seawater samples

The last decade, the development and application of high throughput sequencing technologies have made it possible to analyze the gene content and gene expression patterns of complex microbial communities in their natural environment, i.e. metagenomics and metatranscriptomics (Handelsman et al. 2007). These approaches have given us fundamentally new insights and better understanding of factors that regulate microbial community composition, ecological functions, biogeochemical processes and metabolic pathways for aquatic microorganism (Satinsky et al. 2014, Gifford et al. 2014, Gifford et al. 2013). However, current and developing sequencing techniques produce very large amounts of data, and analyses of such data typically produce highly intricate networks of interdependent relations between genes. This poses major challenges for data handling and interpretation.

Analysis of genomics and transcriptomics data sets from marine bacterioplankton can be done by two complementary approaches (both of which will be used in the BLUEPRINT project). First, an unsupervised approach, where patterns of presence/absence and abundance of all genes in samples are analyzed in relation to each other and in relation to environmental variables (without previous assumptions of which genes are present or expressed). Second, a targeted approach, where genes of known ecological function and/or relevance are selected for analyses in particular samples. Interestingly, these two approaches can be combined to give comprehensive and pertinent information regarding the status and dynamics of desired ecosystems.

This report presents a list of total 225 genes where 54 have been nominated as potentially useful indicator/marker genes to be used in targeted analysis and evaluations of natural samples from the Baltic Sea. The listed genes are known for their implied relevance in bacterially driven biogeochemical processes and for defining the physiology and ecology of marine bacteria. For example, relevance in carbon cycling, inorganic nutrient turnover, nutrient limitation and stress. The proposed indicator genes listed have been assembled from a number of recent publications dedicated to identifying genes that are responsive to changes in environmental conditions (Satinsky et al. 2014, Gifford et al. 2013, Shilova et al. 2014, Saito et al. 2014, Doxey et al. 2014, Harke et al. 2013, Penn et al. 2014 and Smith et al. 2013). Although not directly used here, due to difference in output format, we would like to include mentioning of the modeling work by Lauro et al. (2009) on defining characters separating oligotrophic and copiotrophic bacteria. Still, it should be recognized that knowledge of the function and physiological relevance of these genes for bacteria builds on the enormous efforts done on a series of model organisms in the field of microbiology and molecular genetics since nearly a half-century back (e.g. Cashel et al. 1996).

This list of 54 nominated indicator/marker genes will be used in the BLUEPRINT project as a tool to study targeted genes with potential relevance as indicators; for example by finding correlations with environmental variables, measured process rates and growth conditions both in natural seawater in the Baltic Sea and in experiments with natural bacterial assemblages and specific bacterial isolates.

The present report will be publicly available on the BLUEPRINT website (http://blueprint-project.org/) whereas the gene list inserted below will also be available to BLUEPRINT partners in an Excel format on the internal page of the BLUEPRINT website.

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Target genes

Number	ID	Gene/Protein	Description	Reference	Metabolism	EC number
1		Cobalamin B12-binding domain protein	Enzyme use by prokaryotic and eukaryotic species to catalyze rearrangement-reduction or methyl transfer reactions involved primarily in amino acid synthesis	Doxey et al. 2014/Gifford et al. 2013	Amino acid metabolism	-
2	phaC	Polyhydroxyalkanoate synthase	Catalyzes the polymerization of (R)-3-hydroxybutyryl-CoA to form the polyhydroxyalkanoate polymer, the last step in polyhydroxyalkanoate biosynthesis	Satinsky et al. 2014/Gifford et al. 2013	Carbon metabolism	2.3.1.-
3	pepA	Glutamyl aminopeptidase	Calcium-stimulated exopeptidase that selectively hydrolyze acidic amino acid residues with a preference for certain Glutamine	Satinsky et al. 2014	Carbon metabolism	3.4.11.-
4	pepL	Leucyl aminopeptidase	Hydrolytic exopeptidase with a preference for certain Leucine and hydrophobic amino acid substrates	Satinsky et al. 2014	Carbon metabolism	3.4.11.-
5	pepM/map	Methionyl aminopeptidase	Ubiquitous, essential exopeptidase that cleaves N-terminal / Methionine residues from cellular proteins	Satinsky et al. 2014	Carbon metabolism	3.4.11.18
6	pepN	Alanyl aminopeptidase	Broad specificity exopeptidase that cleaves amino acid residues from the N-terminus of peptides and protein substrates with a preference for certain Alanine	Satinsky et al. 2014	Carbon metabolism	3.4.11.2
7	pepP/pepX	Prolyl aminopeptidase (PAP) or Xaa-Pro aminopeptidase (XAP)	PAPs preferentially cleave N-terminal proline residues from cellular proteins; XAPs are prolidases that catalyze the cleavage of Xaa-Prodipeptides or act on aminoacyl-hydroxyproline analogs but does notact on Pro-Pro bonds	Satinsky et al. 2014	Carbon metabolism	3.4.11.9
8	phaR	Polyhydroxyalkanoate regulator	Transcriptional regulator of polyhydroxyalkanoate biosynthesis	Satinsky et al. 2014/Gifford et al. 2013	Carbon metabolism	-
9	mxaF (moxF)	Methanol dehydrogenase	Catalyzes the oxidation of primary alcohols including methanol (Uniprot.org)	Shilova et al. 2014/Gifford et al. 2013	Carbon metabolism	1.1.2.7
10	GAPDH/gap	Glyceraldehyde-3-phosphate dehydrogenase	Catalyzes the reversible interconversion of glyceraldehyde-3-phosphate and 1,3-diphosphoglycerate	Satinsky et al. 2014/Shilova et al. 2014	Carbon metabolism	1.2.1.59
11	rbcL (IA)	Ribulose 1,5-bisphosphate carboxylase/oxygenase form IA (RuBisCO IA)	Catalyzes the first, rate-limiting step of the Calvin cycle, the primary pathway for photosynthetic carbon reduction in the oceans; rbcL IA has been found in α, β, and γ-proteobacteria, cyanobacteria and prochlorales	Satinsky et al. 2014/Shilova et al. 2014/Gifford et al. 2013	Carbon metabolism	4.1.1.39
12	rbcL (II)	Ribulose 1,5-bisphosphate carboxylase/oxygenase form II (RuBisCO II)	Catalyzes the first, rate-limiting step of the Calvin cycle, the primary pathway for photosynthetic carbon reduction in the oceans; rbcL II has been found in α, β, and γ-proteobacteria, and eukaryotes	Satinsky et al. 2014/Shilova et al. 2014/Gifford et al. 2014	Carbon metabolism	4.1.1.39
13	afuA/futA/hitA/idiA	Periplasmic Fe(III) ABC transporter	Iron-deficiency-induced, periplasmic iron-binding protein component of a ferric iron ABC-transporter system	Satinsky et al. 2014	Iron metabolism	-
14	IdiA	Iron deficiency protein/ Iron (III) transporter	Plays an important role in protecting the acceptor side of photosystem II (PSII) against oxidative damage, especially under iron-limiting growth conditions	Saito et al. 2014/Satinsky et al. 2014/Shilova et al. 2014	Iron metabolism	-
15	fldB/isiB	Flavodoxin	Replaces iron-requiring ferredoxin under iron stress	Shilova et al. 2014/Saito et al. 2014	Iron metabolism	-
16	cphA	Cyanophycin synthetase	Catalyzes the synthesis of cyanophycin granule polypeptide (CGP), which is used as a temporary nitrogen reserve.	Satinsky et al. 2014	Nitrogen metabolism	6.3.2.29/6.3.2
17	cphB	Cyanophycinase	Hydrolyzes cyanophicin to the dipeptide β-Asp-Arg, the first step in making stored amino acids available to the cell	Satinsky et al. 2014	Nitrogen metabolism	3.4.15.6
18	glnA	Glutamine synthetase	Catalyzes the ATP-dependent cycle whereby ammonia is incorporated into glutamate to form glutamine, the first step for ammonia assimilation into organic nitrogen	Satinsky et al. 2014/Shilova et al. 2014/Harke et al. 2013	Nitrogen metabolism	6.3.1.2
19	nirK	Nitrite reductase	Key enzyme in the dissimilatory denitrification process that catalyzes the reduction of nitrite to NO (contians coppar (Cu-Nir))	Satinsky et al. 2014/Shilova et al. 2014	Nitrogen metabolism	1.7.2.1

20 nirA	Nitrogen assimilation transcription factor nirA	Pathway-specific regulatory gene of nitrate assimilation; it activates the transcription of the genes for nitrate and nitrite reductases (niaD and niiA) (Uniprot.org)	Harke et al. 2013		
21 narB	nitrate reductase	Nitrate reductase is a key enzyme involved in the first step of nitrate assimilation in plants, fungi and bacteria.	Harke et al. 2013		
22 nirX/nosZ	Homeobox domain, in the nirA	Nitrous-oxide reductase is part of a bacterial respiratory system which	Shilova 2014	Nitrogen metabolism	1.7.2.4
23 nirS	Dissimilatory nitrite reductase	Key enzyme in the dissimilatory denitrification process that catalyzes	Shilova 2014	Nitrogen metabolism	1.7.2.1/1.7.9
24 nrtA/nrtB/nrtC	Nitrate/nitrite transport binding proteins	Essential compent of the nitrate transporting system. ntrC probably part of a high-affinity binding-protein-dependent transport system for nitrate (Uniprot.org)	Harke et al. 2013	Nitrogen metabolism	3.6.3.-
25 ntcA	N limitation transcriptional regulator	Serves as a transcriptional activator for alternate forms of nitrogen	Shilova et al. 2014/Saito et al. 2014	Nitrogen metabolism	-
26 UrtA/ure	Urea transporter protein	Transports urea	Saito et al. 2014/Shilova et al. 2014	Nitrogen metabolism	-
27 ureA/ureC	Urease subunit gamma/Urease subunit alpha	Catalyzes the hydrolysis of urea to ammonia and carbamic acid**	Shilova et al. 2014/Saito et al. 2014/Gifford et al. 2013	Nitrogen metabolism	3.5.1.5
28 nifH *	Nitrogenase iron protein NifH	The key enzymatic reactions in nitrogen fixation are catalyzed by the nitrogenase complex, which has 2 components: the iron protein and the molybdenum-iron protein (Uniport.org)	Shilova et al. 2014	Nitrogen metabolism	-
29 amt/amtB	Ammonium transporter/Ammonium transporter B	"amtB"- Membrane-bound ammonium/methylammonium transport B protein thought to be required during low [NH(x)]	Shilova et al. 2014/Satinsky et al. 2014/Gifford et al. 2013	Nitrogen metabolism	-
30 amoA	Ammonia monooxygenase subunit A	Catalyzes oxidation of ammonia to hydroxylamine, the first step in the oxidation of ammonia to nitrite.	Shilova et al. 2014/Satinsky et al. 2014/Gifford et al. 2013	Nitrogen metabolism	-
31 napA	Nitrate reductase subunit A	Large subunit of the Nap periplasmic nitrate reductase that catalyzes the first step of the denitrification process by conversion of nitrate to nitrite	Satinsky et al. 2014/Shilova et al. 2014	Nitrogen metabolism	-
32 glnB	N regulatory protein P-II	P-II indirectly controls the transcription of the glutamine synthetase gene (glnA). P-II prevents NR-II-catalyzed conversion of NR-I to NR-I-phosphate, the transcriptional activator of GlnA.	Shilova et al. 2014/Smith et al. 2013	Nitrogen metabolism	-
33 phnD	Phosphonate ABC transporter, periplasmic binding protein	Periplasmic binding protein of an ABC-type transporter system required for utilization of phosphonates and organophosphorus compounds	Satinsky et al. 2014/Shilova et al. 2014	Phosphorus metablolism	-
34 phnE	Phosphonate ABC transporter, integral membrane protein	Integral membrane protein of an ABC-type transporter system required for utilization of phosphonates and organophosphorus compounds	Satinsky et al. 2014	Phosphorus metablolism	-
35 phoD	Alkaline phosphatase	Belongs to the Pho regulon and codes for codes for alkaline phosphatase D (APaseD), which is a secreted phosphodiesterase	Satinsky et al. 2014/Shilova et al. 2014	Phosphorus metablolism	3.1.3.1
36 phoA	Alkaline phosphatase	Dephosphorylates organic phosphates and is induced under phosphate starvation as a means to generate free phosphate groups for uptake and use	Satinsky et al. 2014/Shilova et al. 2014	Phosphorus metablolism	3.1.3.1
37 phoU	Alkaline phosphatase	Serves as a signal transduction mediator, being involved in free inorganic P transport and acting as a regulator of the phosphatespecific transport system	Satinsky et al. 2014/Shilova et al. 2014	Phosphorus metablolism	-
38 phoX	Alkaline phosphatase, Ca2+ binding	Encodes an alkaline phosphatase that uses Ca2+ as a cofactor and can be responsible for extracellular phosphatase activity under phosphorus limitation	Satinsky et al. 2014/Shilova et al. 2014/Harke et al. 2013	Phosphorus metablolism	-
39 phnG/phnH/phnM	C-P lyase	Part of a membrane associated C-P lyase complex required for hydrolysis of C-P bonds to yield inorganic phosphate and the corresponding hydrocarbons	Satinsky et al. 2014	Phosphorus metablolism	-
40 pitA	Low affinity PO4 transporter	Low-affinity inorganic phosphate transporter and when inorganic phosphate is abundant, pitA is its major uptake system	Satinsky et al. 2014	Phosphorus metablolism	-

41 pstA/pstB/pstC/pstS	Phosphate ABC/permease transporter protein/periplasmic binding protein	Operon of the high-affinity phosphate-specific transport (Pst) system. (pstABCS)	Satinsky et al. 2014/Gifford et al. 2013/Harke et al. 2013/Penn et al. 2014	Phosphorus metablolism	3.6.3.27
42 UDP	Sulfoilipid uridine 5-diphosphate/UDP-sulfoquinovose synthase	Replace phospholipids for sulfolipids as an adaptive response to phosphate scarcity	Saito et al. 2014/Gifford et al. 2013	Phosphorus metablolism	-
43 ppk1	Polyphosphate kinase	Reversibly synthesizes inorganic polyphosphate, a storage polymer made up of tens to hundreds of phosphate residues linked together by high-energy bonds	Satinsky et al. 2014	Phosphorus metablolism	2.7.4.1
44 ppk2	Polyphosphate kinase	Can polymerize into an actin-like filament concurrent with its reversible synthesis of inorganic polyphosphate	Satinsky et al. 2014	Phosphorus metablolism	2.7.4.1
45 sphX	Phosphate transport system substrate-binding protein	May be involved in the system for phosphate transport across the cytoplasmic membrane (Uniprot.org)	Harke et al. 2013	Phosphorus metablolism	-
46 dmdA	DMSP demethylase	Catalyzes the first step in the DMSP demethylation pathway - cleavage of a methyl group from DMSP, eventually resulting inmethionine formation and C oxidation	Satinsky et al. 2014/Shilova et al. 2014	Sulfur metabolism	2.1.1.269
47 dddD	Type III acyl coenzyme A transferase	Mediates the cleavage of DMSP forming DMS and a 3-carbon compound	Satinsky et al. 2014/Shilova et al. 2014	Sulfur metabolism	-
48 dddQ	DMSP lyase	Mediates the cleavage of DMSP forming DMS and a 3-carbon compound	Satinsky et al. 2014/Shilova et al. 2014	Sulfur metabolism	-
49 cysI	Sulfite reductase	Assimilatory sulfite reduction enzyme that catalyzes the reaction sulfite to sulfide	Satinsky et al. 2014/Gifford et al. 2013	Sulfur metabolism	1.8.1.2
50 aprA	Adenosine-5'-phosphosulfate reductase (Apr), alpha subunit	Subunit A of dissimilatory adenosine-5'-phosphosulfate (APS) reductase aprAB gene complex that catalyzes the reduction of APS to AMP and sulfite during sulfur reduction	Satinsky et al. 2014	Sulfur metabolism	-
51 aprB	Adenosine-5'-phosphosulfate reductase (Apr), beta subunit	Subunit B of dissimilatory adenosine-5'-phosphosulfate (APS) reductase aprAB gene complex that catalyzes the reduction of APS to AMP and sulfite during sulfur reduction	Satinsky et al. 2014	Sulfur metabolism	-
52 cysK	Cysteine synthase	Involved in sulfur metabolism and synthesizes cysteine, the predominant mechanism by which inorganic sulfur is reduced and incorporated into organic compounds	Satinsky et al. 2014	Sulfur metabolism	2.5.1.47
53 PR/bop	Proteorhodopsin	Mediates light-driven proton pumps for harvesting and conversion of light into energy	Satinsky et al. 2014/Shilova et al. 2014	Other metabolisms	-
54 psbB	Photosystem II CP47 chlorophyll apoprotein	Photosystem II protein that binds to chlorophyll and is found in plants, algae, and cyanobacteria	Satinsky et al. 2014/Shilova et al. 2014/Harke et al. 2013	Other stresses	-

* Other "nif" genes that are of interest				
nifD	Nitrogenase reductase		Shilova et al. 2014	Nitrogen metabolism
nifE	Nitrogenase MoFe cofactor biosynthesis protein NifE		Shilova et al. 2014	Nitrogen metabolism
nifB	Nitrogenase cofactor biosynthesis protein NifB		Shilova et al. 2014	Nitrogen metabolism
nifK	Nitrogenase molybdenum-iron protein beta chain		Shilova et al. 2014	Nitrogen metabolism
nifN	Nitrogenase molybdenum-iron cofactor biosynthesis protein NifN		Shilova et al. 2014	Nitrogen metabolism
nifO	Nitrogenase-associated protein NifO		Shilova et al. 2014	Nitrogen metabolism
nifX	Nitrogenase molybdenum–iron protein NifX		Shilova et al. 2014	Nitrogen metabolism

Other relevant genes

1	pepA	Glutamyl aminopeptidase	Calcium-stimulated exopeptidase that selectively hydrolyze acidic amino acid residues with a preference for certain Glutamine	Satinsky et al. 2014	Carbon metabolism	
2	pepL	Leucyl aminopeptidase	Hydrolytic exopeptidase with a preference for certain Leucine and hydrophobic amino acid substrates	Satinsky et al. 2014	Carbon metabolism	
3	pepM	Methionyl aminopeptidase	Ubiquitous, essential exopeptidase that cleaves N-terminal Methionine residues from cellular proteins	Satinsky et al. 2014	Carbon metabolism	
4	pepN	Alanyl aminopeptidase	Broad specificity exopeptidase that cleaves amino acid residues from the N-terminus of peptides and protein substrates with a preference for certain Alanine	Satinsky et al. 2014	Carbon metabolism	
5	pepP/pepX	Prolyl aminopeptidase (PAP) or Xaa-Pro aminopeptidase (XAP)	PAPs preferentially cleave N-terminal proline residues from cellular proteins; XAPs are prolidases that catalyze the cleavage of Xaa-Pro dipeptides or act on aminoacyl-hydroxyproline analogs but does not act on Pro-Pro bonds	Satinsky et al. 2014	Carbon metabolism	
6	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	Catalyzes the reversible interconversion of glyceraldehyde-3-phosphate and 1,3-diphosphoglycerate	Satinsky et al. 2014	Carbon metabolism	
7	pgi	Glucose-6-phosphate isomerase	Catalyzes the reversible isomerization of glucose-6-phosphate and fructose-6-phosphate	Satinsky et al. 2014	Carbon metabolism	
8	metF	Methylenetetrahydrofolate reductase	Catalyzes the reduction of 5,10-methylenetetrahydrofolate to 5-methyltetrahydrofolate, which is then further used in the final step of methionine biosynthesis	Satinsky et al. 2014	Carbon metabolism	1.5.1.2
9	bglA	Beta-glucosidase	Catalyzes the hydrolysis of terminal non-reducing residues in betaglucosides with release of glucose	Satinsky et al. 2014	Carbon metabolism	
10	pcaH	Protocatechuate 3,4-dioxygenase (3,4-PCD)	Part of the β-ketoadipate pathway that catalyzes the conversion of protocatechuate to citric acid cycle intermediates	Satinsky et al. 2014	Carbon metabolism	
11	vanA	Vanillate demethylase	Involved in vanillate (a lignin-derived monoaryl) degradation by vanillate-utilizing aerobic bacteria	Satinsky et al. 2014	Carbon metabolism	
12	phaC	Polyhydroxyalkanoate synthase	Catalyzes the polymerization of (R)-3-hydroxybutyryl-CoA to form the polyhydroxyalkanoate polymer, the last step in polyhydroxyalkanoate biosynthesis	Satinsky et al. 2014	Carbon metabolism	
13	phaP	Phasin	Coats the surface of the polyhydroxyalkanoate granules, preventing them from coalescing, in turn stabilizing the granules	Satinsky et al. 2014	Carbon metabolism	
14	phaR	Polyhydroxyalkanoate regulator	Transcriptional regulator of polyhydroxyalkanoate biosynthesis	Satinsky et al. 2014	Carbon metabolism	
15	phaZ	Polyhydroxyalkanoate depolymerase	Responsible for intracellular degradation of polyhydroxyalkanoate	Satinsky et al. 2014	Carbon metabolism	
16	amoA	Ammonia monooxygenase subunit A	Catalyzes oxidation of ammonia to hydroxylamine, the first step in the oxidation of ammonia to nitrite.	Satinsky et al. 2014	Nitrogen metabolism	
17	amtB	Ammonium transporter B	Membrane-bound ammonium/methylammonium transport B protein thought to be required during low [NH(x)]	Satinsky et al. 2014	Nitrogen metabolism	
18	cphA	Cyanophycin synthetase	Catalyzes the synthesis of cyanophycin granule polypeptide (CGP), which is used as a temporary nitrogen reserve.	Satinsky et al. 2014	Nitrogen metabolism	
19	cphB	Cyanophycinase	Hydrolyzes cyanophicin to the dipeptide β-Asp-Arg, the first step in making stored amino acids available to the cell	Satinsky et al. 2014	Nitrogen metabolism	
20	glnA	Glutamine synthetase	Catalyzes the ATP-dependent cycle whereby ammonia is incorporated into glutamate to form glutamine, the first step for ammonia assimilation into organic nitrogen	Satinsky et al. 2014/Saito. 2014	Nitrogen metabolism	
21	napA	Nitrate reductase subunit A	Large subunit of the Nap periplasmic nitrate reductase that catalyzes the first step of the denitrification process by conversion of nitrate to nitrite	Satinsky et al. 2014	Nitrogen metabolism	

22 nirK	Nitrite reductase	Key enzyme in the dissimilatory denitrification process that catalyzes the reduction of nitrite to NO	Satinsky et al. 2014	Nitrogen metabolism
23 phnD	Phosphonate ABC transporter, periplasmic binding protein	Periplasmic binding protein of an ABC-type transporter system required for utilization of phosphonates and organophosphorus compounds	Satinsky et al. 2014	Phosphorus metablolism
24 phnE	Phosphonate ABC transporter, integral membrane protein	Integral membrane protein of an ABC-type transporter system required for utilization of phosphonates and organophosphorus compounds	Satinsky et al. 2014	Phosphorus metablolism
25 phnG	C-P lyase	Part of a membrane associated C-P lyase complex required for hydrolysis of C-P bonds to yield inorganic phosphate and the corresponding hydrocarbons.	Satinsky et al. 2014	Phosphorus metablolism
26 phnH	C-P lyase	Part of a membrane associated C-P lyase complex required for hydrolysis of C-P bonds to yield inorganic phosphate and the corresponding hydrocarbons	Satinsky et al. 2014	Phosphorus metablolism
27 phnM	C-P lyase	Part of a membrane associated C-P lyase complex required for hydrolysis of C-P bonds to yield inorganic phosphate and the corresponding hydrocarbons	Satinsky et al. 2014	Phosphorus metablolism
28 phoA	Alkaline phosphatase	Dephosphorylates organic phosphates and is induced under phosphate starvation as a means to generate free phosphate groups for uptake and use	Satinsky et al. 2014	Phosphorus metablolism
29 phoD	Alkaline phosphatase	Belongs to the Pho regulon and codes for codes for alkaline phosphatase D (APaseD), which is a secreted phosphodiesterase	Satinsky et al. 2014	Phosphorus metablolism
30 phoU	Alkaline phosphatase	Serves as a signal transduction mediator, being involved in free inorganic P transport and acting as a regulator of the phosphatespecific transport system	Satinsky et al. 2014	Phosphorus metablolism
31 phoX	Alkaline phosphatase, Ca2+ binding	Encodes an alkaline phosphatase that uses Ca2+ as a cofactor and can be responsible for extracellular phosphatase activity under phosphorus limitation	Satinsky et al. 2014	Phosphorus metablolism
32 pitA	Low affinity PO4 transporter	Low-affinity inorganic phosphate transporter and when inorganic phosphate is abundant, pitA is its major uptake system	Satinsky et al. 2014	Phosphorus metablolism
33 ppk1	Polyphosphate kinase	Reversibly synthesizes inorganic polyphosphate, a storage polymer made up of tens to hundreds of phosphate residues linked together by high-energy bonds	Satinsky et al. 2014	Phosphorus metablolism
34 ppk2	Polyphosphate kinase	Can polymerize into an actin-like filament concurrent with its reversible synthesis of inorganic polyphosphate	Satinsky et al. 2014	Phosphorus metablolism
35 pstA	Phosphate ABC transporter, permease	Membrane permease in the high-affinity phosphate-specific transport (Pst) system that facilitates the transport of phosphate across the membrane	Satinsky et al. 2014	Phosphorus metablolism
36 pstC	Phosphate ABC transporter, permease	Membrane permease in the high-affinity phosphate-specific transport (Pst) system that facilitates the transport of phosphate across the membrane	Satinsky et al. 2014	Phosphorus metablolism
37 pstS	Phosphate ABC transporter, periplasmic binding protein	Phosphate-binding lipoprotein found within the periplasm of the it is part of the high-affinity phosphate-specific transport (Pst) system	Satinsky et al. 2014	Phosphorus metablolism
38 aprA	Adenosine-5'-phosphosulfate reductase (Apr), alpha subunit	Subunit A of dissimilatory adenosine-5'-phosphosulfate (APS) reductase aprAB gene complex that catalyzes the reduction of APS to AMP and sulfite during sulfur reduction	Satinsky et al. 2014	Sulfur metabolism
39 aprB	Adenosine-5'-phosphosulfate reductase (Apr), beta subunit	Subunit B of dissimilatory adenosine-5'-phosphosulfate (APS) reductase aprAB gene complex that catalyzes the reduction of APS to AMP and sulfite during sulfur reduction	Satinsky et al. 2014	Sulfur metabolism
40 cysI	Sulfite reductase	Assimilatory sulfite reduction enzyme that catalyzes the reaction sulfite to sulfide	Satinsky et al. 2014	Sulfur metabolism

41 cysK	Cysteine synthase	Involved in sulfur metabolism and synthesizes cysteine, the predominant mechanism by which inorganic sulfur is reduced and incorporated into organic compounds	Satinsky et al. 2014	Sulfur metabolism
42 dddD	Type III acyl coenzyme A transferase	Mediates the cleavage of DMSP forming DMS and a 3-carbon compound	Satinsky et al. 2014	Sulfur metabolism
43 dddQ	DMSP lyase	Mediates the cleavage of DMSP forming DMS and a 3-carbon compound	Satinsky et al. 2014	Sulfur metabolism
44 dmdA	DMSP demethylase	Catalyzes the first step in the DMSP demethylation pathway - cleavage of a methyl group from DMSP, eventually resulting inmethionine formation and C oxidation	Satinsky et al. 2014	Sulfur metabolism
45 soxA	Cytochrome c (diheme)	One of the seven structural proteins involved in sulfur oxidation combines with the SoxX protein form a cytochrome c complex that is located in the periplasm of the cell and is involved in electron transport	Satinsky et al. 2014	Sulfur metabolism
46 soxB	Sulfate thiohydrolase	One of the seven structural proteins involved in sulfur oxidation a type of cytochrome c protein that is located in the periplasm and involved in the electron transport chain	Satinsky et al. 2014	Sulfur metabolism
47 fliC	Filament protein; flagellin	Structural filament protein, synthesized in the cytosol, composed monomeric subunits that are polymerized into the long helical filament of the bacterial flagellum	Satinsky et al. 2014	Chemotaxis and Motility
48 fliF	MS-ring protein	Transmembrane flagellar MS-ring protein, part of the flagellar basal body, that anchors the flagellum to the cytoplasmic membrane	Satinsky et al. 2014	Chemotaxis and Motility
49 fliG	Flagellar motor switch protein	Essential for assembly, rotation and clockwise/counter-clockwise switching of the bacterial flagellum	Satinsky et al. 2014	Chemotaxis and Motility
50 motA	Flagellar motor protein	Along with MotB couples flagellar rotation to proton/sodium motive force across the membrane and forms the stator elements of the rotary flagellar machine, required for flagellar rotation	Satinsky et al. 2014	Chemotaxis and Motility
51 motB	Flagellar motor protein	Along with MotA couples flagellar rotation to proton/sodium motive force across the membrane and forms the stator elements of the rotary flagellar machine, required for flagellar rotation	Satinsky et al. 2014	Chemotaxis and Motility
52 cheA	Histidine kinase	A cytoplasmic histidine kinase that donates phosphate groups to CheY and CheB, which control flagellar responses and sensory adaptation, respectively	Satinsky et al. 2014	Chemotaxis and Motility
53 cheB	Methylesterase	A phosphorylation-activated response regulator involved in reversible modification of bacterial chemotaxis receptors. It is required for tumbling movement and regulates tumbling frequency based on perceived tumble-modulating signals (i.e. Nutrient concentration) formed by the chemoreceptors	Satinsky et al. 2014	Chemotaxis and Motility
54 cheR	Methyltransferase	Involved in reversible modification of bacterial chemotaxis receptors, it plays a role in the chemosensory response and adaptation of the cell to chemical stimuli	Satinsky et al. 2014	Chemotaxis and Motility
55 cheW	Signaling protein	Plays a role in coupling methyl-accepting chemotaxis proteins, it regulates motility behavior by two distinct signals, one that stimulates and one that inhibits the intracellular phosphorylation cascade by its effect on the histidine kinase CheA	Satinsky et al. 2014	Chemotaxis and Motility
56 thiC	Phosphomethylpyrimidine synthase	Catalyzes the pyrimidine branch of the Thiamin biosynthesis pathway, converting 5-aminoimidazole ribonucleotide to hydroxymethylpyrimidine phosphate	Satinsky et al. 2014	Vitamins
57 thiL	Thiamin-monophosphate kinase	Catalyzes the final step of the thiamin pyrophosphate biosynthesis pathway	Satinsky et al. 2014	Vitamins

58 pdxH	Pyridoxine 5'-phosphate oxidase	Catalyzes the oxidation of pyridoxine 5'-phosphate to pyridoxal 5'-phosphate in the final step of vitamin B6 biosynthesis	Satinsky et al. 2014	Vitamins	
59 pdxJ	Pyridoxine 5'-phosphate synthase	Catalyzes the condensation of 1-deoxy-d-xylulose-5-phosphate and 1-amino-3-oxo-4-(phosphohydroxy)propan-2-one to pyridoxine 5'-phosphate, a reaction involved in de novo biosynthesis of pyridoxine (vitamin B6) and pyridoxal phosphate	Satinsky et al. 2014	Vitamins	
60 fecA	Ferric dicitrate transporter	TonB-ExbB-dependent ferric-siderophore specific outer membrane receptor protein. When intracellular iron is low, exogenous ferric citrate binds to the FecA receptor, which signals for and aids in translocation of ferric citrate into the cell	Satinsky et al. 2014	Iron metabolism	
61 feoB	Fe(II) G protein-like transporter	Membrane-bound G protein-like transporter, essential for Fe(II) uptake in bacteria during conditions of low oxygen	Satinsky et al. 2014	Iron metabolism	
62 Ftr1	High affinity Fe(II) permease	Permease component of a high-affinity Fe(II) uptake system. Expression may be increased during Fe limitation	Satinsky et al. 2014	Iron metabolism	
63 afuA/futA/hitA/idiA	Periplasmic Fe(III) ABC transporter	Iron-deficiency-induced, periplasmic iron-binding protein component of a ferric iron ABC-transporter system	Satinsky et al. 2014	Iron metabolism	
64 afuB/futB	Fe(III) ABC transporter permease	Hydrophobic ferric iron ABC transporter permease protein	Satinsky et al. 2014	Iron metabolism	
65 PR	Proteorhodopsin	Mediates light-driven proton pumps for harvesting and conversion of light into energy	Satinsky et al. 2014	Other metabolism	
66 bchX	Chlorophyll iron protein	Part of a photosynthetic gene cluster involved in redox reactions of the bacteriochlorophyll biosynthesis pathway	Satinsky et al. 2014	Photoautotrophy and Phototrophy	
67 pufL	Photosynthetic reaction center subunit L	The light subunit of the photosynthetic reaction center, it helps provide the scaffolding for the chromophore in the reaction center	Satinsky et al. 2014	Photoautotrophy and Phototrophy	
68 pufM	Photosynthetic reaction center subunit M	The medium subunit of the photosynthetic reaction center, it helps provide the scaffolding for the chromophore in the reaction center	Satinsky et al. 2014	Photoautotrophy and Phototrophy	
69 psbB	Photosystem II CP47 chlorophyll apoprotein	Photosystem II protein that binds to chlorophyll and is found in plants, algae, and cyanobacteria	Satinsky et al. 2014	Photoautotrophy and Phototrophy	
70 cpcD	Phycocyanin-assoc. linker polypeptide	Structural component of the phycobilisome	Satinsky et al. 2014	Photoautotrophy and Phototrophy	
71 α-ca	α carbonic anhydrase	Zinc metalloenzyme found in bacteria, archaea, and eukaryota that participates in CO_2 diffusion, interconversion of CO_2 and HCO_3 during photosynthesis, pH homeostasis, and ion transport	Satinsky et al. 2014	Photoautotrophy and Phototrophy	
72 ε-ca	ε carbonic anhydrase	Zinc metalloenzyme found in cyanobacteria carboxysomes and chemolithoautotrophs that participates in CO_2 diffusion, interconversion of CO_2 and HCO_3 during photosynthesis, pH homeostasis, and ion transport	Satinsky et al. 2014	Photoautotrophy and Phototrophy	
73 rbcL (IA)	Ribulose 1,5-bisphosphate carboxylase/oxygenase form IA (RuBisCO IA)	Catalyzes the first, rate-limiting step of the Calvin cycle, the primary pathway for photosynthetic carbon reduction in the oceans; rbcL IA has been found in α, β, and γ-proteobacteria, cyanobacteria and prochlorales	Satinsky et al. 2014	Carbon metabolism	
74 rbcL (II)	Ribulose 1,5-bisphosphate carboxylase/oxygenase form II (RuBisCO II)	Catalyzes the first, rate-limiting step of the Calvin cycle, the primary pathway for photosynthetic carbon reduction in the oceans; rbcL II has been found in α, β, and γ-proteobacteria, and eukaryotes	Satinsky et al. 2014	Carbon metabolism	
75 cdcA	Cadmium containing carbonic anhydrase		Shilova et al. 2014	Carbon metabolism	
76 chpX	CO_2 hydration protein ChpX		Shilova et al. 2014	Carbon metabolism	
77 dca1	Delta carbonic anhydrase		Shilova et al. 2014	Carbon metabolism	
78 dxs	1-deoxy-D-xylulose-5-phosphate synthase		Shilova et al. 2014	Carbon metabolism	1.1.1.267

79	fae	Formaldehyde-activating enzyme	Shilova et al. 2014	Carbon metabolism	
80	fhcD	Formylmethanofuran-tetrahydromethanopterin formyltransferase	Shilova et al. 2014	Carbon metabolism	
81	gidA	Glucose-inhibited division protein A	Shilova et al. 2014	Carbon metabolism	
82	icd	Isocitrate dehydrogenase	Shilova et al. 2014	Carbon metabolism	1.1.1.42
83	mch	Methenyltetrahydromethanopterin cyclohydrolase	Shilova et al. 2014	Carbon metabolism	
84	mtdB	Methylenetetrahydromethanopterin dehydrogenase	Shilova et al. 2014	Carbon metabolism	
85	mxaF	Methanol dehydrogenase	Shilova et al. 2014	Carbon metabolism	
86	pmoA	Methane monooxygenase	Shilova et al. 2014	Carbon metabolism	
87	ppc	Phosphoenolpyruvate carboxylase	Shilova et al. 2014	Carbon metabolism	
88	prsA	Ribose-phosphate pyrophosphokinase	Shilova et al. 2014	Carbon metabolism	
89	pyk	Pyruvate kinase	Shilova et al. 2014	Carbon metabolism	2.7.1.4
90	sbtA	Sodium-dependent bicarbonate transporter	Shilova et al. 2014	Carbon metabolism	
91	dddL	DMSP lyase	Shilova et al. 2014	Sulfur metabolism	
92	dddP	DMSP lyase	Shilova et al. 2014	Sulfur metabolism	
93	hao	Hydroxylamine oxidoreductase	Shilova et al. 2014	Nitrogen metabolism	
94	metC	Cystathionine beta-lyase family protein involved in Al resistance	Shilova et al. 2014	Nitrogen metabolism	
95	narB	Assimilatory nitrate reductase in bacteria	Shilova et al. 2014	Nitrogen metabolism	
96	nifB	Nitrogenase cofactor biosynthesis protein NifB	Shilova et al. 2014	Nitrogen metabolism	
97	nifD	Nitrogenase reductase	Shilova et al. 2014	Nitrogen metabolism	
98	nifE	Nitrogenase MoFe cofactor biosynthesis protein NifE	Shilova et al. 2014	Nitrogen metabolism	
99	nifH	Nitrogenase iron protein NifH	Shilova et al. 2014	Nitrogen metabolism	
100	nifK	Nitrogenase molybdenum-iron protein beta chain	Shilova et al. 2014	Nitrogen metabolism	
101	nifN	Nitrogenase molybdenum-iron cofactor biosynthesis protein NifN	Shilova et al. 2014	Nitrogen metabolism	
102	nifO	Nitrogenase-associated protein NifO	Shilova et al. 2014	Nitrogen metabolism	
103	nifX	Nitrogenase molybdenum–iron protein NifX	Shilova et al. 2014	Nitrogen metabolism	
104	nirA	Ferredoxin-nitrite reductase	Shilova et al. 2014	Nitrogen metabolism	
105	nirS	Dissimilatory nitrite reductase	Shilova et al. 2014	Nitrogen metabolism	
106	nirX	Homeobox domain, in the nirA operon	Shilova et al. 2014	Nitrogen metabolism	
107	nrtP	Nitrate transporter	Shilova et al. 2014	Nitrogen metabolism	
108	ntcA	N limitation transcriptional regulator	Shilova et al. 2014	Nitrogen metabolism	
109	slc17A	Amino-acid transporter	Shilova et al. 2014	Nitrogen metabolism	

110	ureA	Urease alpha subunit	Shilova et al. 2014	Nitrogen metabolism	
111	ureB	Urease beta subunit	Shilova et al. 2014	Nitrogen metabolism	
112	ureC	Urease	Shilova et al. 2014	Nitrogen metabolism	
113	ureD	Urease accessory protein UreD	Shilova et al. 2014	Nitrogen metabolism	
114	ureE	Urease accessory protein UreE	Shilova et al. 2014	Nitrogen metabolism	
115	ureF	Urease accessory protein UreF	Shilova et al. 2014	Nitrogen metabolism	
116	ureG	Urease accessory protein UreG	Shilova et al. 2014	Nitrogen metabolism	
117	ureH	Urease accessory protein UreH-like protein	Shilova et al. 2014	Nitrogen metabolism	
118	ureX	urease subunit	Shilova et al. 2014	Nitrogen metabolism	
119	urtA	Urea ABC transporter, substrate-binding protein	Shilova et al. 2014	Nitrogen metabolism	
120	amt	Ammonium transporter	Shilova et al. 2014	Nitrogen metabolism	
121	arg	N-acetyl transferase	Shilova et al. 2014	Nitrogen metabolism	
122	carA	Carbamoyl-phosphate synthase	Shilova et al. 2014	Nitrogen metabolism	
123	cynA	Cyanate transporter	Shilova et al. 2014	Nitrogen metabolism	
124	sodC	Cu–Zn superoxide dismutase	Shilova et al. 2014	Nitrogen metabolism	
125	acr3	Arsenite transport (efflux)	Shilova et al. 2014	Phosphorus metablolism	
126	arsC	Arsenate reductase	Shilova et al. 2014	Phosphorus metablolism	1.2.4.1
127	glpQ	Glycerophosphoryl diester phosphodiesterase	Shilova et al. 2014	Phosphorus metablolism	
128	phnA	Phosphonoacetate hydrolase	Shilova et al. 2014	Phosphorus metablolism	
129	phnJ	Phosphonate lyase	Shilova et al. 2014	Phosphorus metablolism	
130	phoH	P stress-inducible protein	Shilova et al. 2014	Phosphorus metablolism	
131	polyP1	Poly-phosphate accumulation	Shilova et al. 2014	Phosphorus metablolism	
132	psiP	Highly expressed under low P	Shilova et al. 2014	Phosphorus metablolism	
133	ptrA	Possible P transcriptional regulator	Shilova et al. 2014	Phosphorus metablolism	
134	sqdB	Sulfolipid biosynthesis protein	Shilova et al. 2014	Phosphorus metablolism	
135	sit	Silicon transporter	Shilova et al. 2014	Silica transport	
136	sit1	Silicon transporter	Shilova et al. 2014	Silica transport	
137	sit2	Silicon transporter	Shilova et al. 2014	Silica transport	
138	sit3	Silicon transporter	Shilova et al. 2014	Silica transport	
139	cirA	Ferric iron-catecholate outer membrane transporter	Shilova et al. 2014	Iron metabolism	
140	dpsA	Ferritin-like diiron-binding domain	Shilova et al. 2014	Iron metabolism	
141	feoA	Ferrous iron transport protein A	Shilova et al. 2014	Iron metabolism	
142	fepB	ABC-type Fe3 + - hydroxamate transport system	Shilova et al. 2014	Iron metabolism	
143	fepC	ABC-type cobalamin/Fe3 + - siderophores transport systems	Shilova et al. 2014	Iron metabolism	
144	fepD	Fe3 + siderophore transport system	Shilova et al. 2014	Iron metabolism	
145	fldA (isiB)	Flavodoxin eukaryotic	Shilova et al. 2014	Iron metabolism	
146	fldB/isiB	Flavodoxin	Shilova et al. 2014/Saito et al. 2014	Iron metabolism	
147	fur	Ferric transcriptional regulator	Shilova et al. 2014	Iron metabolism	
148	idiA	Iron (III) transporter	Shilova et al. 2014	Iron metabolism	
149	isiA	Iron stress-induced chlorophyll-binding protein	Shilova et al. 2014	Iron metabolism	
150	isiP	Iron stress-induced protein	Shilova et al. 2014	Iron metabolism	

151	pep_m20	Possible Peptidase family M20/M25/M56	Shilova et al. 2014	Iron metabolism	
152	petF	Ferredoxin	Shilova et al. 2014	Iron metabolism	
153	piuC	Uncharacterized iron-regulated protein	Shilova et al. 2014	Iron metabolism	
154	pmm1359	Predicted membrane protein, ironstress responsive	Shilova et al. 2014	Iron metabolism	
155	pvsB	Vibrioferrin biosynthesis protein PvsB	Shilova et al. 2014	Iron metabolism	
156	sam	SAM-methyltransferase	Shilova et al. 2014	Iron metabolism	
157	chrA	Chromate transporter	Shilova et al. 2014	Other metabolism	
158	cobN	Cobaltochelatase CobN	Shilova et al. 2014	Other metabolism	
159	mopA	Heme-binding region from putitive Mn-oxidase	Shilova et al. 2014	Other metabolism	
160	mfs	Multidrug efflux transporter, proline/betaine transporter	Shilova et al. 2014	Other stresses	
161	NiSOD	Putative nickel-containing superoxide dismutase precursor	Shilova et al. 2014	Other stresses	
162	NUDIX	nudix hydrolase	Shilova et al. 2014	Other stresses	
163	phrB	DNA photolyase	Shilova et al. 2014	Other stresses	
164	pip	Proline iminopeptidase	Shilova et al. 2014	Other stresses	
165	pmm1148	EF-1 guanine nucleotide exchange	Shilova et al. 2014	Other stresses	
166	pmm1462	Conserved hypothetical protein PMM1462	Shilova et al. 2014	Other stresses	
167	ptox	Plastoquinol terminal oxidase	Shilova et al. 2014	Other stresses	
168		Peptide/nickel transport	Gifford et al. 2013		
169		Sorbitol/mannitol transport	Gifford et al. 2013		
170		Benzoate degradation	Gifford et al. 2013		
171		Carbon-monoxide dehydrogenase	Gifford et al. 2013		
172		Methanesulfonate trans. and met.	Gifford et al. 2013		
173		Formate dehydrogenase	Gifford et al. 2013		1.2.1.2
174		Iron(III) ABC transport	Gifford et al. 2013		
175		peptide/nickel ABC transport	Gifford et al. 2013		
176		Glucose-methanol-choline oxidoreductase	Gifford et al. 2013		
177		Sulfonate/nitrate/taurine ABC transport	Gifford et al. 2013		
178		Alpha-ketoglutarate-dependent taurine dioxygenase	Gifford et al. 2013		
179		Carboxymethylenebutenolidase	Gifford et al. 2013		
180		5-aminolevulinate synthase	Gifford et al. 2013		2.3.1.37
181		Branched-chain amino acid ABC transport	Gifford et al. 2013		
182		Sulfur oxidation	Gifford et al. 2013		
183		TRAP dicarboxylate transporter	Gifford et al. 2013		
184		Putative enoyl-CoA hydratase/isomerase	Gifford et al. 2013		

185	Beta-ketoacyl synthase family protein	Gifford et al. 2013	
186	Taurine--pyruvate aminotransferase	Gifford et al. 2013	
187	Polyhydroxyalkonate synthesis repressor	Gifford et al. 2013	
188	C4-dicarboxylate TRAP transporter	Gifford et al. 2013	
189	Tricarboxylic TRAP transport	Gifford et al. 2013	
190	Glycine betaine/proline transport	Gifford et al. 2013	
191	Ectoine/hydroxyectoine ABC transporter	Gifford et al. 2013	
192	Adenylylsulfate reductase	Gifford et al. 2013	1.8.99.2
193	Taurine transport system periplasmic protein	Gifford et al. 2013	
194	Spermidine/putrescine-binding periplasmic protein	Gifford et al. 2013	
195	TRAP mannitol/chloroaromatic transport	Gifford et al. 2013	
196	Phosphonate transport substrate-binding protein	Gifford et al. 2013	
197	Ferrous iron permease EfeU	Gifford et al. 2013	
198	Poly3-hydroxyalkanoate polymerase (PHAsynthase)	Gifford et al. 2013	
199	Putative Na+/solute symporter	Gifford et al. 2013	
200	Taurine dioxygenase	Gifford et al. 2013	
201	Putative tricarboxylic transport	Gifford et al. 2013	
202	Type 4 fimbrial biogenesis related protein	Gifford et al. 2013	
203	Na+:H+ antiporter	Gifford et al. 2013	
204	Aerobic anoxygenic photosynthesis	Gifford et al. 2013	
205	Choline transporter	Gifford et al. 2013	
206	TonB dependant receptors	Gifford et al. 2013	
207	Cellobiosidase	Gifford et al. 2013	
208	Glucosidases	Gifford et al. 2013	
209	Betalactamase	Gifford et al. 2013	
210	Lipid A export ATP-binding/permease MsbA	Gifford et al. 2013	
211	biotin/lipoyl attachment containing protein	Gifford et al. 2013	
212	bacilysin biosynthesis oxidoreductase BacC	Gifford et al. 2013	
213	Nucleoside transport (NupC)	Gifford et al. 2013	
214	2-methylcitrate dehydratase	Gifford et al. 2013	
215	Citrate lyase	Gifford et al. 2013	
216	Bacterioferritin	Gifford et al. 2013	
217	Ecotine synth. (diaminobutyrate-2-oxoglutarate AT)	Gifford et al. 2013	
218	Citrate transporter	Gifford et al. 2013	

219		Na+/solute symporter	Gifford et al. 2013	
220		Na+-transporting NADH:ubiquinone oxid.red.	Gifford et al. 2013	
221		H+transporting two-sector ATPase	Gifford et al. 2013	
222		Vitamin B6 biosynthesis protein	Gifford et al. 2013	
223		Cobalamin B12-binding domain protein	Gifford et al. 2013	
224	glnB	N regulatory protein P-II	Shilova et al. 2014/Smith et al. 2013	Nitrogen metabolism
225	UrtA	Urea transporter	Saito et al. 2014	

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