

ДОПОЛНИТЕЛЬНЫЕ МАТЕРИАЛЫ

ЭКСПЕРИМЕНТАЛЬНЫЕ СТАТЬИ

**ОБРАЗОВАНИЕ МЕТАНА В ПРЕСНОМ ОЗЕРЕ УМЕРЕННОГО ПОЯСА В
ПЕРИОД ИНТЕНСИВНОГО ЦВЕТЕНИЯ ЦИАНОБАКТЕРИЙ**

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Table S1. Потенциальные гомологи генов синтеза и разложения фосфоната в геноме *Ca. “Fonsibacter ubiquis”* (CP024034.1).

gene locus tag	cdd profile	rpsblast percent identity	profile length	alignment length	e-value
CR143_RS00060	cd03256, ABC_PhnC_transporter, ATP-binding cassette domain of the binding protein-dependent phosphonate transport system. Phosphonates are a class of organophosphorus compounds characterized by a chemically stable carbon-to-phosphorus (C-P) bond. Phosphonates are widespread among naturally occurring compounds in all kingdoms of wildlife, but only prokaryotic microorganisms are able to cleave this bond. Certain bacteria such as <i>E. coli</i> can use alkylphosphonates as a phosphorus source. ABC transporters are a subset of nucleotide hydrolases that contain a signature motif, Q-loop, and H-loop/switch region, in addition to, the Walker A motif/P-loop and Walker B motif commonly found in a number of ATP- and GTP-binding and hydrolyzing proteins.	32,895	241	228	8,53E-39
CR143_RS00315	cd03256, ABC_PhnC_transporter, ATP-binding cassette domain of the binding protein-dependent phosphonate transport system. Phosphonates are a class of organophosphorus compounds characterized by a chemically stable carbon-to-phosphorus (C-P) bond. Phosphonates are widespread among naturally occurring compounds in all kingdoms of wildlife, but only prokaryotic microorganisms are able to cleave this bond. Certain bacteria such as <i>E. coli</i> can use alkylphosphonates as a phosphorus source. ABC transporters are a subset of nucleotide hydrolases that contain a signature motif, Q-loop, and H-loop/switch region, in addition to, the Walker A motif/P-loop and Walker B motif commonly found in a number of ATP- and GTP-binding and hydrolyzing proteins.	38,636	241	220	2,4E-59
CR143_RS00315	TIGR02315, Phosphonates_import_ATP-binding_protein_PhnC, phosphonate ABC transporter, ATP-binding protein. Phosphonates are a class of phosphorus-containing organic compound with a stable direct C-P bond rather than a C-O-P linkage. A number of bacterial species have operons, typically about 14 genes in size, with genes for ATP-dependent transport of phosphonates, degradation, and regulation of the expression of the system. Members of this protein family are the ATP-binding cassette component of tripartite ABC transporters of phosphonates. [Transport and binding proteins, Anions].	37,156	243	218	8,8E-51
CR143_RS00315	TIGR03265, PhnT2, putative 2-aminoethylphosphonate ABC transporter, ATP-binding protein. This ABC transporter ATP-binding protein is found in a number of genomes in operon-like contexts strongly suggesting a substrate specificity for 2-aminoethylphosphonate (2-AEP). The characterized PhnSTUV system is absent in the genomes in which this system is found. These genomes encode systems for the catabolism of 2-AEP, making the need for a 2-AEP-specific transporter likely. [Transport and binding proteins, Amino acids, peptides and amines].	37,745	353	204	2,61E-46
CR143_RS00315	COG4778, PhnL, ABC-type phosphonate transport system, ATPase component [Inorganic ion transport and metabolism].	31,527	235	203	6,86E-34
CR143_RS00315	PRK11701, phnK, phosphonate C-P lyase system protein PhnK; Provisional.	25,214	258	234	2,57E-23
CR143_RS00315	COG4107, PhnK, ABC-type phosphonate transport system, ATPase component [Inorganic ion transport and metabolism].	28,986	258	207	8,07E-23
CR143_RS00315	COG1101, PhnK, ABC-type uncharacterized transport system, ATPase component [General function prediction only].	26,923	263	234	1,25E-21
CR143_RS00375	cd00377, ICL_PEPM, Members of the ICL/PEPM enzyme family catalyze either P-C or C-C bond formation/cleavage. Known members are phosphoenolpyruvate mutase (PEPM), phosphonopyruvate hydrolase	28,571	243	315	2,98E-77

	(PPH), carboxyPEP mutase (CPEP mutase), oxaloacetate hydrolase (OAH), isocitrate lyase (ICL), and 2-methylisocitrate lyase (MICL). Isocitrate lyase (ICL) catalyzes the conversion of isocitrate to succinate and glyoxylate, the first committed step in the glyoxylate pathway. This carbon-conserving pathway is present in most prokaryotes, lower eukaryotes and plants, but has not been observed in vertebrates. PEP mutase (PEPM) turns phosphoenolpyruvate (PEP) into phosphonopyruvate (P-pyr), an important intermediate in the formation of organophosphonates, which function as antibiotics or play a role in pathogenesis or signaling. P-pyr can be hydrolyzed by phosphonopyruvate hydrolase (PPH) to form pyruvate and phosphate. Oxaloacetate acetylhydrolase (OAH) catalyzes the hydrolytic cleavage of oxaloacetate to form acetate and oxalate, an important pathway to produce oxalate in filamentous fungi. 2-methylisocitrate lyase (MICL) cleaves 2-methylisocitrate to pyruvate and succinate, part of the methylcitrate cycle for the alpha-oxidation of propionate.				
CR143_RS00375	cd06556, ICL_KPHMT, Members of the ICL/PEPM_KPHMT enzyme superfamily catalyze the formation and cleavage of either P-C or C-C bonds. Typical members are phosphoenolpyruvate mutase (PEPM), phosphonopyruvate hydrolase (PPH), carboxyPEP mutase (CPEP mutase), oxaloacetate hydrolase (OAH), isocitrate lyase (ICL), 2-methylisocitrate lyase (MICL), and ketopantoate hydroxymethyltransferase (KPHMT).	22,523	240	333	1,47E-49
CR143_RS01045	cd03256, ABC_PhnC_transporter, ATP-binding cassette domain of the binding protein-dependent phosphonate transport system. Phosphonates are a class of organophosphorus compounds characterized by a chemically stable carbon-to-phosphorus (C-P) bond. Phosphonates are widespread among naturally occurring compounds in all kingdoms of wildlife, but only prokaryotic microorganisms are able to cleave this bond. Certain bacteria such as E. coli can use alkylphosphonates as a phosphorus source. ABC transporters are a subset of nucleotide hydrolases that contain a signature motif, Q-loop, and H-loop/switch region, in addition to, the Walker A motif/P-loop and Walker B motif commonly found in a number of ATP- and GTP-binding and hydrolyzing proteins.	29,255	241	188	8,43E-21
CR143_RS01650	cd03256, ABC_PhnC_transporter, ATP-binding cassette domain of the binding protein-dependent phosphonate transport system. Phosphonates are a class of organophosphorus compounds characterized by a chemically stable carbon-to-phosphorus (C-P) bond. Phosphonates are widespread among naturally occurring compounds in all kingdoms of wildlife, but only prokaryotic microorganisms are able to cleave this bond. Certain bacteria such as E. coli can use alkylphosphonates as a phosphorus source. ABC transporters are a subset of nucleotide hydrolases that contain a signature motif, Q-loop, and H-loop/switch region, in addition to, the Walker A motif/P-loop and Walker B motif commonly found in a number of ATP- and GTP-binding and hydrolyzing proteins.	29,96	241	247	6,5E-41
CR143_RS01650	COG1101, PhnK, ABC-type uncharacterized transport system, ATPase component [General function prediction only].	27,004	263	237	9,74E-27
CR143_RS01655	cd03256, ABC_PhnC_transporter, ATP-binding cassette domain of the binding protein-dependent phosphonate transport system. Phosphonates are a class of organophosphorus compounds characterized by a chemically stable carbon-to-phosphorus (C-P) bond. Phosphonates are widespread among naturally occurring compounds in all kingdoms of wildlife, but only prokaryotic microorganisms are able to cleave this bond. Certain bacteria such as E. coli can use alkylphosphonates as a phosphorus source. ABC transporters are a subset of nucleotide hydrolases that contain a signature motif, Q-loop, and H-loop/switch region, in addition to, the Walker A motif/P-loop and Walker B motif commonly found in a number of ATP- and GTP-binding and hydrolyzing proteins.	29,555	241	247	9,6E-44
CR143_RS01655	COG1101, PhnK, ABC-type uncharacterized transport system, ATPase component [General function prediction only].	23,704	263	270	7,88E-23
CR143_RS01655	PRK11701, phnK, phosphonate C-P lyase system protein PhnK; Provisional.	23,137	258	255	1,97E-17

CR143_RS01700	TIGR02315, Phosphonates_import_ATP-binding_protein_PhnC, phosphonate ABC transporter, ATP-binding protein. Phosphonates are a class of phosphorus-containing organic compound with a stable direct C-P bond rather than a C-O-P linkage. A number of bacterial species have operons, typically about 14 genes in size, with genes for ATP-dependent transport of phosphonates, degradation, and regulation of the expression of the system. Members of this protein family are the ATP-binding cassette component of tripartite ABC transporters of phosphonates. [Transport and binding proteins, Anions].	30,303	243	231	4,79E-45
CR143_RS01700	cd03256, ABC_PhnC_transporter, ATP-binding cassette domain of the binding protein-dependent phosphonate transport system. Phosphonates are a class of organophosphorus compounds characterized by a chemically stable carbon-to-phosphorus (C-P) bond. Phosphonates are widespread among naturally occurring compounds in all kingdoms of wildlife, but only prokaryotic microorganisms are able to cleave this bond. Certain bacteria such as E. coli can use alkylphosphonates as a phosphorus source. ABC transporters are a subset of nucleotide hydrolases that contain a signature motif, Q-loop, and H-loop/switch region, in addition to, the Walker A motif/P-loop and Walker B motif commonly found in a number of ATP- and GTP-binding and hydrolyzing proteins.	27,586	241	232	2,55E-44
CR143_RS01700	COG1101, PhnK, ABC-type uncharacterized transport system, ATPase component [General function prediction only].	30,263	263	228	8,75E-34
CR143_RS01970	cd00377, ICL_PEPM, Members of the ICL/PEPM enzyme family catalyze either P-C or C-C bond formation/cleavage. Known members are phosphoenolpyruvate mutase (PEPM), phosphonopyruvate hydrolase (PPH), carboxyPEP mutase (CPEP mutase), oxaloacetate hydrolase (OAH), isocitrate lyase (ICL), and 2-methylisocitrate lyase (MICL). Isocitrate lyase (ICL) catalyzes the conversion of isocitrate to succinate and glyoxylate, the first committed step in the glyoxylate pathway. This carbon-conserving pathway is present in most prokaryotes, lower eukaryotes and plants, but has not been observed in vertebrates. PEP mutase (PEPM) turns phosphoenolpyruvate (PEP) into phosphonopyruvate (P-pyr), an important intermediate in the formation of organophosphonates, which function as antibiotics or play a role in pathogenesis or signaling. P-pyr can be hydrolyzed by phosphonopyruvate hydrolase (PPH) to form pyruvate and phosphate. Oxaloacetate acetylhydrolase (OAH) catalyzes the hydrolytic cleavage of oxaloacetate to form acetate and oxalate, an important pathway to produce oxalate in filamentous fungi. 2-methylisocitrate lyase (MICL) cleaves 2-methylisocitrate to pyruvate and succinate, part of the methylcitrate cycle for the alpha-oxidation of propionate.	46,531	243	245	4,73E-107
CR143_RS01970	cd06556, ICL_KPHMT, Members of the ICL/PEPM_KPHMT enzyme superfamily catalyze the formation and cleavage of either P-C or C-C bonds. Typical members are phosphoenolpyruvate mutase (PEPM), phosphonopyruvate hydrolase (PPH), carboxyPEP mutase (CPEP mutase), oxaloacetate hydrolase (OAH), isocitrate lyase (ICL), 2-methylisocitrate lyase (MICL), and ketopantoate hydroxymethyltransferase (KPHMT).	19,072	240	194	1,58E-13
CR143_RS02060	cd22359, SfsA-like_bacterial, Sugar fermentation stimulation protein A and similar proteins. Sugar fermentation stimulation protein A may bind to DNA in a non-specific manner and may act as a regulatory factor involved in the metabolism of sugars such as maltose. However, it contains a well-conserved PDDEXK nuclease active site and may have hydrolytic activity towards an unknown target. The putative catalytic domain belongs to a superfamily of PDDEXK nucleases including very short patch repair (Vsr) endonucleases, archaeal Holliday junction resolvases, MutH methyl-directed DNA mismatch-repair endonucleases, and catalytic domains of many restriction endonucleases, such as EcoRI, BamHI, and FokI. The N-terminus of SfsA resembles a DNA-binding OB-fold domain.	44,292	218	219	6,13E-109

CR143_RS02060	cd22358, SfsA-like_archaeal, Sugar fermentation stimulation protein A and similar nucleases. Sugar fermentation stimulation protein A may bind to DNA in a non-specific manner and may act as a regulatory factor involved in the metabolism of sugars such as maltose. However, it contains a well-conserved PDDEXK nuclease active site and may have hydrolytic activity towards an unknown target. The putative catalytic domain belongs to a superfamily of PDDEXK nucleases including very short patch repair (Vsr) endonucleases, archaeal Holliday junction resolvases, MutH methyl-directed DNA mismatch-repair endonucleases, and catalytic domains of many restriction endonucleases, such as EcoRI, BamHI, and FokI.	29,333	221	225	2,48E-50
CR143_RS02060	cd22357, SfsA-like, Sugar fermentation stimulation protein A and similar nucleases. Sugar fermentation stimulation protein A may bind to DNA in a non-specific manner and may act as a regulatory factor involved in the metabolism of sugars such as maltose. However, it contains a well-conserved PDDEXK nuclease active site and may have hydrolytic activity towards an unknown target. The putative catalytic domain belongs to a superfamily of PDDEXK nucleases including very short patch repair (Vsr) endonucleases, archaeal Holliday junction resolvases, MutH methyl-directed DNA mismatch-repair endonucleases, and catalytic domains of many restriction endonucleases, such as EcoRI, BamHI, and FokI.	30,909	213	220	5,07E-46
CR143_RS02845	COG1235, PhnP, Metal-dependent hydrolases of the beta-lactamase superfamily I [General function prediction only].	25,103	269	243	3,32E-28
CR143_RS03070	cd03256, ABC_PhnC_transporter, ATP-binding cassette domain of the binding protein-dependent phosphonate transport system. Phosphonates are a class of organophosphorus compounds characterized by a chemically stable carbon-to-phosphorus (C-P) bond. Phosphonates are widespread among naturally occurring compounds in all kingdoms of wildlife, but only prokaryotic microorganisms are able to cleave this bond. Certain bacteria such as E. coli can use alkylphosphonates as a phosphorus source. ABC transporters are a subset of nucleotide hydrolases that contain a signature motif, Q-loop, and H-loop/switch region, in addition to, the Walker A motif/P-loop and Walker B motif commonly found in a number of ATP- and GTP-binding and hydrolyzing proteins.	33,871	241	248	7,45E-68
CR143_RS03070	TIGR02315, Phosphonates_import_ATP-binding_protein_PhnC, phosphonate ABC transporter, ATP-binding protein. Phosphonates are a class of phosphorus-containing organic compound with a stable direct C-P bond rather than a C-O-P linkage. A number of bacterial species have operons, typically about 14 genes in size, with genes for ATP-dependent transport of phosphonates, degradation, and regulation of the expression of the system. Members of this protein family are the ATP-binding cassette component of tripartite ABC transporters of phosphonates. [Transport and binding proteins, Anions].	36,667	243	240	1,1E-60
CR143_RS03070	TIGR03265, PhnT2, putative 2-aminoethylphosphonate ABC transporter, ATP-binding protein. This ABC transporter ATP-binding protein is found in a number of genomes in operon-like contexts strongly suggesting a substrate specificity for 2-aminoethylphosphonate (2-AEP). The characterized PhnSTUV system is absent in the genomes in which this system is found. These genomes encode systems for the catabolism of 2-AEP, making the need for a 2-AEP-specific transporter likely. [Transport and binding proteins, Amino acids, peptides and amines].	40,517	353	232	3,4E-58
CR143_RS03070	COG4778, PhnL, ABC-type phosphonate transport system, ATPase component [Inorganic ion transport and metabolism].	34,158	235	202	1,22E-30
CR143_RS03280	cd03256, ABC_PhnC_transporter, ATP-binding cassette domain of the binding protein-dependent phosphonate transport system. Phosphonates are a class of organophosphorus compounds characterized by a chemically stable carbon-to-phosphorus (C-P) bond. Phosphonates are widespread among naturally occurring compounds in all kingdoms of wildlife, but only prokaryotic microorganisms are able to cleave this bond. Certain bacteria such as E.	33,796	241	216	1,81E-46

	coli can use alkylphosphonates as a phosphorus source. ABC transporters are a subset of nucleotide hydrolases that contain a signature motif, Q-loop, and H-loop/switch region, in addition to, the Walker A motif/P-loop and Walker B motif commonly found in a number of ATP- and GTP-binding and hydrolyzing proteins.				
CR143_RS03280	TIGR02315, Phosphonates_import_ATP-binding_protein_PhnC, phosphonate ABC transporter, ATP-binding protein. Phosphonates are a class of phosphorus-containing organic compound with a stable direct C-P bond rather than a C-O-P linkage. A number of bacterial species have operons, typically about 14 genes in size, with genes for ATP-dependent transport of phosphonates, degradation, and regulation of the expression of the system. Members of this protein family are the ATP-binding cassette component of tripartite ABC transporters of phosphonates. [Transport and binding proteins, Anions].	32,018	243	228	3,22E-41
CR143_RS03280	COG4778, PhnL, ABC-type phosphonate transport system, ATPase component [Inorganic ion transport and metabolism].	36,923	235	195	8,31E-34
CR143_RS03280	TIGR03265, PhnT2, putative 2-aminoethylphosphonate ABC transporter, ATP-binding protein. This ABC transporter ATP-binding protein is found in a number of genomes in operon-like contexts strongly suggesting a substrate specificity for 2-aminoethylphosphonate (2-AEP). The characterized PhnSTUV system is absent in the genomes in which this system is found. These genomes encode systems for the catabolism of 2-AEP, making the need for a 2-AEP-specific transporter likely. [Transport and binding proteins, Amino acids, peptides and amines].	33,898	353	177	2,16E-32
CR143_RS03280	TIGR03258, PhnT, 2-aminoethylphosphonate ABC transport system, ATP-binding component PhnT. This ATP-binding component of an ABC transport system is found in Salmonella and Burkholderia lineages in the vicinity of enzymes for the breakdown of 2-aminoethylphosphonate.	32,323	362	198	4,67E-26
CR143_RS03280	COG1101, PhnK, ABC-type uncharacterized transport system, ATPase component [General function prediction only].	24,885	263	217	8,65E-18
CR143_RS03735	cd06556, ICL_KPHMT, Members of the ICL/PEPM_KPHMT enzyme superfamily catalyze the formation and cleavage of either P-C or C-C bonds. Typical members are phosphoenolpyruvate mutase (PEPM), phosphonopyruvate hydrolase (PPH), carboxyPEP mutase (CPEP mutase), oxaloacetate hydrolase (OAH), isocitrate lyase (ICL), 2-methylisocitrate lyase (MICL), and ketopantoate hydroxymethyltransferase (KPHMT).	36,916	240	214	1,36E-43
CR143_RS04070	cd03256, ABC_PhnC_transporter, ATP-binding cassette domain of the binding protein-dependent phosphonate transport system. Phosphonates are a class of organophosphorus compounds characterized by a chemically stable carbon-to-phosphorus (C-P) bond. Phosphonates are widespread among naturally occurring compounds in all kingdoms of wildlife, but only prokaryotic microorganisms are able to cleave this bond. Certain bacteria such as E. coli can use alkylphosphonates as a phosphorus source. ABC transporters are a subset of nucleotide hydrolases that contain a signature motif, Q-loop, and H-loop/switch region, in addition to, the Walker A motif/P-loop and Walker B motif commonly found in a number of ATP- and GTP-binding and hydrolyzing proteins.	30,4	241	250	8,12E-41
CR143_RS04070	COG1101, PhnK, ABC-type uncharacterized transport system, ATPase component [General function prediction only].	26,407	263	231	4,06E-26
CR143_RS04070	COG4778, PhnL, ABC-type phosphonate transport system, ATPase component [Inorganic ion transport and metabolism].	31,683	235	202	8,34E-15
CR143_RS04075	cd03256, ABC_PhnC_transporter, ATP-binding cassette domain of the binding protein-dependent phosphonate transport system. Phosphonates are a class of organophosphorus compounds characterized by a chemically stable carbon-to-phosphorus (C-P) bond. Phosphonates are widespread among naturally occurring compounds in all kingdoms of wildlife, but only prokaryotic microorganisms are able to cleave this bond. Certain bacteria such as E.	31,878	241	229	1,85E-42

	coli can use alkylphosphonates as a phosphorus source. ABC transporters are a subset of nucleotide hydrolases that contain a signature motif, Q-loop, and H-loop/switch region, in addition to, the Walker A motif/P-loop and Walker B motif commonly found in a number of ATP- and GTP-binding and hydrolyzing proteins.				
CR143_RS04075	PRK11701, phnK, phosphonate C-P lyase system protein PhnK; Provisional.	28,326	258	233	4,66E-25
CR143_RS04075	COG4107, PhnK, ABC-type phosphonate transport system, ATPase component [Inorganic ion transport and metabolism].	29,004	258	231	1,02E-24
CR143_RS04075	COG1101, PhnK, ABC-type uncharacterized transport system, ATPase component [General function prediction only].	30,882	263	204	1,24E-24
CR143_RS04075	COG4778, PhnL, ABC-type phosphonate transport system, ATPase component [Inorganic ion transport and metabolism].	27,753	235	227	3,38E-22
CR143_RS04655	cd03256, ABC_PhnC_transporter, ATP-binding cassette domain of the binding protein-dependent phosphonate transport system. Phosphonates are a class of organophosphorus compounds characterized by a chemically stable carbon-to-phosphorus (C-P) bond. Phosphonates are widespread among naturally occurring compounds in all kingdoms of wildlife, but only prokaryotic microorganisms are able to cleave this bond. Certain bacteria such as E. coli can use alkylphosphonates as a phosphorus source. ABC transporters are a subset of nucleotide hydrolases that contain a signature motif, Q-loop, and H-loop/switch region, in addition to, the Walker A motif/P-loop and Walker B motif commonly found in a number of ATP- and GTP-binding and hydrolyzing proteins.	31,092	241	238	2,32E-33
CR143_RS04655	COG1101, PhnK, ABC-type uncharacterized transport system, ATPase component [General function prediction only].	26,809	263	235	2,11E-21
CR143_RS04995	cd03256, ABC_PhnC_transporter, ATP-binding cassette domain of the binding protein-dependent phosphonate transport system. Phosphonates are a class of organophosphorus compounds characterized by a chemically stable carbon-to-phosphorus (C-P) bond. Phosphonates are widespread among naturally occurring compounds in all kingdoms of wildlife, but only prokaryotic microorganisms are able to cleave this bond. Certain bacteria such as E. coli can use alkylphosphonates as a phosphorus source. ABC transporters are a subset of nucleotide hydrolases that contain a signature motif, Q-loop, and H-loop/switch region, in addition to, the Walker A motif/P-loop and Walker B motif commonly found in a number of ATP- and GTP-binding and hydrolyzing proteins.	30,556	241	252	1,12E-39
CR143_RS04995	TIGR02315, Phosphonates_import_ATP-binding_protein_PhnC, phosphonate ABC transporter, ATP-binding protein. Phosphonates are a class of phosphorus-containing organic compound with a stable direct C-P bond rather than a C-O-P linkage. A number of bacterial species have operons, typically about 14 genes in size, with genes for ATP-dependent transport of phosphonates, degradation, and regulation of the expression of the system. Members of this protein family are the ATP-binding cassette component of tripartite ABC transporters of phosphonates. [Transport and binding proteins, Anions].	29,268	243	246	5,92E-32
CR143_RS04995	COG1101, PhnK, ABC-type uncharacterized transport system, ATPase component [General function prediction only].	26,068	263	234	3,06E-23
CR143_RS05220	cd03256, ABC_PhnC_transporter, ATP-binding cassette domain of the binding protein-dependent phosphonate transport system. Phosphonates are a class of organophosphorus compounds characterized by a chemically stable carbon-to-phosphorus (C-P) bond. Phosphonates are widespread among naturally occurring compounds in all kingdoms of wildlife, but only prokaryotic microorganisms are able to cleave this bond. Certain bacteria such as E. coli can use alkylphosphonates as a phosphorus source. ABC transporters are a subset of nucleotide hydrolases that	32,273	241	220	7,62E-39

	contain a signature motif, Q-loop, and H-loop/switch region, in addition to, the Walker A motif/P-loop and Walker B motif commonly found in a number of ATP- and GTP-binding and hydrolyzing proteins.				
CR143_RS05220	TIGR02315, Phosphonates_import_ATP-binding_protein_PhnC, phosphonate ABC transporter, ATP-binding protein. Phosphonates are a class of phosphorus-containing organic compound with a stable direct C-P bond rather than a C-O-P linkage. A number of bacterial species have operons, typically about 14 genes in size, with genes for ATP-dependent transport of phosphonates, degradation, and regulation of the expression of the system. Members of this protein family are the ATP-binding cassette component of tripartite ABC transporters of phosphonates. [Transport and binding proteins, Anions].	33,636	243	220	1,53E-38
CR143_RS05220	TIGR03265, PhnT2, putative 2-aminoethylphosphonate ABC transporter, ATP-binding protein. This ABC transporter ATP-binding protein is found in a number of genomes in operon-like contexts strongly suggesting a substrate specificity for 2-aminoethylphosphonate (2-AEP). The characterized PhnSTUV system is absent in the genomes in which this system is found. These genomes encode systems for the catabolism of 2-AEP, making the need for a 2-AEP-specific transporter likely. [Transport and binding proteins, Amino acids, peptides and amines].	30,651	353	261	5,07E-33