

Aryl Coenzyme A Ligases, a Subfamily of the Adenylate-Forming Enzyme Superfamily

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Applied and Environmental

AMERICAN SOCIETY FOR

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ABSTRACT Aryl coenzyme A (CoA) ligases belong to class I of the adenylate-forming enzyme superfamily (ANL superfamily). They catalyze the formation of thioester bonds between aromatic compounds and CoA and occur in nearly all forms of life. These ligases are involved in various metabolic pathways degrading benzene, toluene, ethylbenzene, and xylene (BTEX) or polycyclic aromatic hydrocarbons (PAHs). They are often necessary to produce the central intermediate benzoyl-CoA that occurs in various anaerobic pathways. The substrate specificity is very diverse between enzymes within the same class, while the dependency on Mg²⁺, ATP, and CoA as well as oxygen insensitivity are characteristics shared by the whole enzyme class. Some organisms employ the same aryl-CoA ligase when growing aerobically and anaerobically, while others induce different enzymes depending on the environmental conditions. Aryl-CoA ligases can be divided into two major groups, benzoate: CoA ligase-like enzymes and phenylacetate:CoA ligase-like enzymes. They are widely distributed between the phylogenetic clades of the ANL superfamily and show closer relationships within the subfamilies than to other aryl-CoA ligases. This, together with residual CoA ligase activity in various other enzymes of the ANL superfamily, leads to the conclusion that CoA ligases might be the ancestral proteins from which all other ANL superfamily enzymes developed.

KEYWORDS 2-naphthoate-CoA ligase, 2-phenanthrene-CoA ligase, ANL superfamily, BTEX degradation, PAH degradation, adenylate-forming enzymes, aryl-CoA ligases, benzoate-CoA ligase, hydrocarbon degradation, phenylacetate-CoA ligase

Thioester, amide, and ester bonds are very common in nature and are often part of typical chemical building blocks. Enzymes catalyzing the formation of these bonds occur in nearly all forms of life. Many of these enzymes belong to the superfamily of adenylate-forming enzymes, which were structured into a novel order of classes and subclasses by S. Schmelz and J. H. Naismith in 2009 (1). Class I of this superfamily is composed of three subclasses: subclass Ia comprises nonribosomal peptide synthetase (NRPS) adenylation domains, subclass Ib includes acyl and aryl coenzyme A (CoA) synthetases/ligases, and subclass Ic includes oxidoreductases (1).

Class I enzymes can serve various functions. For example, they are involved in fatty acid metabolism and transport (2, 3), cell signaling (4), biofilm formation (e.g., in *Candida albicans*) (5), the synthesis of antibiotic compounds (e.g., in *Streptomyces coelicolor*) (6), protein transport (2, 7, 8), and many others.

This review focuses on aryl-CoA ligases (ACLs). ACLs catalyze the formation of a thioester bond between aromatic compounds and CoA using ATP. Their general mechanism is equivalent to that of acyl-CoA ligases, and the first reaction is shared among most adenylate-forming enzymes. In this step, the negatively charged oxygen of the carboxylate substrate performs a nucleophilic attack on the more positive α -phosphorous to form an aryl-adenylate intermediate and release pyrophosphate (PP_i) (Fig. 1)

Citation Arnold ME, Kaplieva-Dudek I, Heker I, Meckenstock RU. 2021. Aryl coenzyme A ligases, a subfamily of the adenylate-forming enzyme superfamily. Appl Environ Microbiol 87:e00690-21. https://doi.org/10.1128/AEM 00690-21.

Editor Shuang-Jiang Liu, Chinese Academy of Sciences

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Accepted manuscript posted online 14 July 2021 Published 26 August 2021



FIG 1 Mechanism of benzoyl-CoA formation by benzoate-CoA ligase. In the first reaction, adenylation, the carboxylic acid of benzoate attacks the α -phosphate of ATP to form a reactive benzoate-AMP intermediate and PP_i. In the second reaction, thioesterification, the benzoate-AMP intermediate reacts with the thiol group of the CoA and releases AMP by forming the CoA thioester. Ad, adenosyl group.

(for a comprehensive and detailed review of the mechanism, see reference 9; for a review about adenylate-forming enzymes of all classes, see reference 1).

In the second reaction, the intermediate is attacked by a nucleophile, in the case of the aryl-CoA ligases the thiol group of CoA, with AMP as the leaving group (Fig. 1) (1, 10, 11). For 4-chlorobenzoate:CoA ligase, it is proposed that AMP becomes activated as a leaving group by the interaction of its oxygen atoms with hydroxyl groups of two surrounding threonine residues of the enzyme (11).

CoA thioesters are formed by many organisms and serve various purposes. In many bacteria degrading aromatic or polycyclic aromatic compounds, such as, for example, *Rhodopseudomonas palustris*, the formation of a CoA thioester helps to accumulate substrates inside the cell (12). This accumulation comes to pass for two reasons. First, aromatic substrates entering the cell by diffusion through the membrane are converted to CoA thioesters, maintaining a downhill concentration gradient between the cytoplasm and the outside (12). Second, the CoA group prevents back-diffusion out of the cell due to its bulky size and polar structure (13).

Furthermore, the formation of the CoA thioester activates the substrate for further reactions or degradation steps because the CoA thioester group potentially draws electrons from the aromatic ring, facilitating, for example, the reduction of the ring system (14–16).

In some enterobacteria as well as eucaryotes, membrane-bound acyl-CoA ligases mediate long-chain fatty acid transport into the cell as well as activating the substrate by CoA ligation (3, 17, 18; for a comprehensive review on the role of class I adenylate-forming enzymes in the *trans*-membrane movement of long-chain fatty acids, see reference 2).

ARYL-CoA LIGASES FROM ANAEROBICALLY AND AEROBICALLY GROWN BACTERIA

Aryl-CoA ligases have been found in a variety of bacteria that grow not only anaerobically but also aerobically with aromatic substrates. All these CoA ligases catalyze a comparable thioesterification reaction that depends on Mg²⁺, ATP, and free CoA. All aryl-CoA ligases are oxygen insensitive and have an alkaline pH optimum of between 7.0 and 9.3 (Table 1).

Anaerobic degradation of aromatic acids always involves the formation of the corresponding CoA thioester by an aryl-CoA ligase. CoA thioester formation facilitates the uptake of aromatic hydrocarbons (12, 13, 19) and is certainly crucial for further degradation (15, 16, 20, 21). Genes encoding these aryl-CoA ligases are mostly located adjacent to genes for enzymes involved in the anaerobic degradation pathway, such as reductases (Fig. 2) (22).

Bacteria grown aerobically with aromatic substrates usually use oxygenases to activate the aromatic compound through the formation of a hydroxylated intermediate that is oxygenolytically cleaved (23). In several bacteria, however, the aerobic metabolism of aromatic acids occurs via a novel type of aerobic degradation pathway (*box* pathway). These aromatic acids are activated via an aryl-CoA ligase, similar to anaerobic degradation, and are further hydrolytically cleaved (23). It is proposed that the produced CoA thioester acts as an inducer for the expression of the downstream enzymes in aerobic and anaerobic degradation (24).

TABLE 1 Characteris	tics of different aryl-CoA liga	ses						
Aryl-CoA ligase	Microorganism	Growth condition	Native protein form	Subunit size (kDa) ^a	pH optimum	$K_m (\mu M)^b$	Substrate affinity	Reference
Benzoate:CoA ligase	Rhodopseudomonas palustris	Anaerobic	Monomer	60	8.4–8.9	0.6–2	Benzoate and 2- and 4-fluorobenzoate	44
	Azoarcus evansii	Anaerobic	Homodimer	120	9.3	11	Benzoate, 2- ,3-, and	25, 26
		Aerobic	Homodimer	56 (130)	6	11	4-fluorobenzoate, and 2-aminohenzoate	
	Thauera aromatica	Aerobic/anaerobic	Monomer	58	8.5	16	Benzoate, 2- ,3-, and	34
							4-fluorobenzoate, and 2-aminobenzoate	
	Magnetospirillum sp. strain TS-6	Aerobic/anaerobic	Homodimer	60 (120)	6	30	Benzoate and 2- and 4-fluorobenzoate	35
4-Chloroben zoate: CoA ligase	Pseudomonas sp. strain CBS3	Aerobic	Homodimer	57	7.5	8.5 ± 0.09	4-Chlorobenzoate, benzoate, 4-bromobenzoate, 4-methvlbenzoate, and	45
-	:	:	:	L	L			
2-Aminobenzoate: CoA ligase	Azoarcus evansii	Aerobic	Monomer	65	8.5	10	2-Aminobenzoate and benzoate	29
		Anaerobic	Monomer	60	8.5–9.2	13	2-, 3-, and 4-fluorobenzoate	25
4-Hydroxybenzoate: CoA ligase	Rhodopseudomonas palustris	Anaerobic	Dimer	61 (117)	6~	22	4-Hydroxybenzoate, benzoate, and cyclohex- 1,4-dienecarboxylate	79
	Thauera aromatica	Aerobic	Monomer	48	8.5	37	4-Hydroxybenzoate and 4-aminobenzoate	36
Phenylacetate:CoA	Pseudomonas putida	Aerobic	Monomer	48 ± 1	7.0-8.5	16.5	Phenylacetate	39
ligase	Azoarcus evansii	Anaerobic	Monomer	52 ± 2	8.5	60		31
		Aerobic	Monomer	52	8-8.5	14		32
	Burkholderia cenocepacia Paak1/Paak2	Aerobic	Homodimer	48 (82)	7.5	62 ± 4/150 ± 7		72
3-Hydroxybenzoate: CoA ligase	Thauera aromatica	Anaerobic	Monomer	60	≥9	60 ± 5	3- and 4-hydroxybenzoate	37
^a Subunit sizes in parenth ${}^{b}K_{m}$ values given here ref	eses denote the size of the full dir er to the main substrate.	ler.						

Minireview

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FIG 2 Organization of gene clusters involved in the anaerobic or/and aerobic catabolism of benzoate, 4-hydroxybenzoate, 2-aminobenzoate, or phenylacetate in *Rhodopseudomonas palustris, Azoarcus evansii, Thauera aromatica,* or *Pseudomonas putida* KT2440, created using Gene Graphics (80). Genes are represented by tags: green, genes encoding CoA ligases (*badA, bzdA*, and *bclA*, benzoate:CoA ligase; *hbadA*, 4-hydroxybenzoate:CoA ligase; *abmG*, 2-aminobenzoate:CoA ligase; *paaK*, phenylacetate:CoA ligase); violet, genes encoding the subunits of the corresponding reductases for anaerobic degradation; orange, genes encoding ferredoxin; pink, regulatory genes; yellow, putative transport genes; gray, genes encoding enzymes for the downstream degradation pathway; white, genes of unknown function. Two vertical lines indicate that the genes are not adjacent in the genome.

There are a few bacteria known that are able to degrade certain aromatic acids such as benzoate, 2-aminobenzoate, and also phenylacetate aerobically and anaerobically using aryl-CoA ligases. This is considered an adaptation of these bacteria to changes between anoxic and oxic conditions (16). The denitrifying bacterium Azoarcus evansii is a great example of a bacterium that induces two distinct aryl-CoA ligases for several aromatic acids, depending on the availability of oxygen during growth. Benzoate:CoA ligases expressed in anaerobically or aerobically grown Azoarcus evansii cells are homodimers with different molecular masses (25, 26) and gene locations on the chromosome. One benzoate:CoA ligase, BzdA, is encoded in the cluster coding for enzymes involved in anaerobic degradation (bzd cluster), whereas the other one, BclA, is located within the cluster for enzymes required for aerobic degradation (box cluster) (Fig. 2) (27, 28). Two other monomeric aryl-CoA ligases were found in A. evansii growing with 2-aminobenzoate: one is induced under oxic conditions (29), and the other is found in anaerobically grown cultures (25). Two very similar clusters encoding enzymes for the aerobic degradation of 2-aminobenzoate, including the 2-aminobenzoate:CoA ligase, are present in the genome (30), while genes involved in anaerobic degradation are barely known. A. evansii grown anaerobically on 2-aminobenzoate also expresses a small amount of the aerobically induced 2-aminobenzoate:CoA ligase (25). The expression of both 2-aminobenzoate:CoA ligases during anaerobic growth indicates that A. evansii is able to switch rapidly from anaerobic to aerobic degradation of 2-aminobenzoate. Furthermore, this implies that the expression of both ligases is not exclusively under the control of the availability of oxygen and is thus regulated by other factors.

A. evansii also expresses two distinct aryl-CoA ligases in aerobic or anaerobic cultures grown with phenylacetate. Both phenylacetate:CoA ligases are monomers, have similar molecular masses and nearly the same pH optima, and are active only with phenylacetate. Furthermore, both ligases require glycerol for stability. Despite this similarity, both phenylacetate:CoA ligases have totally different N-terminal amino acid sequences and are encoded in the vicinity of enzymes required for aerobic or anaerobic degradation pathways, respectively (22, 31–33).

Based on the position of these aryl-CoA ligase genes in the genome of *A. evansii*, it might be that all these aryl-CoA ligases are expressed together with the enzymes required for the corresponding degradation pathway, as has been shown for the aerobically induced 2-aminobenzoate:CoA ligase (30).

In contrast to *A. evansii*, the denitrifying bacteria *Thauera aromatica* and *Magnetospirillum* sp. strain TS-6 expressed the same benzoate:CoA ligase (BclA) when the cultures were grown aerobically or anaerobically with benzoate (34, 35). The gene for benzoate:CoA ligase of *Thauera aromatica* was found as a part of the gene cluster for the novel aerobic benzoate oxidation pathway (*box* pathway) and not in the gene cluster for anaerobic benzoyl-CoA metabolism (Fig. 2) (34). In contrast, the *bclA* gene of *Magnetospirillum* sp. is located in neither the *bzd* cluster nor the *box* cluster (35). This indicates that the benzoate:CoA ligase is expressed independently from enzymes involved in the corresponding degradation pathway. Thus, the presence or absence of oxygen induces the expression of the respective downstream enzymes (34, 35). This opportunity may enable these bacteria to survive in environments where the oxygen conditions are changing rapidly and they need to switch between anaerobic and aerobic degradation pathways.

SUBSTRATE SPECIFICITY

Even though all aryl-CoA ligases utilize the same reaction mechanism, substrate specificities differ widely (Table 1). Eight different aryl-CoA ligases have been found in the denitrifying bacterium A. evansii alone: two benzoate:CoA ligases, two 2-aminobenzoate: CoA ligases, two phenylacetate:CoA ligases, a 3-hydroxybenzoate:CoA ligase, and a 4hydroxybenzoate:CoA ligase (25, 26, 29, 31, 32). Each of these aryl-CoA ligases is encoded in the vicinity of its corresponding downstream genes. A. evansii grown anaerobically in a batch culture with 2-aminobenzoate showed the presence of 2-aminobenzoate:CoA ligase, benzoate:CoA ligase, and a small amount of the 2-aminobenzoate:CoA ligase usually produced during aerobic growth. All three aryl-CoA ligases prefer the same substrates (25). Even benzoate:CoA ligase induced under oxic conditions with benzoate as the substrate showed similar substrate affinities (26). This suggests a regulatory function of these ligases in the downstream degradation pathway and, due to the similar substrate specificities, may also allow switching easily from one degradation pathway to another. Interestingly, A. evansii expresses four enzymes with nearly the same substrate specificity and not only one as in the denitrifying bacterium T. aromatica. The benzoate:CoA ligase induced during aerobic and anaerobic growth on benzoate or 2-aminobenzoate in T. aromatica has a broad substrate specificity (34). This may enable T. aromatica to alternate rapidly between different degradation pathways depending on the occurrence of the substrates. Two further aryl-CoA ligases were identified in T. aromatica, the distinct monomeric aryl-CoA ligases for the isomers 3-hydroxybenzoate and 4-hydroxybenzoate (36, 37). These two aryl-CoA ligases have a very narrow substrate specificity compared to the benzoate:CoA ligase. This suggests that 3-hydroxybenzoate: CoA ligase and 4-hydroxybenzoate:CoA ligase, in contrast to the benzoate:CoA ligase, are involved in the regulation of the downstream genes and are able to activate only their corresponding degradation pathway.

The phototrophic bacterium *R. palustris* grown with 4-hydroxybenzoate in the absence of oxygen showed 4-hydroxybenzoate:CoA ligase activity. In contrast to the high substrate specificity of the 4-hydroxybenzoate:CoA ligase of *T. aromatica*, this ligase has a broad substrate affinity. The gene for 4-hydroxybenzoate:CoA ligase (*hbadA*) is located adjacent to the gene clusters coding for enzymes involved in 4-hydroxybenzoate degradation as well as enzymes required for benzoate degradation (Fig. 2) (38). This high substrate diversity may enable *R. palustris* to also regulate the expression of enzymes required for the downstream degradation of other aromatic acids such as benzoate.

A highly substrate-specific aryl-CoA ligase is the phenylacetate:CoA ligase induced in *A. evansii* and *Pseudomonas putida* when grown with phenylacetate. The aerobically and anaerobically induced phenylacetate:CoA ligases from *A. evansii* and the aerobically induced one from *P. putida* could convert only phenylacetate to phenylacetyl-CoA. No other substrates were converted to their corresponding CoA thioesters (31, 32, 39), indicating a potential regulatory function in the expression of enzymes exclusively involved in the downstream degradation of phenylacetate.

This shows that the substrate specificity of monoaromatic aryl-CoA ligases differs from ligase to ligase, even if they are expressed during growth with the same substrate; this may indicate different regulatory functions.

The substrate specificity of polycyclic aromatic aryl-CoA ligases is under investigation. The polycyclic aromatic aryl-CoA ligases expressed in the naphthalene-degrading, sulfate-reducing culture N47 (40) or NaphS2 (41) showed broad substrate specificity. They can convert fluorinated naphthoates to their corresponding CoA thioester at the same rate as naphthoate, similar to what is known for all benzoate:CoA ligases. Several hydroxylated naphthoates were also used by the naphthoate:CoA ligase but with lower conversion rates (M. E. Arnold, F. Kaschani, and R. U. Meckenstock, unpublished results). In the sulfate-reducing, phenanthrene-degrading enrichment culture TRIP1 (42, 43), the phenanthroate:CoA ligase is very specific for 2-phenanthroate. Only 3-phenanthroate was utilized by the phenanthroate: CoA ligase as well but with a much lower conversion rate (I. Kaplieva-Dudek, F. Kaschani, and R. U. Meckenstock, unpublished results).

INFLUENCE OF CATIONS AND THIOL GROUP-MODIFYING AGENTS ON ARYL-CoA LIGASE ACTIVITY

All known adenylate-forming enzymes require magnesium ions for their catalytic reaction. The absence or replacement of magnesium by other cations leads to a loss of enzyme activity. For example, the addition of the known inhibitor of magnesium-dependent enzymes NaF to phenylacetate:CoA ligase of A. evansii decreased the ligase activity by up to 20% (31). The 4-chlorobenzoate:CoA ligase of Pseudomonas sp. strain CBS3 has 12-fold-lower activity without Mg^{2+} (11), indicating that magnesium is necessary for optimal enzyme activity. Magnesium ions neutralize the charge of ATP and later the charge of the leaving group pyrophosphate. Furthermore, magnesium ions can interact with and stabilize the acyl-AMP intermediate. In nearly all aryl-CoA ligases, Mg²⁺ can be replaced only by Mn²⁺ without loss of activity (25, 29, 31, 39, 44). For the 4-chlorobenzoate:CoA ligase from *Pseudomonas* sp. strain CBS-31, it was also shown that Mg²⁺ can be replaced by Co²⁺ as a cofactor (45). In most cases, other cations such as Zn²⁺, Cu²⁺, Ni²⁺, Hg²⁺, and Mo⁵⁺ have strong inhibitory effects on ligase activity. Copper ions can probably interact with the thiol group and thus prevent the CoA from binding to the substrate. Monovalent cations like K⁺, Na⁺, Li⁺, and Rb⁺ have no effect on aryl-CoA ligase activity (25, 29, 31, 39, 44). In contrast to monocyclic aromatic aryl-CoA ligases, polycyclic aromatic aryl-CoA ligases were also active with either Na⁺ or K⁺ instead of Mg²⁺ when using cell extracts (Arnold et al., unpublished; Kaplieva-Dudek et al., unpublished). However, it cannot be excluded that a sufficient amount of Mq^{2+} is present in the ligase assays since a cell extract was used and not purified enzymes. So far, similar findings have also been reported for xenobiotic/medium-chain fatty acid:CoA ligases of bovine liver mitochondria and cinnamate:CoA ligase of Hypericum calycinum cell cultures (46-48). The phenanthroate: CoA ligase from the sulfate-reducing, phenanthrene-degrading culture TRIP1 showed higher ligase activity when Na⁺ or K⁺ was added to cell extracts instead of Mg²⁺. With a combination of Mg²⁺ and K⁺, the greatest conversion of 2-phenanthroate was measured. Furthermore, phenanthroate:CoA ligase was inhibited with increasing Mg²⁺ concentrations (Kaplieva-Dudek et al., unpublished). This indicates a difference between aryl-CoA ligases converting monocyclic aromatic and polycyclic aromatic hydrocarbon (PAH)-carboxylic acids regarding the influence of cations on ligase activity. Other strong inhibitory effects on monocyclic aromatic aryl-CoA ligases were detected by thiol group-modifying agents such as N-ethylmaleimide, iodoacetamide, p-hydroxymercuribenzoate, 5,5'-dithiobis-(2-nitrobenzoic acid), and p-chloromercuribenzoic acid, which indicates that a free thiol group of the CoA is necessary for enzyme activity (25, 32, 36).

ARYL-CoA LIGASES FORM TWO MONOPHYLETIC CLADES

A neighbor-joining phylogenetic tree of amino acid sequences of the adenylate-forming enzyme superfamily (ANL superfamily) was recently constructed by L. Clark et al. (49), aligning in total 374 protein sequences of the ANL superfamily, of which 49 belonged to aryl-CoA ligases. The unrooted tree classified the proteins into nine distinct groups: luciferases, three groups of fatty acyl-CoA synthetases, nonribosomal peptide synthetases (NRPSs), fatty acid-AMP ligases, methylmalonyl-CoA synthetases, mycobacterial FadD10 long-chain fatty acyl-CoA ligases, and aryl-CoA ligases. The alignment of the sequences yielded 5 amino acids conserved in all groups: Glu328, Gly384, Asp418, Arg433, and Lys524 (residue positions correspond to the *Thermus thermophilus* sequence as noted in this paper). Conserved residues were mostly found surrounding the active site of the enzymes containing the AMP- and CoA-binding site rather than the protein surface. Group-specific residues were identified using the GEnt program (50), calculating the conservation of specific residues inside the aryl-CoA group of proteins versus the whole alignment. Two of the eight identified residues interacted directly with the substrate: Asn411 of the 4-chlorobenzoate:CoA ligase from *Alcaligenes* forms a hydrogen bond to the α -phosphate of AMP in the thioesterification conformation, and His207 interacts with the substrate during the adenylation reaction.

Recently, Robinson et al. (51) used a machine-learning approach to identify enzymes of the ANL superfamily and construct a maximum likelihood phylogenetic tree of the characterized proteins. This tree shows that β -lactone synthetases, NRPSs, as well as luciferases form very distinct monophyletic clades. In contrast to the study by L. Clark et al. (49), especially the aryl/acyl-CoA ligases are distributed widely throughout the phylogenetic clades and show a closer relationship to the enzyme subfamilies than to each other. Hence, aryl/acyl-CoA ligases seem to be clearly polyphyletic, and those authors conclude that the ANL superfamily developed from enzymes with an active site comparable to that of modern aryl/acyl-CoA ligases using CoA-SH as a cofactor. In this case, divergent evolution from ancestral CoA ligase-like scaffolds led to the diverse specialized functions of the ANL superfamily. A similar radial topology and common ancestor have been shown previously for the nitroreductase superfamily, where evidence suggests divergent evolution from an ancestral minimal flavin-binding scaffold (52). This line of reasoning is supported by experiments showing low-level CoA-ligase activity in members of the ANL superfamily, specialized primarily toward other functions. Five NRPS A domains were bifunctional, showing CoA ligase activity (53), similar to luciferases (54). Moreover, the fact that single point mutations were able to restore CoA ligase activity in ANL superfamily members strengthens the hypothesis of an ancestral CoA ligase-like scaffold (51). Nonetheless, the alternative of CoA ligase activity developing independently at several times throughout ANL superfamily evolution, as shown with other superfamilies, cannot be conclusively excluded at this point.

We constructed a maximum likelihood phylogenetic tree with Mega-X (55, 56) using 39 amino acid sequences of the aryl-CoA enzyme family (Fig. 3). Here, the group of the aryl-CoA ligases was divided into two phylogenetically distinct subgroups: benzoate: CoA ligase-like enzymes and phenylacetate:CoA ligase-like enzymes. In this tree, not only do benzoate:CoA ligases and phenylacetate:CoA ligases cluster into separate clades, but putative polycyclic aromatic compound ligases for naphthoate (57, 58) and phenanthroate (43) are also part of the phenylacetate:CoA ligase-like monophyletic clade. The only relatively conserved residues of the aryl-CoA ligases, leading to clustering according to their substrate spectrum inside these two major phylogenetic clades, can be found surrounding the substrate-binding pocket (49).

STRUCTURAL FEATURES AND CONSERVED RESIDUES OF ARYL-CoA LIGASES

Overall, benzoate:CoA ligase-like and phenylacetate:CoA ligase-like enzymes conform to the general two-domain structure of ANL enzymes, with a larger N-terminal domain with parallel β -sheets forming the core surrounded by α -helices and the active site situated in the linker region between the N- and C-terminal domains. A 140° rotation of the C-terminal domain enables the enzyme to catalyze the two distinct reactions of adenylation and thioesterification (9, 59). During the first reaction, the enzyme



0.50

FIG 3 Maximum likelihood phylogenetic tree of aryl-CoA ligases of the ANL superfamily. The tree was constructed in Mega-X using 39 amino acid sequences of the aryl-CoA enzyme family (see GenBank accession numbers at the right). Enzymes (Continued on next page)

adopts the adenylation conformation when ATP and the carboxylate bind to the active site in the N-terminal region. This configuration places the carboxylate in the ideal position to attack the α -phosphate, which leads to the release of PP_i and the formation of the adenylate intermediate (60). For the second reaction, a rotation of the C-terminal domain is necessary because the pantetheine tunnel, which is part of the CoA-binding site, is blocked in the adenylation conformation. The pantetheine or thiol group of CoA needs to be close to the intermediate to form the thioester bond and displace the AMP. During the C-terminal domain rotation and the subsequent formation of the thiolation conformation, the pantetheine tunnel is open, and CoA can be placed correctly into the binding pocket, leading to the formation of the aryl-CoA product (61).

The study of the adenylation domain of NRPSs yielded 10 conserved motifs, 9 of which can be found in the wider ANL superfamily (A1 to A8 and A10) (9, 62). Three of these motifs have been previously described (63). A recent publication by L. Clark et al. (49) compared 374 amino acid sequences of the ANL family and found 10 conserved motifs, corresponding partially to the previously established motifs. A comparison of these different motifs and their function can be found in Table 2.

Crystal structures of the 4-chlorobenzoate:CoA ligase elucidated the role of conserved amino acids in these motifs (64, 65). One of the most conserved regions found in all enzymes of this superfamily is the ATP-binding site. Motif A7, containing a conserved aspartic acid residue, as well as motif A8, containing an arginine residue, interact with ribose hydroxyls. The ATP molecule is further stabilized via the A5 motif. In the 4-chlorobenzoate:CoA ligase, an aromatic tyrosine is the key residue for this interaction. The key catalytic residue lysine in motif A10 interacts in the adenylation conformation of the enzyme with the α -phosphate during the nucleophilic attack on ATP. This lysine is highly conserved in all aryl-CoA ligases and throughout the acyl-CoA and fatty acid acyl-CoA ligases. The lysine residue is the target of acetylation as a posttranslational regulation mechanism (66, 67). Reversible lysine acylation in prokaryotes is a relatively new field of study. The earliest mention of this regulatory mechanism in bacteria was in 2002 (68). The benzoate: CoA ligase BadA from Rhodopseudomonas palustris is one example of regulation through the interaction of acetyltransferases and deacetylases (66). Another, possibly related regulatory mechanism was found in Azoarcus sp. strain CIB. Here, the genes for benzoate degradation are located in one operon. Gene expression is regulated by the repressor BzdR, which is dependent on the benzoyl-CoA concentration in the cell (69). Posttranslational lysine acetylation might be a possible way to regulate not just ligase activity but also the expression of aryl-CoA ligase genes through the benzoyl-CoA concentration. This might provide a diverse toolset for bacteria to regulate an energy-consuming reaction.

The position of the CoA-binding site is not well conserved within the group of aryl-CoA ligases, but it consists of a nucleotide-binding site on the protein surface and a pantetheine tunnel interacting with motif A8. The substrate-binding site within this group shows almost no conservation and is highly diverse even between enzymes with the same main substrate (9). The alignment created for the phylogenetic tree (Fig. 3) has been searched for the motifs described here (Table 2). The sequence alignments containing at least 50% sequence identity with these motifs are marked in Fig. 4.

C. K. Thornburg et al. (59) elucidated the structure of the benzoate:CoA ligase BadA from *R. palustris* (Fig. 5) and determined the reaction mechanism and wild-type substrate specificity through mutations of the active center. BadA shows a preference for *ortho*-substituted substrates in contrast to *meta* or *para* isomers. Steric effects influence kinetics more than electrostatic interactions. The enzyme shows a two-domain structure with the N-terminal domain containing the benzoate-binding site, typical for the ANL superfamily. The substrate is centered in the active site with the help of charged

FIG 3 Legend (Continued)

marked with an asterisk are listed in Table 1. BCL, benzoate:CoA ligase; 4-HBCL, 4-hydroxybenzoate:CoA ligase; 3/4-CBCL, 3/4chlorobenzoate:CoA ligase; 2-ABCL, 2-aminobenzoate:CoA ligase; 2-PACL, 2-phenanthroate:CoA ligase; 2-NACL, 2-naphthoate: CoA ligase; PCL, phenylacetate:CoA ligase.

TABLE 2 Const	erved sequence motifs in the	e ANL superfamily ^a			
Motif	Motif described by	Amino acid sequence [¢]			
described by Clark et al. ⁶	Marahiel et al., ^c A1–A10, and Chang et al., ^d I–III	1–10	A1-A10 (I-III)	Function(s) and result(s) of mutation ^f	Motif found in aryl-CoA ligases ^g
Q	A1	(B/K)LANA xxxLG(V/J/L)K(K/P)GD(B/V)V(A/G)(L/V/J)L	Ψ(S/T)Ωx(E/Q)Ψ	Structural	
10	A2	(A/I)GA(V/I)VVP(L/I)NPRx _x (Y/L)TPK(E/D)(I/L)XYR(L/I)N	(R/K/F)ΨGΨ	Structural	
m	A3 (I)	(T/S)SG(T/S)TGLPKGV(M/L)(L/H)(T/S)H	ΨΨx(S/T)(S/T/G)	P-loop	X (Gly189)
			G(S/T)TGxPK	Thr161, 2,000-fold-lower activity	
				Gly163, 1,000-fold-lower activity	
				Pro168, no activity	
				Lys169, 4-fold-lower activity	
	A4		C	Aromatic residue, part of the acyl-binding	
				pocket in the active center	
				His207, 500-fold-lower activity	
6 7		(I/L)(E/Q)K(Y/E)(K/R)(V/I))Tx(L/E)xG(V/A)PTIYR(E/A)L(L/A)(K/Q) DI SSI (R/K)xI VS(G/A)(G/A)(A/E)(P/A)I N(P/K)E(V/I)xE			X (Pro278) X
	A5 (11)			Desitioning of ΔTD and hinding of $M\alpha^{2+}$	<
				Tyr304, no change in activity Thr307, 100-fold-lower activity	< c
				Glu306, 50-fold-lower activity	
8	:	ExkPGSVG(K/R)(P/V)VP(G/N)V(E/D)V(K/R)(I/V/L)(V/I)DP		-	
τ,	A6	GE(I/L)C(V/I)(R/K)x ₅ GPG(V/I/L)(M/F/A)KGY(W/Y/L)N	GEX ₁₀₋₁₄ GY	Structural	
_	A/ (III)	(Y/L/F)H(1/S)GU(L/I)(G/A)(Y/K)XUEUGY(F/L)(W/F)(I/F)(V/1) (G/D)Rx(K/D)D(L/N)I(K/I)S(G/K/S)G(Y/E/F)(R/N/O)(1/V)	(1/S)	Positioning of ATP, binding/interacting with the ribose hydroxyls of ATP	X (Arg424)
	A8	GPAE(I/V/L)ESAL	Rx(D/K)x ₆ G	Asp385, 500-fold-lower activity	
				Arg400, 100-fold-lower activity	
4 c	Δ10	HPA(V/I)A(E/D)AAV(V/I)G(V/I)P(D/H)(P/E)x(W/A/R)G(E/Q)V(P/V) D(P/D)×/V/I)/E/A/IEI/DE/I /I)DK/T/AI/YD /A)/S/C/F/S/KII /D//R/KI			Y (1 we 518)
N					V (LYSJIO)
^a A1–A10, conserv	ed motifs of the adenylation doma	in of NRPS (62); I–III, conserved sequences of the acyl ligase family (63); 1–10,	conserved motifs of the	ANL superfamily (49); P-loop, phosphate-binding loo	pp.
^b See reference 49.					
^c See reference 62. dSee reference 63					

Minireview

⁹Amino acids used in the phylogenetic analysis of aryl-CoA ligases (Fig. 3) were aligned using the MUSCLE algorithm (Mega-X) and examined for conserved sequences. The 100% conserved amino acids and their positions in the benzoate:CoA ligase of *Thauera aromatica* (GenBank accession number AAN32623.1) are written in three-letter code. A motif was considered present if 50% of the amino acid code was concurrent with the described motifs.

 $^{e}\Omega$, aromatic amino acid (F, Y, H, or W); Ψ , aliphatic amino acid (A, V, L, I, or M); x, any amino acid.

^fSee references 9, 11, and 63.

 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 	MS	SVKFLFTEEN	VGKRHGVYPD	EEQDRTK	PYSEKFWSKV	ETLPIERI	REIQMER-FR	NIVQFAYARS	[80]
<pre>2. putative_2-NACL_N47_CBX27264.1</pre>				MRLYTQK	ATESPYWNEY	M-ETMPREKL	DQLHLRR-LQ	RLIKYAYENI	[80]
 PCL_(aerobic)_Azoarcus_evansii_WP_169132234.1* 				MPVKT	PSPGDLEP	I-EKASQDEL	RALQLER-LK	WSVRHAYENV	[80]
 PCL_Pseudomonas_putida_WP_059394932.1* 				MNMY	HDADRALLDP	M-ETASVDAL	RQHQLER-LR	WSLKHAYDNV	[80]
 BCL_Thauera_aromatica_AAN32623.1* 		MYTLS	VADHSNTPPA	IKIPERY	NAADDLIGRN	L-LAGRGGKT	VYIDDAGS	YTYDELALRV	[80]
BCL_Magnetospirillum_spTS-6_BAE91925.1*		M	TSPNASSEHA	LDIPRDY	NAATWFIDRH	L-KDGRADKV	AFIDADGS	HTYGQLADKV	[80]
7. 4-HBCL Thauera aromatica K172 AVR88075.1*		MPTLS	AADHTASPPE	IRIPRHY	NAADDLIGRN	L-DAGRGPKI	AYIDDEGR	YSFDELARRV	[80]
 4-HBCL/BCL Rhodopseudomonas palustris 053005.1* 			MP-	LRDY	NAAVDEVDRN	V-AEGRGGKI	AFIDPORS	LSYGELRDAV	[80]
9. 4-CBCL Pseudomonas sp. CBS3 AB044579.1*				M	OTVHEMLRRA	VSRVPHRW	AIVDAAR-ST	FDICRTGETS	[80]
10.3-HBCL Thauera aromatic K172 AVR88779.1*			MSEO	LOP005M	NAADEIIGRP	L-AOGLGEOT	AMLCAER S	ITYRELDAAT	[80]
11.2-ABCL Azoarcus evansii AAL02077.1*	MTSHVDTF	ARDRLPPPEO	OPEFLFELPS	LOFPPLM	NCAVELLDRR	V-LGGEGERV	CLRAPGG-LR	WTYRDLLGHA	1 801
1 putative 2-PACL PITCH v1 a1100006 TRTP SPD71907 1	PEVERTUD-N	AGTKPED						TRGUDD-	[160]
2 putative 2-NACL N47 CBY27264 1	PMYOEL YD-K	AHVKPED						TKMI DDY	[160]
2. pulative_2-mace_m4/_cbx2/204.1	PHYREAED-A	KGVHPDD						IKALODI	[160]
4 DCL Decudemente nutide UD 050204022 1*	DI VROBEA E	CCAUDDD						LTCLED	[160]
4. PCL_PSeudomonas_putida_WP_0595944952.1*	PLTRQRFA-E	CGAMPUD	VOUL DOTOTO	TTELCATUCC	LOCTATINT!!	TECOVENINT		ALL DI CADI	[100]
5. BCL_Inauera_aromatica_AAN32623.1*	NRCGSALRII	LGLQPKDRVL	VCVLDGIDFP	TIFLGAIKGG	VVPIAINILL	TESDYEYMLT	DSAARVAVVS	QELLPLFAPM	[100]
BCL_Magnetospirillum_spTS-6_BAE91925.1*	NRAGNALK-G	LGLHMENRIA	MIMLDTVDFP	AVFWGAVKAG	IVPIPLNTLL	TTGDYGYMLS	DSRARVLVIS	EELFDKVEPI	[160]
7. 4-HBCL_Thauera_aromatica_K172_AVR88075.1*	NRCGSALGEV	LGLRREERVL	MCVHDTIDFP	TVFLGAIRAG	IVPIAVNTLL	TASDYEYMLT	DSRARVAIVS	EPLMAVFGPL	[160]
 4-HBCL/BCL_Rhodopseudomonas_palustris_Q53005.1* 	ARVGPMLA-R	LGVEQENRIA	LVLKDTVDFP	ILFWGAIRAG	IVPVLLNTRL	TADQYRYLLE	DSRSRVVFAS	SEFLPVIEEA	[160]
9. 4-CBCL_Pseudomonas_spCBS3_ABQ44579.1*	RNEGSATA-R	LWPQPARPLA	VVSGNSVEAV	IAVLALHRLQ	AVPALMNPRL	KPAEISELVA	RGEMARAVVA	ND-AGVMEAI	[160]
10.3-HBCL_Thauera_aromatic_K172_AVR88779.1*	NRHGNALR-A	HGVGKGDRVL	FLMDDSPELV	AAYLGTLRIG	AVAVALNVRL	APRDVLYVIQ	DSACRLLYID	AEFLHLYQQI	[160]
<pre>11.2-ABCL_Azoarcus_evansii_AAL02077.1*</pre>	NRIANVLVHE	LGVVPGNRVL	LRGPNSPMLA	ACWFAIMKAG	AIAVATMPLL	RAKELGQILD	KGRITHALCA	HALRGELDEA	[160]
							A3/3	3	
1. putative 2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1	IRHIPIVTKY	DFG		-DDQKENPPY	GTAFTSPPNT	QLKYW	QTSGTTA	KPRLWTETKE	[240]
2. putative 2-NACL N47 CBX27264.1	VEKIPSIDKP	DIL		-RYOAANPPF	GGSIVRDSDE	YLTFF	FOTSGTTG	TPMKEIGYYR	[240]
3. PCL (aerobic) Azoarcus evansii WP 169132234.1*	LAKEPETAKG	DL		RDNYPF	GMFAVPRE	KVARV	HASSGTTG	KPTVVGYTLK	[240]
4. PCL Pseudomonas putida WP 059394932.1*	LAKEPETGKN	DL		RDNYPY	GMEAVPOE	EVVRL	HASSGTTG	KPTVVGYTON	[240]
5 BCL Thauera aromatica AAN32623 1*	I GKVPTI EHI	WA-GGA-	GEDSLA	ALLATGSEOF	E AAPTRPD	DHCEW	I VSSGSTG	APKGTVHTHS	[240]
6 BCL Magnetosninillum en TS-6 RAE01025 1*	I DDI DMI EHV	VTS-GENAH-	GLUDLA	DITAKVEDKI	KTAETTPD	DVAEN	LIVESGETG	APKGAVHLOP	[240]
7 A-HRCI Thauera anomatica V173 AVR00075 1	L GKUDTI COT	TVA-GDDAA	GADELA	ALLAOGREAT	P==AADTWAD	DACEN	LIVESCETC	APKGTUUTUC	[240]
A-HPCI /PCI Phodoneaudorenes palustais OFSOOF 11	AADI DUI DTT	TAV-CDADA	DTLOLA	NULATEOREAP	A DAATCAD	DTAVL	-0VSSCTTC	MDKCVMINALC	[240]
a. +-nbct/bct_knodopseddomonas_paiustris_053005.1*	AADLPHLKII	ALD	PILQLA	RELATEQEGG	APAATCAD	DIATW		L DKCALTER	[240]
9. 4-CBCL_PSeudomonas_spCBS3_ABQ44579.1*	RIKVPSVCVL	ALD	DLVSGS	RVPEVAGKSL	PPPPCEPE	QAGEV	FYISGIIG	LPKGAVIPQR	[240]
10.3-HBCL_Thauera_aromatic_K172_AVR88779.1*	AGELEQPPQV	VVR-GDEAP-	APAIIAFK	HFLDGQAATL	ESVQVAPD	DVAYW	LYSSGTTG	KPKAVMHAHR	[240]
11.2-ABCL_Azoarcus_evansii_AAL02077.1*	VATRPSVAHV	VSF-GDPAG-	AGLE	AAMARQSGEF	DNVATASD	DTCIL	AFTSGTTG	QPKATMHFHR	[240]
1. putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1	-DWENGIFLY	SRGLYAHGIR	PGWRGFFG	FSYPPFIAFW	LCHSACESMG	CQIVPKGP-L	STKAWLGL	IKNLSTTG	[320]
2. putative_2-NACL_N47_CBX27264.1	-DMLSTGWVF	KWWAHGIR	PADIFYFA	FPFGTFMAFW	CAYYDAVAMG	AQVITSGG-M	TTEQRVRO	ILELKPT-	[320]
3. PCL (aerobic) Azoarcus evansii WP 169132234 1*	-DIDTWATVV	ARSIRASGGR	AGDMVHTA	YGYGLFTGGI	GAHYGAEKLG	CTVVPMSG-G	QTEKOIOL	IQDEKPD-	[320]
4. PCL Pseudomonas putida WP 059394932 1*	-DINTWANNA	ARSTRAAGGP	KGDKVHVS	YGYGLETGGI	GAHYGAFRIG	CTVIPMSG-G	OTEKOVOL	IRDEOPD-	[320]
5. BCL Thauera aromatica AAN32623 1*	-DI THTAFI V	ARPTIGTR	EGDIAVESA	AKI FEAVGLG	NGI TEPI AVG	ATAVI MAERP	TPAAVEER	I RRHOPD-	[320]
6 BCL Magnetecninillum cn. TC 6 RAE0103E 1*	DIDATAVIN	GOOVI GTR	ED DUTYEA	AKLEFAYOLO	NGMTESI HVG	ATCVILLEDRD	TDEAVMEN	LKDHODT	[320]
6. BCL_MagnetOspiriium_spIS-6_BAE91925.1*	-DLPATAVHY	GQQVLGIR	EDDVIYSA	AKLFFAYGLG	NGMIFSLAVG	ATSVLLKDRP	TPEAVMKL	LKDHQPT-	[320]
7. 4-HBCL_Inauera_aromatica_K172_AVK88075.1*	-SLIHIAELY	ARPVLGIR	EDDVVFSA	AKLFFAYGLG	NGLIFPLAVG	ATAVLMAERP	TPAAVFER	LRQHRPT-	[320]
 4-HBCL/BCL_Rhodopseudomonas_palustris_Q53005.1* 	-SPRVMAENA	GRRIGYR	EDDVVFSA	AKLFFAYGLG	NAMECOMOIG	ATSVLYPERP	TADSVFDT	LRLHQPT-	[320]
<pre>9. 4-CBCL_Pseudomonas_spCBS3_ABQ44579.1*</pre>	-AAESRVLFM	ATQAGLR	HGSHNVVLGL	MPLYHTIGFF	AVLVAAMAFD	GTYVVVEE-F	DAGNVLKL	IERERVT-	[320]
10.3-HBCL_Thauera_aromatic_K172_AVR88779.1*	SVLIADRL	EREYFGIK	PGDRVFTT	SKMFFGWSLG	HSLMGGLQCG	ATVIVAPGWP	DAERVMAT	AARHRPT-	[320]
11.2-ABCL_Azoarcus_evansii_AAL02077.1*	-DVIAACRCW	PPHVLRPQ	PDDVFIGS	PPLAFTFGLG	GMLLFPMSVG	ASTVLLEQ-A	SPPKLLDA	IGEFGAT-	[320]
	1.00								
	9			7			A5		
 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 	VDSFLAATPT	FTMRHVEMAE	ELGINLKELN	-IKVLTMAGE	PGACVPSTKK	YLENAWAAKA	-HDQLGSVET	SGPVMYSC	[400]
<pre>2. putative_2-NACL_N47_CBX27264.1</pre>	VLVATPT	YAMRIAEMAR	EMGVDIAHSS	-IKYITSAGE	AGYVLPTVRD	AVEKAWGAKA	-LDLYGISDL	WGSTSWHC	[400]
 PCL_(aerobic)_Azoarcus_evansii_WP_169132234.1* 	IIMVTPS	YMLTVLDEME	RMGIDPHQTS	-LKVGIFGAE	PWT QAMRA	AMEARAGIDA	-VDIYGLSEV	MGP-GVANEC	[400]
4. PCL Pseudomonas putida WP 059394932.1*	IIMVTPS	YMLNLADEIE	ROGIDPHDLK	-LRLGIFGAE	PWTDELRR	SIEORLGINA	-LDIYGLSEI	MGP-GVAMEC	[400]
			COVE CELD	-I PACTSAGE	AL P EDVGR	RWOAREGVDT	-I DGTGSTEM	I HT-EL SNRA	1001
 BCL Thauera aromatica AAN32623.1* 	IFYGVPT	LYASMLANPD	CPKEGELK	- LINACI SAGE					14001
5. BCL_Thauera_aromatica_AAN32623.1* 6. BCL_Magnetospirillum_spTS-6_BAF91925.1*	IFYGVPT		VRRET-ASTR	-I RACVSAGE	ALPEDVGR	RWEEREGAAT	-LDGLGSTEM	LHT-FLSNRH	[400]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4_HE0L_Thauera_aromatica_K122_AVR980475_1* 	IFYGVPT		YRRET-ASTR	-LRACVSAGE	ALPEDVGR	RWEERFGAAI	-LDGLGSTEM	LHI-FLSNRH	[400]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* HECL_Thauera_aromatica_K172_AVR88075.1* HECL_FIAUERA_AROMANNE_AROMANNNE_AROMANNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNN AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNE_AROMANNNNE_AROMANNNE_AROMANNNNE_AROMANNNE_AROMANNNNE_AROMANNNNNNE_AROMANNNN	IFYGVPT IFYGVPT IFYGVPT	LYASMLANPD LYGTILADPQ LYASMLASPD	YRRET-ASTR CPARGELN	-LRACVSAGE -LRACVSAGE	ALPEDVGR ALPEEIGR	RWEERFGAAI RWTERYGLDI	-LDGLGSTEM -LDGIGSTEM	LHI-FLSNRH LHI-FLSNRP	[400] [400] [400]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_Q53005.1* 	IFYGVPT IFYGVPT IFYGVPT LLFAVPT	LYASMLANPD LYGTILADPQ LYASMLASPD LYAAMLADPR	YRRET-ASTR CPARGELN SRTET-LPDR	-LRACVSAGE -LRACVSAGE -LRACVSAGE -LRLCVSAGE	ALPEDVGR ALPEEIGR PLPAQVGL	RWEERFGAAI RWTERYGLDI NWRNRFGHDI	-LDGLGSTEM -LDGIGSTEM -VNGVGSTEM	LHI-FLSNRH LHI-FLSNRP GHL-FLTNLP	[400] [400] [400] [400]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88095.1* 4-HBCL_PSeudomonas_palustris_Q53005.1* 4-CBCL_Pseudomonas_psCBS3_ABQ44579.1* 	IFYGVPT IFYGVPT IFYGVPT LLFAVPT AMFATPT	LYASMLANPD LYGTILADPQ LYASMLASPD LYAAMLADPR HLDALTTAVE	YRET-ASTR CPARGELN SRTET-LPDR QAGARLES	-LRACVSAGE -LRACVSAGE -LRLCVSAGE -LEHVTFAGA	ALPEDVGR ALPEEIGR PLPAQVGL TMPDTVLE	RWEERFGAAI RWTERYGLDI NWRNRFGHDI RVNRFIPGEK	-LDGLGSTEM -LDGIGSTEM -VNGVGSTEM -VNIYGTTEA	LHI-FLSNRH LHI-FLSNRP GHL-FLTNLP MNSLYMRAVR	[400] [400] [400] [400] [400]
 BCL_Thauera_aromatica_AN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_QS3005.1* 4-CBCL_Thauera_aromatic_K172_AVR88779.1* 	IFYGVPT IFYGVPT IFYGVPT LLFAVPT AMFATPT ILFSTPV	LYASMLANPD LYGTILADPQ LYASMLASPD LYAAMLADPR HLDALTTAVE MYRNLLREGA	YRRET-ASTR CPARGELN SRTET-LPDR QAGARLES GESAAMRD	- LRACTSAGE - LRACTSAGE - LRLCVSAGE - LEHVTFAGA - IRHFVSAGE	ALPEDVGR ALPEEIGR PLPAQVGL TMPDTVLE KLPENIGQ	RWEERFGAAI RWTERYGLDI NWRNRFGHDI RVNRFIPGEK QWLDTFGIPI	-LDGLGSTEM -LDGIGSTEM -VNGVGSTEM -VNIYGTTEA -TEGIGASET	LHI-FLSNRH LHI-FLSNRP GHL-FLTNLP MNSLYMRAVR VFL-FLCARP	[400] [400] [400] [400] [400] [400]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_BCL_Rhodopseudomonas_pulstris_Q53005.1* 4-CBCL_Pseudomonas_spCBS3_ABQ44579.1* 10.3-ABCL_Thauera_aromatic_K172_AVR88779.1* 11.2-ABCL_Tavaercus_evani_AAL02077.1* 	IFYGVPT IFYGVPT IFYGVPT LLFAVPT AMFATPT ILFSTPV ILFTAPT	LYASMLANPD LYASMLASPD LYAAMLADPR HLDALTTAVE MYRNLLREGA SYRAMAEGAR	YRRET-ASTR CPARGELN SRTET-LPDR QAGARLES GESAAMRD ERRLGAPLGG	- LRACTSAGE - LRACTSAGE - LRACTSAGE - LRLCVSAGE - LEHVTFAGA - IRHFVSAGE PLVKCVSAGE	ALPEDVGR ALPEEIGR PLPAQVGL TMPDTVLE KLPENIGQ VLPAATRA	RWEERFGAAI RWTERYGLDI NWRNRFGHDI RVNRFIPGEK QWLDTFGIPI LWKDATGIEI	-LDGLGSTEM -LDGIGSTEM -VNGVGSTEM -VNIYGTTEA -TEGIGASET -IDGIGATEM	LHI-FLSNRH LHI-FLSNRP GHL-FLTNLP MNSLYMRAVR VFL-FLCARP FHI-FISADE	[400] [400] [400] [400] [400] [400] [400]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_Q53005.1* 4-CBCL_Pseudomonas_psCB53_ABQ44579.1* 3-HBCL_Thauera_aromatic_K172_AVR88779.1* 2-ABCL_Azoarcus_evansii_AAL02077.1* 	IFYGVPT IFYGVPT IFYGVPT LLFAVPT AMFATPT ILFSTPV ILFTAPT	LYASMLANPD LYASMLASPD LYAAMLADPR HLDALTTAVE MYRNLLREGA SYRAMAEGAR	YRET-ASTR CPARGELN SRTET-LPDR QAGARLES GESAAMRD ERRLGAPLGG	- LRACVSAGE - LRACVSAGE - LRACTSAGE - LRLCVSAGE - LEHVTFAGA - IRHFVSAGE PLVKCVSAGE	ALPEDVGR ALPEEIGR PLPAQVGL TMPDTVLE KLPENIGQ VLPAATRA	RWEERFGAAI RWTERYGLDI NWRNRFGHDI RVNRFIPGEK QWLDTFGIPI LWKDATGIEI	-LDGLGSTEM -LDGIGSTEM -VNGVGSTEM -VNIYGTTEA -TEGIGASET -IDGIGATEM	LHI-FLSNRH LHI-FLSNRP GHL-FLTNLP MNSLYMRAVR VFL-FLCARP FHI-FISADE	[400] [400] [400] [400] [400] [400] [400]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_GAC_BAC0pseudomonas_pulstris_053065.1* 4-BCL_PSeudomonas_sp0E53_ABQ44579.1* 10.3-HBCL_Thauera_aromatic_K172_AVR88779.1* 11.2-ABCL_Azoarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 	IFYGVPT IFYGVPT LLFAVPT LLFAVPT ILFSTPV ILFTAPT AEQAEEENMS	LYASMLANPD LYGTILADPQ LYASMLASPD LYAAMLADPR HLDALTTAVE MYRNLLREGA SYRAMAEGAR DHLNLDSF	YRRET-ASTR CPARGELN SRTET-LPDR QAGARLES GESAAMRD ERRLGAPLGG LVELVDPDT-	- LRACVSAGE - LRACVSAGE - LRLCVSAGE - LEHVTFAGA - IRHFVSAGE PLVKCVSAGE LKPVGDGE	ALPEDVGR ALPEEIGR PLPAQVGL TMPDTVLE KLPENIGQ VLPAATRA PGATVVTA	RWEERFGAAI RWTERYGLDI NWRNRFGHDI RVNRFIPGEK QWLDTFGIPI LWKDATGIEI LTRFGMPTIR	-LDGLGSTEM -LDGLGSTEM -VNGVGSTEM -VNIYGTTEA -TEGIGASET -IDGIGATEM FLLGDW	LHI-FLSNRH LHI-FLSNRP GHL-FLTNLP MNSLYMRAVR VFL-FLCARP FHI-FISADE MTISYEKCRC	[400] [400] [400] [400] [400] [400] [400] [400]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_Q53005.1* 4-CBCL_PSeudomonas_psCBS3_ABQ44579.1* 11.2-ABCL_Azoarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a100006_TRIP_SPD71907.1 putative_2-NACL_N47_CBX27264.1 	IFYGVPT IFYGVPT LLFAVPT LLFAVPT ILFSTPV ILFSTPV ILFTAPT AEQAEEENMS PVHP	LYASMLANPD LYGTILADPQ LYASMLASPD LYAAMLADPR HLDALTTAVE MYRNLLREGA SYRAMAEGAR DHLNLDSF DRLHLTETIA	YRRET-ASTR CPARGELN SRTET-LPDR QAGARLES GESAAMRD ERRLGAPLGG LVELVDPDT- YPLVLDKEG-	-LRACVSAGE -LRACVSAGE -LRACTSAGE -LRLCVSAGE -LEHVTFAGA -IRHFVSAGE PLVKCVSAGE LKPVGDGE KLVPDGG	ALPEDVGR ALPEEIGR PLPAQVGL TMPDTVLE KLPENIGQ VLPAATRA PGATVVTA IGEWTLTN	RWEERFGAAI RWTERYGLDI NWRNRFGHDI RVNRFIPGEK QWLDTFGIPI LWKDATGIEI LTRFGMPTIR Y-STVMPLIK	-LDGLGSTEM -LDGIGSTEM -VNGVGSTEM -VNIYGTTEA -TEGIGASET -IDGIGATEM FLLGDW YRTHDT	LHI-FLSNRH LHI-FLSNRP GHL-FLTNLP MNSLYMRAVR VFL-FLCARP FHI-FISADE MTISYEKCRC VEWHKETCEC	[400] [400] [400] [400] [400] [400] [400] [400] [480] [480]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_Thauera_aromatica_K172_AVR88079.1* 3-HBCL_Thauera_aromatic_K172_AVR88779.1* 11.2-ABCL_Thauera_aromatic_K172_AVR88779.1* 11.2-ABCL_Thauera_aromatic_K172_AVR88779.1* 11.2-ABCL_Thauera_aromatic_K172_AVR88779.1* 11.2-ABCL_Thauera_aromatic_K172_AVR88779.1* 11.2-ABCL_Thauera_aromatic_K172_AVR8779.1* 11.2-ABCL_Thauera_aromatic_K172_AVR8779.1* 11.2-ABCL_Thauera_aromatic_K172_AVR8779.1* 11.2-ABCL_TOPACL_PITCH_v1_a1100006_TRIP_SPD71907.1 12.2-DACL_M47_CBX27264.1 PCL_Gerobic_Acarous_evansii_MP_169132234.1* 	IFYGVPT IFYGVPT LFYGVPT LLFAVPT ILFAVPT ILFSTPV ILFTAPT AEQAEEENMS PVHP IEAK	LYASMLANPD LYGTILADPQ LYASMLASPD LYAAMLADPR HLDALTTAVE MYRNLLREGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DGPVIWEDHF	YRRET-ASTR CPARGELN SRTET-LPDR QAGARLES GESAAMRD ERRLGAPLGG LVELVDPDT- YPLVLDKEG- YPEIIDPHT-	- LRACTSAGE - LRACTSAGE - LRACTSAGE - LRLCVSAGE - LEHVTFAGA - IRHFVSAGE PLVKCVSAGE LKPVGDGE KLVPDGG GEVLPDGS	ALPEDVGR ALPEEIGR PLPAQVGL TMPDTVLE KLPENIGQ VLPAATRA PGATVVTA IGEWTLTN EGELVFTT	RWEERFGAAI RWTERYGLDI NWRNRFGHDI RVNRFIPGEK QWLDTFGIPI LWKDATGIEI LTRFGMPTIR Y-STVMPLIK LTKEAMPVIR	-LDGLGSTEM -LDGLGSTEM -VNGVGSTEM -VNIYGTTEA -TEGIGASET -IDGIGATEM FLLGDW YRTHDT YRTRDL	LHI-FLSNRH LHI-FLSNRP GHL-FLTNLP MNSLYMRAVR VFL-FLCARP FHI-FISADE MTISYEKCRC VEWHKETCEC TRLLPPTARS	[400] [400] [400] [400] [400] [400] [400] [400] [480] [480] [480]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_Pseudomonas_palustris_Q53005.1* 3-HBCL_Thauera_aromatic_K172_AVR88779.1* 11.2-ABCL_Azoarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-NACL_N47_CBX27264.1 PCL_(aerobic)_Azoarcus_evansii_WP_169132234.1* PCL_Seudomonas_putida_WP_6594932.1* 	IFYGVPT IFYGVPT LLFAVPT LLFAVPT ILFSTPV ILFSTPV ILFTAPT AEQAEEENMS PVHP IEAK IEK	LYASMLANPD LYGTILADPQ LYASMLASPD LYASMLASPD LYAAMLADPR HLDALTTAVE MYRNLLREGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DGPVIWEDHF DGPVIWEDHF	YRET-GELK YRET-ASTR CPAR-GELN SRTET-LPDR QAGA-RLES GESA-AMRD ERRLGAPLGG LVELVDPDT- YPLVLDKEG- YPEIIDPHT- YPEIIDPUT-	-LRACVSAGE -LRACVSAGE -LRLCVSAGE -LEHVTFAGA -IRHFVSAGE PLVKCVSAGE KLVPDGG GEVLPDGS GEVLPDGS	ALPEDVGR ALPEDVGR ALPEEIGR PLPAQVGL TMPDTVLE KLPENIGQ VLPAATRA PGATVVTA IGEWTLTN EGELVFTT LGELVFTS	RWEERFGAAI RWTERYGLDI NWRNRFGHDI RVNRFIPGEK QWLDTFGIPI LWKDATGIEI LTRFGMPTIR Y-STVMPLIK LTKEAMPVIR LSKEALPMVR	-LDGLGSTEM -LDGIGSTEM -VNGVGSTEM -VNIYGTTEA -TEGIGASET -IDGIGATEM FLLGDW YRTHDT YRTRDL YRTRDL	LHI-FLSNRH LHI-FLSNRP GHL-FLTNLP MNSLYMRAVR VFL-FLCARP FHI-FISADE MTISYEKCRC VEWHKETCCC TRLLPPTARS TRLLPGTARP	[400] [400] [400] [400] [400] [400] [400] [400] [480] [480] [480] [480]
 BCL_Thauera_aromatica_AM32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_Thauera_aromatica_K172_AVR88079.1* 3-HBCL_PSeudomonas_spCBS3_ABQ44579.1* 11.2-ABCL_Azoarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-NACL_M47_CBX27264.1 PCL_PSeudomonas_putida_WP_059394932.1* SLC_Thauera_aromatica_AM32623.1* 	IFYGVPT IFYGVPT IFYGVPT LLFAVPT LLFAVPT ILFSTPV ILFSTPV ILFTAPT AEQAEEENMS PVHP I-EAK GDVHYG-T	LYASMLANPD LYASMLASPD LYASMLASPD LYAAMLADPR HLDALTTAVE MYRNLLREGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DGPTIWEDHF DGPTIWEDHF SGKPVPGY	VRET-GELN VRET-ASTR CPAR-GELN SRTET-LPDR QAGARLES GESA-AMRD ERRLGAPLGG LVELVDPDT- YPLVLDKEG- YPEIIDPTT- RLRLIDEDG-	LRACVSAGE -LRACVSAGE -LRLCVSAGE -LRLVSAGE -LEHVTFAGA -IRHFVSAGE PLVKCVSAGE KLVPDGG GEVLPDGS GEVLPDGQ AEITTAGV	ALPEDVGR ALPEDVGR PLPAQVGL TMPDTVLE KLPENIGQ VLPAATRA PGATVVTA IGEWTLTN EGELVFTS AGEL0ISG	RWEERFGAAI RWTERYGLDI NWRNRFGHDI RVNRFIPGEK QWLDTFGIPI LWKDATGIEI LTRFGMPTIR Y-STVMPLIK LTKEAMPVIR LSKEALPMVR PSSAVMYWNN	-UDGLGSTEM -UDGIGSTEM -VNGVGSTEM -VNIYGTTEA -TEGIGASET -IDGIGATEM FLLGDW YRTRDL YRTRDL YRTRDL	LHI-FLSNRH LHI-FLSNRP GHL-FLTNLP MNSLYMRAVR VFL-FLCARP FHI-FISADE MTISYEKCRC VEWHKETCEC TRLLPPTARS ATFMGEMTRS	[400] [400] [400] [400] [400] [400] [400] [400] [480] [480] [480] [480] [480] [480]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_sp.Ts-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_Pseudomonas_palustris_Q53005.1* 4-CBCL_Pseudomonas_psp.CBS3_ABQ44579.1* 11.2-ABCL_Azoarcus_evansii_AAL02077.1* putative_2-PACL_NI7C_NI27264.1 PCL_(aerobic)_Azoarcus_evansii_MP_169132234.1* PCL_C_aromatica_AN32623.1* PCL_Thuera_aromatica_AN32623.1* BCL_Thauera_aromatica_AN32623.1* BCL_Thauera_aromatica_AN32623.1* 	IFYGVPT IFYGVPT LLFAVPT LLFAVPT ILFATPT ILFSTPU AEQAEEENMS P VHP IEAK IETK G DVHYG-T GEVRYG-T	LYASMLANPD LYASMLASPD LYAAMLASPD LYAAMLASPD HLDALTTAVE MYRNLLREGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DGPVIWEDHF GGPVIWEDHF SGKPVPGY SGKPVPGY	VRET-ASTR VRET-ASTR CPAR-GELN SRTET-LPDR QAGA-RLES GESAANRD ERRLGAPLGG LVELVDPDT- YPLVLDKEG- YPEIIDPHT- YPEIIDPUT- RLRLIDEDG- ELKICSDDG-	LRACVSAGE -LRACVSAGE -LRLCVSAGE -LEHVTFAGA IRHFVSAGE PLVKCVSAGE KLVPVGGE KLVPDGG GEVLPDGG GEVLPDGG AEITTAGV HEV-POGE	ALP EDVGR ALP EDVGR ALP EDVGR PLP AQVGL TMP DTVLE KLP ENIGQ VLP AATRA PGATVV TA IGEWTL TN EGELVF TS AGELQI SG MGELVV RG	RWEERFGAAI RWTERYGLDI NWRNRFGHDI RVNRFIPGEK UWKDATGIEI LWKDATGIEI LTRFGMPTIR Y-STVMPLIK LTKEAMPVIR LSKEALPMVR PSSATAYNNO	-UDGLGSTEM -UDGIGSTEM -VNGVGSTEM -VNIVGTTEA -TEGIGASET -IDGIGATEM YRTHDT YRTHDT YRTRDL PEKTA	LHI-FLSNRH LHI-FLSNRP GHL-FLTNLP MNSLYMRAVR VFL-FLCARP FHI-FISADE MTISYEKCRC VEWHKETCEC TRLLPPTARS TRLLPGTARP ATFMGEWTRS	[400] [400] [400] [400] [400] [400] [400] [480] [480] [480] [480] [480]
 BCL_Thauera_aromatica_AM32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_FACL_BAC0pscudomonas_pulstris_Q53005.1* 4-HBCL_PSeudomonas_spCBS3_ABQ44579.1* 11.2-ABCL_Aroarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-NACL_M47_CBX27264.1 PCL_PSeudomonas_putida_W7_059394932.1* BCL_Thauera_aromatica_AM32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Magnetospirillum_spTS-6_BAE91925.1* 	IFYGVPT IFYGVPT LLFAVPT LLFAVPT ANFATPT ILFTAPT AEQAEEENMS PVHP IETK GDVHYG-T GOVHYG-T GOVRYG-T	LYASMLANPD LYASMLASPD LYASMLASPD LYAAMLASPD LYAAMLASPD HLDALTTAVE MYRNLLREGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DGPVIWEDHF SGKPVPGY SGKPVPGY SGMPVPGY	VRET-ASTR VRET-ASTR CPAR-GELN SRTET-LPDR QAGA-RLES GESA-AMRD ERRLGAPLGG VPLUDPDT- YPLUDKEG- YPEIIDPHT- YPEIIDPHT- XLRIDEDG- ELKICSDDG- ELKICSDDG-	LRACVSAGE -LRACVSAGE -LRLCVSAGE -LRLVTFAGA IRHFVSAGE PLVKCVSAGE KLVPDGG GEVLPDGG GEVLPDGQ AEITTAGV NEITAPGE	ALP EDVGR ALP EDVGR PLP AQVGL KLP ENIGQ VLP AQVGL KLP ENIGQ VLP AATRA PGATVV TA IGEWTL TN EGELVF TS AGELQI SG MGELVV RG MGELVV RG	RWEERFGAAI RWTERYGLDI NWRNRFGHDI RVNRFIPGEK UWLDTFGIPI LWKDATGIEI LTRFGMPTIR Y-STVMPLIK LTKEAMPVIR LSKEALPMVR PSSATAYWNQ PTSAVCYWNN	LDGLGSTEM -UDGLGSTEM -VNGVGSTEM -VNGVGSTEA -TEGIGASET -IDGIGATEM FLLGDW YRTHDT YRTHDT YRTRDL PEKTA REKSR	LH1-FLSNRH LH1-FLSNRP GHL-FLSNRP GHL-FLSNRP VFL-FLCARP FH1-FISADE MTISYEKCRC VEWHKETCEC TRLLPDTARS ATFMGEWTRS KTFRGEWTRS STFLGEUTRS	[400] [400] [400] [400] [400] [400] [400] [480] [480] [480] [480] [480]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_BCL_Rhodopseudomonas_palustris_Q53005.1* 4-CBCL_Pseudomonas_psCBS3_ABQ44579.1* 10.3-HBCL_Thauera_aromatic_K172_AVR880770.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 PCL_(aerobic)_Azoarcus_evansii_MP_169132234.1* RCL_Thauera_aromatica_AAN32623.1* BCL_Manetospirillum_spTS-6_BAE91925.1* ALBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 	IFYGVPT IFYGVPT LLFAVPT LLFAVPT LLFAVPT ILFSTPV ILFTAPT AEQAEEENMS PVHP I EAK G DVHYG-T G EVRYG-T G EVRYG-T H AVEYG-T	LYASMLANPD LYASTLADPQ LYASMLASPD LYAAMLADPR HLDALTTAVE MYRNLLREGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DGPTIWEDHF DGPTIWEDHF DGPTIWEDHF SGKPVPGY SGKPVPGY SGWPVGY	VRET-ASTR VRRET-ASTR CPAR-GELN SRTET-LPDR QAGARLES GESAAVRD ERRLGAPLGG LVELVDPDT- YPLVLDKEG- YPEIIDPVT- YPEIIDPVT- YPEIIDPVT- RLRLIDEDG- ELKICSDDG- RVRLIDDAG- RLRLVGDRG-	LRACVSAGE -LRACVSAGE -LRLCVSAGE -LEHVTFAGA -IRHFVSAGE PLVKCVSAGE KLVPDGG GEVLPDGQ GEVLPDGQ AEITTAGV HEV-PQGE NEITAPGE	ALP EDVGR ALP EDVGR ALP EDVGR PLP AQVGL KLP ENIGQ VLP AQVGL KLP ENIGQ VLP AATRA IGEWTL TN EGELVF TT IGEWTL SG MGELVV RG PGELQI SG MGELVV RG	RWEERFGAAI RWTERYGLDI NWRNRFGHDI RVNRFIPGEK QWLDTFGIPI LWKDATGIEI LTRFGMPTIR Y-STVMPLIK LTKEAMPUIR LSKEALPMVR PSSAVMYUNN PSSATAYUNQ PTSAVCYUNN	LDGLGSTEM -UGLIGSTEM -VNGYGSTEM -VNIYGTTEA -TEGIGASET -IDGIGATEM FLLGDW YRTRDL YRTRDL YRTRDL YRTRDL PEKTA REKSR REKSR	LH1-FLSNRH LH1-FLSNRP GHL-FLTNLP GHL-FLTNLP MNSLYMRAVR VFL-FLCARP FH1-FISADE MTISYEKCRC VEWHKETCEC TRLLPPTARS ATFMGEMTRS TFLLGEMTRS TFLGEWTRS	[400] [400] [400] [400] [400] [400] [400] [480] [480] [480] [480] [480] [480] [480]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_Q53005.1* 4-CBCL_PSeudomonas_prils_AVR88779.1* 11.2-ABCL_AZOarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a100006_TRIP_SPD71907.1 putative_2-NACL_M47_CBX27264.1 PCL_Gaerobic)_Azoarcus_evansii_MP_169132234.1* PCL_Gaerobic)_Azoarcus_evansii_MP_169132234.1* BCL_Thauera_aromatica_K172_AVR88075.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL/BAUerodopseudomonas_palustris_Q53005.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_Q53085.1* 	IFYGVPT IFYGVPT IFYGVPT ANFATPT ANFATPT ANFATPT ILFSTPV ILFTAPT AEQAEEENMS P VHP I EAK I ETK G DVHYG-T H AVEYG-T H AVEYG-T I	LYASMLANPD LYGTILADPQ LYASMLASPD LYAAMLADPR HLDALTTAVE MYRNLLREGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DGPVIWEDHF DGPTIWEDHF DGPTIWEDHF SGKPVPGY SGMPVPGY SGVPVDGY	VRET-ASTR VRET-ASTR CPAR-GELN SRTET-LPDR QAGARLES GESA-AMRD ERRLGAPLGG LVELVDPDT- YPEIIDPVT- RLRLIDEDG- RVRLIDDAG- RVRLIDDAG- RVRLIDDAG- RVRLIDDAG- RVRLIDDAG-	LIRACVSAGE LRACVSAGE -LRACVSAGE -LRHVTFAGA IRHFVSAGE PLVKCVSAGE LKPVGDGE GEVLPDGQ GEVLPDGQ GEVLPDGQ AELTTAGV NEITAPGE NEITAPGE NEITAPGE	ALP EDVGR ALP EDVGR PLP AQVGL TMP DTVLE KLP ENIGQ VLP AAVRA PGATVV TA IGEWTL TN IGEWTL TN LGELVF TS AGELQI SG IGELLV SG IGELLV SG IGELLV SG	RWEERFGAAI RWTERYGLDI NWRNRFGHDI RVNRFIPGEK QWLDTFGIPI LWKDATGIEI LTRFGMPTIR Y-STVMPLIK LSKEALPMVR PSSATAYUNQ PTSAVCYWNN GSSAAGYUNQ -RRRMRPFAA	LDGLGSTEM -UDGLGSTEM -VNGVGSTEM -VNGYGSTEA -TEGIGASET -IDGIGATEM FLLGDW YRTRDL YRTRDL YRTRDL PEKTA REKSR REKSR REKSR	LHI-FLSNRH LHI-FLSNRP GHL-FLTNLP GHL-FLTNLP FHI-FLSADE MTISYEKCRC VEWHKETCEC VEWHKETCEC TRLLPFTARS TRLLPGTARP ATFMGEWTRS STFLGEWTRS TTFVGEWTRT	[400] [400] [400] [400] [400] [400] [400] [400] [480] [480] [480] [480] [480] [480] [480] [480]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_BCL_Rhodopseudomonas_palustris_Q53005.1* 4-CBCL_Pseudomonas_psCBS3_ABQ44579.1* 1.2-ABCL_Thauera_aromatic_K172_AVR880770.1* 1.2-ABCL_ATAGE_VITA_VITA1100006_TRIP_SP071907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 PULTATIVE_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 PULTATIVE_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 PCL_(aerobic)_Azoarcus_evansii_MP_169132234.1* RCL_Thauera_aromatica_AAN32623.1* BCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 	IFYGVPT IFYGVPT LIFAVPT AMFATPT AMFATPT AMFATPT ILFSTPV ILFTAPT AEQAEEENMS P VHP I EAK G DVHYG-T G EVRYG-T G QVRYG-T I AVEYG-T I AVEYG-T I AVEYG-T	LYGSTLAPPQ LYGSTLAPPQ LYASMLASPD LYAAMLAPR HLDALTTAVE MYRNLLREGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DGPTIWEDHF SGKPVPGY SGKPVPGY SGVPVDGY GTVMRPGFFS CGVPVDGY	VRET-ASTR VRRET-ASTR CPARGELN SRTET-LPDR GESAAMRD ERRLGAPLGG LVELVDPDT- YPEULDPUT- RLRLIDEDG- ELKICSDDG- ELKICSDDG- RURLIDDAG- RURLIDDAG- EVRILDDAG- EVRILDDAG-	LRACVSAGE -LRACVSAGE -LRACVSAGE -LRHCVSAGE PLVKCVSAGE KLVPDGG GEVLPDGS GEVLPDGG AEITTAGV HEV-PQGE NEITAPGE QDV-ADDE DVDDGCPTVK	ALP EDVGR ALP EDVGR ALP EDVGR TMP DTVLE KLP ENIGQ VLP ANTRA PGATVVTA IGEWTVTA IGEWTVTA IGEWTVTA GELVFTT LGELVFTS MGELVFSG MGELVVSG RASWRV CITATPM	RWEERFGAAI RWTERFGHDI RVNRFIPGHDI RVNRFIPGEK QWLDTFGIPI LWKDATGIEI LTRFGMPTIR Y-STVMPLIK LTKEAMPVIR LSKEALPHVR PSSAVMYUNN PSSAVMYUNN PSSATAYUNQ PTSAVCYUNU GSSAAGYUNQ -RRRNPFGA ASOEVCYUNU	LDGLGSTEM -LDGLGSTEM -VNGYGSTEM -VNGYGSTEM -VNIYGTTEA -TEGIGASET FLLGDW YRTRDL YRTRDL YRTRDL YRTRDL REKSL REKSL REKSL RDKTR RINTR	LHI-FLSNRH LHI-FLSNRP GHL-FLTNLP MINSLYMRAVR VFL-FLCARP FHI-FISADE MTISYEKCRC VEWHKETCEC TRLLPPTARS TRLLPGTARP ATFMGEMTRS XTFMGEMTRS STFLGEWTRS STFLGEWTRS TFVGEWTRT RLLQKSFRKA	[400] [400] [400] [400] [400] [400] [400] [480] [480] [480] [480] [480] [480] [480] [480] [480]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_FAC_BAC_BACOMONAS_SPLISTIS_053065.1* 3-HBCL_PSeudomonas_spCBS3_ABQ44579.1* 11.2-ABCL_Aroarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-NACL_M47_CBX27264.1 PCL_PSeudomonas_putida_WP_059394932.1* BCL_Mauera_aromatica_AAN32623.1* BCL_Mauera_aromatica_AAN32623.1* BCL_Mauera_aromatica_AAN32623.1* BCL_Mauera_aromatica_AAN3263.1* 4-HBCL/BAUera_aromatica_AAN3263.1* 4-HBCL_PSeudomonas_ppCBS3_ABQ44579.1* 10.3-HBCL_Thauera_aromatica_X172_AVR88075.1* 3-HBCL_Thauera_aromatica_X172_AVR88075.1* 	IFYGVPT IFYGVPT IFYGVPT LIFAVPT ANFATPT ILFSTPV ILFSTPV ILFTAPT AEQAEEENMS P VHP I ETK G DVHYG-T G QVRYG-T G QVRYG-T H AVEYG-T I	LYGSTLAPPQ LYGSTLAPPQ LYASMLASPD LYAAMLAPPR HLDALTTAVE MYRNLLREGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DGPJIWEDHF SGKPVPGY SGKPVPGY SGKPVPGY SGVPVDGY SGVPVDGY SGVPVDGY SGVPVDGY SGVPVDG-Y SGVPVDG-Y SGVPVDG-Y SGVPVDG-Y SGVPVDG-Y SGVPVDG-Y SGVPVDG-Y SGVPVDG-Y SGVPVDG-Y SGVPVDG-Y SGVPVDG-Y SGVPVDG-Y SGVPVDG-Y SGVPVDG-Y SGVPVDG-Y SGVPVDG-Y	VRET-ASTR VRRET-ASTR CPAR-GELN SRTET-LPDR QAGARLES GESA-AMRD ERRLGAPLGG UVELVDPDT- YPLUDHT- YPEIIDPHT- YPEIIDPHT- RLRLIDEDG- RVRLIDDAG- RVRLIDDAG- EVRLINEVGDF	LRACVSAGE LRACVSAGE LRACVSAGE LLRLVSAGE LLHVTFAGA IRHFVSAGE PLVKCVSAGE KLVPDGG KLVPDGG GEVLPDGG GEVLPDGG AEITTAGV NEITAPOE NEITAPOE NEITAPOE PVDDGCPTVK NEITAPOE PVDDCCPTVK NEITAPOE BUV-ADDE	ALP EDVGR ALP EDVGR ALP EDVGR PLP AQVGL TMP DTVLE KLP ENIGQ VLP AATRA PGATVV TA IGEWTL TN IGEWTL TS AGELQI SG IGELLV SG IGELLV SG IGELLV SG IGELLV SG	RWEERFGAAI RWTERYGLDI NWRNRFGHDI NWRNFFGHDI LWKDATGIPI LWKDATGIPI LWKDATGIPI LWKDATGIPI LTRFGMPTIR LSKEALPMVR PSSATAYNNQ PSSATAYNNQ GSSAAGYNNU GSSAAGYNNU GSSAAGYNNU GSSAY	LDGLGSTEM -UDGLGSTEM -UNGYGSTEM -UNGYGSTEM -UNGYGTEA -TEGIGASET -IDGIGATEM FLLGDW YRTRDL YRTRDL YRTRDL PEKTA PEKTA REKSR REKSR REKSR REKSR	LHT-FLSNRH LHT-FLSNRP MNSLYMRAVR VFL-FLSNRP MNSLYMRAVR VFL-FLCARP HTI-FISADE MTISYEKCRC VEWHKETCEC TRLLPPTARS ATFMGEWTRS XFFRGEWTHS STFLGEWTRS TTFVGEWTRT KLLQKSFRKA KALRDGWYP	[400] [400] [400] [400] [400] [400] [400] [400] [480] [480] [480] [480] [480] [480] [480] [480]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_BCL_Rhodopseudomonas_palustris_Q53005.1* 4-CBCL_Pseudomonas_psCBS3_ABQ44579.1* 1.2-ABCL_Aroarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 PCL_(aerobic)_Azoarcus_evansii_MP_169132234.1* PCL_(aerobic)_Azoarcus_evansii_MP_169132234.1* BCL_Thauera_aromatica_AAN32623.1* BCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 3-HBGL_Thauera_aromatica_K172_AVR88779.1* 11.2-ABCL_Apcarcus_evansii_ARL02077.1* 	IFYGVPT IFYGVPT IFYGVPT ILFX0VPT ILFX0VPT ILFX0VP ILFX0VPT ILFX0VPT EAK	LYGSTLAPPQ LYGSTLAPPQ LYAAMLADPR HLDALTTAVE MYRNLLREGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DGPTIWEDHF DGPTIWEDHF DGPTIWEDHF SGKPVPGY SGKPVPGY SGVPVGY GTVMRPGFFS CGKRVPWA TGTVVPGY	VPRET-ASTR VPRET-ASTR CPAR-GELN SRTET-LPDR QAGARLES GESA-AMRD ERRLGAPLGG VPLUDPT- VPLVLDKEG- VPEIIDPVT- VPLUDKEG- RURLIDDAG- RURLIDDAG- RURLUGDAG- EVRLLDELG- RARIVDDEG-	LRACVSAGE LRACVSAGE LRLCVSAGE LLEHVTFAGA IRHFVSAGE PLVKCVSAGE KLVPDGG GEVLPDGQ GEVLPDGQ KLTAPGE QDV-ADDE DVDDGCPTVK REV-PAGT	ALP EDVGR ALP EDVGR ALP EDVGR PLP AQVGL TMP DTVLE KLP ENIGQ VLP ATRA PGATVV TA IGEWT TN EGELVF TT IGEWT TN EGELVF TT IGEUT SG MGELVV RG IGELLV SG RASWRW PGLIAI RM VGRLAV KG	RWEERFGAAI RWTERFGHDI RVNRFIPGEK QWLDTFGIPI LWKDATGIEI LTRFGMPTIR Y-STVMPLIK LTKEAMPUTR LSKEALPMVR PSSAVMYVNNN PSSATAYINQ GSSAAGYWNQ -RRRNRPFQA ASQFVGYWKL PTGCRYLD	LDGLGSTEM LDGLGSTEM -VNGVGSTEM -VNIYGTTEA TEGIGASET FLLGDW YRTHDT YRTHDT YRTHDT YRTRDL Y	LHI-FLSNRH LHI-FLSNRH CHI-FLTNLP MNSLYMRAVR VFL-FLCARP FHI-FISADE MTISYEKCRC VEWHKETCEC TRLLPPTARS TRLLPPTARS XTFMGEMTRS XTFMGEMTRS TFLGEHTRS TTFVGEWTRT RLLQKSFRKA KALRDGMYYP NYVGDGWNYT	[400] [400] [400] [400] [400] [400] [400] [480] [480] [480] [480] [480] [480] [480] [480] [480] [480]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_sp.Ts-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_Brhodopseudomonas_palustris_Q53005.1* 4-CBCL_Pseudomonas_privationas_palustris_Q53005.1* 9.4-CBCL_Pseudomonas_privationas_palustris_Q53005.1* 9.4-BCL_Thauera_aromatic_K172_AVR880779.1* 11.2-ABCL_Azoarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 PCL_Gaerobic)_Azoarcus_evansii_MP_169132234.1* PCL_Gaerobic)_Azoarcus_evansii_MP_169132234.1* PCL_Gaerobic_Jazoarcus_evansii_MP_169132234.1* PCL_Thauera_aromatica_K172_AVR88075.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-CBCL_Thauera_aromatica_K172_AVR88075.1* 4-BCL_Thauera_aromatic_K172_AVR88779.1* 11.2-ABCL_Azoarcus_evansii_AAL02077.1* 		LYGSTLADPQ LYGSTLADPQ LYASMLASPR HLDALTTAVE MYRNLLREGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DGPTIWEDHF SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGVPVDGY TGTVNRPGFFS	VRET-ASTR VRRET-ASTR CPAR-GELM SRTET-LPDR QAGARLES GESAAWRD ERRLGAPLGG LVELVDPDT- YPEIIDPHT- RLRLIDEDG- ELKICSDDG- RVRLIDDAG- RURLUGDRG- EVRLURVGG- EVRLUDELG- RARIVDDEG-	LRACVSAGE LRACVSAGE LRLCVSAGE LRLCVSAGE -LRLVPKGGE -LKLVPDGG -GEVLPDGG -GEVLPDGS -GEVLPDGG -GEVLPDGG -AETTAGC -NEITAPGE DVDOGCPTVK -NEITPDT -REV-PAGT	ALPEDVGR ALPEDVGR ALPEDVGR TMPDTVLE KLPENIGQ VLPAATRA PGATVVTA IGEWTLTN EGELVFTT LGEUFFTS AGELQISG IGELLVSG IGELLVSG IGELLVSG	RWEERFGAAI RWTERFGHDI NWRNRFGHDI RVNRFIPGEK QWLDTFGIPI LWKDATGIEI LTRFGMPTIR Y-STVMPLIK LTKEAMPVIR LSKEALPHVR PSSATAYUNQ PTSAVCYUNN GSSAAGYUNQ -RRNRFQA ASQFVGYWKL PTGCRYLD	- LDGLGSTEM - LDGIGSTEM - VNGVGSTEM - VNGVGSTEM - VNGVGSTEM - TEGIGASET - TEGIGASET - TEGIGASET - TEGIGASEM - TEG	LHI-FLSNRH LHI-FLSNRH UHI-FLSNR MNSLYMRAVR VFL-FLCARP MNSLYMRAVR VFL-FLCARP MTISYEKCRC VEWHKETCEC TRLLPPTARS TRLLPGENTRS TRLPGENTRS TFLGGENTRS TFFVGEWTRT RLLQKJSRKA KALRDGWYYP NYVGDGWNYT	[400] [400] [400] [400] [400] [400] [400] [480] [480] [480] [480] [480] [480] [480] [480] [480]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_SCAC_MONDAS_SD_NEWSTANDASSD_NEWSTAND	IFYGVPT IFYGVPT IFYGVPT IFYGVPT AIFATPT 	LYASHLAND LYGTLLADP LYAANLASPD LYAANLASPD LYAANLAPR HLDALTTAV MYRNLREGA SYRAMAEGAR DHLNLDSF DHLNLTS-S SYRAMAEGAR DHLNLTS-S SYRAMAEGAR DGPLNEDHF SGKPVPGY SGVPVGY GTVMRPGFFS GGKRVPGY TGTVVPGY AT/BB	VRET-ASER CPAR-GELN SRTET-LPDR QAGA-RLES GESA-ANRD ERRLGAPLGG UVELVDPDT- YPEIIDPHT- YPEIIDPHT- RLRLIDEDG- ELKICSDDG- RURLIDDGG- RURLIDGDG- RURLIDGG RURLIDGG- RURLIDGG- RURLIDGG- RURLIDGG- NALVOGG	-LRACV3AGE -LRACV3AGE -LRACV3AGE -LRUCV3AGE -LRUVTAGA -TRHVSAGE PUKCV3AGE -GEVLP0G -GEVLP0G -GEVLP0G -AEITTAGV -AEITTAGV -AEITTAGV -NEITAGE -NEITAG	ALPEDVGR ALPEDVGR ALPELGR TMPDTVLE KLPENIGQ VLPATVL IGENTLTN IGENTLTN IGENTLTN IGENTLTN IGENTLTS AGELQISG IGELLVSG IGELLVSG IGELLVSG IGELIARASHRI PGLIAIRM VGRLAVKG	RWEERFGAAI RWTERYGLDI NWRRNFGHOL LWRANFGHOL LWRANFGIPG LLWRATGIEL LTKFGMPTIR Y-STVMPLIK LTKEAMPVIR LSKEALPWN SSSAWTWWNN GSSAAGVWNQ -ARRWRPFDA ASQFVGYWKL PTGCRYLD	- LDGLGSTEM - LDGLGSTEM - VNGYGSTEM - VNGYGSTEM - TEGIGASET - IDGIGATEM FLLGDW YRTRDL YRTRDL YRTRDL YRTRDL PEKTA PEKTA PEKTA PEKTA PEKTA PEKTA PEKTA PEKTA PERTA DSRQR	LHI-FLSNRH LHI-FLSNRP MNSLYMRAVR GHL-FLTNLP MNSLYMRAVR VFL-FLCARP FHI-FISADE MTISYEKCRC VEWHKETCEC VEWHKETCEC ATFMGENTRS TRLLPGTARS TRLLPGTARS TRLLPGTARS TRLLPGTARS STFLGEWTRS STFLGEWTRS STFLGEWTRS STFLGEWTRS STFLGEWTRS MCKSFRKA KALRDGMYYP NYVGDGWNYT	[400] [400] [400] [400] [400] [400] [400] [480] [480] [480] [480] [480] [480] [480] [480] [480]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_BCL_Rhodopseudomonas_palustris_Q53005.1* 4-CBCL_Pseudomonas_ppCBS3_ABQ44579.1* 11.2-ABCL_Pseudomonas_ppCBS3_ABQ44579.1* 11.2-ABCL_Atoarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_V1_a1100006_TRIP_SPD71907.1 putative_2-NACL_N47_CBX27264.1 PCL_(aerobic)_Azoarcus_evansii_MP_169132234.1* RCL_Mauera_aromatica_AN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_BCL_Rhodopseudomonas_palustris_Q53065.1* 4-CBCL_Pseudomonas_prCBS3_ABQ44579.1* 3-HBCL_Thauera_aromatic_X172_AVR88077.1* putative_2-PACL_PITCH_V1_a1100006_TRIP_SPD71907.1 		LVASHLAND LVASTLADP LVASHLASPD LVASHLASPD LVASHLASPD HLDALTTAVE MYRHLLREA SYRAPAEGAR SYRAPAEGAR DHLNLDSF DRLHLTETTA DGPVIWEDHF DGPVIWEDHF DGPVIWEDHF SGKPVPGY SGWPVGY SGWPVGY GTVMRPGFFS CGKRVPWA TGTVVPGY ATAB KGGIKAR	UPRE-GELR VPRET-ASTR CPAR-GELN SRTET-LPDR QAGARLES GESA-AMRD ERNLGAPLGE LVELVDPDT- VPLVLDKEG- VPEIIDPTT RLRLUPDRG- EVRLUDDAG- EVRLUDDAG- EVRLUDDLGG- MI SDDLITLKGT	- LRACY3AGE - LRACY3AGE - LRACY3AGE - LRLCY3AGE - LLKPVGDGE - LLKPVGDGE - LKVPGDGE LKVPGGGE KLVPDGG GEVLPDGQ GEVLPDGQ GEVLPDGQ MEX-TAPGE MEX-TAPGE MEX-TAPGE NEXTTPDT REV-PAGT	ALPEDVGR ALPEDVGR ALPEIGR TMP-DTVLE KLPAUGU VLPAATGA PGATVVTA IGEWTLTN LGELVFTS AGELQISG MGELVURG VGELXKG VGRLAVKG	RIVERFGAAI RIVTERVGLDI NVIRRIFGHU RVIRRIFIGEK QWLDTFGIPI LIKKANTGIEI LITRFGMPTIR LSKEALPMVR PSSAVNVNIN PSSATAVNQ -RRRNRPFQA ASQFVGVWLL PTGCRVD- YKIRVKRT	-LDGLGSTEM -LDGLGSTEM -UNGVGSTEM -VNGVGSTEA -VNGVGTEA -TEGLGASET FEGLGASET FEGLGASET FUNCTION 	LILI FLISHA LILI FLISHA GILI FLISHAP GULI FLISHAP MISLYMRAUR VEL-FLCARP FHI-FISADE MTISYEKCRC VENHKETCEC TRILPGTARP TRILPGTARP TRILPGTARP TRILPGTARP TFIGEWITS TRILPGTARP TFIGEWITS TRILPGTARP TFIGEWITS TFIGEWITS	[400] [400] [400] [400] [400] [400] [400] [400] [480] [480] [480] [480] [480] [480] [480] [480] [480] [480] [480]
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 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_BCL_Rhodopseudomonas_palustris_Q53005.1* 4-CBCL_Pseudomonas_ppCBS3_ABQ44579.1* 11.2-ABCL_ACL_PACTURE_aromatic_K172_AVR88079.1* putative_2-PACL_PITCH_V1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_V1_a1100006_TRIP_SPD71907.1* PCL_(aerobic_Azaarcus_evansii_MAL02077.1* BCL_Mauera_aromatica_AM32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_FACL_PACUdomas_pulstris_Q53005.1* 4-CBCL_Pseudomonas_p1_CBS3_ABQ44579.1* 3-HBCL_Thauera_aromatic_K172_AVR880779.1* 3-HBCL_Thauera_aromatic_K172_AVR880779.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 		LVASHLAND LVASTLADP LVASHLASPD LVASHLASPD LVASHLASPD HLDALTTAVE MYRNLLREGA SYRAMAEGAR DHLNLDSF DRLHLTETA DRLHLTETA DGPVIKUPH DGPTIWEDHF DGPTIWEDHF DGPVIKUPHC-Y SGMPUPCY SGMPUPCY GTVMPG-FS CGKRVPMA TGTVPGY AT/AB KGGXLAR RGGXLAR	UVRET-AST CPAR-GELN XRTET-LPD QAGARLES GESAAMRD ERRLGAPLEG ERRLGAPLEG LVELVDPDT- VPLUDNTEG VPEIIDPVT- RLRLUGDRG- EVRLUDAGE EVRLUDAGE EVRLUDAGE VI SDDLIIKGT SDDLIIKGT	-LRACV3AGE -LRACV3AGE -LRACV3AGE -LRLCV3AGE -LRLVTFAGA -LRLVTFAGA PLVKCV5AGE PLVKCV5AGE -CKLVPDGG -GEVLPDGQ -GEVLPDGQ -GEVLPDGQ -AEV17AG -AEV17AG -NEVTPAG -NEVTPAG NIVPSLIENS NIVPSLIENS NLPFTQVEEL	ALPEDVER ALPEDVER ALPEIGR PLP-AQVG VLPALVG VLPATRA PGATWTA IGENTL-TN IGENTL-TN IGENTL-TN EGELVFTT LGELVFTT LGELVFTT LGELVFTT RGELQI-SG MGELWKG VGRLAVKG VGRLAVKG	RHEERFGAAT RNTERYGLDI NVNRFGHOT RVNRFINGEK QMLDTFGDIT LWKDATGIEI LWKDATGIEI LKKDATWIT SSAVMYWWN SSAVWWC SSAVWC SSAVWWC SSAVC SSAVWC SSAVC	-LDGLGSTEM -LDGLGSTEM -VNGVGSTEM -VNGVGSTEM -VNGVGTTEA -TEGGGASET -TEGGGASET -TEGGGASET -TEGGGASET -TUTNL 	LHI-FLSNRR LHI-FLSNRP GHI-FITSLOND WISLYRRAVR VEL-FLCARP FHI-FISADE MTISYEKCRC VEMHKETCE TRLLPGTARP TRLUEGTARE THTFUSENTR TRLUEGTARE KITRGEWITS TTFVGEWITS TLLQKSFRKG KALROGWYP NYVGDOGNIYT AK-PGIK AA-PDVP AA-PDVF	[400] [400] [400] [400] [400] [400] [400] [480] [480] [480] [480] [480] [480] [480] [480] [480] [480] [480] [560] [560]
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 BCL_Thauera_aromatica_AN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_BCL_Rhodopseudomonas_palustris_Q53085.1* 4-BCL_Seudomonas_ppCBS3_ABQ44579.1* 11.2-ABCL_Pseudomonas_ppCBS3_ABQ44579.1* putative_2-PACL_PITCH_V1_a1100006_TRIP_SP071907.1 putative_2-NACL_PITCH_V1_a1100006_TRIP_SP071907.1 PCL_(aerobic)_Azoarcus_evansii_MA102075.1* BCL_Thauera_aromatica_AN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_X172_AVR88075.1* 4-HBCL_FACL_PACL_PITCH_V1_A1100006_TRIP_SP071907.1 putative_2-PACL_PITCH_V1_A102077.1* putative_2-PACL_PITCH_V1_A102077.1* putative_2-PACL_PITCH_V1_A102077.1* putative_2-PACL_PITCH_V1_A102077.1* putative_2-PACL_PITCH_V1_A102077.1* putative_2-PACL_PITCH_V1_A102077.1* 	IFYGVPT IFYGVPT IFYGVPT 	LVASHLAND LVASTLADP LVASHLASPD LVASHLASPD LVASHLASPD HLDALTTAVE WRNLLREGA SYRAMAEGAR DHLNLDSF DR.HLTETLA DR.HLTETLA SKIPVPGY SKIPVPGY SKIPVPG-Y SKIPVFG-Y SKIPVF	UPREGELR VPRET-ASTR QAGARLES GESAARR GESAARR ERRLGAPLGG VPEIIDPHT- VPEIIDPHT- VPEIIDPHT- VPEIIDPHT- VPLVLXEG VPEIIDPHT- RLRLIDEG ELKICSDOG- RURVIDDGG- RURVIDDGG- RURVIDDGG- VPLIDELG- SDDMLIXGG SDDMLIXGG SDDMLIXGG SDDMLIXGG	LINCI SAGE - LRACVSAGE - LRACVSAGE - LRACVSAGE - LLRUYFAGA - LLRUYFAGA - LLRUYFAGA - LLRUYGDE - LLRUYGDE - CLVPUGDE - GEVLPDGG - GEVLPDGG - GEVLPDGG - GEVLPDGG - GEVLPDGG - GEVLPDGG - AEITTAGV - NEITAFG NUPGIEG NUFPTAGGI NUFPTAGGI NUFPTQIEG VVSPTQIESC VVSPTQIESC - MVSPTQIESC - MVSPTQI	ALPEDVGR ALPEDVGR ALPEIGR PLP-AQVG VLPATRA PGATWTA IGEVTLT IGEVTLT EGELVPTT EGELVPTT EGELVPTT EGELVPTT EGELVPTT EGELVFTT EGELVFTT EGELVFTT EGELVFTT IGEULTL-SG IGELLVSG IGELLVSG IGELLVSG IGELLVSG IGELLVSG IGELLVSG IGELLVSG IGELLVSG IGELLVSG IGELLVSG IGELLVSG IGELLVSG IGEDLTN VGRLAVKG UVKIKQLSFM UVKIKQLSFM UVKIKQLSFM UVKIKQLSFM	RINE ERFGAAT RITERYGLDI RIVERFLIGEK QWLDTFGDIT LIKKDATSIEL LIKRORMTIR V-STWHDLK LIKRAMPUTR LSKEALPWR SSAVRYWWN SSAVRYWN SSAVRYWWN SSAVRYWWN SSAVRYN SSAVRYWN SSAVRYWN SSAVRYWN SSAVRYWN SSAVRYWN SSAVRYWN SSAVRYN	-LDGLGSTEM -LDGLGSTEM -VNGVGSTEM -VNGVGSTEM -VNGVGTEA -TEGGGASET -TEGGGASET -TEGGGASET -TEGGGASET -TUTNL 	LHI-FLSNRH LHI-FLSNRH GHI-FITNLP MMSLYMRAVR VFL-FLCARP FHI-FISADE MTISYEKCRC VEMHKETCE TRLLPGTARP TRLLPGTARP TRLLPGTARP TRLLPGTARP TRLSKENT KITRGEWITS TFFGEWITS KALROGWYP NYVGDOBWIYT AA-PDVP	[400] [400] [400] [400] [400] [400] [400] [400] [480] [480] [480] [480] [480] [480] [480] [480] [480] [480] [560] [560] [560] [560]
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_SCL_Rhodpseudomonas_pulstris_Q53005.1* A-BCL_Thauera_aromatic_K172_AVR880770.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-NACL_M47_CBX27264.1 PCL_Pseudomonas_putida_WP_059394932.1* BCL_Thauera_aromatic_K172_AVR88075.1* PCL_Pseudomonas_putida_WP_059394932.1* BCL_Thauera_aromatic_AAN32623.1* BCL_Thauera_aromatic_A172_AVR88770.1* a.+BBCL_Thauera_aromatic_A172_AVR8875.1* A-HBCL_Thauera_aromatic_K172_AVR8875.1* A-HBCL_Thauera_aromatic_K172_AVR8875.1* A-HBCL_Thauera_aromatic_K172_AVR8875.1* A-HBCL_Thauera_aromatic_K172_AVR8875.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1* PUtL_(aerobic)_Azoarcus_evansii_MP_169132234.1* PCL_Geudomonas_putida_WP_659394932.1* BCL_Thauera_aromatic_K172_AVR8877.1* PCL_Geudomonas_pn_G539A932.1* BCL_Thauera_aromatic_K172_AVR8875.1* PCL_Geudomonas_pn_G535_6_BAE91225.1* 	IFYGVPT IFYGVPT IFYGVPT 	LYASHLAND LYASTLADPC LYASHLASPD LYAANLAPP HLDALTTAVE MYRNLIEGA SYRAMAEGAR DHLNLDSF DRLHLTETTA DGPTIKEDHF DGPTIKEDHF DGPTIKEDHF SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY TGTVNPGFF5 GGV-TVKAR RGGTXKR RGGTXLG TGT DEGYTVVAGR DEGYTVVAGR	UVRET-ASTR CPAR-OELN STET-LPDR QAGARLES GESAARLB GESAARLB ERRLGAPLGG ULVELVDPDT- VPLUDATG VPEIDPHT- VPEIDPHT- VPEIDPT- RURLDEGG RURLDDAG RURLDDAG SDDLIIKGT SDDLIIKGT SDDLIIKGT SDDMLIIKGV SDDMLIIKGV SDDMLIIKGV SDDMLIIKGV	LINCISAGE -LRACVSAGE -LRACVSAGE -LRUTFAGA -LRUTFAGA -LKPVGDGE -LKVVGDGE -LKVVGDGE -LKVVDGG -GEVLPDQ -GEVLP	ALPEUVER ALPEUVER ALPEIGE PLPAQVG VLPALVG VLPALTA GEMTUTN GEMTUTN GEMTUTN GEGLVFTT GEGLVFTT GEGLVFTS GEGLVFTS GEGLVSG GEGLVSG GEGLVSG GEGLVSG GEGLVSG GEGLVSG GEGLVSG GEGLVSG GEGLSPE IGGIDGLTEN JCKNPKLAPQ VLKIQLSE LIJSHKVLKA	RNEERFGAAI RNTERVGLDI NVIRRIFGEK WINRIFGEK WUNRIFGEK WULDTFGIDI LWKDATGIEI LIKEAMPUTR LSKEALPMVR PSSATVNWN PSSATVAWN PSSATVAWN PSSAVTVAWN SSAAGVWNU C-RRRINRFGA ASQFVGWNL PTGCRYLD VRIRVKRT LEIHIITG-E VLEVDKD-G VYLEVDKD-G VYLEVDKD-G VYLEVDKD-G VYLEVDKD-G AVVGED-L	-LDGLGSTEM -LDGLGSTEM -VNG/GSTEM -VNG/GSTEM -VNG/GSTEM -VNG/GSTEM -TEGGASET	LILI-FLSNRH LHI-FLSNRP GRIL-FITNLP MNSLYMRAUR VEL-FLCARP HII-FISADE MTISYEKCRC VEWHKETCEC TRLLPPTARS TRLLPTARS TRLLPTARS TFLGENTRS TFLGENTRS TFLGENTRS TFLGENTRS TFLGENTS TFLGENTS TFLGENTS TFLGENTS	[400] [400] [400] [400] [400] [400] [400] [400] [480] [480] [480] [480] [480] [480] [480] [480] [480] [480] [560] [560] [560] [560] [560] [560] [560]
 BCL_Thauera_aromatica_AN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL/Thauera_aromatica_K172_AVR88075.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_Q53085.1* 4-KBCL/SEL_Rhodopseudomonas_palustris_Q53085.1* 1.2-ABCL_Pseudomonas_psCBS3_ABQ44579.1* 1.2-ABCL_Thauera_aromatic_K172_AVR88077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 putative_2-NACL_M47_CBX27264.1 PCL_(aerobic)_Azoarcus_evansii_NP_169132234.1* RCL_Mauera_aromatica_AN432623.1* BCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 putative_2-PACL_PITCH_V1_a1100006_TRIP_SP071907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 putative_2-PACL_PITCH_V1_a1100006_TRIP_SP071907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 BCL_Mauera_aromatica_K3223.1* BCL_Lauera_aromatica_AV32623.1* BCL_Lauera_aromatica_AV32623.1* BCL_Mauera_aromatica_AV32623.1* BCL_Mauera_aromatica_AV3263.1* BCL_Mauera_aromatica_AV3263.1* BCL_Mauera_aromatica_AV3263.1* BCL_Mauera_aromatica_AV3263.1* BCL_Mauera_aromatica_AV3263.1* BCL_Mauera_aromatica_AV3263.1* 		LVASHLAND LVASTLADP LVASHLASPD LVASHLASPD LVASHLASPD LVAAHLADP HLDALTTAVE WRNLLREGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DGPTIMEDHF DGPTIMEDHF DGPTIMEDHF DGPTIMEDHF SGKPVPGY SGKPVDGY GGVVPGG-Y SGVPVDG-Y GTVNPGCF CGKRVPHA TGTVVPGY SGVPVDG-Y TGTVPGY SGVPVDG-Y TGTVPG-T SGVPVDG-Y GTVNPGCF DGYVYAGR DGYVYKAGR DGYVYKAGR	UPREGELR VPRET-ASTR QAGARLES GESAARLS GESAARLS GESAARLS PLVLUXEG RERLGAPLGG ERRLGAPLGG VPLVLVKGRG RLRLIDEDG- ELKICSDDG- RURLIDDHT- VPEIIDPHT- VP	LINCISACE LIRACVSAGE -LRACVSAGE -LRACVSAGE -LRACVSAGE PLIKCVSAGE PLIKCVSAGE PLIKCVSAGE -GEVLPDGC -GEVLPDGC -GEVLPDGC -GEVLPDGC -GEVLPDGC -GEVLPDGC -GEVLPDGC -GEVLPDGC NUPPILIEN NUPPILIEN NUPPILIEN NUPPILIEN NUPPILIEN VIPPILIEN	ALPEDVGR ALPEDVGR ALPEIGR PIPAQVG VLPATRA PGATWTA IGEVTLTS AGELVPTT AGELVPTT AGELVPTT AGELVFTT AGELVFTT AGELVFTT AGELVSG TGELLVSG TGELLVSG TGELLVSG TGELLVSG TGGLDGLTEN IGGIDGLTEN IGGIDGLTEN ICKNPKLAP VLATKQLSEN LIAHEAVLEA	RINE ERFGAAT RITERYGLDT RIVERFLIGEK QWLDTFGDTL LIKKDATSIEL LIKRGHPTIR V-STWHDLK LIKEAMPUTR LSKEALPWR SSAVHYWIN SSAARWING SSAAGVWING	-LDGLGSTEM -LDGLGSTEM -VNGVGSTEM -VNGVGSTEM -VNGVGSTEM -TEGGGASET -TEGGGASET -TEGGGASET -TEGGGASET -TEGGASET -TUTNU 	LHI-FLSNRR LHI-FLSNRP GHI-FITNLP MMSLYMRAVR VFL-FLCARP FHI-FISADE MTISYEKCRC VEHNEKTCCE TRLLPPTARS TRLLPGTARS TRLLPGTARS TRLSWRTR KITRGEWITT TFVGEWITT KLLQKSRRKA KALRDGWYYP NVVGDGWIYT AA-PDIV	(400) (500) (50) (5
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_SCAC_MONTAL_ARR80770.1* JHBCL_Thauera_aromatic_K172_AVR880770.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-VACL_M47_CBX27264.1 PCL_0erobic_Arcorus_evansii_AAL2023.1* BCL_Mauera_aromatica_AN32623.1* BCL_Mauera_aromatica_ARA32623.1* BCL_Mauera_aromatica_ARA32623.1* BCL_Thauera_aromatica_ARA32623.1* BCL_Thauera_aromatica_ARA32623.1* A-HBCL_Thauera_aromatica_ARA3267.1* J-CABCL_PSeudomonas_plustris_033065.1* A-HBCL_Thauera_aromatica_K172_AVR88779.1* 2-ABCL_Azoarcus_evansii_ANE7877.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1* PUtative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1* PUtative_2-PACL_PITCH_v1_a1100006_TRIP_SD71907.1* BCL_Thauera_aromatica_K172_AVR88775.1* BCL_Thauera_aromatica_K172_AVR8875.1* BCL_Thauera_aromatica_K172_AVR8875.1* BCL_Thauera_aromatica_K172_AVR8875.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* A-HBCL_Thauera_aromatica_K172_AVR8875.1* 	IFYGVPT IFYGVPT IFYGVPT 	LYASHLAND LYASHLAND LYASHLASPD LYASHLASPD LYAAMLAPP HLDALTTAVE MYRNLLEEGA SYRAMAEGAR DHLNLDSF DRLHLTETTA DGFTIKEDHF GGFTIKEDHF GGFTIKEDHF SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGVPVDGY GTWNRPGFFS GGKRVPKA TGTVVPGY LYAD GTWNRPGFS GGC-VLGR RGGLYLGR 	UPREGELN VRRET-ASTR QAGARLES GESAANE GESAANE ERRLGAPLGG ERRLGAPLGG UVELVDPDT- VPEUIDPT- VPEUIDPT- VPEIIDPT- VPEIIDPT- RLRLIDEG- RLRLVGDRG- EVRLIDAG- RLRLVGDRG- RLRLVGDRG- RLRLVGDRG- RLRLVGDRG- SDDLLIIKGT SDDMLIIKGS SDDMLIIKGS SDDMLIIKVSGI SDDMLIKVSGI SDDMLIKVSGI	-LRACV3AGE -LRACV3AGE -LRACV3AGE -LRACV3AGE -LRUTFAGA -LRUTFAGA -LKPVGDGE -LKPVGDGE -LKPVGDGE -LKVPDGS -GEVLPDGS -GE	ALPEDVGR ALPEDVGR ALPEIGR PLPAQVG VLPATRA PGATWTA IGENTLTN GENTLTN GEGLVFTT LGELVFTT GGLVF-TS GGLVF-TS GGLVF-TS GGLVF-GT GGLGL-FA GGLGL-TA GGLVSG UKJRLAVKG VRSIEGLSPE IGGIDGLTEN IGKJRKLAPQ VLKIRQLSP LIAHEAVLEA LIAHEAVLEA LIAHEAVLEA LIAHEAVLEA	RIVERPRGAI RIVERPGLIA RUTERPGLI RVIREIPGEK QMLDTFGIDI LWKDATGIEI LIKEAMPUTR V-STVMPLIK LIKEAMPUTR DSSAUTVMWN SSSALAPMUR PSSAUTVMWN SSSAGVMWQ SSSAQGVMQ SSSAQGVMQ PTSAVCVMW PTSAVCVM PTS	-LDGLGSTEM -LDGLGSTEM -UNG/GSTEM -UNG/GSTEM -UNG/GSTEM -UNG/GSTEM -TEG/GASET -IDG/GATEM FLLGDM FLLGDM REKSL 	LII-FLSNRH LII-FLSNRP GUL-FLTNLP MNSLYMRAVR VEL-FLCARP FHI-FISADE MTISYEKCRE VEWKETCEC VEWKETCEC VEWKETCEC TRLIPPTARS TRLIPPTARS TRLIPPTARS TRLIPPTARS TRLIPPTARS TRLIPTARS TRLIPTARS ALARDGWYP NVVGDGWLYT AK-PGIK	(400) (500) (50) (5
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL/Thauera_aromatica_K172_AVR88075.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_Q53005.1* 4-CBCL_Pseudomonas_psCBS3_ABQ44579.1* 1.2-ABCL_Aroarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 PULative_2-NACL_M47_CBX27264.1 PCL_(aerobic)_Azoarcus_evansii_MP_169132234.1* RCL_Breudomonas_putida_WP_659394932.1* BCL_Thauera_aromatica_K172_AVR88075.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 3-HBCL_Thauera_aromatic_K172_AVR88779.1* 11.2-ABCL_Azoarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 putative_2-PACL_PITCH_V1_a1100006_TRIP_SP071907.1 BCL_daerobic)_Azoarcus_evansii_WP_169132234.1* PCL_(aerobic)_Azoarcus_evansii_WP_169132234.1* PCL_Gerobic)_Azoarcus_evansii_WP_169132234.1* PCL_Gerobic)_Azoarcus_evansii_WP_169132234.1* PCL_Gerobic)_Azoarcus_evansii_WP_169132234.1* PCL_Gerobic)_Azoarcus_evansii_WP_169132234.1* PCL_Gerobic)_Azoarcus_evansii_WP_169132234.1* PCL_Gerobic)_Azoarcus_evansii_WP_16913223.1* BCL_Thauera_aromatica_AXB2623.1* PCL_Gerobic)_Azoarcus_evansii_WP_16913225.1* A-HBCL/BAUER_BESS_SUMESSUMES		LVASHLANDD LVASHLANDD LVASHLASDD LVASHLASDD LVAAHLADD HLDALTTAVE WRNLLREGA SYRAMAEGAR DHLNLDSF DR.HLTETLA DR.HLTETLA SKIPVPGY SKIPVFGY SK	UPRET-GELR CPAR-GELN SRTET-LPDR QAGARLES GESAARR ERRLGAPLGG VPEIIDPHT- VPEIIDPHT- VPEIIDPHT- VPEIIDPHT- VPEIIDPHT- VPEIIDPHT- RLRLIDEGC VPEIIDPHT- VPEIIDPHT- VPLVDKGGRG- VPLVDKGGRG- VPLVDKGGRG- VPLVDKGGRG- SDDMLIXGG GDDMLKVGGI GDDMLKVGGI TDDIFKVSGI VDMMIISGG	LIKALYJAGE - LRALYJAGE - LRALYJAGE - LRUTFAGA - LRUTFAGA - LEHVTAGA - LKVPGDE - LKVPGDE - CKVPGDE - GEVLPDGS - GEVLPDS - GEVLPDS - GEVLPDS	ALP EDVRR ALP EDVRR ALP EEIGR PIP AQVGL TMP DTVLE KLP EHIGR VLP AATRA PGATW TA IGENTL TN IGENTL	RINE ERFGAAT RINTERYGLDI RIVTRETINGEK QWLDTFGDIT LIKKDATSIEL LIKRGAMPUTR LSKALPWPT SSAVMYWAN PSSATAVMQ PSSAVMYWAN PSSATAVMQ SSAAGVWW CSSAAGVWW CSSAVGVWKL PTGCYUD- YRIRVKRT YRIRVKRT QYEIRUKRT QYEIRUKRT AVVGEDE-C AVVGEDE-C AVVGEDE-C AVVGEDE-C	-LDGLGSTEM -LDGLGSTEM -UNG/GSTEM -VNG/GSTEM -VNG/GSTEM -VNG/GSTEM -TEGGGASET -TEGGGASET -TEGGASET -LLGBW FLLGBW 	LHI-FLSNRR LHI-FLSNRR GHI-FLTNL WMSLYWRAVR VFL-FLCARP FHI-FISADE MTISYEKCRC VEWHKETCE TRLLPDTARS TRLLPGTARE TRLLPGTARE TRLLPGTARE TRLSKENT KITRGEWITS TFFUGEWITS KITRGEWITS KALROGWYP NYVGDOBWIYT AA-PDVP	(400) (500) (50) (5
 BCL_Thauera_aromatica_AM32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_Thauera_aromatica_K172_AVR88079.1* 3-HBCL_Thauera_aromatica_K172_AVR88079.1* 3-HBCL_Thauera_aromatica_K172_AVR88079.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-VACL_M47_CBX27264.1 PCL_Pseudomonas_putida_WP_059394932.1* BCL_Thauera_aromatica_AVR32623.1* BCL_Thauera_aromatica_AVR32623.1* A-HBCL/SL_Rhodpseudomonas_palustris_Q53065.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1* PUtL_Gerobic_Acoarcus_evansii_MP_169132234.1* PCL_Gerobic_Acoarcus_evansii_MP_169132234.1* PCL_Gerobic_Acoarcus_evansii_MP_169132234.1* PCL_Gerobic_Acoarcus_evansii_MP_169132234.1* PCL_Gerobic_ACOARCUS_VANSII_VANS2053.1* BCL_Thauera_aromatica_K172_AVR8075.1* BCL_Magnetospirillum_spTS-6_BA591325.1* A-HBCL_Thauera_aromatica_K172_AVR8075.1* BCL_Magnetospirillum_spTS-6_BA591325.1* A-HBCL_Thauera_aromatica_K172_AVR8075.1* BCL_Magnetospirillum_spTS-6_BA591325.1* A-HBCL_Thauera_aromatica_K172_AVR8075.1* 		LYASHLAND LYASHLAND LYASHLASPD LYASHLASPD LYAAMLADP HLDALTTAVE MYRNLLEEGA SYRAMAEGAR DHLNLDSF DRLHITETIA DGFINEDHF DGFINEDHF DGFINEDHF DGFINEDHF SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVFG-Y SGKPVFGKFGKFGKFGKFGKFGKFGKFGKFGKFGKFGKFGKFGKF	UPREGELR VPRET-ASTR CPARGELN SRTET-LPDR QAGARLES GESAARLES GESAARLES GESAARLES GESAARLES RELATIONE ERRLGAPLG UVELVDPDT- VPEIIDPHT- VPEIIDPUT- RLRLIDEG- ELKICSDDG- RURLIDDAG RURLIDAG SDDLIIKGT TDQMVTKGT SDDMLIKVSGI SDDMLIKVSGI SDDMLIKVSGI SDDMLKVSGI VDDFKVSGI SDDMLKVSGI	-LRACV3AGE -LRACV3AGE -LRACV3AGE -LRACV3AGE -LRUTFAGA -LRUVGDE -LEHVTFAGA -LRUVGDE -LKVPGDE -CEVLPDGS KUVPGDE KUVPGC 	ALPEDVGR ALPEDVGR ALPEEIGR PIPAQVG VLPAATRA PGATVVTA IGEMTLTN EGELVFTT LGELVFTT LGELVFTT AGELQTST IGELVSG IGELLVSG IG	RUEERFGAAT RUTERVGLDI NUTRETVGLDI NUTRETJGEK QULDTFGDIT LWKDATGIEI LIKEAMPUIR LIKEAMPUIR LIKEAMPUIR LIKEAMPUIR LIKEAMPUIR SSAARGWING GSSAAGGWING GSSAAGGWING GSSAAGGWING CSSAA	-LDGLGSTEM -LDGLGSTEM -UNG/GSTEM -UNG/GSTEM -UNG/GSTEM -UNG/GSTEM -UNG/GSTEM -TEG/GASET -IDG/GATEM FCLLGOW 	LILI-FLSNRH LHI-FLSNRP GUL-FLTNLP MNSLYNRAVR VEL-FLCARP FHI-FISADE MTISYEKCRC VEWHETCEC VEWHETCEC VEWHETCEC TRLIPPTARS TR	(400) (500) (50) (5
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_BCL_Rhodopseudomonas_pulstris_Q53005.1* 4-CBCL_Pseudomonas_psCBS3_ABQ44579.1* 1.2-ABCL_Aroarous_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 PCL_Garobic_Azoarous_evansii_MP_169132234.1* PCL_Grenobic_Azoarous_evansii_MP_169132234.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 3-HBCL_RSCL_Rhodopseudomonas_pulstris_Q53005.1* 9.4-CBCL_Pseudomonas_spCBS3_ABQ44579.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SP071907.1* PUL_Gaerobic_Azoarous_evansii_AAL02077.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* HCL_Gaerobic_Azoarous_evansii_AVP_169132234.1* PCL_Gaerobic_Azoarous_evansii_AVP_169132234.1* PCL_Gaerobic_Azoarous_evansii_AVP_169132234.1* PCL_Gaerobic_Bacoarous_evansii_AVP_169132234.1* PCL_Gaerobic_Bacoarous_evansii_AVP_169132234.1* PCL_Gaerobic_Bacoarous_evansii_AVP_169132234.1* PCL_Gaerobic_Bacoarous_evansii_AVP_169132234.1* PCL_Gaerobic_Bacoarous_evansii_AVP_169132234.1* PCL_Gaerobic_Bacoarous_evansii_Bacoarous_evansii_AVP_169132234.1* PCL_FSeudomonas_putcia_VP_059304932.1* ALHBCL_Thauera_aromatic_K172_AVR88075.1* A-HBCL_Thauera_aromatic_K172_AVR88075.1* A-HBCL_Thauera_aromatic_K172_AVR88075.1* A-HBCL_Thauera_aromatic_K172_AVR88075.1* A-HBCL_Thauera_aromatic_K172_AVR88075.1*		L'ASHLAND L'YGTLLADP L'YGTLLADP L'YASHLASPD L'YASHLASPD L'YASHLASPD L'YASHLASPD HLDLTTAVE MYRNLLEGS SYRAMAEGAR DHLNLDSF DRLHLTETIA DGPTINEDHF DGPTINEDHF DGPTINEDHF DGPTINEDHF SGKPVPGY SGKPVGY SGKPVGK	UPRET-GELR CPAR-GELN STET-LPDR QAGA-RLES GESA-ARD ERRLGAPLGG EKSL-ARD FRILGAPLGG ELKICSDDG- ELKICSDDG- ELKICSDDG- ELKICSDDG- ELKICSDDG- ELKICSDDG- RVRLIDDAG- RVRLIDDAG- RVRLIDDAG- SDDLIIKGT SDDMLITKGS SDDMLITKGS SDDMLIKVSGI SDDMLIKVSGI SDDMLKVSGI SDDMLKVSGI SDDMLKVSGI SDDMLKVSGI SDDMLKVSGI	-LRACV3AGE -LRACV3AGE -LRACV3AGE -LRACV3AGE -LRUTFAGA -LRUTFAGA -LKVPOGGE -LKVVGDGE -LKVVGDGE -LKVVPOG -GEVLPDQ -GEVLPDQ -AEVTAQ -REV-PQGE -NETTPO -REV-PQGE NVFPTALQGI NUFPTALQGI NUFPTALQGI NUFPTALQGI NUFPTALQGI VSPFEVEA VSPFEVEA VSPFEVEA VSPFEVEA VSPFEVEA NUFPTELGQ NUFPSEVESA	ALP-EDVER ALP-EDVER ALP-EDVER ALP-EIGR PIP-AQVE TMP-DTVLE KLP-ENICO VLP-AATRA PGATVV-TA IGENTL-TM IGENTL-TM IGENTL-TM EGELVF-TT IGENTL-TM FGLI-SG MGELVV-TG MGELV TG MGELV TG	RIFERFGAAT RWTERYGLDI RWTRFJIGEK QWLDTFGDIT LWKDATSIEL LKKDATSIEL LKKDATSIEL LKKDATWIN SSATAVWIQ SSATAVVIQ	-LDGLGSTEM -LDGLGSTEM -UNG/GSTEM -VNG/GSTEM -VNG/GSTEM -VNG/GSTEM -TEGGASEM -TEGGASEM -TEGGASEM -LLGBW 	LHI -FLSNRR LHI -FLSNR GUL -FLSNR GUL -FLSNR FWI-SLSNR FHI -FLSNR FHI -FLSA FHI -FLSA	(400) (500) (50) (5
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_Thauera_aromatica_K172_AVR88079.1* 3-HBCL_Thauera_aromatic_K172_AVR88079.1* 11.2-ABCL_Azoarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-NACL_M47_CBX27264.1 PCL_Pseudomonas_putida_WP_059394932.1* BCL_Thauera_aromatica_AAN32623.1* BCL_Thauera_aromatica_AAN32623.1* BCL_Thauera_aromatica_AAN32623.1* A-HBCL/BL_Rhodopseudomonas_palustris_Q53005.1* 4-HBCL/BCL_Rhodopseudomonas_plustris_Q53085.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_Q53085.1* 9.4-CBCL_Pseudomonas_pCBS3_ABQ44579.1* 11.2-ABCL_Azoarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1* PCL_Pseudomonas_putida_WP_059394932.1* SCL_Thauera_aromatica_ATX2_AVR88075.1* SCL_Thauera_aromatica_ATX2_AVR88075.1* SCL_Thauera_aromatica_ATX2_AVR88075.1* SCL_Thauera_aromatica_ATX2_AVR88075.1* SCL_Thauera_aromatica_ATX2_AVR88075.1* SCL_Thauera_aromatica_ATX2_AVR8875.1* SCL_Thauera_aromatica_ATX2_AVR8875.1* SCL_Thauera_aromatica_ATX2_AVR8875.1* A-HBCL/BCL_Rhodopseudomonas_putstis_Q53085.1* A-HBCL/BCL_Rhodopseudomonas_putstis_Y1 SCL_TAUERA_BAROMASES.1* SCL_TAUERA_BAROMASES.2* A-HBCL/TAUERA_BAROMASES.1* A-HBCL_Thauera_aromatica_ATX2_AVR8875.1* A-HBCL_Thauera_aromatica_ATX2_AVR8875.1* A-HBCL_ThaUERA_BAROMASES.2* A-HBCL_TAUERA_BAROMASES.2* A-BCL_ACUE_Rhodopseudomonas_putstis_Q53085.1* 		L'ASHLAND L'YGTLADP L'YGTLADP L'YAMLASPD L'YAMLASPD L'YAMLASPD L'YAMLASPD DHLNLDSF DRLHLTATAV MYRNLEEG SGVPVGY S	UPREGELR VPRET-ASTR CPARGELN SRTET-LPDR QAGARLES GESAARLES GESAARLES GESAARLES GESAARLES RELATEDRUT VPEIIDPHT- RIRLIDEGE ELKICSDG- RURLIDGE- ELKICSDG- EVRLIDELG- EVRLIDGEG EVRLIDELG- SDDLIIKGT SDDLIIKGT SDDMLITKGG SDDMLIKVGGI SDDMLIKVGGI SDDMLIKVGGI SDDMLIKVGGI SDDMLIKVGGI SDDMLIKVGGI SDDMLIKVGGI SDDMLKVGI SDDMLKVGI SDDMLKVGI SDDMLKVGI SDDMLKVGI SDDMLKVGI SDDMLKVGI SDDMLKVGI SDDMLKVGI SDDMLKVGI SDDMLK	- LRACY3AGE - LRACY3AGE - LRACY3AGE - LRACY3AGE - LRUTFAGA - LRUYAGE - LEHVTFAGA - LRUYAGE - LEHVTFAGA - LRUYAGE - CLVPGDE KLVPGDE 	ALPEDVGR ALPEDVGR ALPEIGR PLPAQVG VLPAATRA PGATVVTA IGGHTLTN EGELVFTT LGELVFTT LGELVFTT AGEQIST GGLJAITN PGLJAI-SC IGELLVSG IGEL	RIVEERFGAAT RIVEERFGAAT RIVTERFGLD RIVTRETIGEK QUIDTFGDT LIKKDATGIEI LIKEAMPVIR LSKEALPHYR PSSAVTWINN PSSATAVHIQ PSSAVTWINN SSAAGWHQ ASQFVGYHKL PTGCRYLD YRIRVKRT LEIHLIG-E VRIRVKRT LEIHLIG-E VYLLEVKDC- AVVGGEDE-C AVVGGETA-E AVVGGEDE-C AVVGCDE-R	-LDGLGSTEM -LDGLGSTEM -UNG/GSTEM -UNG/GSTEM -UNG/GSTEM -UNG/GSTEM -TEGGASET -TEGGASET -TEGGASET -LLGOW 	LILI-FLSNRH LHI-FLSNRP GUL-FLTNLP MNSLYNRAVR VEL-FLCARP HII-FISADE MTISYEKCRE VELWKETCE TRLIPPTARS TRLIPPTARS TRLIPPTARS TRLIPFTARS TRLIPSTRA KTFRGEWTRS TFFGGWTRS KTFRGEWTRS KTFRGEWTRS LLQXSFRKA KALRDGHVP NVVGDGWNYT AK-PGIK LA-PGET LA-PGET LA-PGET LA-PGET LA-PGET LA-PGET LA-PGET LA-PGET PR-PGHG PR-PGHG	(400) (500) (50) (5
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* A+BGL_Thauera_aromatica_K172_AVR88075.1* A+BGL/BGL_Rhodpseudomonas_pulstris_Q5005.1* A+BGL/BGL_Rhodpseudomonas_pulstris_Q5005.1* A+BGL/Thauera_aromatic_K172_AVR880770.1* Putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 PUtative_2-NACL_M47_CBX27264.1 PCL_Pseudomonas_putida_WP_059394932.1* BCL_Thauera_aromatica_K172_AVR88075.1* BCL_Thauera_aromatica_K172_AVR88075.1* A+BGL/Thauera_aromatica_K172_AVR88075.1* A+BGL/BAUC_M47_CBX27264.1 PCL_(aerobic)_Azoarcus_evansii_MP_169132234.1* PCL_Garobic)_Azoarcus_evansii_MP_169132234.1* PCL_Garobic)_Azoarcus_evansii_MP_169132234.1* PCL_(aerobic)_Azoarcus_evansii_MP_169132234.1* PCL_Garobic)_Azoarcus_evansii_MP_169132234.1* PCL_Garobic)_Azoarcus_evansii_MP_169132234.1* PCL_Garobic_Max02623.1* BCL_Mauera_aromatica_K172_AVR88075.1* PCL_Garobic)_Azoarcus_evansii_MP_169132234.1* PCL_Garobic_Max02623.1* BCL_Mauera_aromatica_K172_AVR88075.1* HHSCL/GL_Rhodpseudomasa_palustris_Q53085.1* 4-HBCL/Thauera_aromatica_K172_AVR88075.1* HHSCL/BL_Rhodpseudomasa_palustris_Q53085.1* A+HBCL/BL_Rhodpseudomasa_palustris_Q53085.1* A+HBCL/BL_Rhodpseudomasa_palustris_Q53085.1* A+HBCL/BL_Rhodpseudomasa_palustris_Q53085.1* A+HBCL/BL_Rhodpseudomasa_palustris_Q53085.1* A+HBCL/BL_Rhodpseudomasa_palustris_Q53085.1* A+HBCL/PSULTANUER_aromatica_K172_AVR88779.1* A+HBCL/PSULTANUER_aromatica_K172_AVR88779.1* A+HBCL/PSULTANUER_aromatica_K172_AVR88779.1* A+HBCL/PSULTANUER_aromatica_K172_AVR88779.1* A+HBCL/P		L'ASHLAND L'ASTLLADE L'ASHLASPD L'ASHLASPD L'AAMLADE HLDALTTAVE MINNELLEGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DGPTINEDHF DGPTINEDHF DGPTINEDHF SGMPVPGY SGMPVPGY SGMPVPGY SGMPVPGY SGMPVPGY SGMPVPGY SGMPVPGY SGMPVPGY SGMPVPGY SGMPVPGY SGMPVPGY SGMPVPGY SGMPVPGY SGMPVPGY SGMPVFGY GTWNRPGFFS CGCLIKAR KGGLIKAR KGGLIKAR CGC-VLGG DGYYVYAGR DGGYYVYAGR DGGYYVYAGR DGGYYVYAGR ADGYFHYGG ADGYFHYGG ADGYFHYGG ADGYFHYGG ADGYFHYGG ADGYFHYGG ADGYFHYGG ADGYFHYGG ADGYFHYGG ADGYFHYGG	UPREGELR VPRET-ASTR CPARGELN STET-LPDR QGGRLES GESAARLES GESAARLES GESAARLES GESAARLES GESAARLES RESAARLES CESAARLES VPEIDPHT- VPEIDPHT- VPEIDPHT- VPEIDPHT- VPEIDPHT- VPEIDPHT- SDDLIIKGT SDDMLIIKGT SDDMLIIKGT SDDMLIIKGT SDDMLIIKGT SDDMLIIKGT SDDMLIKSGI SDDMLKYSGI VDDHFYSGI VDDHFYSGI VDDHFYSGI VDDHFYSGI	LINCISACE LRACV3AGE -LRACV3AGE -LRACV3AGE -LRUTFAGA -LRUTFAGA -LKVVGDGE -LKVVGDGE -LKVVGDGE -LKVVDGG -LKVVPGGE -LKVVPGGE -GEVLPDG -GEVLPDG -GEVLPDG -GEVLPDG -GEVLPDG -REVVPGE -NETTPD -REV-PAGT NVFPIALGEI NVFPIALGEI NVFPIALGEI VVSPEVEAS VVSPEVEAS VVSPEVEAS VVSPEVEAS VVSPEVEAS VVSPEVEAS VVSPEVEAS VVSPEVEAS VVSPEVEAS VVSPEVEAS	ALPEDVRR ALPEDVR ALPEDVR ALPEIGR PIPAQVG VLPAATRA PGATVVTA IGBNTLTN EGELVFTT LGELVFTT LGELVFTS GAELQISG IGELVSG IGELVSG IGELVSG IGELVSG IGELVSG IGELVSG IGELGISG IGELGUSG IGELGI-SP IGGIGGLTEM URARAVLEA LIAMEAVLEA LIAMEAVLEA LAAMFGAKE ASAVFGIE	RIFERFGAAT RWTERYGLDI RWTRFJIGEK QWLDTFGDIT LWKDATGIEI LWKDATGIEI LKKDATGIEI LKKDATWIN SSATAVNIQ PSSATAVNQ PSSATAVNQ PSSATAVNQ PSSATAVNQ RSSATAVNQ	-LDGLGSTEM -LDGLGSTEM -VNG/GSTEM -VNG/GSTEM -VNG/GSTEM -VNG/GSTEM -TEG/GASET	LII - FLSNRH LII - FLSNRP GUL - FLTNLP MNSLYMRAUR VEL - FLSNRP FHI - FISADE MTISYEKCRC VEWHKETCEC TRLLPFTARS TRLLPGTARP ATFMGEUTRS STFLGEHTRS STFLGEHTRS STFLGEHTRS AKALROW/YP NYYGDGMNYT M-PGLS- LA-PGEY LA-PGEY LA-PGE LA-PGE PE-DPSA PR-DGH	(400) (500) (50) (5
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RRRWRFPGA ASQFVGYWKL PTGCRYLD YRIRVKRT LETHITG-E YRIRVKRT LETHITG-E VYLEVKAC AVVGEDED-C AVVGEDED-C AVVGEDFD-C AVVGEDFD-C AVVGEDFD-C AVVGEDFD-C AVGGVDE-F BURKK</td><td>-LDGLGSTEM -LDGLGSTEM -UNGVGSTEM -VNGVGSTEM -VNGVGSTEM -TEGGGASET -TEGGGASET -TEGGGASET -TEGGGASET -TUTNU </td><td>LHI-FLSNRH LHI-FLSNRP GRI-FLTNLP MMSLYMRAVR VFL-FLCARP HHI-FISADE MTISYEKCRE VEHWETCEC TRLLPPTARS TRLLPPTARS TRLLPPTARS TRLLPPTARS TRLLPTARS TRLSVERKCRE VEHWETCEC TRLLPPTARS TRLLPTARS TRLSVERKCRE VEHWETCEC TRLLPPTARS TRLSVERKCRE VEHWETCEC TRLLPPTARS TRLSVERKCRE VEHWETCEC TRLLPPTARS TRLSVERKCRE VEHWETCEC TRLSVERKCRE TRLSVERKCRE VEHWETCEC TRLSVERKCRE VEHWETCEC TRLSVERKCRE VEHWETCEC TRLSVERKCRE VEHWETCEC TRLSVERKCRE VEHWETCEC TRLSVERKCRE VEHWETCEC TRLSVERKCRE T</td><td>(400) (500) (50) (5</td>		LVASHLANPD LVASHLANPD LVASHLASPD LVASHLASPD LVASHLASPD LVASHLASPD HLDALTTAVE WRNLIEGES SYRAMAEGAR DHLNLDSF DRLHITTATA DRLHIETTA DGFINEDHF DGFINEDHF DGFINEDHF CGKRVPGY SKVPVGY SKVVVGY SKVVVGY SKVVVGY SKVVVGY SKVVVGY SKVVVGY SKVVVGY SKVVVGY SKVVVGY SKVVVGY SKVVVGY SKVVVGY SKVVVGY SKVVVGY SKVVVGY SKVVVVGY SKVVVGY SKVVVGY SKVVVGY SKVVVGY SKVVVVGY SKVVVVGY SKVVVVGY SKVVVVGY SKVVVVGY SKVVVVGY SKVVVVGY SKVVVVVGY SKVVVVVGY SKVVVVGY SKVVVVVGY SKVVVVVGY SKVVVVGY SKVVVVVGY SKVVVVGY SKVVVVGY SKVVVVGY SKVVVVGY SKVVVVGY SKVVVVGY SKVVVVGY SKVVVVGY SKVVVVGY SKVVVVGY SKVVVVGY SKVVVVGY SKVVVVGY SK	UPRE-GELR CPAR-GELN SRTET-LPDR QAGARLES GESAARLES GESAARLES GESAARLES GESAARLES RILLORDG ERRLGAPLGG ERRLGAPLGG ERRLGAPLGG EVRLIDPUT- RURLIDDG- EVRURDGG- EVRLIDELG- EVRLIDELG- EVRLIDELG- EVRLIDELG- SDDLIIIKGT SDDLIIKGT SDDMILKVGGI SDDMILKVGG SDDMILKVG SDDMILKVGG SDDMILKVG SDDMILKVG SDDMILKVG SDDMILKVG SDDMILKVG SDDMILKVG SDDMILKVG SDDMILKVG	-LRACV3AGE -LRACV3AGE -LRACV3AGE -LRACV3AGE -LRUTFAGA -LRUTFAGA -LRUTFAGA -LRUTFAGA -LRUTFAGA -LRUTPAGE KUPPGDE KUPPGDE KUPPGDE KUPPGDE WEITFOT RETA NUPSLIENS NVFPTALGGI NVFPTALGGI NVFPTALGGI NVFPTALGGI NVFPTALGGI NVFPTALGGI NVFPTEEQA VVSPFELEQA NIMSSFELEQA NIMSSFELEQA NIMSSFELEQA NIMSSFELEQA NIMSSFELEQA NIMSSFELEQA NIMSSFELEQA NIMSSFELEQA NIMSSFELEQA NIMSSFELEQA NIMSSFELEQA NIMSSFELEQA NIMSSFELEQA	ALPEDVGR ALPEDVGR ALPEDVGR ALPEIGR PIPAQVG VLPAATRA PGATWTA IGHTLTN IGGHTLTN IGGHTLTN IGGHTLTN IGGHTLTN PGLQISG IGELVS	RINE ERFGAAT RINTER REGAT RUTER YGLDI NVIRR I I PIGEK QWLDTFGDIT LIKKDATGIEI LIKEGAMPTIR V-STWHOLTK LITKEAMPVIR LSKEAL PMYR PSSAVTWWN PSSATAVWNQ PSSAVTWWN SSAAGWWQ - 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 BCL_Thauera_aromatica_AM32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_Thauera_aromatica_K172_AVR88079.1* 3-HBCL_Thauera_aromatic_K172_AVR88779.1* 11.2-ABCL_Azoarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-NACL_M47_CBX27264.1 PCL_0erobic_Azoarcus_evansii_WP_169132234.1* PCL_0erobic_Azoarcus_evansii_WP_169132234.1* PCL_Dseudomonas_putida_WP_059394932.1* BCL_Thauera_aromatica_AX132623.1* BCL_Thauera_aromatica_AX13263.1* A-HBCL/Thauera_aromatica_X122.4VR88075.1* 4-HBCL_Thauera_aromatic_K172_AVR88077.1* 11.2-ABCL_Azoarcus_evansii_MP_169132234.1* PCL_0erobic_Azoarcus_evansii_MP_169132234.1* PCL_0erobic_Azoarcus_evansii_MP_169132234.1* PCL_0erobic_Azoarcus_evansii_MP_169132234.1* PCL_0erobic_Azoarcus_evansii_MP_169132234.1* PCL_Pseudomonas_putida_WP_059394932.1* SCL_Thauera_aromatica_K172_AVR8875.1* PCL_Pseudomonas_putida_MP_059394932.1* BCL_Thauera_aromatica_AX122X64.1 PCL_0erobic_Azoarcus_evansii_MP_169132234.1* PCL_0EROBICS_DEMOMENAS_palustris_053065.1* 4-HBCL/Thauera_aromatica_AX122X07.1* PLTABUER_aromatica_AX122X07.1* PLTABUER_aromatica_AX122X07.1* PLTABUER_AROMATICA_AUX088075.1* A-HBCL_Thauera_aromatica_X172_AVR8875.1* A-HBCL_RUERABUENDEMOMENS_palustris_05308.1* A-HBCL_RUERABUENDEMOMENS_palustris_05308.1* A-HBCL_RUERABUENDEMOMENS_palustris_05308.1* PLEACL_RUERABUENDEMOMENS_palustris_05308.1* PLEACL_RUERABUENDEMOMENS_palustris_05308.1* PLEACL_RUERABUENDEMOMENS_palustris_05308.1* PLEACL_RUERABUENDEMOMENS_palustris_05308.1* 		LVASHLAAND LVASTLAADQ LVASHLASPD LVASHLASPD LVAAMLADP HLDALTTAVE WRNLIEEGA SYRAMAEGAR DHLNLDSF DRLHLTETTA DGVTIKEDHF DGVTIKEDHF DGVTIKEDHF DGVTIKEDHF SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVFGKY SGKPVFGY S	UPRE-GELR CPAR-GELN STET-LPDR QAGARLES GESAARLES GESAARLES GESAARLES GESAARLES RELADADES PRELADADES RELADADES VPEIDPHT- RIRLIDEDG- ELKICSDDG- RURLIDGR- EVRLIDELG- RARIVODEG- EVRLIDELG- EVRLIDELG- EVRLIDELG- EVRLIDELG- SDDLIIIKGT SDDLIIKGT SDDMILKVGGI SDDMILKVG	-LRACV3AGE -LRACV3AGE -LRACV3AGE -LRACV3AGE -LRUTFAGA -LRUTFAGA -LRUTFAGA -LRUTFAGA -LRUTFAGA -LRUTPAGE KUPPGDE 	ALPEDVGR ALPEDVGR ALPEDVGR ALPEIGR PIPAQVG VLPAATRA PGATWTA IGGHTL-TM IGGHTL-TM IGGHTL-TM EGELVFTT IGGHTL-TM EGELVFTT IGGHTL-TM EGELVFTT IGGHTL-TM EGELVFTT IGGHTL-TM EGELVFTT IGGHTL-TM EGELVFTT IGGHTL-TM EGELVFTT IGGHTL-TM EGELVFTT IGGHTL-TM IGGH	RINE ERFGAAT RINTER REGAT RUTERYGLDI RVINRE I I PGEK QWLDTFGDIT LIKKDATGIEI LIKEGAMPTIR V-STWHOLTK LIKEAL PM/R PSSAVT/WWL PSSAVTWWL PSSA	-LDGLGSTEM -LDGLGSTEM -VNGVGSTEM -VNGVGSTEM -VNGVGSTEM -TEGGGASET -TEGGGASET -TEGGGASET -TEGGGASET -TUTNU 	LHI -FLSNRH LHI -FLSNRP GRIL-EITLING WISLYRRAVR VEL-FLCARP HII -FISADE MTISYEKCRE VEHWETCEC TRLLPPTARS TRLLPPTARS TRLLPPTARS TRLLPPTARS TRLSVERKER KTFRGEWITR TFYGEWITR KLLQSSRRKA KALRDGWYP NVVGDGWIVT AK-PGIK LA-PGET-	(400) (500) (50) (5
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 BCL_Thauera_aromatica_AM32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_Thauera_aromatica_K172_AVR88079.1* 3-HBCL_Thauera_aromatic_K172_AVR88779.1* 11.2-ABCL_Azoarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-NACL_M47_CBX27264.1 PCL_0erobic_Azoarcus_evansii_WP_169132234.1* PCL_0erobic_Azoarcus_evansii_WP_169132234.1* PCL_Dseudomonas_putida_WP_059394932.1* BCL_Thauera_aromatica_AX32623.1* BCL_Thauera_aromatica_X172_AVR88075.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_Thauera_aromatic_K172_AVR8877.1* 2-ABCL_Azoarcus_evansii_MP_169132234.1* PCL_0erobic_Azoarcus_evansii_MP_169132234.1* PCL_0erobic_Azoarcus_evansii_MP_169132234.1* A-HBCL/BCL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 PCL_0erobic_Azoarcus_evansii_MP_169132234.1* PCL_Pseudomonas_putida_MP_059394932.1* BCL_Thauera_aromatica_AX72_AVR88075.1* A-HBCL/BCL_Rhodopseudomonas_palustris_053065.1* 4-HBCL_Thauera_aromatica_AX72_AVR88075.1* A-HBCL_Thauera_aromatica_AX72_AVR88075.1* A-HBCL_Thauera_aromatica_AX72_AVR88075.1* A-HBCL_Thauera_aromatica_X72_AVR88075.1* A-HBCL_Thauera_aromatica_AX72_AVR88075.1* A-HBCL_Thauera_aromatica_X72_AVR88075.1* A-HBCL_Thauera_aromatica_X72_AVR88075.1* A-HBCL_Thauera_aromatica_X72_AVR88075.1* A-HBCL_Thauera_aromatica_X72_AVR8875.1* A-HBCL_Thauera_aromatica_X72_AVR8875.1* A-HBCL_Thauera_aromatica_X72_AVR8875.1* A-HBCL_RevEQUERDMANA_S92032.1* PUTATive_2-PACL_PITC		LVASHLAAND LVASTLADPD LVASHLASPD LVASHLASPD LVASHLASPD LVASHLASPD LVASHLASPD MURNLIEGES SYRAMAEGAR DHLNLDSF DRLHLTETIA DGPTINEDHF DGPTINEDHF DGPTINEDHF DGPTINEDHF SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVFGY SGKFFGS SGKPVFGY SGKFFGS SGKPVFGY SGKFFGS SGKPVFGY SGKFFGS SGKPVFGY SGKFFGS SGK	UPRE-GELR VPRET-ASTR CPAR-GELN SRTET-LPDR QAGARLES GESAARLES GESAARLES GESAARLES RELADATES VPEIDPHT- RIRLIDEDG- ELKICSDDG- RURLIDDVT- RURLIDDEG- ELKICSDDG- EVRURDGR- EVRLIDELG- RARIVODEG- VMUDDEG- SDDMIIIKGT SDDMIIIKGT SDDMIIIKGT SDDMIIKGS DDMILKVSGI TDDIFKVSGI VDDIFKVSGI VDDIFKVSGI VDDIFKVSGI VDDIFKVSGI VDDIFKVSGI VDDIFKVSGI VDDIFKVSGI VDDIFKVSGI VDTVISGS VDMIKVGV -FRIGVKWLMI -FRIGVKWLMI	-LRACV3AGE -LRACV3AGE -LRACV3AGE -LRACV3AGE -LRUTFAGA -LRUTFAGA -LRUTFAGA -LRUTFAGA -LRUTFAGA -LRUTFAGA KUTPAGE KUPPAGE KUPPAGE WFIATAGE NUPPSLIENS NVFPTALQGI NVFPTALQGI NVFPTALQGI NIFPSEVEA VVSPTEVEA VVSPTEVEA VVSPTEVEA NIFPSEVEA NIFFSEVEA NIFFSEVEA NIFFSEV	ALPEDVGR ALPEDVGR ALPEDVGR ALPEIGR PIPAQVG VLPAATRA PGATWTA IGGHTLTM IGGHTLTM IGGHTL-TM EGELVFTT IGGHTL-TM EGELVFTT IGGHTL-TM EGELVFTT IGGHTL-TM EGELVFTT IGGHTL-TM EGELVFTT IGGHTL-TM EGELVFTT IGGHTL-TM EGELVFTT IGGHTL-TM EGELVFTT IGGHTL-TM EGELVFTT IGGHTL-TM I	RINE ERFGAAT RINTER REGAT RUTERYGLDI RVINRE I I I GEK WURNTR FENDE RVINRE I I GEK WULDT FEIDT LIKKDAT SIEL LIKEAL PMVR PSSATYAWIQ PS	-LDGLGSTEM -LDGLGSTEM -UNGVGSTEM -VNGVGSTEM -VNGVGSTEM -TEGGGASET -TEGGGASET -TEGGGASET -LLGOW 	LHI -FLSNRH LHI -FLSNRP GRIL-FLTNLP MMSLYMRAVR VFL-FLCARP HII -FISADE MTISYEKCRE VEHNETCEC TRLLPPTARS TRLLPPTARS TRLLPPTARS TRLLPPTARS TRLSPTARP ATFMGEUTRS KTFRGEWTRS TTFVGEWTRS KLLQSSFRKA KALROGWYP NVVGDGMIVT AK-PGIK LA-PGET R-PGHG	(400) (500) (50) (5
 BCL_Thauera_aromatica_AM32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_SCL_PSeudomonas_pulstris_053005.1* A-CBCL_Pseudomonas_pr_CBS3_ABQ44579.1* J.PABCL_Thauera_aromatic_K172_AVR880770.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 PUt_Live_2-NACL_M47_CBX27264.1 PCL_Pseudomonas_puida_WP_059394932.1* BCL_Thauera_aromatic_AX12_AVR88075.1* BCL_Thauera_aromatic_AX12_AVR88779.1* JHBCL_Thauera_aromatica_AVA32623.1* CL_CL_Seudomonas_puida_WP_059394932.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* J-HBCL_ACL_RAOPSeudomonas_pulstris_053085.1* J-HBCL_Thauera_aromatic_K172_AVR88075.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-NACL_M47_CBX27264.1 PCL_Gaerobic_Azoarcus_evansii_WP_169132234.1* PCL_Gaerobic_Azoarcus_evansii_WP_169132234.1* PCL_Gaerobic_Azoarcus_evansii_WP_169132234.1* PCL_Gaerobic_Azoarcus_evansii_WP_169132234.1* PCL_Gaerobic_Azoarcus_evansii_AR_2053.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_X172_AVR88075.1* J-HBCL_Thauera_aromatica_X172_AVR88075.1* J		L'ASHLAND L'ASHLAND L'ASHLASPD L'ASHLASPD L'AAMLAPP L'AAMLAPP L'AAMLAPP HLDALTTAVE MYRNLIEGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DGFTIKBDHF DGFTIKBDHF DGFTIKBDHF DGFTIKBDHF SGKPVPGY SGKPVF SGKPVGY	UVRET-ASTR CPAR-OELN STET-LPDR QAGARLES GESAARLS GESAARLS GESAARLS GESAARLS CRACK PFLIDPT- VPLUDKEG- VPEIDPT- VPEIDPT- VPEIDPT- VPEIDPT- VPEIDPT- VPEIDPT- SDDLIIKGT SDDLIIKGT SDDLIIKGT SDDMLIIKGS SDDMLIIKGS SDDMLIIKGS SDDMLIIKGS SDDMLIIKGS SDDMLIKSGE ADDMLVSGI SDMLVSGI SDDMVVSGI SDDMVVSGI SDDMVVSGI SDDMVVSGI SDDMVVSGI SDDMVVSGI SDDMVV	-LRACV3AGE -LRACV3AGE -LRACV3AGE -LRACV3AGE -LRUTFAGA -LRUVFAGA -LKPVGDGE -LLKVPGGE -LLKVPGGE -LKVPGGE -LKVPGGE -GEVLPDQ	ALPEDVGR ALPEDVGR ALPEDVGR ALPEIGR PUPAQVGL YMPDTVLE KLPENIGQ VLPAATRA PGATVVTA IGENTLTN EGELVFTT GGTVVTG GGTVVTG GGTVVTG GGTVVTG GGTVVTG GGTGL-TC IGGTGL-TC VGRLAVKG VGRLAV	RIVERPRGAI RIVERPSGAI RUTERPSGLI RVIREIPGEK WIRNFRGHU RVIREIPGEK WILDTFGIEI LIVEGAMUTTEGEK V-STWIPLIK LIVEGAMUTTEGEK V-STWIPLIK LIVEGAMUTTEGEK PSSAVNYWIN PSSATAVING PSSAVNYWIN	-LDGLGSTEM -LDGLGSTEM -UNGVGSTEM -VNGVGSTEA -VNGVGSTEA -TEGGGASET -TEGGGASET -TEGGGASET -TEGGGASET -TEGGGASET -TEGGA	LILI -FLSNRH LHI -FLSNRP GRIL-EITNLP MNSLYMRAVR VFL-FLCARP HII-FISADE MTISYEKCRC VEJWKETCEC TRLIPPTARP ATFMGEUTRS TFLGEUTRS TFLGEUTRS TFLGEUTRS TFLGEUTRS ALADOWINT NVVGD0WIVT AK-PGIK LA-PGEI	(400) (500) (50) (5
 BCL_Thauera_aromatica_AM32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL_Thauera_aromatica_K172_AVR88079.1* 3-HBCL_Thauera_aromatic_K172_AVR88779.1* 11.2-ABCL_Azoarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-NACL_M47_CBX27264.1 PCL_0erobic_Azoarcus_evansii_WP_169132234.1* PCL_0erobic_Azoarcus_evansii_WP_169132234.1* PCL_Dseudomonas_putida_WP_059394932.1* BCL_Thauera_aromatica_AX32623.1* BCL_Thauera_aromatica_X172_AVR88075.1* 4-HBCL/BCL_Thauera_aromatica_X172_AVR88075.1* 4-HBCL/BCL_Thauera_aromatica_X172_AVR88075.1* 9.4-BCL_Pseudomonas_p_C853_ABQ44579.1* 11.2-ABCL_Azoarcus_evansii_MP_169132234.1* PCL_0erobic_Azoarcus_evansii_MP_169132234.1* 4-CBCL_Pseudomonas_p_C853_ABQ44579.1* 11.2-ABCL_Azoarcus_evansii_MP_169132234.1* PCL_0erobic_Azoarcus_evansii_MP_169132234.1* PCL_0erobic_Azoarcus_evansii_MP_169132234.1* PCL_Pseudomonas_putida_WP_059394932.1* BCL_Thauera_aromatica_X172_AVR8875.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_053065.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_0530805.1* 4-LBCL_Pseudomonas_put_GBSTRIS_S030805.1* <		L'ASMLAND L'ASMLAND L'ASMLASPD L'ASMLASPD L'ASMLASPD L'ASMLASPD L'ASMLASPD L'ASMLASPD DILHITETIA DENTIFENT DENTIFENT SCRUPCE-1	UPRE-GELR CPAR-GELN SRTET-LPDR QAGARLES GESAARLES GESAARLES GESAARLES GESAARLES GESAARLES RURLDRDG- ERRLGAPLGG UPELUPPUT- RURLDRDG- ELKICSDDG- RURLDRDG- EVRLUBELG- RURLDRDG- EVRLUBELG- RURLDRDG- SDDLIIKGT TDDIFVIKGRG DDMLIKGGE DDMLIKGE	-LRACV3AGE -LRACV3AGE -LRACV3AGE -LRACV3AGE -LRACV3AGE PLVKCV3AGE PLVKCV3AGE PLVKCV3AGE PLVKCV3AGE -LKVPVGDCE KVVPGDCE KVVPGVA HEVVPGV 	ALPEDVGR ALPEDVGR ALPEDVGR ALPEIGG PIPAQVG VLPAATRA PGATWTA IGGWTLTM IGGWTLTM IGGWTLTM IGGWTLTM IGGWTLTM IGGWTLTM IGGWTLTM IGGWTLTM IGGWTLTM IGGWTLTM IGGWTLTM IGGWTLTM IGGWTLTM IGGWTLTG IGGUTLGM IGGUTLSG IGGUTLSG IGGUTLSG IGGUTLSG IGGUTLSG IGGWTLTG IGG	RINE ERFGAAT RINE REFGAAT RUTERYGLDI RVINRE INGEK QWLDTFGDIT LIKKDATGIEI LIKRGAMPTIR V-STWHDLK LIKEAMPVIR LSKEALPMVR PSSANTWINQ PSSANT PSSANTWI	-LDGLGSTEM -LDGLGSTEM -UNGVGSTEM -VNGVGSTEM -VNGVGSTEM -TEGGGASET -TEGGGASET -TEGGGASET -LLGRW 	LHI -FLSNRH LHI -FLSNRH GUL -FLTLINRP GUL -FLTLINRP FHI -FLSADE MTISYEKCRE VEL-FLCARP FHI -FLSADE MTISYEKCRE VEHNETCEC TRLLPPTARS TRLLPPTARS TRLLPPTARS TRLSENT RTFNGEWTRS TRLSENT RTFNGEWTRS TRLGKSTRS KTFNGEWTRS TLLQKSFRKA KALROS/WYP NVVGDGWIVT AK-PGIK LA-PGET	(4406) (4406) (4406) (4406) (4406) (4406) (4406) (4406) (4406) (4406) (4406) (4406) (4406) (4406) (4406) (4406) (4406) (5
 BCL_Thauera_aromatica_AM32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_SCL_Rhodpseudomonas_pulstris_Q53005.1* 4-CBCL_Pseudomonas_pr_CBS3_ABQ44579.1* J.PABCL_Thauera_aromatic_K172_AVR880770.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-NACL_M47_CBX27264.1 PCL_Pseudomonas_putida_WP_059394932.1* BCL_Thauera_aromatic_K172_AVR88075.1* BCL_Thauera_aromatic_AM32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatic_K172_AVR88075.1* A-HBCL_Thauera_aromatic_K172_AVR88075.1* A-HBCL_Thauera_aromatic_K172_AVR88075.1* putative_2-NACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-NACL_M47_CBX27264.1 PCL_(aerobic)_Azoarcus_evansii_MP_169132234.1* PCL_Genedomonas_pn_CBS3_ABQ44579.1* PCL_Genedomonas_canstic_K172_AVR88075.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* A-HBCL_Thauera_aromatic_K172_AVR88779.1* PCL_Genedomas_canomatic_K172_AVR88779.1* PCL_Genedomas_pn_UBS3_A0932.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* A-HBCL_Thauera_aromatic_K172_AVR88779.1* JABCL_Thauera_aromatic_K172_AVR88779.1* JABCL_Thauera_aromatic_K172_AVR88779.1* JABCL_Thauera_aromatic_K172_AVR88779.1* A-HBCL_Thauera_aromatic_K172_AVR88779.1* A-HBCL_Thauera_aromatic_K172_AVR8875.1* GL_Magnetospirillum_spTS-6_BAE91925.1* GL_Mauera_aromatic_K172_AVR8875.1* BCL_Mauera_aromatica_AVR32623.1* BCL_Mauera_aromatica_KAVR22623.1* BCL_Mauera_aromatica_K172_AVR88075.1* BCL_Mauera_aromatic_K172_AVR88075.1* BCL_Mauera_aromatic_K172_AV		L'ASMLAND L'ASMLAND L'ASMLASPD L'ASMLASPD L'AAMLAPD L'AAMLAPD L'AAMLAPD HLDALTTAVE MYRNLIEGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DGFTIMEDHF GGFTIKEDHF DGFTIMEDHF DGFTIMEDHF DGFTIMEDHF SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVFG-S SGNPVGY ATAB KGGTLKEDIR 	UVRET-ASTR CPAR-OELN STTET-LPDR QAGARLES GESAARLS GESAARLS GESAARLS GESAARLS UVELVDPDT- VPLUDAT- VPLUDATG VPLUDATG VPLUDATG RLRUTEDG RLRUTEDG RLRUTEDG RLRUTEDG SDDLITKGT SDDLIT	-LRACY3AGE -LRACY3AGE -LRACY3AGE -LRACY3AGE -LRUTFAGA -LRUTFAGA -LRUYAGDE -LLKPVGDE -LLKPVGDE -LKPVGDE -LKVPDGG KUPDG -GEVLPDQ -GEVLPDQ -GEVLPDQ -GEVLPDQ -GEVLPDQ -GEVLPDQ -GEVLPDQ -GEVLPDQ -GEVLPDQ -GEVLPDQ -GEVLPDQ -GEVLPDQ -GEVLPDQ -GEVLPDQ -GEVLPDQ -GEVLPDQ -GEVLPDQ -RUPFQ -RUPFQ -GEVLPDQ -RUPFQ -GEVLPDQ -GEVLP	ALPEUVGR ALPEUVGR ALPEUGR PLPAQVG VLPATRA PGATWTA IGENTLTN IGEN	RIVERPRGAI RIVERPGLOI RUTRETIGEK WURRIFGHU RUTRETIGEK WULDTFGIDI LIKEAPUTL LIKEAPUTL LIKEAPUTL LIKEAPUTL SKALAPUR PSSAUTVINU S	-LDGLGSTEM -LDGLGSTEM -UNGVGSTEM -VNGVGSTEA -VNGVGSTEA -TEGGGASET -TEGGGASET -TEGGGASET -TEGGGASET -TEGGGASET -TEGGA	LILI - FLSNRH LHI - FLSNRP GUL - FLTNLP MNSLYMRAVR VEL-FLCARP FHI - FISADE MTISYEKCRE VEWKETCEC VEWKETCEC VEWKETCEC TRLIPPTARS TRLIPPTARS TRLIPPTARS TRLIPPTARS TRLIPPTARS TRLIPPTARS TRLIPPTARS TRLIPTARS ALARDGWYP NVVGDGWLYT MLASEQU- LLA-PGET LA-PGEL LASRGDI PR-PGHG PR-PGHG ALYGRVVAGN	(400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (50) (5
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 BCL_Thauera_aromatica_AM32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_SCL_Rhodpseudomonas_pulstris_Q53065.1* 4-CBCL_Pseudomonas_pr_CBS3_ABQ44579.1* JavABCL_Thauera_aromatic_K172_AVR880770.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 PUtLive_arotus_evansii_AAL2623.1* PCL_Pseudomonas_putida_WP_859394932.1* BCL_Thauera_aromatic_A172_AVR88075.1* BCL_Thauera_aromatica_AM32623.1* BCL_Thauera_aromatica_AVR3267.1* A-HBCL_Thauera_aromatica_X172_AVR88075.1* A-HBCL_Thauera_aromatica_X172_AVR88075.1* A-HBCL_Thauera_aromatica_X172_AVR88075.1* A-HBCL_Thauera_aromatica_X172_AVR88075.1* Putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1* PCL_Gaerobic_Azoarcus_evansii_MP_169132234.1* PCL_Gaenobic_Macarcus_evansii_AAL02077.1* Putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 RCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_X172_AVR88075.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL_Thauera_aromatica_K172_AVR88075.1* BCL_Mauera_aromatica_K172_AVR88075.1* BCL_Mauera_aromatica_K172_AVR88075.1* BCL_Thauera_aromatica_K172_AVR88075.1* BCL_Mauera_aromatica_K172_AVR88075.1*		LYASHLAND LYASTLADPC LYASHLASPD LYASHLASPD LYAAMLADPC LYAAMLADPC HLDALTTAVE WRNLLEEGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DGFTIMEDHF GGFTIKBOHF GGFTIKBOHF GGFTIKBOHF SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVFGY SG	UPKEGELN VRRET-ASTR CPARGELN SRTET-LPDR QAGARLES GESAARL ERRLGAPLGG GESAARL PFLIDPUT- VPLUDKEG- VPEIDPUT- VPEIDPUT- VPEIDPUT- VPEIDPUT- VPEIDPUT- VPEIDPUT- VPEIDPUT- VPEIDPUT- SDDLIIKGT SDDMLIIKGS SDDMLIIKGS SDDMLIIKGS SDDMLIIKSGE LDDMIVSAGY -DKTSVRLMI -FRIGVKMKV -TVIGISTQV -NLLAPVKYP -SLLAPVKYP -SLADPVKYP -SALAPVKYP -SALAPVKYP -SALAPVKYP -SALAPVKYP -SALAPVKYP	-LRACV3AGE -LRACV3AGE -LRACV3AGE -LRACV3AGE -LRUTFAGA -LRUTFAGA -LRUTFAGA -LRUTFAGA -LRUTPAGE -LEHUTFAGA -LRUTPAGE -CEVLPDGG -GEVLPDGG -GEVLPDG -GE	ALPEVVGR ALPEVVGR ALPEVGR IMPDVLE KLPELIGR PUPAQVL IMPDVLE KLPENIGO VLPAATRA PGATVVTA IGENTLTN EGELVFTT GELVFTT LGELVFTT LGELVFTT GELVFTT GELVFTT GELVFTT GELVFTT GELVFTS GELVF-	RIVERPRGAI RIVERPGLOI RUTRETIGEK QULDTFGIDI LIKEAPUTL LIKEAPUTL LIKEAPUTL LIKEAPUTL STAVHUQ PSSAVTWHIK SSAARGWHQ SSA	-LDGLGSTEM -LDGLGSTEM -UNGVGSTEM -VNGVGSTEM -VNGVGSTEM -VNGVGSTEM -TEGGASET -TEGGASET -LGGNGATEM FLLGOW 	LHI -FLSNRH LHI -FLSNRP GRIL-FLTNLP MNSLYWRAVR VEWHKEYCEG VEWHKEYCEG VEWHKEYCEG VEWHKEYCEG VEWHKEYCEG KTFRGEWTR TRLIPPTARS TRLIPPTARS TRLIPPTARS TRLIPPTARS TRLIPPTARS TRLIPTARS	(400) (500) (50) (5
 BCL_Thauera_aromatica_AM32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 3-HBCL_Thauera_aromatica_K172_AVR88779.1* 11.2-ABCL_Azoarcus_evansii_AAL02077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-NACL_M47_CBX27264.1 PCL_0erobic_Azoarcus_evansii_MP_169132234.1* ACL_Pseudomonas_putida_WP_059394932.1* BCL_Thauera_aromatica_K172_AVR88077.1* PUtative_araromatica_AM32623.1* BCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL/BCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL/BCL_Thauera_aromatica_K172_AVR88075.1* A-HBCL/BCL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1* Putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 PUtLavera_aromatica_K172_AVR8877.1* PCL_0erobic_Azoarcus_evansii_MP_169132234.1* PCL_0erobic_Azoarcus_evansii_MP_169132234.1* PCL_Pseudomonas_putida_WP_059394932.1* BCL_Thauera_aromatica_K172_AVR8875.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_053065.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_05005.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_050305.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_050305.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_050305.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_050305.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_050305.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_050305.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_050305.1* 4-HBCL/BCL_Rhodopseudomonas_palustris_050305.1* 4-HBCL/BCL_Rhodopseudomonas_palustr		LVASHLAAND LVASTLADPD LVASHLASPD LVASHLASPD LVASHLASPD LVASHLASPD LVASHLASPD HLDALTTAVE WRNLLEEGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DGPTIMEDHF DGPTIMEDHF DGPTIMEDHF DGPTIMEDHF SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVFG-Y SGKPVFG-Y SGKPVGY SGKFVGS SGKPVGX SGK	UPRE-GELR VARET-ASTR CPAR-GELN SRTET-LPDR QAGARLES GESAARLES GESAARLES GESAARLEY PFLIDPHT- RIRLIDEDG- EIKICSDDG- RURLIDDET- ELKICSDDG- RURLIDDET- ELKICSDDG- EVRLIDELG- RURLIDDEG- EVRLIDELG- RURLIDGG SDDLIIIKGT SDDLIIKGT SDDLIIKGT SDDLIIKGT SDDMILKVGGI GDDMLKVGGI GDDMLKVGGI DDMILSGGE ADDMI	-LRACV3AGE -LRACV3AGE -LRACV3AGE -LRACV3AGE -LRACV3AGE -LRACV3AGE PLVKCV3AGE PLVKCV3AGE PLVKCV3AGE PLVKCV3AGE -LKVPGDCE -CVVPGDCE -CVVPGDCE -GEVLPDGS -GEVLP	ALPEDVRR ALPEDVRR ALPEDVRR ALPEIGR PIPAQVG VLPAATRA PGATWTA IGGWTLTN IGGWTLTN IGGWTLTN IGGWTLTN IGGWTLTN EGELVFTT IGGWTLTN EGELVFTT IGGWTLTN EGELVFTT IGGWTLTN EGELVFTT IGGWTLTN EGELVFTT IGGWTLTN FGLIALRA VRSIEGLSPE IGGIDGLTEN IGGIDGLTEN IGGIDGLTEN IGGIDGLTEN IGGWTLTG IGG	RIVEERFGAAT RIVEERFGAAT RIVERFGAAT RIVERFGAAT RIVERFGAAT RIVERFLINGEK QMLDTFGDIT LIKKDATGIEI LIKKDATGIEI LIKKDATGIEI LIKKDATGIEI LIKKDATGIEI PSSANYMUN PSSATAVMQ PSSANYMUN PSSATAVMQ PSSANYMUN PSSANYMUN PSSATAVMQ PSSANYMUN PSSAN	-LDGLGSTEM -LDGLGSTEM -VNGVGSTEM -VNGVGSTEM -VNGVGSTEM -TEGGGASET -TEGGGASET -TEGGGASET -TGGGASET -TGGGASET -TLTNL 	LHI -FLSNRH LHI -FLSNRH GUL -FLSNRP GUL -FLSNRP GUL -FLSNRP FHI -FLSADE MIISYEKCRE VEL-FLCARP FHI -FLSADE MIISYEKCRE VEHNETCEC TRLLPPTARS TRLLPGTARP ATFMGEUTRS TRLLPGTARP ATFMGEUTRS TFLGEWTRS TRLLQSTARKA KALROSWYP NVVGDGMVYT AK-PGIK LA-PGET	(400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (400) (50) (5
 BCL_Thauera_aromatica_AAN32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* A-HBCL_Thauera_aromatica_KI72_AVR88075.1* A-HBCL_SCAC_MONDELS_NELSTIS_053065.1* A-BCL_Thauera_aromatic_KI72_AVR88077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-NACL_MA7_CBX27264.1 PCL_0erobic_Arcorus_evansii_AAL2023.1* BCL_Mauera_aromatic_KI72_AVR88075.1* BCL_Thauera_aromatic_AAN32623.1* BCL_Thauera_aromatica_AAN32623.1* BCL_Thauera_aromatica_AAN32623.1* BCL_Thauera_aromatica_AAN32623.1* BCL_Thauera_aromatica_AAN32623.1* BCL_Thauera_aromatica_AAN3263.1* A-HBCL_Thauera_aromatica_AAN3263.1* A-HBCL_Thauera_aromatica_AAN3263.1* A-HBCL_Thauera_aromatica_KI72_AVR88779.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1* PCL_(aerobic)_Azoarcus_evansii_MP_169132234.1* PCL_GEUROMONAS_spC853_A8Q44579.1* BCL_Thauera_aromatica_KI72_AVR88775.1* BCL_Thauera_aromatica_KI72_AVR8875.1* A-HBCL_Thauera_aromatica_KI72_AVR8875.1* A-HBCL_Thauera_aromatica_KI72_AVR8875.1* A-HBCL_Thauera_aromatica_KI72_AVR8875.1* A-HBCL_Thauera_aromatica_KI72_AVR8875.1* A-HBCL_Thauera_aromatica_KI72_AVR8875.1* A-HBCL_Thauera_aromatica_KI72_AVR8875.1* A-HBCL_Thauera_aromatica_KI72_AVR8875.1* A-HBCL_Azoarcus_evansii_API69132234.1* PCL_QecoloC_APICAUCENCES2.1* A-HBCL_Azoarcus_evansii_API69132234.1* PCL_PSeudomonas_ppC53_ABQ44579.1* 2-ABCL_Azoarcus_evansii_API69132234.1* ACL_PSeudomonas_ppC53_ABQ457.1* A-HBCL_Rhodopseudomonas_palvstris_053005.1* <li< td=""><td></td><td>LYASHLAND LYASHLAND LYASHLASPD LYASHLASPD LYASHLASPD LYASHLASPD LYASHLASPD DHLNLDSF DRLHLTETIA DRYNLEDEG DGYINEDH DGFTIMEDHF DGFTIMEDHF DGFTIMEDHF DGFTIMEDHF DGFTIMEDHF SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVFG-Y SGKPVFGKFG SGKPVFG-Y</td><td>UPKEGELR VRRET-ASTR CPARGELN SRTET-LPDR QAGARLES GESAARL ERRLGAPLGG GESAARL PFLIDPHT- VPEILDPHT- VPEILDPHT- VPEILDPHT- VPEILDPHT- RLRLIDEG- RLRLIDEG- RLRLIDEG- RRLVGDRG- RLRLIDEG- SDDMLITKGT SDDMLITKGT SDDMLITKGT SDDMLITKGSE SDDMLITKGSE SDDMLITKGSE SDDMLITKGSE LDDMIVSAGY -KTSVRLMI -FRIGVKMKV -TFIGISTQV -NLLAPYKYP -SALAPYKYP -SALAPYKYP -SALAPYKYP -SALAPYKYP -SALAPYKYP</td><td>LINCISAGE LRACVSAGE -LRACVSAGE -LRACVSAGE -LRACVSAGE PLVKCVSAGE PLVKCVSAGE PLVKCVSAGE PLVKCVSAGE KUPDGG GEVLPDGS GEVLPDGS GEVLPDGS GEVLPDGS MEITAPG -</td><td>ALPEDVGR ALPEDVGR ALPEDVGR ALPEIGR PIPAQVGL YLPALTRA DFDQVLE EGLVFTT LGELVFTT LGELVFTT GGIDGLTEN CGLVF-TT GGIDGLTEN GGIDGLTEN GGIDGLTEN CKINKLAQ-KG VKSIEGLSPE IGGIDGLTEN IGGIDGLTEN LIAHEAVLEA LIAHEAVL</td><td>RIVERPIGAAI RIVERPIGAAI RIVERPIGAI RIVERPIGEN WINRINGFOH WINRINGFOH WINDIGEN VINRINGFOH VINTIGEN VINTIGEN VINTIGEN STANTANING PSSANTANING PSSANTANING PSSANTANING PSSANTANING SSAAGAWING SS</td><td>-LDGLGSTEM -LDGLGSTEM -UNGVGSTEM -VNGVGSTEM -VNGVGSTEM -TEGGGASET -TGGGASET -TGGGASET -TGGGASET -TGGGASET -TGGGASET -TGG</td><td>LHI -FLSNRH LHI -FLSNRP GRIL-FLTNLP MNSLYNRAVR VEL-FLCARP FHI -FISADE MTISYEKCRC VEWHETCEC VEWHETCEC VEWHETCEC TRLIPPTARS</td><td>[400] [500] [500]</td></li<>		LYASHLAND LYASHLAND LYASHLASPD LYASHLASPD LYASHLASPD LYASHLASPD LYASHLASPD DHLNLDSF DRLHLTETIA DRYNLEDEG DGYINEDH DGFTIMEDHF DGFTIMEDHF DGFTIMEDHF DGFTIMEDHF DGFTIMEDHF SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVFG-Y SGKPVFGKFG SGKPVFG-Y	UPKEGELR VRRET-ASTR CPARGELN SRTET-LPDR QAGARLES GESAARL ERRLGAPLGG GESAARL PFLIDPHT- VPEILDPHT- VPEILDPHT- VPEILDPHT- VPEILDPHT- RLRLIDEG- RLRLIDEG- RLRLIDEG- RRLVGDRG- RLRLIDEG- SDDMLITKGT SDDMLITKGT SDDMLITKGT SDDMLITKGSE SDDMLITKGSE SDDMLITKGSE SDDMLITKGSE LDDMIVSAGY -KTSVRLMI -FRIGVKMKV -TFIGISTQV -NLLAPYKYP -SALAPYKYP -SALAPYKYP -SALAPYKYP -SALAPYKYP -SALAPYKYP	LINCISAGE LRACVSAGE -LRACVSAGE -LRACVSAGE -LRACVSAGE PLVKCVSAGE PLVKCVSAGE PLVKCVSAGE PLVKCVSAGE KUPDGG GEVLPDGS GEVLPDGS GEVLPDGS GEVLPDGS MEITAPG -	ALPEDVGR ALPEDVGR ALPEDVGR ALPEIGR PIPAQVGL YLPALTRA DFDQVLE EGLVFTT LGELVFTT LGELVFTT GGIDGLTEN CGLVF-TT GGIDGLTEN GGIDGLTEN GGIDGLTEN CKINKLAQ-KG VKSIEGLSPE IGGIDGLTEN IGGIDGLTEN LIAHEAVLEA LIAHEAVL	RIVERPIGAAI RIVERPIGAAI RIVERPIGAI RIVERPIGEN WINRINGFOH WINRINGFOH WINDIGEN VINRINGFOH VINTIGEN VINTIGEN VINTIGEN STANTANING PSSANTANING PSSANTANING PSSANTANING PSSANTANING SSAAGAWING SS	-LDGLGSTEM -LDGLGSTEM -UNGVGSTEM -VNGVGSTEM -VNGVGSTEM -TEGGGASET -TGGGASET -TGGGASET -TGGGASET -TGGGASET -TGGGASET -TGG	LHI -FLSNRH LHI -FLSNRP GRIL-FLTNLP MNSLYNRAVR VEL-FLCARP FHI -FISADE MTISYEKCRC VEWHETCEC VEWHETCEC VEWHETCEC TRLIPPTARS	[400] [500] [500]
 BCL_Thauera_aromatica_AM32623.1* BCL_Magnetospirillum_spTS-6_BAE91925.1* 4-HBCL_Thauera_aromatica_K172_AVR88075.1* 3-HBCL_Thauera_aromatica_K172_AVR88075.1* 3-HBCL_Thauera_aromaticAL02077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-NACL_MA7_CBX27264.1 PCL_0erobic_h2corcus_evansii_MP_169132234.1* BCL_Thauera_aromatica_K172_AVR88075.1* BCL_Thauera_aromatica_K172_AVR88075.1* BCL_Thauera_aromatica_K172_AVR88075.1* BCL_Thauera_aromatica_K172_AVR88075.1* BCL_Thauera_aromatica_K172_AVR88075.1* BCL_Thauera_aromatica_K172_AVR88075.1* 4-HBCL/BCL_Thauera_aromatica_K172_AVR88075.1* 4-BCL_Pseudomonas_pLICAN_AUR402077.1* putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_A100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_A100006_TRIP_SPD71907.1* PUtative_2-PACL_PITCH_v1_a1100006_TRIP_SPD71907.1 putative_2-PACL_PITCH_v1_A100006_TRIP_SPD71907.1* PCL_0erobic_h2coarcus_evansii_MP_169132234.1* PCL_0erobic_h2coarcus_evansii_AAL02077.1*<td></td><td>L'ASMLAND L'AGTLLADPE L'AGMLASPD L'AGMLASPD L'AGMLASPD L'AGMLASPD HLDALTTAVE WRNLLREGA SYRAMAEGAR DHLNDSF DRLHLTETIA DRLHLTETIA DGPTIMEDHF GGFUNPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVFGY GGTVNFG- CGKRVPL-A TGTVFG- CGKRVFH-A CGSKTVVLGR CSGNTVVLGR CSGNTVVLGR CSGNTVVLGR LELSKQTK LELSKQTK </td><td>UPKE-GELK VRRET-ASTR CPAR-GELN SRTET-LPDR QAGARLES GESAARLB GESAARLB GESAARLB RRLBIDEDG ERRLGAPLGG ERRLGAPLGG ERRLGAPLGG VPEIIDPHT- RLRLIDEDG- ELKICSDDG- RURLIDDHT- RURLIDDEG- EVRLIDPUT- RURLIDDEG- EVRLIDELG- RARLVOBGG- EVRLIDELG- RARLVOBGG- VMUTISGG SDDMILIKGT SDDMILIKGT SDDMILIKGT SDDMILIKGT SDDMILIKGT SDDMILIKGT SDDMILIKGT SDDMILIKGT SDDMILIKGT SDDMILIKGT SDDMILKVGGI SDDMILKVGGI SDDMILKVGGI SDDMILKVGGI SDDMILKVGGI SDDMILKVGGI SDDMILKVGGI SDDMILKVGGI SDDMILKVGGI SNDMIKVGGI SNDMILKVGGI SNDMIKVGGI SNDMIKVGGI SNDMIKVGGI SNDMIKVGGI SSLAPKYW ASALADFKP ASALADFKP SALAPKYW SALADFKP SALADFKP</td><td>LINCI VIAGE - IRACV3AGE - IRACV3AGE - IRACV3AGE - IRACV3AGE - IRACV3AGE - IRACV3AGE - LEMVTFAGA - IRACV3AGE - GEVLPOSC - METATAGE NVFPTALGEI NVFPTALGEI NVFPTALGEI NVFPTALGEI NVFPTALGEI NIFPSEIEC VISPEIEC VISPEIEC NIFSEIEC - RAVEVELEL RAVEFVELEL RAUGINOLE RAUGINGLEELF RAIEFROSLE</td><td>ALP-EDVR ALP-EDVR ALP-EDVR ALP-EIGR PIP-AQVG VLP-AATA PGATWTA IGEVITS IGEVITS IGEVITS AGEQI-SG IGELVTS IGE</td><td>RINE ERFGAAT RINE REFGAAT RITERYGLDI RIVER FLOGEK QUIDTFGDIT LIKKDATGIEI LIKKDATGIEI LIKKDATGIEI LIKKDATGIEI LIKKDATGIEI LIKKDATGIEI LIKKDATGIEI SKALDWYG SSAARGVING</td><td>-LDGLGSTEM -LDGLGSTEM -VNGVGSTEM -VNGVGSTEM -VNGVGSTEM -TEGGGASET -TEGGGASET -TEGGGASET -TEGGGASET -TUTNU </td><td>LHI-FLSNRR LHI-FLSNRP HII-FLSNRP GRI-FLTNLP MMSLYMRAVR VFL-FLCARP MMSLYMRAVR VFL-FLCARP HII-FISADE MTISYEKCRC VEHNETCCC TRLLPPTARS TRLLPGTARP ATFINGEWTRS TRLLOGTARP ATFINGEWTRS TTFVGEWTRS TTFVGEWTRS TTFVGEWTRS TTFVGEWTRS TLLQCSRRKC KALROGWYP NVVGDGWIVT AK-PGIK</td><td>(400) (500) (50) (5</td>		L'ASMLAND L'AGTLLADPE L'AGMLASPD L'AGMLASPD L'AGMLASPD L'AGMLASPD HLDALTTAVE WRNLLREGA SYRAMAEGAR DHLNDSF DRLHLTETIA DRLHLTETIA DGPTIMEDHF GGFUNPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVPGY SGKPVFGY GGTVNFG- CGKRVPL-A TGTVFG- CGKRVFH-A CGSKTVVLGR CSGNTVVLGR CSGNTVVLGR CSGNTVVLGR LELSKQTK LELSKQTK 	UPKE-GELK VRRET-ASTR CPAR-GELN SRTET-LPDR QAGARLES GESAARLB GESAARLB GESAARLB RRLBIDEDG ERRLGAPLGG ERRLGAPLGG ERRLGAPLGG VPEIIDPHT- RLRLIDEDG- ELKICSDDG- RURLIDDHT- RURLIDDEG- EVRLIDPUT- RURLIDDEG- EVRLIDELG- RARLVOBGG- EVRLIDELG- RARLVOBGG- VMUTISGG SDDMILIKGT SDDMILIKGT SDDMILIKGT SDDMILIKGT SDDMILIKGT SDDMILIKGT SDDMILIKGT SDDMILIKGT SDDMILIKGT SDDMILIKGT SDDMILKVGGI SDDMILKVGGI SDDMILKVGGI SDDMILKVGGI SDDMILKVGGI SDDMILKVGGI SDDMILKVGGI SDDMILKVGGI SDDMILKVGGI SNDMIKVGGI SNDMILKVGGI SNDMIKVGGI SNDMIKVGGI SNDMIKVGGI SNDMIKVGGI SSLAPKYW ASALADFKP ASALADFKP SALAPKYW SALADFKP SALADFKP	LINCI VIAGE - IRACV3AGE - IRACV3AGE - IRACV3AGE - IRACV3AGE - IRACV3AGE - IRACV3AGE - LEMVTFAGA - IRACV3AGE - GEVLPOSC - METATAGE NVFPTALGEI NVFPTALGEI NVFPTALGEI NVFPTALGEI NVFPTALGEI NIFPSEIEC VISPEIEC VISPEIEC NIFSEIEC - RAVEVELEL RAVEFVELEL RAUGINOLE RAUGINGLEELF RAIEFROSLE	ALP-EDVR ALP-EDVR ALP-EDVR ALP-EIGR PIP-AQVG VLP-AATA PGATWTA IGEVITS IGEVITS IGEVITS AGEQI-SG IGELVTS IGE	RINE ERFGAAT RINE REFGAAT RITERYGLDI RIVER FLOGEK QUIDTFGDIT LIKKDATGIEI LIKKDATGIEI LIKKDATGIEI LIKKDATGIEI LIKKDATGIEI LIKKDATGIEI LIKKDATGIEI SKALDWYG SSAARGVING	-LDGLGSTEM -LDGLGSTEM -VNGVGSTEM -VNGVGSTEM -VNGVGSTEM -TEGGGASET -TEGGGASET -TEGGGASET -TEGGGASET -TUTNU 	LHI-FLSNRR LHI-FLSNRP HII-FLSNRP GRI-FLTNLP MMSLYMRAVR VFL-FLCARP MMSLYMRAVR VFL-FLCARP HII-FISADE MTISYEKCRC VEHNETCCC TRLLPPTARS TRLLPGTARP ATFINGEWTRS TRLLOGTARP ATFINGEWTRS TTFVGEWTRS TTFVGEWTRS TTFVGEWTRS TTFVGEWTRS TLLQCSRRKC KALROGWYP NVVGDGWIVT AK-PGIK	(400) (500) (50) (5
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IRACV3AGE - IRACV3AGE - IRACV3AGE - IRACV3AGE - IRACV3AGE - LEHVTFAGA - LEHVTFAGA - LEHVFAGE - GEVLPDGS - GEVLPDGS - GEVLPDGS - GEVLPDGS - GEVLPDGS - GEVLPDGS - GEVLPDGS - GEVLPAGE - NETAFOS NVFPTAIGGT NVFPTAIGGT NVFPTAIGGT NVFPTAIGGT NVFPTAIGGT NVFPTAIGGT NVFPTAIGGT NVFPTAIGGT NVFPTAIGGT NVFPTAIGGT NVFPTAIGGT NIFSEVERA NIFSEVERA RVFVFUELP RVFVFUELP RNVFVGELFS RVFVFUELP RNVFVGELFS - RNVFVGELFS - RNVFVGE - RNVFVGE - RNVFVGE - RNVFVGE - RNVFVGE - RNVFVGE - RNVFVGE - RNVFVGE</td><td>ALP EDVRR ALP EDVRR ALP EDVRR ALP EIGR PIP AQVGL YLP AATRA PGATVV TA IGEVTL TT IGEVTL TT IGEVTL</td><td>RIVEERFGAAT RIVEERFGAAT RIVERFGAAT RIVERFGAAT RIVERFLIGEK QUIDTFGIDT LIKKDATSIEI LIKRGATSIEI LIKRGANPUTR LSKEALPWR SSAVMYWWN PSSATAWNQ PSSAVMYWWN PSSATAWNQ SSAAGWNQ -ASQFVGYWKL PTGCRYLD- PTSAVCWN PTGCRYLD- PTSAVCWN PTGCRYLD- RRWRPFGA VILEVNLO- ASQFVGYWKL PTGCRYLD- RRWRPFGA VILEVNLO- AVGGEDE- BURKKET- VVARPND-D AVGGEDE- EDHRKKK- VVGRVDC- RE- VVARPND-D AVGGEDE- CHURYKET- VVRAVGEDE- CHURYKET- VVRAVGEDE- CHURYKE- VVRAVGEDE- LIREFTLGGKA- LIREFTLGGK QLIQHVSATS RLRDMLQATL RLREGKP</td><td>-LDGLGSTEM -LDGLGSTEM -VNGVGSTEM -VNGVGSTEM -VNGVGSTEM -TEGGGASET -TEGGGASET -TEGGGASET -TGGGASE</td><td>LHI -FLSNRR LHI -FLSNRR HII -FLSNRP GRI -FLSNRP MISLYRRAVR VFL -FLCARP MISLYRRAVR MTISYEKCRC VFL-FLCARP FHI -FLSADE MTISYEKCRC VFL-FLCARP FHI -FLSADE MTISYEKCRC VFL-FLCARP FHI -FLSADE TRLUEGTARE ATFMGEWTRS TRLUEGTARE ATFMGEWTRS TTFVGEWTRS TTFVGEWTRS TTFVGEWTRS TTFVGEWTRS TLLQSTRRC ALAPODY</td><td>(400) (500) (50) (5</td>		L'ASMLAND L'ASTLADOR L'ASMLASPD L'ASMLASPD L'AAMLADR HLDALTTAVE WRNLLREGA SYRAMAEGAR DHLNLDSF DRLHLTETIA DRLHLTETIA DGPTIMEDHF GGFUNPDGY SGKPUPGY SG	UVRET-ASTR CPAR-OELN XYRET-ASTR QAGARLES GESAANR ERRLGAPLGG GESAARL PVLUDXEG ERRLGAPLGG ERRLGAPLGG ERRLGAPLGG ERRLGAPLGG ERRLGAPLGG VPLUDXEG ELKICSDG- RURLIDDHT- VPEIIDPHT- VPEIIDPHT- VPEIIDPHT- RURLIDDEG- ELKICSDG- RURLIDGG EVRLLDELG- RARLVGGRG SDDMILIKGT SLDMILYGAGY -REIGVRWA -FRIGVRWA SALADFKP ASALADFKP -RIGIKWCP SALADFKP -RIGIKWCP SALADFKP -RIGIKWCP	LINCI VAGE - 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 10.3-HBCL_Thauera_aromatic_KI72_AVR88779.1*
 ---- [644]

 11.2-ABCL_Azoarcus_evansii_AAL02077.1*
 ---- [644]

FIG 4 Alignment of 11 out of 39 aryl-CoA ligase protein sequences, with structural motifs highlighted in blue. The protein sequences were taken out of the alignment of 39 aryl-CoA ligases used for the maximum likelihood phylogenetic (Continued on next page)



FIG 5 Crystal structures of benzoate:CoA ligases (a and b) and phenylacetate:CoA ligases (c and d). (a) Crystal structure of benzoate:CoA ligase (BadA) from *Rhodopseudomonas palustris* with benzoyl-AMP (PDB accession number 4ZJZ) (46). (b) Crystal structure of benzoate:CoA ligase from *Paraburkholderia xenovorans* LB400 (PDB accession number 2V7B) (47). (c and d) Crystal structures of the phenylacetate:CoA ligases PaaK1 (PDB accession number 2Y4N) and PaaK2 (PDB accession number 2Y4O) from *Burkholderia cenocepacia* J2315 with phenylacetyl adenylate (49). Images were created using Mol* Viewer (78) from the RCSB PDB database.

interactions between a lysine residue contained in the C-terminal domain and the carboxylate group of the benzoate. Contrary to other benzoate:CoA ligases, which adopt the adenylation conformation during cocrystallization with benzoate (65, 70), BadA takes on the thiolation conformation even in the absence of CoA. This indicates two possible subgroups of benzoate:CoA ligases: enzymes with a resting state in the thiolation conformation and those in the adenylation conformation. Those authors propose a multistep reaction mechanism for BadA, analogous to that of the human mediumchain acyl-CoA synthetase ACSM2A (71). Here, the carboxylate binds to the enzyme in the thiolation conformation, followed by a domain rearrangement to the adenylation conformation in which ATP binds to the substrate and acyl-AMP is formed. The last step is the typical domain movement to the thiolation conformation for the thioesterification reaction with CoA.

Crystallization studies of the phenylacetate:CoA ligases PaaK1 and PaaK2 from *Burkholderia cenocepacia* J2315 (72) (Fig. 5) show the phenylacetate:CoA ligases as a distinct subgroup of the aryl-CoA ligases besides the benzoate:CoA ligases. PaaK1 and PaaK2 show structures similar to those of homologous aryl-CoA ligases apart from one additional feature in the N-terminal domain of these enzymes, a novel microdomain of ~70 residues. This microdomain is built with a leucine-zipper-like organization and forms a continuous three-helical bundle structure. The microdomain is stabilized by the hydrophobic interactions of 6 leucine residues and Tyr30, Phe44, and Phe63 of PaaK1. This alteration in the N-terminal domain leads to a change in the typical conformation of the group of four

FIG 4 Legend (Continued)

tree in Fig. 3. The whole alignment can be found in the supplemental material. The structural motifs found in aryl-CoA ligases (Table 2) are highlighted in blue. Amino acids that are 100% conserved in the whole alignment are marked in yellow.

 β -sheets surrounded by five α -helices as can be found in the benzoate:CoA ligase from *Burkholderia xenovorans* (70) or the 4-chlorobenzoate:CoA ligase of *Pseudomonas* sp. (63). The monomeric N-terminal domain of PaaK1 is comprised of three β -sheets surrounded by nine α -helices, which leaves the phosphate-binding loop (P-loop) (motif A3) isolated, leading to the necessary dimerization of this domain. Cocrystallization of PaaK1 with ATP further proved the binding of the phosphates from ATP to the P-loop. Hydrogen bonds formed between the amide backbone of the P-loop and the phosphates from ATP reinforce this coupling, with additional stabilization through hydrogen bonds with Ser94, Thr96, and Thr97. As mentioned above, the lysine residue of the A10 motif is highly conserved in these two enzymes as well as in other aryl-CoA ligases.

PHENYLACETATE: CoA LIGASES, AN EXPANDING GROUP

Recent studies have elucidated new enzymes, expanding the group of phenylacetate:CoA ligases with substrates outside the already known aryl carboxylates. The 2-hydroxyisobutyric acid:CoA ligase from *Aquincola tertiaricarbonis* L108 (73) shows a closer relationship to the phenylacetate:CoA ligases PaaK1 and PaaK2, with 34% and 33% coverages of homologous sequences, compared to 20% with other short- and medium-chain acid ANL ligases. The enzyme shows a similar tertiary structure typical of phenylacetate:CoA ligases, forming a dimer with a sevenstranded β -sheet connecting the two subunits. The acyl-binding pocket contains the unique active-site residues Tyr164 and Ser239, leading to a smaller and more polar environment.

A unique set of enzymes from the benzoxazole biosynthesis pathway has recently been identified as a subset of the phenylacetate:CoA ligase family (74, 75). The enzymes AjiA1 and the closely related ligase NatL2 show 30% sequence identity with PaaK1 but do not undergo a domain alteration; instead, these newly described enzymes feature a domain-swapping reaction involving a C-terminal loop constricting the enzymes to one conformation.

As described above in this review, phylogenetic analyses of putative 2-phenanthroate:CoA and 2-naphthoate:CoA ligases (43, 76, 77) (Fig. 3) indicate that they belong to the monophyletic clade of phenylacetate:CoA ligases. These ligases show a sequence similarity of ~20 to 25% with the described benzoate:CoA ligases, compared to ~30% sequence similarity with phenylacetate:CoA ligases.

CONCLUSION

The group of aryl-CoA ligases is a central group of the ANL superfamily. Recent evidence even suggested an aryl-CoA ligase-like enzyme as an ancestral enzyme from which the more specialized functions of the ANL superfamily have evolved (51).

Most aryl-CoA ligases are encoded either in the same operon as or close to the corresponding degradation genes of their respective pathways (22). The regulation of these genes is still not fully understood, as some aryl-CoA ligases are regulated by oxygen availability (24), while others are regulated by posttranslational acetylation of a C-terminal conserved lysine residue (66). This in turn influences benzoyl-CoA levels and might be used in some cases to regulate the gene expression of aryl-CoA ligases through a transcription repressor (69).

Acetylation of catalytic residues in prokaryotes is still a relatively new topic, and as such, further research is necessary. It is still unclear what factors influence the expression of acetyltransferases and deacetylases, as many times, these enzymes are not encoded near their corresponding genes. In the future, more aryl-CoA ligases as well as other ANL superfamily enzymes need to be examined for signs of acetylation, as the lysine residue is highly conserved throughout the family.

Crystallization studies give further insights into and elucidate the key residues responsible for reaction mechanisms while also showing new strategies emerging from newly identified members of this group. The aryl-CoA ligases are divided into two major groups, the benzoate:CoA ligase-like and the phenylacetate:CoA ligase-like enzymes, with their members clustering according to their substrate specificity, as the active site contains most of the conserved amino acid residues (9).

The newly discovered ligases from anaerobic polycyclic aromatic hydrocarbon degradation pathways fall into the second group of phenylacetate:CoA ligases, which expands our knowledge of the essential requirements of these enzymes. In recent years, the group of aryl-CoA ligases has been steadily growing, with more and more enzymes being identified. These enzymes share little sequence similarity, but newly emerging bioinformatic tools and the expansion of machine-learning approaches demonstrate new ways of identifying possible candidate enzymes (51). Future studies will have to focus on these enzymes and their role in the aryl-CoA ligase family as well as the importance of this group in the context of the wider ANL superfamily.

SUPPLEMENTAL MATERIAL

Supplemental material is available online only. **SUPPLEMENTAL FILE 1**, PDF file, 0.1 MB.

ACKNOWLEDGMENTS

I. Kaplieva-Dudek and R. U. Meckenstock acknowledge support by the EU-Horizon 2020 program through the ERC advanced grant EcOILogy number 666952.

We declare no conflict of interest.

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