Oxidative opening of the aromatic ring: tracing the natural history of a large superfamily of dioxygenase domains and their relatives

Supporting Information

Alexander M. Burroughs[1], Margaret E. Glasner[2], Kevin P. Barry[3], Erika A. Taylor*[3], L Aravind*[1]

[1]-National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD 20894, USA
[2]-Department of Biochemistry and Biophysics, Texas A&M University, College Station, TX 77843, USA
[3]-Department of Chemistry, Wesleyan University, Middletown, CT 06459, USA

*-corresponding authors

*To whom correspondence should be addressed: L Aravind: Building 38A, Room 5N503, 8600 Rockville Pike, Bethesda, MD 20894 USA; aravind@ncbi.nlm.nih.gov; Tel. (301)594-2445; Fax. (301)435-7794. Erika A. Taylor: 52 Lawn Avenue, Hall-Atwater, Room 142, Middletown, CT 06459 USA; eataylor@wesleyan.edu; Tel. (860)685-2739; Fax. (860)685-2211.

Table of Contents

I. Supporting Figure Legends.
II. Supporting Table S1.
III. Supporting Figure S1.
IV. Supporting Figure S2.
V. Supporting Data.

I. Supporting Figure Legends

Supporting Figure S1. Sequence logo representation of the Figure 3 multiple sequence alignment. Top and bottom panels correspond to the top and bottom regions of the Figure 3 alignment. Height of letters depicts the information content for the columns in the alignment, measure in bits. Coloring of letters corresponds to amino acid biochemical properties: small, green; hydrophobic, yellow; negatively-charged, red; positively-charged, purple; hydroxyl group-bearing, cyan; otherwise polar, blue. Secondary structure elements corresponding to the conserved core of the domain are provided below each panel. Active site residue positions are marked with an asterisk and the conserved aspartate discussed in the text is marked with a caret symbol.

Supporting Figure S2. (A) Presence/absence plot for three-gene island and related domain families in prokaryotic phylogenies. Presence/absence is colored by percentage of genomes within a taxon (labeled to left of plot) which contain a given component (see legend). Purple boxes flag taxons wherein at least a subset of genomes display mutual exclusivity between the classical Memo family and the AMMECR1 fusion PCAD family. Red boxes flag taxons where some mutual exclusivity is observed between the presence of the three-gene island and the SelU domain. (B) Linear line plot depicting presence/absence of a given domain family across individual prokaryotic genomes, with each point representing presence in a genome and all genomes aligned in columns along the horizontal axis, grouped according to taxon. Points are colored by taxon, legend provided below. Size of point corresponds to total number of domain family representatives in a genome; as most genomes contain only a single member of the listed domain families, little variation in point size is observed. Mutual exclusivity observed in firmicutes and γ-proteobacteria are highlighted in black boxes.

II. Supporting Table S1

Lineage name	Family name	Higher-order	PDBID	N-term stacking hairpin	Core strand order	C-term α/β unit	S3 loop catalytic residue^	VR1 (forest green)	VR2 (sand)	VR3 (light blue)
Germination protease	HybD-like	HybD-like	1C8B_A	descending helix	21364	absent, possible displacement by N-term insert	--	2 helical turns, extended loop	ascending loop	small loop extension
HybD	HybD-like	HybD-like	1CFZ_A	none	21364	absent	--	none	ascending helix	small loop extension
peptidyl hydrolase	pth	pth-like	2PTH_A	present, first strand is poorly-formed	21364	possible compensatory β-helix from Cterm ext	--	none	ascending minimal loop	extended loop
5'-methylthio-adenosine nucsidase	MTAN	PNP-like	6AYM_A	present	213645	present	H (absent in MTAN family)	none	poorly-structured extended loop	none
YgiD-like	PCAD	PCAD-Memo	2PW6A	present, both strands broken	213645 162534cp	present	H	extended loop	extended loop	extended loop, helix 5 and 6a-b
Memo	Memo	PCAD-Memo	3BCZ_A	present, elongated at turn	213645 162534cp	present	H	none	extended loop housing 2 strands which stack in a barrel-like structure w/ third strand from Nterm	extended loop, helix 5 and 6
tRNA deacylase	tRNA deacylase	tRNA deacylase	1YQE_A	present, somewhat	213645	present	--	2 α-helical turns	extended loop with poorly-	none

				smaller than typical					defined structure	
bacPAC2	bacPAC2	PAC2-like	2P90_A	present	213645	present, not prominent: both strand and helix are primitive	--	slight bulge-like extension	none	slight bulge-like extension
endolysin Ply	amidase-like	Zn-dep. exo-peptidase assemblage	1XOV_A	absent	213645	present	--	none	none	slightly elongated loop
carboxy-peptidaseA	carboxy-peptidaseA	Zn-dep. exo-peptidase assemblage	1M4L_A	Nterm stacking	213645	present	N	large poorly-structure loop with 1-2 helices	somewhat elongated loop	slight bulge in loop
leucine amino-peptidase	leucine amino-peptidase	Zn-dep. exo-peptidase assemblage	1LAM_A	Nterm stacking	213645	present	N	extended loop with β-hairpin	none	extended loop, helical segment
amino-peptidase	dinuclear Zn exo-peptidase	Zn-dep. exo-peptidase assemblage	1RTQ_A	Nterm stacking	213645	present	EE	α-helical turn	none	extended loop
transferrin receptor protease	FolH-like	Zn-dep. exo-peptidase assemblage	1DE4_C	Nterm stacking, elongated strands	213645	present, strand considerably degraded	D	slight loop extension	none	extended loop
Succinyl-glutamate desucci-nylase AstE	AstE/AspA-like	Zn-dep. exo-peptidase assemblage	2G9D_A	Nterm stacking, additional N-term strand	213645	present	N	single helix leading into extended loop	slightly extended loop	slightly extended loop

Glutaminyl-peptide cyclo-transferase	Glutaminyl-peptide cyclo-transferase like	Zn-dep. exo-peptidase assemblage	2AFW_A	Nterm stacking, slightly elongated strands	213645 (S4 and S5 degraded)	present, strand considerably degraded	EE	extended loop with bulge-like structure	none	striking extended loop pointing upwards
N-formyl-glutamate amido-hydrolase	FGase-like	Zn-dep. exo-peptidase assemblage	2Q7S_A	single stacking strand at N-terminus	213645	present	N	highly elaborate extended loop with little structure	small extended bulge loop	mostly extended loop with 1-2 helical elements
pyro-glutamate amino-peptidase	pyro-glutamate amino-peptidase	pyro-glutamate amino-peptidase	1A2Z_A	none	213645	present	--	none	very long extended loop with flap-like β-element. reminiscent of Memo	extended, upwards-pointing loop

Lineage name	Family name	Higher-order grouping	'VR4'	core strand 5 insert	Hairpin insert	Comments	HHPRED search	DALI search
Germination protease	HybD-like	HybD-like	helical cap with flap (dimerizing domain?)	n/a	n/a	elaborate version of other HybD	returns pth family profiles	hits to pth structures recovered first, often PNP structures are observed next
HybD	HybD-like	HybD-like	extended loop	n/a	n/a	minimal HybD	returns pth family profiles	pth is strongest, maybe pyro-glutamyl amino-peptidase is next? Then PNP hits
peptidyl hydrolase	pth	pth-like	helix cap	n/a	n/a	reverse reciprocity with HybD	returns HybD family profiles	PNP and minimal HybD structures recovered with about the same scores

5'-methylthio-adenosine nucsidase	MTAN	PNP-like	extended loop	helix with strand stacking between S3 and S5	none	barrelizing structure formed at S5 insert with C-terminal strands	returns exclusively PNP family profiles	returns several families with similar scores including PAC2, Zn-dep. exo-peptidases, and deacylases
YgiD-like	PCAD	PCAD-Memo	none	none	elongation at turn	--	PCAD tends to return low-scoring hits with tRNA deacylase profiles and some Zn-dep. exo-peptidases	difficult to discern, PCAD members return several other families with roughly equal scores
Memo	Memo	PCAD-Memo	none	lateral shelf has strongly helicized	elongation at turn	VR2 insert forms something like a barrel… distinct from PNP barrel	low-scoring hits to tRNA deacylase family profiles	difficult to discern, returns several families including PNP and the Zn-dep. exopeptidases with roughly equal scores
tRNA deacylase	tRNA deacylase	tRNA deacylase	small loop has helicized	some extension, interactions with VR1 and VR2	none	C-term domain helix stacks at the Cterm α/β unit	returns PCAD family profiles with strongest scores, Zn-dep. exo-peptidases at borderline significance	returns PNP and several other families at roughly equal scores
bacPAC2	bacPAC2	PAC2-like	1-2 α-helical turns	standard lateral shelf	poorly-formed helix gives way to hairpin insert	Nterm ext. stacks small strand against Nterm hairpin	none	PAC2-like family members and PNPs tend to be the best-scoring hits, followed by scattered Zn-dep. exo-peptidase assemblage hits
endolysin Ply	amidase-like	Zn-dep. exo-	helix cap	none	n/a	--	detects tRNA deacylase family profiles and other	after detecting amidases, appears to largely detect other families of the Zn-

		peptidase assemblage					exopeptidases, notably the AstE_AspA family	dep. exopeptidase assemblage
carboxy-peptidaseA	carboxy-peptidaseA	Zn-dep. exo-peptidase assemblage	slightly extended loop	lateral shelf with 1-2 α-helical turns	none	--	detects other peptidase families, with AstE_AspA, SpoIIP, and amidases as outgroups	sees other peptidase families with some PNP and polyglutamyl aminopeptidase structures also scoring well
leucine amino-peptidase	leucine amino-peptidase	Zn-dep. exo-peptidase assemblage	extended loop that folds back on itself	helicized lateral shelf with extended loop tracing backwards	2-helix insert	4th sandwich layer formed by core S5, VR1, Nterm hairpin	returns "classical" Zn-dep. exo-peptidase profiles (top assemblage in Fig. 4)	mostly returns hits with other Zn-dep. exopeptidase family members
amino-peptidase	dinuclear Zn exo-peptidase	Zn-dep. exo-peptidase assemblage	extended cap-like loop with some helicity	lateral shelf with extended bulge	none	S6 is 'broken' by strange kind of spreading of core sheet	returns "classical" Zn-dep. exo-peptidase profiles (top assemblage in Fig. 4)	mostly returns hits with other Zn-dep. exopeptidase family members
transferrin receptor protease	FolH-like	Zn-dep. exo-peptidase assemblage	extended cap-like structure with at least 1 helix	extended lateral shelf with helical segment	PA (protease-associated) domain insertion	--	returns "classical" Zn-dep. exo-peptidase profiles (top assemblage in Fig. 4)	mostly returns hits with other Zn-dep. exopeptidase family members
Succinyl-glutamate desucci-nylase AstE	AstE/AspA-like	Zn-dep. exo-peptidase assemblage	small loop extension	standard lateral shelf	none	Cterm fusion to barrel sandwich hybrid domain	returns profiles from Fig. 4 bottom assemblage of the zn-dep. exo-peptidases	mostly returns hits with other Zn-dep. exopeptidase family members
Glutaminyl-peptide cyclo-transferase	Glutaminyl-peptide cyclo-transferase	Zn-dep. exo-peptidase assemblage	extended loop folding back over active site	standard lateral shelf	none, slightly extended	unusual extended loop after H1	returns "classical" Zn-dep. exo-peptidase profiles	sees other peptidase families before detecting some PNP and other

	like				strands and loop		(top assemblage in Fig. 4)	family structures with Z-scores ~5-6
N-formyl-glutamate amido-hydrolase	FGase-like	Zn-dep. exo-peptidase assemblage	small extended loop folding back over active site	lateral shelf with notable bulge	n/a	--	mostly detects AstE/AspA and SpoIIP before other peptidases	strongest hits are with Fig. 4 bottom assemblage of Zn-dep. exo-peptidase structures
pyro-glutamate amino-peptidase	pyro-glutamate amino-peptidase	pyro-glutamate amino-peptidase	extended, upwards-pointing loop w/α-like elements	standard lateral shelf	n/a	--	nothing recovered outside of this family	strongest hits with PNPs

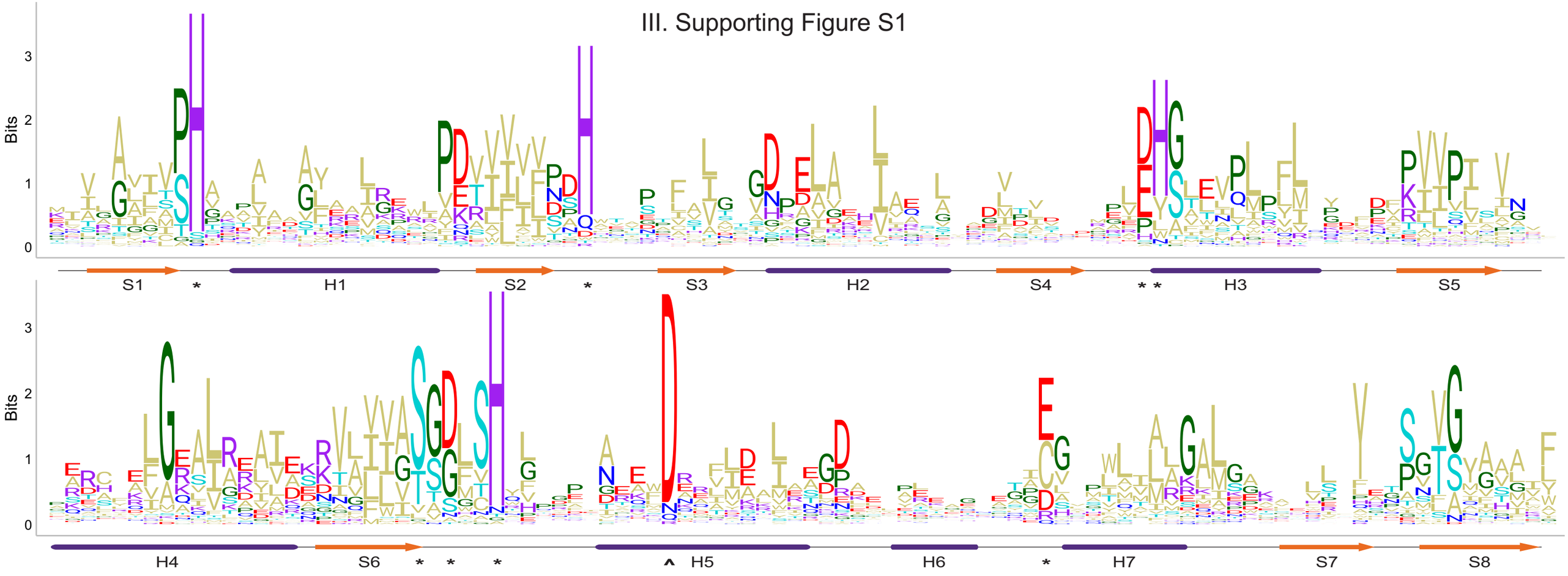
Lineage name	Family name	Higher-order grouping	phyletic distributions
Germination protease	HybD-like	HybD-like	mostly firmicutes, some scattered in tenericutes and bacteroidetes
HybD	HybD-like	HybD-like	largely pan-bacteria, pan-archaeal (including Asgardian)
peptidyl hydrolase	pth	pth-like	absolutely conserved in bacteria, eukaryotes with mitochondria
5'-methylthio-adenosine nucsidase	MTAN	PNP-like	PNP-like has a branch clearly traceable to LUCA
YgiD-like	PCAD	PCAD-Memo	bacteria, some eukaryotes
Memo	Memo	PCAD-Memo	universal
tRNA deacylase	tRNA deacylase	tRNA deacylase	pan-archaeal, land plants, scattered bacteria
bacPAC2	bacPAC2	PAC2-like	pan-archaeo-eukaryotic, pan-actinobacteria and a scattering of other bacterial lineages

endolysin Ply	amidase-like	Zn-dep. exo-peptidase assemblage	largely pan-bacterial, quite a bit of caudovirus representation
carboxy-peptidaseA	carboxy-peptidaseA	Zn-dep. exo-peptidase assemblage	pan-eukaryotic, largely pan-bacterial with notable underrepresentation in cyanos. Limited euryarchaeal presence
leucine amino-peptidase	leucine amino-peptidase	Zn-dep. exo-peptidase assemblage	pan-bacterial, largely pan-eukaryotic with basal lineages in question. Limited archaea look like horizontal transfers
amino-peptidase	dinuclear Zn exo-peptidase	Zn-dep. exo-peptidase assemblage	probably pan-eukaryote and pan-bacteria. Archaea found sporadically across many lineages but relatively strong presence in Asgard
transferrin receptor protease	FolH-like	Zn-dep. exo-peptidase assemblage	see above row for joint phylogenetic distribution, but this specific family appears pan-euk with some scattered bacteria
Succinyl-glutamate desucci-nylase AstE	AstE/AspA-like	Zn-dep. exo-peptidase assemblage	pan-euryarchaea, a few other archaeal sequences (Bathyarcheaota), euk: vertebrates, scattered fungi, SAR representation. bac: pan-bacteria with likely underrepresentation in actinos
Glutaminyl-peptide cyclo-transferase	Glutaminyl-peptide cyclo-transferase like	Zn-dep. exo-peptidase assemblage	core family involved in peptide cyclotransferase reaction (e.g. neuropeptide processing in animals) is crown group euk, sporadic bacterial distribution, and Asgardian archaea. Considering the broader assemblage of related families, could probably be considered pan-bacteria and sporadically present across archaea
N-formyl-glutamate amido-hydrolase	FGase-like	Zn-dep. exo-peptidase assemblage	found in most bacterial lineages but often sporadic (concentrated in α-proteos, but underrepresented in firmicutes and cyanos)

pyro-glutamate amino-peptidase	pyro-glutamate amino-peptidase	pyro-glutamate amino-peptidase	sporadic in bacteriodetes, otherwise pan-bacteria. pan-euk but absent in giardia and probably apicomplexa. Sporadic presence in eury- and cren-archaea, only a single Asgardian.

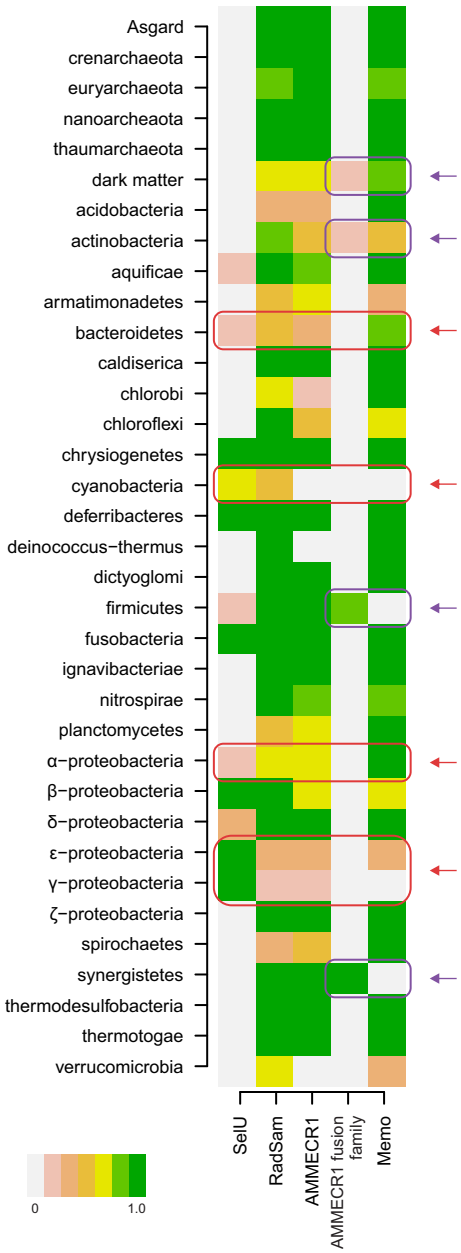
^: S3 here refers to core strand ordering across the PNP-pth fold; from the vantage of the PCAD-Memo superfamily this is S1

III. Supporting Figure S1

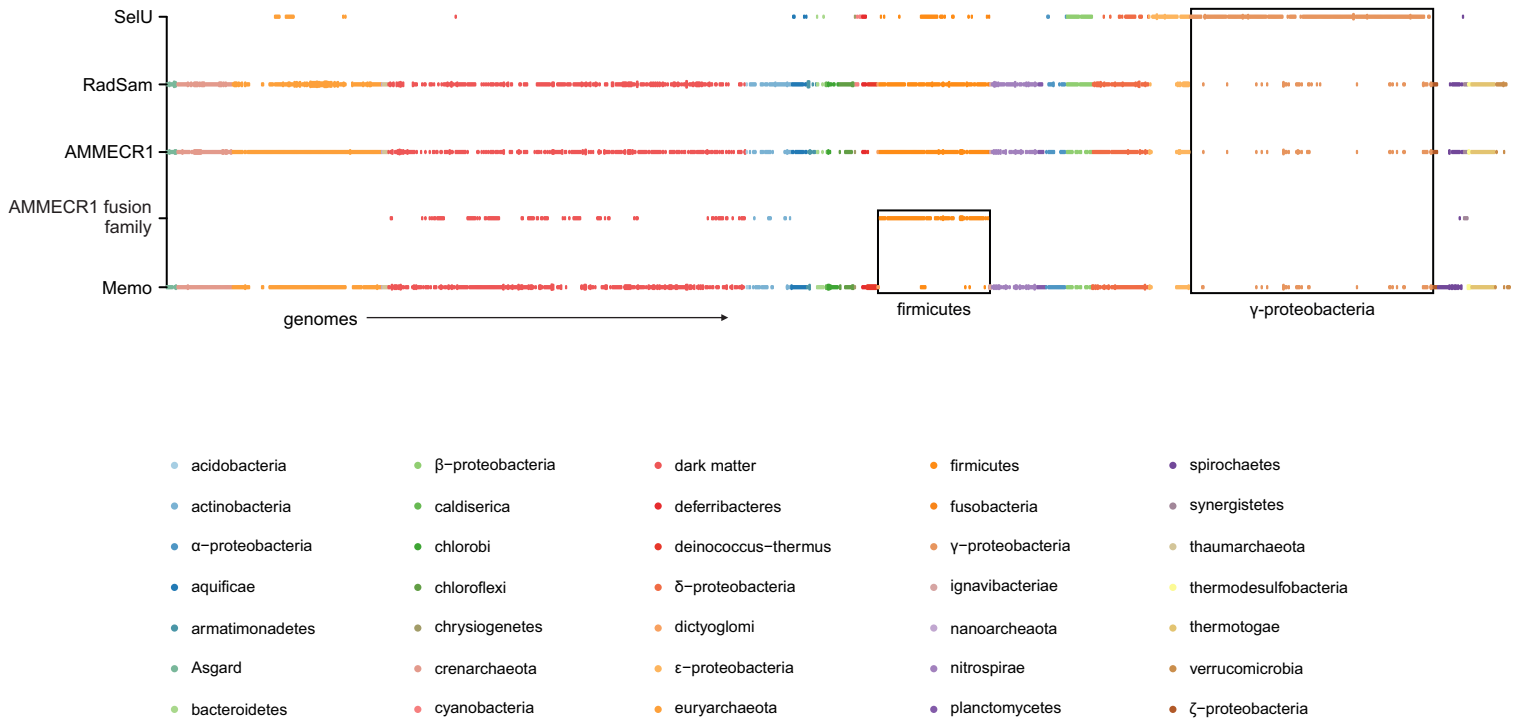


IV. Supporting Figure S2

A



B



SUPPORTING DATA

Natural history of the protoporphyrinogen dioxygenases superfamily: emergence of a pervasive bacterial catabolic ring opening function from an ancestral RNA-modification function

A. Ben Hassine[1], Manjo E. Siswanto[1], Kevin P. Battaile[2], Eliza A. Taylor[3], L Bertrand[1]

1 - National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health
2 - Department of Biochemistry and Biophysics, College of Agriculture and Life Sciences, Texas A&M University
3 - Chemistry Department and Molecular Biophysics Program, College of Integrated Sciences and Environmental Studies, Wesleyan University

ABSTRACT

A diverse collection of enzymes comprising the protoporphyrinogen dioxygenases (PCDOs) have been characterized in a range of extracellular aromatic compound degradation pathways. These enzymes have been shown to catalyze the oxidation of a wide range of substrates, including environmental pollutants, and are implicated in a variety of human and plant diseases. To better understand the evolution of this RIDCHEMBL protein superfamily, we explored their structure and function determinants to establish a unified evolutionary framework for the PCDO/Mem superfamily, identifying 15 closely/moderately related families including a previously/undesignated diversity in 5 described families of the Mem family. Our analysis suggests that the Mem family is a pervasive bacterial catabolic ring opening function from an ancestral RNA-modification function that has been retained in a wide range of common accessory loci(s) of all extant organisms. In addition to identifying enzymatic active site residues across the superfamily, we describe three distinct structurally variable regions emanating from the core scaffold which often house conserved residues specific to individual families. These are predicted to contribute to the active site architecture of each family and to modulate substrate specificity and catalysis. Finally, we describe the genomic contexts of representatives of each family, providing insight into potentially previously/unrecognized aromatic ring substrates in PCDO clade families. We greatly extend the known range of conserved contextual associations for the Mem family, and we describe novel associations with the AMMECR1 domain and a Radical SAM family member. Together, these observations point to two distinct yet potentially related functions for members of the Mem family, which may be the result of a single ancestral function that has been retained in two lineages after the emergence of two distinct yet potentially related functions. In total, this report throws light on the functions of the large swaths of both the PCDO and Mem branches of the superfamily which remain experimentally uncharacterized.

TABLE OF CONTENTS

I. Accession numbers for PCDO domain-containing proteins with their domain architectures, conserved gene neighborhoods, and phylogenies
  A. Tip1-like family
    B. Classical Mem family
      C. Mem/Tip1-like fusion, paired and independent associations
        1. AMMECR1 Island-independent associations
        2. AMMECR1 Island-proximal-component association
      C. Classical LigB family
        1. LigB-associating subfamily
        2. LigB-associating subfamily
    b. Hpd/Hgd-like family 1
    b. Hcd/Dhc-like family
    b. Hpd/Hgd-like family 2
    b. HPD12 family
    b. Hpd/Hgd-like family 3
    c. LigB-like family
    d. Hpd/Hgd-like family
    e. HPD (Proteobacteria) L-Dopachrome family
    e. CapA/TpbAA-associating family
    f. Hpd/Hgd-like family
    g. Orf4 CDS family
    h. CTL400 family

II. Alignments
  a. Structural superimposed of all PCDO families
    b. Classical LigB family
    b. Mem/Tip1 fusion alignment
    b. AMMECR1 fusion family alignment
    b. CapA/TpbAA fusion family alignment
    b. Hpd/Hgd-like family alignment
    c. Two-like domain found in gene neighborhoods of Tip1 family alignment
    d. LigB-like family
    e. Mem/Tip1-like/Carrich region fused to AMMECR1 in eukaryotes
    f. Predicted actinomycetal phosphomevalonate decarboxylase of DMP kinase fold
    g. Orf4 CDS family
    h. ATC family
    i. Hpd/Hgd-like family
    j. Hpd/Hgd-like family 1
    k. Hpd/Hgd-like family 2
    l. HPD12 family
    m. p-cresol decarboxylase family
    n. Hpd/Hgd-like family
    o. CTL400 family

III. Accession numbers for PCDO domain-containing proteins with their domain architectures, conserved gene neighborhoods, and phylogenies

Accession numbers which were included in the analyses presented in the paper are provided below in clusters which correspond to the mentioned family for each sequence. Accession numbers are further annotated by the following columns in order from left to right: domain architecture (abbreviated), genome accession, protein accession, and taxonomy. Where a protein sequence could not be found in the RefSeq database, when possible, further annotation/organization within individual families are provided above groups of sequences, preceded by hashes ('#').

A. Tip1-like family

```
# neighborhood containing conserved association with membrane-bound protein with the DNRR_synthase and glutaminine_synthase_Tpi2
# neighborhoods lacking the glutaminine_synthase_Tpi2
WP_081890394.1    ><PCAD><[LigB_pgdc]><DNRR_synthase_rlbB><DNRP_Tpi2>                                   260   bacteria;proteobacteria;gammaproteobacteria
```

MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium
MF_00987(28)	[->PCAP]<-[->TM_rich_Dual_Dual<]	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium leguminosarum
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium leguminosarum bv. viciae
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium leguminosarum
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Methylobacterium nodulans (strain LMG 21967 / CNCM I-1324)
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium sp. PW
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium sp. CF142
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium multihospitum A2391
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium sp. Pop5
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobacter capsulatus DE 1003
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium cryolite ZP-5
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium sp. AC44/96
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobacter capsulatus
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium sp. CF080
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium mesoamericanum
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium sp. Pop5.1
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium sp. CF122
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium sp. Pop5.2
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium sp. CF142
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium wilt Sv. Acacias etc. NGA1
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium wilt ITR KZ
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Rhizobium sp. CF080 KOLGEN
MF_00987(28)	[->PCAP]<-[->TM_rich_Dual_Dual<]	282	bacteria;proteobacteria;alphaproteobacteria	Sphingomonas laterium
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Sphingomonas sp. LK11
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Tistrella mobilis KA08S20-065
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	282	bacteria;proteobacteria;alphaproteobacteria	Tistrella mobilis KA
MF_01824(28)	[->PCAP]<-[->Dual	282	bacteria;proteobacteria;alphaproteobacteria	Rhodopseudomonas palustris
MF_00987(28)	[->Dual<-STP+>PCAP	283	bacteria;cyanobacteria	Rhodopirellula baltica
MF_00987(28)	[->Dual<-STP+>PCAP	283	bacteria;cyanobacteria	Rhodopirellula europaea
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria;Nostocales	Nodularia spumigena CCY9414 S24
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria;Nostocales	Anabaena(Nostocales) Nostocales;
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Pseudanabaena sp. PCC 7429
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Pseudanabaena
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Pseudanabaena
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Leptolyngbya sp. KIOST-1
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Nostoc punctiforme PCC 73102
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Nostoc sp. PCC 7120 = FACHB-418
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena cylindrica PCC 7122
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr1
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr2
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr3
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr4
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr5
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr6
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr7
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr8
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr9
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr10
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr11
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr12
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr13
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr14
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr15
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr16
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr17
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr18
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr19
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr20
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr21
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr22
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr23
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr24
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr25
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr26
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr27
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr28
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr29
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr30
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr31
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr32
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr33
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr34
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr35
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr36
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr37
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr38
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr39
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr40
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr41
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr42
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr43
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr44
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr45
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr46
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr47
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr48
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr49
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr50
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr51
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr52
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr53
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr54
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr55
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr56
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr57
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr58
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr59
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr60
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr61
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr62
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr63
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr64
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr65
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr66
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr67
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr68
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr69
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr70
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr71
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr72
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr73
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr74
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr75
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr76
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr77
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr78
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr79
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr80
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr81
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr82
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr83
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr84
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr85
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr86
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr87
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr88
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr89
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr90
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr91
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr92
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr93
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr94
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr95
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr96
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr97
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr98
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr99
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr100
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr101
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr102
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr103
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr104
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr105
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr106
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr107
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr108
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr109
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr110
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr111
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr112
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr113
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr114
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr115
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr116
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr117
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr118
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr119
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr120
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr121
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr122
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr123
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr124
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr125
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr126
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr127
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr128
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr129
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr130
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr131
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr132
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr133
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr134
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr135
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr136
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr137
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr138
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr139
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr140
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr141
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr142
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr143
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr144
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr145
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr146
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr147
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr148
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr149
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cyanobacteria	Anabaena sp. 90chr150
MF_01824(28)	[->TM_rich_Dual_Dual<]-5-[PCAP]<-[->STP+PEP2->	283	bacteria;cy

EAR67327.1	PCAG	239	eukaryota\fungi\ascomycota	Glarea lozoyensis 74030
CCX02384.1	PCAG	202	eukaryota\fungi\ascomycota	Taphrina deformans PYCC 5710
XP_007782860.1	PCAG	202	eukaryota\fungi\ascomycota	Pneumocystis jirovecii RU7 = 42720
EGJ07031.1	PCAG	243	eukaryota\fungi\ascomycota	Colletotrichum gloeosporioides Nara gc5
EGU81763.1	PCAG	243	eukaryota\fungi\ascomycota	Fusarium oxysporum f. sp. vasinfectum
GHG63021.1	PCAG	244	eukaryota\fungi\ascomycota	Bipolaris sorokiniana ND90Pr
EGU75364.1	PCAG	244	eukaryota\fungi\ascomycota	Fusarium oxysporum f. sp. pisi
EMC78006.1	PCAG	247	eukaryota\fungi\basidiomycota	Botryosphaeria dothidea CBS 115476
XP_013554605.1	PCAG	247	eukaryota\fungi\basidiomycota	Botrytinia fuckeliana B05.10
XP_007916823.1	PCAG	247	eukaryota\fungi\basidiomycota	Colletotrichum higginsianum
EGU74980.1	PCAG	213	eukaryota\fungi\ascomycota	Fusarium oxysporum f. sp. melonis 26406
XP_016211940.1	PCAG	200	eukaryota\fungi\ascomycota	Ustilaginoidea virens UV8b
XP_007599399.1	PCAG	200	eukaryota\fungi\basidiomycota	Pseudozyma hubeiana = Ustilago hubeiana R1-lim-1
EGU47763.1	PCAG	200	eukaryota\fungi\ascomycota	Fusarium oxysporum f. sp. lycopersici 4287
EGU48753.1	PCAG	200	eukaryota\fungi\ascomycota	Fusarium oxysporum f. sp. lycopersici 4287
EGU80295.1	PCAG	315	eukaryota\fungi\ascomycota	Verticillium dahliae VdLs.17
XP_003189599.1	PCAG	200	eukaryota\fungi\ascomycota	Sclerotinia sclerotiorum 1980 UF-70
XP_007916484.1	PCAG	200	eukaryota\fungi\ascomycota	Colletotrichum higginsianum
EGU75511.1	PCAG	200	eukaryota\fungi\ascomycota	Fusarium oxysporum f. sp. melonis 26406
EGU83594.1	PCAG	315	eukaryota\fungi\ascomycota	Verticillium dahliae VdLs.17
XP_003174578.1	PCAG	200	eukaryota\fungi\ascomycota	Trichophyton rubrum CBS 118892
XP_003232363.1	PCAG	200	eukaryota\fungi\ascomycota	Trichophyton rubrum CBS 118892
XP_007916823.1	PCAG	200	eukaryota\fungi\ascomycota	Colletotrichum higginsianum
XP_007599399.1	PCAG	200	eukaryota\fungi\basidiomycota	Pseudozyma hubeiana = Ustilago hubeiana R1-lim-1
EGU47763.1	PCAG	200	eukaryota\fungi\ascomycota	Fusarium oxysporum f. sp. lycopersici 4287
EGU48753.1	PCAG	200	eukaryota\fungi\ascomycota	Fusarium oxysporum f. sp. lycopersici 4287
XP_003189599.1	PCAG	200	eukaryota\fungi\ascomycota	Sclerotinia sclerotiorum 1980 UF-70
XP_007916484.1	PCAG	200	eukaryota\fungi\ascomycota	Colletotrichum higginsianum
EGU75511.1	PCAG	200	eukaryota\fungi\ascomycota	Fusarium oxysporum f. sp. melonis 26406
XP_003174578.1	PCAG	200	eukaryota\fungi\ascomycota	Trichophyton rubrum CBS 118892
XP_003232363.1	PCAG	200	eukaryota\fungi\ascomycota	Trichophyton rubrum CBS 118892

NP_000203856.1	>>PQAP	289	bacteria\proteobacteria\gammaproteobacteria	Alistipedbacter Sensilibacter	aromatic ring-cleaving dioxygenase [Alistipedbacter Sensilibacter];
NP_117624211.1	>>PQAP	291	bacteria\actinobacteria	Streptomyces sp. TOR3209	extradiol ring-cleaving dioxygenase [Streptomyces sp. TOR3209];
NP_000203856.1	>>PQAP	291	bacteria\actinobacteria	Streptomyces sp. TOR3209	extradiol ring-cleaving dioxygenase [Streptomyces sp. TOR3209];
NP_000203856.1	>>PQAP	291	bacteria\actinobacteria	Mycobacterium sp. 141	extradiol ring-cleaving dioxygenase III subunit B [Mycobacterium sp. 141];
NP_000203856.1	>>PQAP	291	bacteria\actinobacteria	Mycobacterium sp. 141	extradiol ring-cleaving dioxygenase III subunit B [Mycobacterium sp. 141];
NP_104265925.1	>>PQAP	275	bacteria\actinobacteria	Methylpiperatum flagellatum	hypothetical protein ETC_1970 [Methylpiperatum flagellatum];
NP_000203856.1	>>PQAP	291	bacteria\proteobacteria\gammaproteobacteria	Pseudomonas sp. Ag1/2a/3a/3b/3c/4a/4b	extradiol ring-cleaving dioxygenase [Pseudomonas sp. Ag1/2a/3a/3b/3c/4a/4b];
NP_000203856.1	>>PQAP	291	bacteria\proteobacteria\gammaproteobacteria	Alistipedbacter indicus\ulmus	aromatic ring-opening dioxygenase, catalytic subunit LigB [Alistipedbacter indicus\ulmus];
NP_102764805.1	>>PQAP	289	bacteria\proteobacteria\gammaproteobacteria	Rhodococcus erythropolis PR4	conserved hypothetical protein [Rhodococcus erythropolis PR4];
NP_000203856.1	>>PQAP	291	bacteria\proteobacteria\gammaproteobacteria	Pseudomonas sp. Ag1/2a/3a/3b/3c	extradiol ring-cleaving dioxygenase [Pseudomonas sp. Ag1/2a/3a/3b/3c];
NAF36001.1	>>PQAP\>>>1\\NTQ\>	287	bacteria\proteobacteria\gammaproteobacteria	Moraxella osloense NCIB07	extradiol ring-cleaving dioxygenase [Moraxella osloense N-2927];
NP_000203856.1	>>PQAP	291	bacteria\proteobacteria\gammaproteobacteria	Corynebacterium ammoniagenes	extradiol ring-cleaving dioxygenase [Corynebacterium ammoniagenes];
EEF47488.1	>>PQAP	289	bacteria\proteobacteria\gammaproteobacteria	Pseudomonas sp. Ag1/2a/3a/3b/3c	extradiol ring-cleaving dioxygenase [Pseudomonas sp. Ag1/2a/3a/3b/3c];
NP_000203856.1	>>PQAP	291	bacteria\proteobacteria\gammaproteobacteria	Alistipedbacter Sensilibacter SI300	hypothetical protein SI300_00_01170 [Alistipedbacter Sensilibacter];
NP_000203856.1	>>PQAP	291	bacteria\proteobacteria\gammaproteobacteria	Pseudomonas sp. Ag1/2a/3a/3b/3c	extradiol ring-cleaving dioxygenase [Pseudomonas sp. Ag1/2a/3a/3b/3c];
NP_000203856.1	>>PQAP	291	bacteria\proteobacteria\gammaproteobacteria	Gordonia polyisoprenivorans	extradiol ring-cleaving dioxygenase [Gordonia polyisoprenivorans];
NP_000203856.1	>>PQAP	291	bacteria\proteobacteria\gammaproteobacteria	Alistipedbacter Sensilibacter	hypothetical protein [Alistipedbacter Sensilibacter Sensilibacter Sensilib

Supporting_Data.INC.txt					
NP_002703875.1	rl-PGAD*	284	bacteria|proteobacteria|alphaproteobacteria	Falsirhizobium sulamanensis PS107	putative fatsdoxi ring-cleavage dioxygenase, class III enzyme, subunit B [Falsirhizobium sulamanensis PS107].
NP_013129445.1	rl-PGAD(+)ETN-PEP2->	299	bacteria|proteobacteria|alphaproteobacteria	Sphingomonas sp. FARC FRG21	aromatic ring-cleaving dioxygenase [Sphingomonas sp. FARC FRG21].
NP_013129446.1	rl-PGAD(+)ETN-PEP2	299	bacteria|proteobacteria|alphaproteobacteria	Sphingomonas sp. FARC FRG21	hypothetical protein [Sphingomonas sp. FARC FRG21].
NP_013129447.1	rl-PGAD*	299	bacteria|proteobacteria|alphaproteobacteria	Pleiomiella coccoides	hypothetical protein [Pleiomiella coccoides].
NP_013760532.1	rl-PGAD*	145	bacteria|proteobacteria|gammaproteobacteria	Pseudomonas sp. Ag1/1 GFP-1	putative fatsdoxi ring-cleavage dioxygenase, class III enzyme, subunit B [Pseudomonas saghalinensis strain Ag1/1].
NP_013760533.1	rl-PGAD*	145	bacteria|proteobacteria|gammaproteobacteria	Melaseria hebeae	aromatic ring-cleaving dioxygenase [Melaseria hebeae].
NP_013760534.1	rl-PGAD*	145	bacteria|proteobacteria|gammaproteobacteria	Pseudomonas sp. Ag1/1 GFP-1	hypothetical protein [Pseudomonas sp. Ag1/1 GFP-1].
NP_013760535.1	rl-PGAD*	145	bacteria|proteobacteria|gammaproteobacteria	Burkholderia pseudomallei NCTC 13179	catalytic LigB subunit of aromatic ring-opening dioxygenase family protein [Burkholderia pseudomallei NCTC 13179].
GCA003351.0	rl-PGAD*	299	bacteria|proteobacteria|alphaproteobacteria	Blond disease bacterium R229	putative fatsdoxi ring-cleavage dioxygenase,class III enzyme, subunit B [Blond disease bacterium R229].
NP_013760536.1	rl-PGAD*	145	bacteria|proteobacteria|gammaproteobacteria	Burkholderia sp. H160	hypothetical protein [Burkholderia sp. H160].
NP_013760537.1	rl-PGAD*	299	bacteria|proteobacteria|alphaproteobacteria	Burkholderia atlas 13780	4,5-DOPA dioxygenase extradiol [Burkholderia atlas 13780].
NP_013760538.1	rl-PGAD*	299	archaea|euryarchaeota	Methanosphaera boonei AGR	extradiol ring-cleavage dioxygenase III subunit B [Methanosphaera boonei AGR].
NP_013760539.1	rl-PGAD*	299	bacteria|proteobacteria|alphaproteobacteria	Rhizobium sp. Pop5 RU7	putative fatsdoxi ring-cleavage dioxygenase, class III enzyme, subunit B [Rhizobium sp. Pop5 RU7].
NP_013760540.1	rl-PGAD*	299	bacteria|proteobacteria|alphaproteobacteria	Jacobiasca sp. AFPC	hypothetical protein [Jacobiasca sp. AFPC].
NP_013760541.1	rl-PGAD*	299	bacteria|proteobacteria|alphaproteobacteria	Rhizobium sp. Pop5 RU7	hypothetical protein [Rhizobium sp. Pop5 RU7].
NP_013760542.1	rl-PGAD*	299	bacteria|proteobacteria|alphaproteobacteria	alpha proteobacterium LLA128	aromatic ring-cleaving dioxygenase [alpha proteobacterium LLA128].
NP_013760543.1	rl-PGAD*	299	bacteria|proteobacteria|alphaproteobacteria	Ilyobacter polytropus DSM 2926 ATCC 15264	putative fatsdoxi ring-cleavage dioxygenase, class III enzyme, subunit B [Ilyobacter polytropus DSM 2926 ATCC 15264].
NP_013760544.1	rl-PGAD*	299	bacteria|proteobacteria	Flagella bizogen	hypothetical protein [Flagella bizogen].
NP_013760545.1	rl-PGAD*	257	bacteria|proteobacteria	Leptospira borgpetersenii serovar Hardjo-bovis str. JB197	catalytic LigB subunit of aromatic ring-opening dioxygenase [Leptospira borgpetersenii serovar Hardjo-bovis str. JB197].
NP_013760546.1	rl-PGAD*	299	bacteria|proteobacteria|alphaproteobacteria	Sphingomonas sp. FARC FRG21	aromatic ring-cleaving dioxygenase [Sphingomonas sp. FARC FRG21].
NP_013760547.1	rl-PGAD*	299	bacteria|proteobacteria|alphaproteobacteria	Sphingomonas sp. FARC FRG21	hypothetical protein [Sphingomonas sp. FARC FRG21].
NP_013760548.1	rl-PGAD*	110	bacteria|firmicutes	Lactobacillus sakei	putative ring-cleavage dioxygenase [Lactobacillus sakei].
NP_013760549.1	rl-PGAD*	110	bacteria|firmicutes	Lactobacillus sakei 5-1	hypothetical protein CNE_BB1p00400 [Lactobacillus sakei 5-1].
NP_013760550.1	rl-PGAD*	110	bacteria|firmicutes	Lactobacillus sakei subsp. sakei	putative ring-cleavage dioxygenase [Lactobacillus sakei subsp. sakei].
NP_013760551.1	rl-PGAD*	299	bacteria|proteobacteria	Oscillibacter Bacterium NA_L4	hypothetical protein [Oscillibacter Bacterium NA_L4].
CCT01610.1	rl-PGAD*	265	bacteria|firmicutes	Megasporilium	putative dioxygenase [Megasporilium].
NP_013760552.1	rl-PGAD*	299	bacteria|proteobacteria	Sphingomonas sp. WDMC7	putative ring-cleavage dioxygenase [Sphingomonas sp. WDMC7].
NP_013760553.1	rl-PGAD*	299	bacteria	Leptospira	MEGLITOMCEB1 aromatic ring-opening dioxygenase, subunit LigB [Leptospira].
NP_013760554.1	rl-PGAD*	299	bacteria|firmicutes	Sphingobium dicaparillatum	aromatic ring-cleaving dioxygenase [Sphingobium dicaparillatum].
NP_013760555.1	rl-PGAD*	299	bacteria|proteobacteria	Sphingomonas sp. FARC FRG21	hypothetical protein [Sphingomonas sp. FARC FRG21].
NP_013760556.1	rl-PGAD*	299	bacteria|proteobacteria	Sphingomonas napomuhon ATCC 15944	extradiol-type ring-opening dioxygenase [Sphingomonas napomuhon ATCC 15944].
NP_013760557.1	rl-PGAD*	299	bacteria|proteobacteria	Sphingomonas sp. FARC FRG21	hypothetical protein [Sphingomonas sp. FARC FRG21].
NP_013760558.1	rl-PGAD*	274	bacteria|firmicutes	Thalassospira lucentensis	extradiol ring-cleavage dioxygenase [Thalassospira lucentensis].
NP_013760559.1	rl-PGAD*	299	bacteria|proteobacteria	Sphingomonas sp. FARC FRG21	hypothetical protein [Sphingomonas sp. FARC FRG21].
NP_013760560.1	rl-PGAD*	299	bacteria|proteobacteria	Sulfolobus tokodaii str. 7	hypothetical protein STK771 [Sulfolobus tokodaii str. 7].
NP_013760561.1	rl-PGAD*	292	bacteria|proteobacteria	Sphingomonas sp. WM-1	catalytic LigB subunit of aromatic ring-opening dioxygenase [Sphingomonas sp. WM-1].
NP_013760562.1	rl-PGAD*	299	bacteria|proteobacteria	Sphingomonas sp. FARC FRG21	hypothetical protein [Sphingomonas sp. FARC FRG21].
NP_013760563.1	rl-PGAD*	261	archaea|euryarchaeota	Methanolinea mazei DSM 5348	extradiol ring-cleavage dioxygenase III subunit B [Methanolinea mazei DSM 5348].
NP_013760564.1	rl-PGAD*	261	bacteria|proteobacteria	Aeropyrum ispfahan 4B	putative dioxygenase [Aeropyrum ispfahan 4B].
NP_013760565.1	rl-PGAD*	299	bacteria|proteobacteria	Sphingomonas sp. FARC FRG21	hypothetical protein [Sphingomonas sp. FARC FRG21].
NP_013760566.1	rl-PGAD*	299	bacteria|proteobacteria	Lamprocystis sp. G10	MEGLITOMCEB1 extradiol ring-cleavage dioxygenase [Lamprocystis].
NP_013760567.1	rl-PGAD*	299	bacteria|proteobacteria	Acidovorax sp. MD-ASD1	putative extradiol dioxygenase [Acidovorax sp. MD-ASD1].
NP_013760568.1	rl-PGAD*	299	bacteria|proteobacteria	Ralstonia solanacearum Po82	putative ring-cleavage dioxygenase, class III enzyme, subunit B [Ralstonia solanacearum Po82].
AAM01287.1	rl-PGAD*	275	bacteria|firmicutes	Agrobacterium vitis	Agrobacterium vitis
NP_013760569.1	rl-PGAD*	299	bacteria|proteobacteria	Pontimonas thermosoma	Pontimonas thermosoma
NP_013760570.1	rl-PGAD(+)ETN-PEP2->	299	bacteria|proteobacteria	Sphingomonas sp. FARC FRG21	hypothetical protein [Sphingomonas sp. FARC FRG21].
NP_013760571.1	rl-PGAD*	299	bacteria|proteobacteria	Agrobacterium vitis B6	Agrobacterium vitis B6
NP_013760572.1	rl-PGAD*	85	bacteria|proteobacteria	Brachybacterium sp. DMS 370	hypothetical protein [Brachybacterium sp. DMS 370].
NP_013760573.1	rl-PGAD*	299	bacteria|proteobacteria	Sphingomonas sp. FARC FRG21	hypothetical protein [Sphingomonas sp. FARC FRG21].
NP_013760574.1	rl-PGAD*	299	bacteria|proteobacteria	Sinomonhabdus thailandensis	hypothetical protein [Sinomonhabdus thailandensis].
NP_013760575.1	rl-PGAD*	299	bacteria|proteobacteria	Sphingomonas sp. FARC FRG21	hypothetical protein [Sphingomonas sp. FARC FRG21].
NP_013760576.1	rl-PGAD*	267	bacteria|proteobacteria	Sphingobium sp. FDS-4	extradiol dioxygenase [Sphingobium sp. FDS-4].
NP_013760577.1	rl-PGAD*	299	bacteria|proteobacteria	Sphingomonas sp. FARC FRG21	hypothetical protein [Sphingomonas sp. FARC FRG21].
NP_013760578.1	rl-PGAD*	299	bacteria|proteobacteria	Ruegeria sp. 108	putative ring-cleavage dioxygenase [Pelobacteraceae medicinal].
NP_013760579.1	rl-PGAD*	257	bacteria|proteobacteria	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	hypothetical protein L0130[B] [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130].
NP_013760580.1	rl-PGAD*	299	bacteria|proteobacteria	Sphingomonas sp. FARC FRG21	hypothetical protein [Sphingomonas sp. FARC FRG21].
NP_013760581.1	rl-PGAD*	299	bacteria|proteobacteria	Agrobacterium albertimagni	aromatic ring-cleaving dioxygenase [Agrobacterium albertimagni].
NP_013760582.1	rl-PGAD*	257	bacteria|proteobacteria	Leptospira alstoni	catalytic LigB subunit of aromatic ring-opening dioxygenase [Leptospira alstoni].
NP_013760583.1	rl-PGAD*	299	bacteria|proteobacteria	Sulfolobus solfataricus P2	putative ring-cleavage dioxygenase [Sulfolobus solfataricus P2].
NP_013760584.1	rl-PGAD*	299	archaea|euryarchaeota	Methanosphaerula palustris E1-9c	hypothetical protein [Methanosphaerula palustris E1-9c].
NP_013760585.1	rl-PGAD*	265	bacteria|firmicutes	Acetofilamen marmgnosphera	possible catalytic LigB subunit of aromatic ring-opening dioxygenase [Acetofilamen marmgnosphera].
NP_013760586.1	rl-PGAD*	299	bacteria|proteobacteria	Sphingomonas sp. FARC FRG21	hypothetical protein [Sphingomonas sp. FARC FRG21].
NP_013760587.1	rl-PGAD*	272	bacteria|firmicutes	Solicola canadensis DSM 5653	hypothetical protein Solca_2148 [Solicola canadensis DSM 5653].
NP_013760588.1	rl-PGAD*	267	bacteria|proteobacteria	Sphingomonas-like bacterium B12	aromatic ring-cleaving dioxygenase, partial [Sphingomonas-like bacterium B12].
NP_013760589.1	rl-PGAD*	299	bacteria|proteobacteria	Sphingomonas sp. FARC FRG21	hypothetical protein [Sphingomonas sp. FARC FRG21].
NP_013760590.1	rl-PGAD*	278	bacteria|firmicutes	Mycobacgrilla cubrum ATCC 11179	putative ring-cleavage dioxygenase III subunit B [Mycobacgrilla cubrum ATCC 11179].
NP_013760591.1	rl-PGAD*	299	bacteria|proteobacteria	Tistlella mobilis KEM0320-065	catalytic LigB subunit of aromatic ring-opening dioxygenase [Tistlella mobilis KEM0320-065].
NP_013760592.1	rl-PGAD*	299	bacteria|proteobacteria	Sphingomonas sp. FARC FRG21	hypothetical protein [Sphingomonas sp. FARC FRG21].
NP_013760593.1	rl-PGAD*	299	bacteria|proteobacteria	Sphingobium chlorophenolicum	putative ring-cleavage dioxygenase [Sphingobium chlorophenolicum].
NP_013760594.1	rl-PGAD*	299	bacteria|proteobacteria	Sphingomonas sp. FARC FRG21	hypothetical protein [Sphingomonas sp. FARC FRG21].
NP_013760595.1	rl-PGAD*	273	bacteria|firmicutes	Martelella mediterranea	hypothetical protein [Martelella mediterranea].
NP_013760596.1	rl-PGAD(+)ETN-PEP2->	299	bacteria|proteobacteria	Phenylobacterium zucineum HLK1	putative ring-cleavage dioxygenase III subunit B [Phenylobacterium zucineum HLK1].
NP_013760597.1	rl-PGAD*	299	bacteria|proteobacteria	Brachybacterium alimentarium DSM 110	hypothetical protein BLIM40 [Brachybacterium alimentarium DSM 110].
NP_013761224.1	PCAD*->	299	bacteria|proteobacteria	Rhodanobacter spathiphylli	aromatic ring-cleaving dioxygenase [Rhodanobacter spathiphylli].
NP_013761225.1	PCAD*->	299	bacteria|proteobacteria	Rhodanobacter denitrificans	aromatic ring-cleaving dioxygenase [Rhodanobacter denitrificans].
NP_013761226.1	PCAD*->	159	bacteria|firmicutes	Oceanicola batamensis	Extradiol ring-cleavage dioxygenase, class III enzyme, subunit B [Oceanicola batamensis].
NP_013761227.1	PCAD*->	299	bacteria|proteobacteria	Rhodanobacter spathiphylli	aromatic ring-cleaving dioxygenase [Rhodanobacter spathiphylli].
NP_013761228.1	PCAD*->	251	bacteria|proteobacteria	Roseovarius sp. 217	aromatic ring-cleaving dioxygenase [Roseovarius sp. 217].
NP_013761229.1	PCAD*->	251	bacteria|proteobacteria	Ruegeria sp. 217	aromatic ring-cleaving dioxygenase [Ruegeria sp. 217].
NP_013761230.1	PCAD*->	251	bacteria|proteobacteria	Ruegeria sp.	aromatic ring-cleaving dioxygenase [Ruegeria sp.].
NP_013761231.1	PCAD*->	251	bacteria|proteobacteria	Stagnicoccus scadinicorne	aromatic ring-cleaving dioxygenase [Stagnicoccus scadinicorne].
NP_013761232.1	PCAD*->	251	bacteria|proteobacteria	Roseobacter litoralis	aromatic ring-cleaving dioxygenase [Roseobacter litoralis].
NP_013761233.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus polymyxa BC2	extradiol ring-cleavage dioxygenase class III protein subunit B [Paenibacillus polymyxa BC2].
NP_013761234.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus polymyxa	MFS transporter [Paenibacillus polymyxa].
NP_013761235.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus polymyxa A681	4,5-DOPA dioxygenase extradiol [Paenibacillus polymyxa A681].
NP_013761236.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus polymyxa	MFS transporter [Paenibacillus polymyxa].
NP_013761237.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus sp. oral taxon 786	MFS transporter [Paenibacillus sp. oral taxon 786].
NP_013761238.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus sp. P22	MFS transporter [Paenibacillus sp. P22].
NP_013761239.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus sp. Aloe-11	MFS transporter [Paenibacillus sp. Aloe-11].
NP_013761240.1	PCAD*->	258	bacteria|firmicutes	Paenibacillus sp. JCM 10914	putative cytoplasmic protein [Paenibacillus sp. JCM 10914].
NP_013761241.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus sp. P26	MFS transporter [Paenibacillus sp. P26].
NP_013761242.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus sp. oral taxon 786	MFS transporter [Paenibacillus sp. oral taxon 786].
NP_013761243.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus sp. Aloe-11	MFS transporter [Paenibacillus sp. Aloe-11].
NP_013761244.1	PCAD*->	258	bacteria|firmicutes	Paenibacillus sp. JCM 10914	putative cytoplasmic protein [Paenibacillus sp. JCM 10914].
NP_013761245.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus polymyxa CR1	MFS transporter [Paenibacillus polymyxa CR1].
NP_013761246.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus sp. P26	MFS transporter [Paenibacillus sp. P26].
NP_013761247.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus sp. FSL H8-227	Extradiol ring-cleavage dioxygenase class III protein subunit B [Paenibacillus sp. FSL H8-227].
NP_013761248.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus sp.	MFS transporter [Paenibacillus sp.].
NP_013761249.1	PCAD*->	258	bacteria|firmicutes	Paenibacillus sp. 541MC03	extradiol ring-cleavage dioxygenase class III protein subunit B [Paenibacillus sp. 541MC03].
NP_013761250.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus polymyxa CR1	MFS transporter [Paenibacillus polymyxa CR1].
NP_013761251.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus sp. FSL H8-227	MFS transporter [Paenibacillus sp. FSL H8-227].
NP_013761252.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus sp. 541MC03	MFS transporter [Paenibacillus sp. 541MC03].
NP_013761253.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus sp. 541MC03	extradiol ring-cleavage dioxygenase class III protein subunit B [Paenibacillus sp. 541MC03].
NP_013761254.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus polymyxa CR1	MFS transporter [Paenibacillus polymyxa CR1].
NP_013761255.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus sp. P26	MFS transporter [Paenibacillus sp. P26].
NP_013761256.1	PCAD*->	263	bacteria|firmicutes	Paenibacillus sp. Aloe-11	MFS transporter [Paenibacillus sp. Aloe-11].
NP_013761257.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter ovatus	aromatic ring-cleaving dioxygenase [Rhodobacter ovatus].
NP_013761258.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter sphaeroides	aromatic ring-cleaving dioxygenase [Rhodobacter sphaeroides].
NP_013761259.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761260.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761261.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761262.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761263.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761264.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761265.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761266.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761267.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761268.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761269.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761270.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761271.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761272.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761273.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761274.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761275.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761276.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761277.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761278.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761279.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761280.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761281.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761282.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761283.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761284.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761285.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761286.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761287.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761288.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761289.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761290.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761291.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761292.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761293.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761294.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761295.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761296.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761297.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761298.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761299.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761300.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761301.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761302.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761303.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761304.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761305.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761306.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761307.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761308.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761309.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761310.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761311.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761312.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761313.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761314.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761315.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761316.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761317.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761318.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761319.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761320.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761321.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761322.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761323.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761324.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761325.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761326.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761327.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761328.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761329.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761330.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761331.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761332.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761333.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761334.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761335.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761336.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761337.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761338.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761339.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761340.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761341.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761342.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761343.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761344.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761345.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761346.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761347.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_013761348.1	PCAD*->	251	bacteria|proteobacteria	Rhodobacter	aromatic ring-cleaving dioxygenase [Rhodobacter].
NP_

NP_000932896.1	PCAP<>	258	bacteria|proteobacteria|alphaproteobacteria	Pseudovibrio sp. JE062
NP_000934893.1	PCAP<>	149	bacteria|proteobacteria|alphaproteobacteria	Plesiomonas shigelloides
NP_000936488.1	PCAP<>	257	bacteria|proteobacteria|alphaproteobacteria	Ruegeria sp. TM1040
NP_000937276.1	PCAP<>	257	bacteria|proteobacteria|alphaproteobacteria	Alistipes sp. JC136
NP_000938000.1	PCAP<>	257	bacteria|proteobacteria|alphaproteobacteria	Alistipes finegoldii
NP_000941000.1	PCAP<>	258	bacteria|proteobacteria|alphaproteobacteria	Alistipes sp. HGB5
NP_000941000.1	PCAP<>	258	bacteria|proteobacteria|alphaproteobacteria	Alistipes finegoldii DSM 17036

```
#similar to the above two contexts, but abbreviated
NF_00179000.1     Ribosomal_S2<Memo*>
NF_00179000.1     Ribosomal_S2<Memo*>
NF_00352996.1     Ribosomal_S2<Memo*>
NF_00352996.1     Ribosomal_S2<Memo*>
NF_00352996.1     Ribosomal_S2<Memo*>
NF_00353675.1     enolase<Ribosomal_S2<Memo*>
NF_00353675.1     enolase<Ribosomal_S2<Memo*>
NF_00353675.1     enolase
```

```
Supporting_Data.INC.txt
GP_004801025.1   Mmar<->                                   287   eukaryotaraphidophyceae                    Babesia equi                                                   hypothetical protein BEWA_027630 [Babesia equi]
ETM39402.1       Mmar<->                                   199   eukaryotaraphidophyceae                    Plasmodium falciparum Tanzania (2000708)                       hypothetical protein PFTANZ_00896 [Plasmodium falciparum Tanzania (2000708)]
ETM39401.1       Mmar<->                                   239   eukaryotaraphidophyceae                    Eimeria maxima                                                 hypothetical protein, conserved [Eimeria maxima]
CDJ56215.1       Mmar<->                                   239   eukaryotaraphidophyceae                    Eimeria maxima                                                 hypothetical protein, conserved [Eimeria maxima]
XP_002549876.1   Mmar<->                                   211   eukaryotaraphidophyceae                    Plasmodium falciparum 7G8                                      hypothetical protein PFPG_00776 [Plasmodium falciparum 7G8]
XP_002549876.1   Mmar<->                                   211   eukaryotaraphidophyceae                    Plasmodium falciparum 7G8                                      hypothetical protein PFPG_00776 [Plasmodium falciparum 7G8]
CDJ56215.1       Mmar<->                                   239   eukaryotaraphidophyceae                    Eimeria tenella Houghton 1                                     hypothetical protein, conserved [Eimeria tenella]
CDJ56215.1       Mmar<->                                   239   eukaryotaraphidophyceae                    Eimeria tenella                                                hypothetical protein, conserved [Eimeria tenella]
ETM39401.1       Mmar<->                                   239   eukaryotaraphidophyceae                    Plasmodium yoelii 17X                                          hypothetical protein PYYGI_00_0348 [Plasmodium yoelii 17X]
CDJ56215.1       Mmar<->                                   239   eukaryotaraphidophyceae                    Eimeria acervulina                                             hypothetical protein, conserved [Eimeria acervulina]
CDJ56215.1       Mmar<->                                   239   eukaryotaraphidophyceae                    Eimeria acervulina                                             hypothetical protein, conserved [Eimeria acervulina]
CDJ56215.1       Mmar<->                                   239   eukaryotaraphidophyceae                    Eimeria brunetti                                               hypothetical protein, conserved [Eimeria brunetti]
CDJ56215.1       Mmar<->                                   239   eukaryotaraphidophyceae                    Eimeria brunetti                                               hypothetical protein, conserved [Eimeria brunetti]
XP_002549876.1   Mmar<->                                   211   eukaryotaraphidophyceae                    Plasmodium falciparum CAMP/Malaysia                            hypothetical protein PFCAMP_00_0776 [Plasmodium falciparum CAMP/Malaysia]
XP_002549876.1   Mmar<->                                   211   eukaryotaraphidophyceae                    Plasmodium falciparum MC(0.5.C12)                              hypothetical protein PFMC_00_0776 [Plasmodium falciparum MC(0.5.C12)]
CCF72926.1       Mmar<->                                   212   eukaryotaraphidophyceae                    Babesia microti strain RI                                      unnamed protein product [Babesia microti strain RI]
XP_002410384.1   Mmar<->                                   239   eukaryotaraphidophyceae                    Plasmodium vivax Sal-1                                         hypothetical protein, conserved [Plasmodium vivax Sal-1]
XP_002410384.1   Mmar<->                                   239   eukaryotaraphidophyceae                    Plasmodium vivax Sal-1                                         hypothetical protein [Plasmodium vivax Sal-1]
XP_746391.1      Mmar<->                                   290   eukaryotaraphidophyceae                    Theileria parva strain Muguga                                  hypothetical protein [Theileria parva strain Muguga]
XP_002368531.1   Mmar<->                                   290   eukaryotaraphidophyceae                    Theileria parva                                                hypothetical protein, conserved [Theileria parva]
XP_002368531.1   Mmar<->                                   290   eukaryotaraphidophyceae                    Plasmodium knowlesi strain H                                   hypothetical protein in Hypoxanthen species [Plasmodium knowlesi strain H]
XP_002549876.1   Mmar<->                                   211   eukaryotaraphidophyceae                    Plasmodium falciparum 3D7                                      Mmar-like protein [Plasmodium falciparum 3D7]
XP_002549876.1   Mmar<->                                   211   eukaryotaraphidophyceae                    Plasmodium falciparum 3D7                                      hypothetical protein, conserved [Plasmodium falciparum 3D7]
CDJ56215.1       Mmar<->                                   239   eukaryotaraphidophyceae                    Eimeria brunetti                                               hypothetical protein, conserved [Eimeria brunetti]
CDJ56215.1       Mmar<->                                   239   eukaryotaraphidophyceae                    Plasmodium falciparum 3D7[0.1                                  hypothetical protein CDS 3D7 [Plasmodium falciparum 3D7]
XP_002549876.1   Mmar<->                                   211   eukaryotaraphidophyceae                    Plasmodium falciparum 3D7[0.1                                  hypothetical protein PFB_0240c [Plasmodium falciparum 3D7]
CDJ56215.1       Mmar<->                                   239   eukaryotaraphidophyceae                    Eimeria tenella                                                hypothetical protein, conserved [Eimeria tenella]
EFC01384.1       Mmar<->                                   316   eukaryotaraphidophyceae                    Reticulomyxa filosa                                            hypothetical protein RF1-0677 [Reticulomyxa filosa]
EFC01384.1       Mmar<->                                   316   eukaryotaraphidophyceae                    Reticulomyxa filosa                                            hypothetical protein RF1-0677 [Reticulomyxa filosa]
XP_002370531.1   Mmar<->                                   285   eukaryotaraphidophyceae                    Giardia lamblia                                                hypothetical protein GLP_Family protein [Giardia lamblia]
XP_002370531.1   Mmar<->                                   285   eukaryotaraphidophyceae                    Giardia lamblia                                                hypothetical protein GLP_Family protein [Giardia lamblia]
EEH50385.1       Mmar<->                                   285   eukaryotaraphidophyceae                    Giardia intestinalis ATCC 50581                                hypothetical protein GLOTRI_1896 [Giardia intestinalis ATCC 50581]
XP_002370531.1   Mmar<->                                   285   eukaryotaraphidophyceae                    Giardia lamblia ATCC 50803                                     hypothetical protein GLP_Family protein [Giardia lamblia ATCC 50803]
XP_001478844.1   Mmar<->                                   285   eukaryotaraphidophyceae                    Paramecium tetraurelia strain d4-2, "Miyakoji 2"               hypothetical protein GSPT_1934 [Paramecium tetraurelia strain d4-2, "Miyakoji 2"]
XP_004196673.1   Mmar<->                                   298   bacteriaproteobacteriaalphaalphaorhizobiales   Desulfovibrio sp. HCG                                          unnamed protein product [Desulfovibrio sp. HCG]
XP_003720371.1   Mmar<->                                   287   bacteriaproteobacteriaalphaalphaorhizobiales   Babesia bovis strain T2Bo                                      hypothetical protein BBOV_I003 [Babesia bovis strain T2Bo]
XP_003720371.1   Mmar<->                                   287   bacteriaproteobacteriaalphaalphaorhizobiales   Babesia pseudoboviseae Shuchi                                  hypothetical protein [Babesia pseudoboviseae Shuchi]
XP_002549876.1   Mmar<->                                   211   bacteriaproteobacteriaalphaalphaorhizobiales   Desulfovibrio sp. A2                                           hypothetical protein [Desulfovibrio sp. A2]
XP_002549876.1   Mmar<->                                   211   bacteriaproteobacteriaalphaalphaorhizobiales   Pelotomaculum thermopropionicum SI                             hypothetical protein Pelotomaculum thermopropionicum SI [Pelotomaculum thermopropionicum SI]
XP_002549876.1   Mmar<->                                   211   bacteriaproteobacteriaalphaalphaorhizobiales   Desulfovibrio sp. A2                                           hypothetical protein [Desulfovibrio sp. A2
```

```
#Conserved linkage to citrate synthase, CoA transferase, and often an alcohol dehydrogenase which, while annotated as a NADP+-quinone oxidoreductase,
#clustering searches indicate closest known relative to Trichomy/CoA carboxylase/hydratase. Possibly a pathway where the PCXD and alcohol dehydrogenase
#catalyze the formation of a substrate for the CoA transferase and the alcohol dehydrogenase works with the CoA transferase and the PCXD directly
#involvinfuscinone as carboxylatelike substrate for citrate synthase.
WP_052872376.1   NTA_lic2lic->>lic2gal->lic2gal->>citrate_synt->CoA_transf_3                                                
```

```
NP_001314486.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase
NP_001317049.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001319457.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320008.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320009.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320010.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320011.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320012.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320013.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320014.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320015.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320016.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320017.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320018.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320019.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320020.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320021.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320022.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320023.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320024.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320025.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320026.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320027.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320028.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320029.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320030.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320031.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320032.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320033.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320034.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320035.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320036.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320037.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320038.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320039.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320040.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320041.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320042.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320043.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320044.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320045.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320046.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320047.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320048.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320049.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320050.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320051.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320052.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320053.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320054.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320055.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320056.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320057.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320058.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320059.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320060.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320061.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320062.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320063.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320064.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320065.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320066.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320067.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320068.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320069.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320070.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320071.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320072.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320073.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320074.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320075.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320076.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320077.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320078.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320079.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320080.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320081.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320082.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320083.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320084.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320085.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320086.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320087.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320088.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320089.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320090.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320091.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320092.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320093.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320094.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320095.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320096.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320097.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320098.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320099.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
NP_001320100.1   <-MFS_transporter>-4-hydroxy-2-oxovalerate_aldolase>-acetaldehyde_dehydrogenase>-2-keto-4-pentenoate_hydratase>-3-hydroxy-4-ketoxoa_C_4-dicarboxylic_acid_hydrolase>-PCAD>-3-(3-hydroxyphenyl)propionate_hydroxylase>HTH_LuxR_1>1>0>
```

Within subset of the Insert-containing Classical LigB clade is specifically involved in catechol degrad

NP_006435681.1	RTA<<<Hpal_2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase>Hpal_2-oxo-hepta-3-ene-1,7-dioic acid hydratase>5-carboxymethyl-2-hydroxymuconate isomerase>PCAD<<<5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase>4-hydroxyphenylacetate isomerase>Decarboxylase>4-hydroxyphenylacetate isomerase>Decarboxylase	289	bacteria\proteobacteria\Betaproteobacteria	Ralstonia pickettii	5,4-dihydroxyphenylacetate 2,3-dioxygenase [Ralstonia pickettii].
NP_005270981.1	>>>carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase>>>PCAD<<<5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase>	289	bacteria\proteobacteria	Saccharothrix espanaensis DSM 44229	5,4-dihydroxyphenylacetate 2,3-dioxygenase [Saccharothrix espanaensis DSM 44229].
NP_006435681.1	RTA<<<Hpal_2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase>Hpal_2-oxo-hepta-3-ene-1,7-dioic acid hydratase>5-carboxymethyl-2-hydroxymuconate isomerase>PCAD<<<5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase>4-hydroxyphenylacetate isomerase>Decarboxylase>4-hydroxyphenylacetate isomerase>Decarboxylase	289	bacteria\proteobacteria\Betaproteobacteria	Burkholderia sp. RPE67	5,4-dihydroxyphenylacetate 2,3-dioxygenase [Burkholderia sp. RPE67].
NP_006435681.1	RTA<<<Hpal_2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase>Hpal_2-oxo-hepta-3-ene-1,7-dioic acid hydratase>5-carboxymethyl-2-hydroxymuconate isomerase>PCAD<<<5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase>4-hydroxyphenylacetate isomerase>Decarboxylase>4-hydroxyphenylacetate isomerase>Decarboxylase	289	bacteria\proteobacteria\Betaproteobacteria	Ralstonia pickettii 12D	5,4-dihydroxyphenylacetate 2,3-dioxygenase [Ralstonia pickettii 12D].
NP_006435681.1	RTA<<<Hpal_2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase>Hpal_2-oxo-hepta-3-ene-1,7-dioic acid hydratase>5-carboxymethyl-2-hydroxymuconate isomerase>PCAD<<<5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase>4-hydroxyphenylacetate isomerase>Decarboxylase>4-hydroxyphenylacetate isomerase>Decarboxylase	289	bacteria\proteobacteria\Betaproteobacteria	Burkholderia sp. H160	5,4-dihydroxyphenylacetate 2,3-dioxygenase [Burkholderia sp. H160].
NP_006435681.1	RTA<<<Hpal_2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase>Hpal_2-oxo-hepta-3-ene-1,7-dioic acid hydratase>5-carboxymethyl-2-hydroxymuconate isomerase>PCAD<<<5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase>4-hydroxyphenylacetate isomerase>Decarboxylase>4-hydroxyphenylacetate isomerase>Decarboxylase	289	bacteria\proteobacteria\Betaproteobacteria	Thiomonas sp. 3As	5,4-dihydroxyphenylacetate 2,3-dioxygenase [Thiomonas sp. 3As].
NP_006435681.1	RTA<<<Hpal_2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase>Hpal_2-oxo-hepta-3-ene-1,7-dioic acid hydratase>5-carboxymethyl-2-hydroxymuconate isomerase>PCAD<<<5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase>4-hydroxyphenylacetate isomerase>Decarboxylase>4-hydroxyphenylacetate isomerase>Decarboxylase	289	bacteria\proteobacteria\Betaproteobacteria	Burkholderia ambifaria AMMD	5,4-dihydroxyphenylacetate 2,3-dioxygenase [Burkholderia ambifaria AMMD].
NP_006435681.1	RTA<<<Hpal_2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase>Hpal_2-oxo-hepta-3-ene-1,7-dioic acid hydratase>5-carboxymethyl-2-hydroxymuconate isomerase>PCAD<<<5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase>4-hydroxyphenylacetate isomerase>Decarboxylase>4-hydroxyphenylacetate isomerase>Decarboxylase	289	bacteria\proteobacteria\Betaproteobacteria	Burkholderia sp. H160	5,4-dihydroxyphenylacetate 2,3-dioxygenase [Burkholderia sp. H160

```
Supporting_Data.txt
NP_008429984.1   ->Cys_rich+Radical_SAM+zinc_ribbon(!?>>>>>>>>>>>PCAD+AMMECR1*   468  bacteria+firmicutes      Clostridium sp. MahGuangXi MGC34-26          putative protein, PHOSS Family (Clostridium sp. MahGuangXi MGC34-26);
NP_007372254.1   PCAD+AMMECR1*->Cys_rich+Radical_SAM+zinc_ribbon->   465  bacteria+firmicutes      Clostridiales bacterium 1_7_47FAA            extracellular ring-cleavage dioxygenase (Clostridiales bacterium 1_7_47FAA);
NP_001076756.1   PCAD+AMMECR1*->Cys_rich+Radical_SAM+zinc_ribbon->   465  bacteria+firmicutes      Bacillus cereus                              hypothetical protein (Bacillus cereus);
NP_001297195.1   PCAD+AMMECR1*->Cys_rich+Radical_SAM+zinc_ribbon->   465  bacteria+firmicutes      Clostridium glycolicum                       hypothetical protein (Clostridium glycolicum);
NP_001076756.1   PCAD+AMMECR1*->Cys_rich+Radical_SAM+zinc_ribbon->   465  bacteria+firmicutes      Bacillus cereus                              hypothetical protein (Bacillus cereus);
NP_001297195.1   PCAD+AMMECR1*->Cys_rich+Radical_SAM+zinc_ribbon->   465  bacteria+firmicutes      Clostridium glycolicum                       hypothetical protein (Clostridium glycolicum);
NP_001297195.1   PCAD+AMMECR1*->Cys_rich+Radical_SAM+zinc_ribbon->   465  bacteria+firmicutes      Clostridium glycolicum                       hypothetical protein (Clostridium glycolicum);
NP_001297195.1   PCAD+AMMECR1*->Cys_rich+Radical_SAM+zinc_ribbon->   465  bacteria+firmicutes      Clostridium glycolicum                       hypothetical protein (Clostridium glycolicum);
NP_001076756.1   PCAD+AMMECR1*->Cys_rich+Radical_SAM+zinc_ribbon->   465  bacteria+firmicutes      Bacillus cereus                              hypothetical protein (Bacillus cereus);
NP_001297195.1   PCAD+AMMECR1*->Cys_rich+Radical_SAM+zinc_ribbon->   465  bacteria+firmicutes      Clostridium glycolicum                       hypothetical protein (Clostridium glycolicum);
NP_001297195.1   PCAD+AMMECR1*->Cys_rich+Radical_SAM+zinc_ribbon->   465  bacteria+firmicutes      Clostridium glycolicum                       hypothetical protein (Clostridium glycolicum);
NP_008429984.1   ->Cys_rich+Radical_SAM+zinc_ribbon(!?>>>>>>>>>>>PCAD+AMMECR1*   468  bacteria+firmicutes      Clostridium sp. MahGuangXi MGC34-26          putative protein, PHOSS Family (Clostridium sp. MahGuangXi MGC34-26);
NP_001076756.1   PCAD+AMMECR1*->Cys_rich+Radical_SAM+zinc_ribbon->   465  bacteria+firmicutes      Bacillus cereus                              hypothetical protein (Bacillus cereus);
NP_001297195.1   PCAD+AMMECR1*->Cys_rich+Radical_SAM+zinc_ribbon->   465  bacteria+firmicutes      Clostridium glycolicum                       hypothetical protein (Clostridium glycolicum);
NP_008429984.1   ->Cys_rich+Radical_SAM+zinc_ribbon(!?>>>>>>>>>>>PCAD+AMMECR1*   468  bacteria+firmicutes      Clostridium sp. MahGuangXi MGC34-26          putative protein, PHOSS Family (Clostridium sp. MahGuangXi MGC34-26
```

```
Supporting_Data.DRC.txt

NP_282692791.1   DP=Regulonas=GNBBCXO:<>DP=Mem?<>DP=CDPI1GC      304          Bacteria|spirochaetes                          Spirochaeta celldoricphila                          AmmoMemoRadiAm system protein B [Spirochaeta celldoricphila]
CBI29504.1       DP=Lalinoiset<>DP=AMMBCXO:<>DP=Mem?<>DP=CDPI1GC  289          Bacteria|spirochaetes                          Spirochaetaceae Genomic SC_154                      AmmoMemoRadiAm system protein B [Spirochaetaceae Genomic SC_154]
CBI29504.1       DP=Lalinoiset<>DP=AMMBCXO:<>DP=Mem?<>DP=CDPI1GC  289          Bacteria|spirochaetes                          Spirochaetaceae Genomic SC_127                      AmmoMemoRadiAm system protein B [Spirochaetaceae Genomic SC_127]

Alternative versions
WP_014135502.1   DP=Mem?<>                                        313          Bacteria|firmicutes                            Anaerotruncus sp. G3(2012)                          hypothetical protein [Anaerotruncus sp. G3(2012)]
WP_009275551.1   DP=Mem?<>                                        289          Bacteria|spirochaetes                          Treponema pedis str. T A4                           hypothetical protein TPE_1713 [Treponema pedis str. T A4]
CBI29504.1       DP=Mem?<>                                        289          Bacteria                                       Treponema pedis str. T A4                           hypothetical protein ACD_22050118G0001 [uncultured Bacteria]
WP_009275551.1   DP=Mem?<>                                        289          Bacteria                                       uncultured Bacterium                                hypothetical protein ACD_52090G00001 [uncultured Bacteria]
WP_009275551.1   DP=Mem?<>                                        287          Bacteria                                       uncultured Bacterium                                hypothetical protein ACD_52090G00002 [uncultured Bacteria]
WP_009275551.1   DP=Mem?<>                                        287          Bacteria                                       uncultured Bacterium                                hypothetical protein ACD_KX00033G0001 [uncultured Bacteria]

Association with alpha-2-macroglobulin, restricted to yet widely present in the scrolled bacterial
A"Rack marker". The alpha-2-macroglobulin typically, but not always, contains a bin domain insert.

A-bin domain inserted into alpha-2-macroglobulin, Mem associates with CapA/PpkA (PSR_cap) domain via direct
Affixes of in the operon
WP_014135502.1   ---DP=Mem<PSR_cap?><alpha-2-macroglobulin_KIRT_insert>  424          Bacteria                                       Microgenomates group bacterium GWC1_OM71_40_22      DUF 1328 2 domain protein [Microgenomates group bacterium GWC1_OM71_40_22]
WP_009275551.1   ---DP=Mem<PSR_cap?><alpha-2-macroglobulin_KIRT_insert>  404          Bacteria                                       Candidatus Nanosalinarum sp. J07AB56 [Candidatus Nanosalinarum sp. J07AB56]  hypothetical protein [Candidatus Nanosalinarum sp. J07AB56]
WP_009275551.1   ---DP=Mem<PSR_cap?><alpha-2-macroglobulin_KIRT_insert>  404          Bacteria                                       Candidatus Moranbacteria bacterium GWC11_OM42_49.19 DUF 1328 2 domain protein [Candidatus Moranbacteria bacterium GWC11_OM42_49.19
```

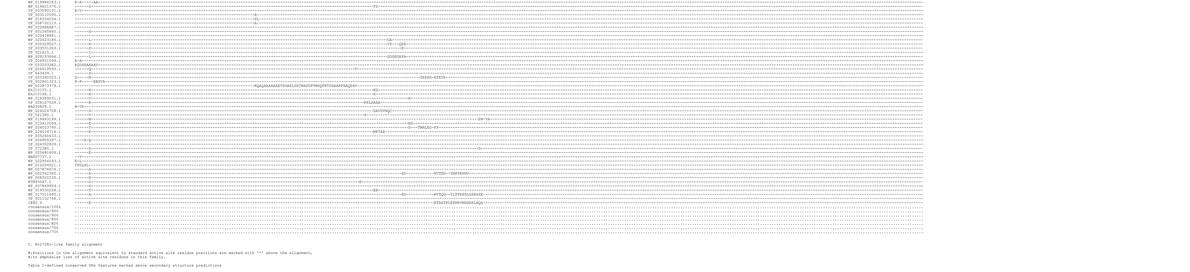
C. PsTKTb-like family alignment

#Positions in the alignment equivalent to standard active site residue positions are marked with '*' above the alignment,
#rin emphasize some of active site residues in this family.

Table 1-defined conserved TM features marked above secondary structure predictions

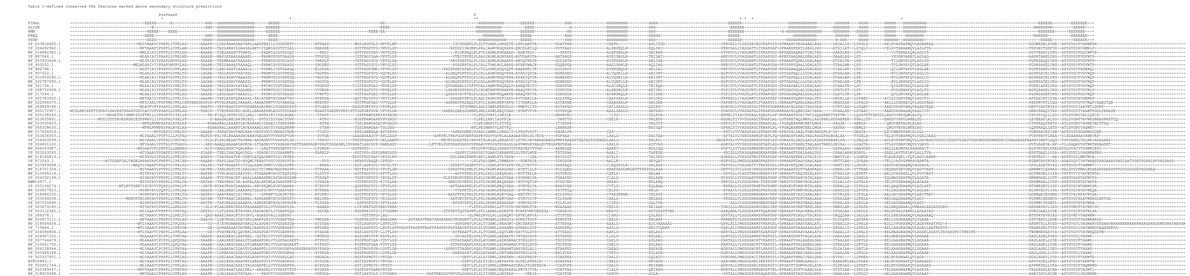
D. ARMHCH1 Pattern family alignment

Table 1-defined conserved TM features marked above secondary structure predictions



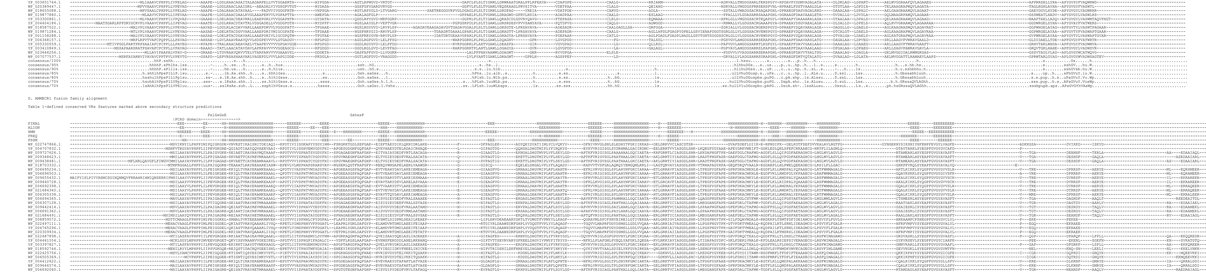
E. CqhD/PqmH Pattern family alignment

Table 1-defined conserved TM features marked above secondary structure predictions



F. PqqB-like Pattern family alignment

Table 1-defined conserved TM features marked above secondary structure predictions



C. Hpd4/Pap4-like family 1

Table 1-defined conserved TRs features marked above secondary structure predictions

D. PTH12 family

Table 1-defined conserved TRs features marked above secondary structure predictions

E. promote degrading family

Table 1-defined conserved TRs features marked above secondary structure predictions

F. Dcn_D29 family

Table 1-defined conserved TRs features marked above secondary structure predictions

G. CT1369 family

Table 1-defined conserved TRs features marked above secondary structure predictions