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Description	RVBD1521_(fadD25)_1712308_1714059
Date	Fri Aug 2 13:30:10 BST 2019
Unique Job ID	f0ec825ff83ce21f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6eqoB_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coenzyme a synthetase; <b>PDBTitle:</b> tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nadp+ and phosphomethylphosphonic acid adenylate ester
2	<a href="#">c5es8A_</a>	 Alignment		100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> linear gramicidin synthetase subunit a; <b>PDBTitle:</b> crystal structure of the initiation module of lgra in the thiolation2 state
3	<a href="#">c6p1jA_</a>	 Alignment		100.0	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> txo2; <b>PDBTitle:</b> the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo2 serine module
4	<a href="#">c5u89A_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> amino acid adenylation domain protein; <b>PDBTitle:</b> crystal structure of a cross-module fragment from the dimodular nrps2 dhbf
5	<a href="#">c5gxdA_</a>	 Alignment		100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> amp-dependent synthetase and ligase; <b>PDBTitle:</b> structure of acryloyl-coa lyase prpe from dinoroseobacter shibae df12 12
6	<a href="#">d1pg4a_</a>	 Alignment		100.0	20	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
7	<a href="#">c5ifiA_</a>	 Alignment		100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coenzyme a synthetase; <b>PDBTitle:</b> crystal structure of acetyl-coa synthetase in complex with adenosine-2 5'-propylphosphate from cryptococcus neoformans h99
8	<a href="#">c5msdA_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylic acid reductase; <b>PDBTitle:</b> structure of the a domain of carboxylic acid reductase (car) from2 nocardia iowensis in complex with amp and benzoic acid
9	<a href="#">d1ry2a_</a>	 Alignment		100.0	19	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
10	<a href="#">c5ja2A_</a>	 Alignment		100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> enterobactin synthase component f; <b>PDBTitle:</b> entf, a terminal nonribosomal peptide synthetase module bound to the2 non-native mbth-like protein pa2412
11	<a href="#">c5wmmA_</a>	 Alignment		100.0	24	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> nrps; <b>PDBTitle:</b> crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios

12	<a href="#">c4wd1A_</a>	Alignment		100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetoacetate-coa ligase; <b>PDBTitle:</b> acetoacetyl-coa synthetase from streptomyces lividans
13	<a href="#">c3kxwA_</a>	Alignment		100.0	33	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> saframycin mx1 synthetase b; <b>PDBTitle:</b> the crystal structure of fatty acid amp ligase from legionella2 pneumophila
14	<a href="#">c5ey8D_</a>	Alignment		100.0	35	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> acyl-coa synthase; <b>PDBTitle:</b> structure of fadd32 from mycobacterium smegmatis complexed to ampc20
15	<a href="#">c2vsgA_</a>	Alignment		100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> surfactin synthetase subunit 3; <b>PDBTitle:</b> structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module
16	<a href="#">c5mstA_</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioester reductase domain-containing protein; <b>PDBTitle:</b> structure of the a domain of carboxylic acid reductase (car) from segniliparus rugosus in complex with amp and a co-purified carboxylic3 acid
17	<a href="#">c6n8eA_</a>	Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> holo-obif1; <b>PDBTitle:</b> crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
18	<a href="#">c3gqwB_</a>	Alignment		100.0	28	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid amp ligase; <b>PDBTitle:</b> crystal structure of a fatty acid amp ligase from e. coli with an acyl2 adenylate product bound
19	<a href="#">c5mssA_</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioester reductase domain-containing protein; <b>PDBTitle:</b> structure of the a-pcp didomain of carboxylic acid reductase (car)2 from segniliparus rugosus in complex with amp
20	<a href="#">c4r0mB_</a>	Alignment		100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> mcyg protein; <b>PDBTitle:</b> structure of mcyg a-pcp complexed with phenylalanyl-adenylate
21	<a href="#">c4zxiA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> enterobactin synthase component f; <b>PDBTitle:</b> crystal structure of holo-entf a nonribosomal peptide synthetase in2 the thioester-forming conformation
22	<a href="#">c4zxiA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyrocidine synthetase 3; <b>PDBTitle:</b> crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine
23	<a href="#">c3e7wA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--poly(phosphoribitol) ligase subunit 1; <b>PDBTitle:</b> crystal structure of dlta: implications for the reaction mechanism of2 non-ribosomal peptide synthetase (nrps) adenylation domains
24	<a href="#">c4r0mA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> mcyg protein; <b>PDBTitle:</b> structure of mcyg a-pcp complexed with phenylalanyl-adenylate
25	<a href="#">d3cw9a1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
26	<a href="#">c3vngA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> nrps adenylation protein cytc1; <b>PDBTitle:</b> co-crystal structure of nrps adenylation protein cytc1 with atp from2 streptomyces
27	<a href="#">d1mdba_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
28	<a href="#">c4wv3A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase/ligase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> anthranilate-coa ligase; <b>PDBTitle:</b> crystal structure of the anthranilate coa ligase auaeii in

					complex2 with anthranoyl-amp <b>PDB header:</b> ligase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein 4-coumarate--coa ligase 1, resveratrol <b>PDBTitle:</b> 4-coumaroyl-coa ligase::stilbene synthase fusion protein
29	<a href="#">c3tsyA_</a>	Alignment	not modelled	100.0	20
30	<a href="#">c5ie2A_</a>	Alignment	not modelled	100.0	21
31	<a href="#">c3ni2A_</a>	Alignment	not modelled	100.0	22
32	<a href="#">c4dg9A_</a>	Alignment	not modelled	100.0	17
33	<a href="#">c5x8gA_</a>	Alignment	not modelled	100.0	23
34	<a href="#">c4eatB_</a>	Alignment	not modelled	100.0	21
35	<a href="#">c4oxiA_</a>	Alignment	not modelled	100.0	16
36	<a href="#">c5wm7A_</a>	Alignment	not modelled	100.0	21
37	<a href="#">c4dg8A_</a>	Alignment	not modelled	100.0	18
38	<a href="#">c6ac3B_</a>	Alignment	not modelled	100.0	17
39	<a href="#">c3iteB_</a>	Alignment	not modelled	100.0	15
40	<a href="#">c4ir7A_</a>	Alignment	not modelled	100.0	21
41	<a href="#">c2d1tA_</a>	Alignment	not modelled	100.0	22
42	<a href="#">c3etcB_</a>	Alignment	not modelled	100.0	17
43	<a href="#">c3eynB_</a>	Alignment	not modelled	100.0	18
44	<a href="#">c6ijbA_</a>	Alignment	not modelled	100.0	14
45	<a href="#">c5aplA_</a>	Alignment	not modelled	100.0	21
46	<a href="#">c3rg2H_</a>	Alignment	not modelled	100.0	18
47	<a href="#">c3r44A_</a>	Alignment	not modelled	100.0	18
48	<a href="#">c5u2aA_</a>	Alignment	not modelled	100.0	18
49	<a href="#">c5keiA_</a>	Alignment	not modelled	100.0	21
50	<a href="#">c4d56A_</a>	Alignment	not modelled	100.0	19
51	<a href="#">c6h1bA_</a>	Alignment	not modelled	100.0	21
52	<a href="#">c5ijgB_</a>	Alignment	not modelled	100.0	20
					<b>PDB header:</b> ligase

53	<a href="#">c3dhvA</a>	Alignment	not modelled	100.0	19	<b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine-poly(phosphoribitol) ligase; <b>PDBTitle:</b> crystal structure of dlta protein in complex with d-alanine2 adenylate
54	<a href="#">c5e7qB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coa synthetase; <b>PDBTitle:</b> acyl-coa synthetase ptma2 from streptomyces platensis
55	<a href="#">c6akdA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> amp-dependent synthetase and ligase; <b>PDBTitle:</b> crystal structure of idn17
56	<a href="#">d1amua</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
57	<a href="#">c4fuqD</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> malonyl coa synthetase; <b>PDBTitle:</b> crystal structure of apo matb from rhodopseudomonas palustris
58	<a href="#">c2v7bB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> benzoate-coenzyme a ligase; <b>PDBTitle:</b> crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
59	<a href="#">c3l8cA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--poly(phosphoribitol) ligase subunit 1; <b>PDBTitle:</b> structure of probable d-alanine--poly(phosphoribitol) ligase subunit-12 from streptococcus pyogenes
60	<a href="#">c1amuB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> peptide synthetase <b>Chain:</b> B: <b>PDB Molecule:</b> gramicidin synthetase 1; <b>PDBTitle:</b> phenylalanine activating domain of gramicidin synthetase 12 in a complex with amp and phenylalanine
61	<a href="#">d1l1cia</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
62	<a href="#">c6ozvA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> txo1; <b>PDBTitle:</b> the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo1 serine module in3 complex with amp
63	<a href="#">c3g7sA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> long-chain-fatty-acid--coa ligase (fadd-1); <b>PDBTitle:</b> crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus
64	<a href="#">d1v25a</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
65	<a href="#">c3nyrA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyl-coa ligase; <b>PDBTitle:</b> malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
66	<a href="#">c5buqA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-succinylbenzoate--coa ligase; <b>PDBTitle:</b> unliganded form of o-succinylbenzoate coenzyme a synthetase (mene)2 from bacillus subtilis, solved at 1.98 angstroms
67	<a href="#">c3iplB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-succinylbenzoate--coa ligase; <b>PDBTitle:</b> crystal structure of o-succinylbenzoic acid-coa ligase from2 staphylococcus aureus subsp. aureus mu50
68	<a href="#">c4gr5B</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> non-ribosomal peptide synthetase; <b>PDBTitle:</b> crystal structure of slgn1deltaasub in complex with ampcpp
69	<a href="#">c5c5hA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-succinylbenzoate--coa ligase; <b>PDBTitle:</b> r195k e. coli mene with bound osb-ams
70	<a href="#">c3e53A</a>	Alignment	not modelled	100.0	61	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty-acid-coa ligase fadd28; <b>PDBTitle:</b> crystal structure of n-terminal domain of a fatty acyl amp2 ligase faal28 from mycobacterium tuberculosis
71	<a href="#">c4w8oA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> luciferase-like enzymeamp-coa-ligase; <b>PDBTitle:</b> structure of the luciferase-like enzyme from the nonluminescent2 zophobas morio mealworm
72	<a href="#">c5jipB</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nonribosomal peptide synthase; <b>PDBTitle:</b> crystal structure of cmis6
73	<a href="#">c3qyaA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> luciferase; <b>PDBTitle:</b> crystal structure of a red-emitter mutant of lampyris turkestanicus2 luciferase
74	<a href="#">c3o82B</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide arylation enzyme; <b>PDBTitle:</b> structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
75	<a href="#">c3o82A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide arylation enzyme; <b>PDBTitle:</b> structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
76	<a href="#">c5n81B</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrocidine synthase 1; <b>PDBTitle:</b> crystal structure of an engineered tyca variant in complex with an o-2 propargyl-beta-tyr-amp analog
77	<a href="#">c3wv4B</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> non-ribosomal peptide synthetase; <b>PDBTitle:</b> crystal structure of vinn
78	<a href="#">c4lncA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> bile acid-coenzyme a ligase;

78	<a href="#">c4gca</a>	Alignment	not modelled	100.0	19	<b>PDBTitle:</b> crystal structure of a bile acid-coenzyme a ligase (baib) from2 clostridium scindens (vpi 12708) at 2.19 a resolution <b>PDB header:</b> ligase
79	<a href="#">c3ivrA</a>	Alignment	not modelled	100.0	22	<b>Chain:</b> A; <b>PDB Molecule:</b> putative long-chain-fatty-acid coa ligase; <b>PDBTitle:</b> crystal structure of putative long-chain-fatty-acid coa ligase from2 rhodospseudomonas palustris cga009
80	<a href="#">c5oe3C</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> anthranilate--coa ligase; <b>PDBTitle:</b> crystal structure of the n-terminal domain of pqsa in complex with2 anthraniloyl-amp (crystal form 1)
81	<a href="#">c6abhG</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> luminescent protein <b>Chain:</b> G; <b>PDB Molecule:</b> red-bioluminescence eliciting luciferase; <b>PDBTitle:</b> structure of a natural red emitting luciferase from phrixothrix hirtus2 (p1 crystal form)
82	<a href="#">c3t5cA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> probable chain-fatty-acid-coa ligase fadd13; <b>PDBTitle:</b> crystal structure of n-terminal domain of facl13 from mycobacterium2 tuberculosis in different space group c2
83	<a href="#">c5burB</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> 2-succinylbenzoate--coa ligase; <b>PDBTitle:</b> o-succinylbenzoate coenzyme a synthetase (mene) from bacillus2 subtilis, in complex with atp and magnesium ion
84	<a href="#">c5jipC</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> nonribosomal peptide synthase; <b>PDBTitle:</b> crystal structure of cmis6
85	<a href="#">c2y4oA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> phenylacetate-coenzyme a ligase; <b>PDBTitle:</b> crystal structure of paak2 in complex with phenylacetyl adenylate
86	<a href="#">c2y27B</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> phenylacetate-coenzyme a ligase; <b>PDBTitle:</b> crystal structure of paak1 in complex with atp from burkholderia2 cenocepacia
87	<a href="#">c4gs5A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> acyl-coa synthetase (amp-forming)/amp-acid ligase ii-like <b>PDBTitle:</b> the crystal structure of acyl-coa synthetase (amp-forming)/amp-acid2 ligase ii-like protein from dyadobacter fermentans dsm 18053
88	<a href="#">c3govD</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> D; <b>PDB Molecule:</b> phenylacetate-coenzyme a ligase; <b>PDBTitle:</b> crystal structure of a hypothetical acyl-coa ligase (bt_0428) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
89	<a href="#">c3hguB</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B; <b>PDB Molecule:</b> ehpf; <b>PDBTitle:</b> structure of phenazine antibiotic biosynthesis protein
90	<a href="#">c3laxA</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> phenylacetate-coenzyme a ligase; <b>PDBTitle:</b> the crystal structure of a domain of phenylacetate-coenzyme2 a ligase from bacteroides vulgatus atcc 8482
91	<a href="#">c5kodA</a>	Alignment	not modelled	98.8	13	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> indole-3-acetic acid-amido synthetase gh3.5; <b>PDBTitle:</b> crystal structure of gh3.5 acyl acid amido synthetase from arabidopsis2 thaliana
92	<a href="#">c4eplA</a>	Alignment	not modelled	98.2	11	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> jasmonic acid-amido synthetase jar1; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana gh3.11 (jar1) in complex2 with ja-ile
93	<a href="#">c4b2gB</a>	Alignment	not modelled	98.1	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> gh3-1 auxin conjugating enzyme; <b>PDBTitle:</b> crystal structure of an indole-3-acetic acid amido synthase from vitis2 vinifera involved in auxin homeostasis
94	<a href="#">c4ewvB</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> 4-substituted benzoates-glutamate ligase gh3.12; <b>PDBTitle:</b> crystal structure of gh3.12 in complex with ampcpp
95	<a href="#">c6avhA</a>	Alignment	not modelled	96.9	14	<b>PDB header:</b> ligase, plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> gh3.15 acyl acid amido synthetase; <b>PDBTitle:</b> gh3.15 acyl acid amido synthetase
96	<a href="#">c4z1oB</a>	Alignment	not modelled	46.9	7	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> phosphoribosyltransferase; <b>PDBTitle:</b> hypoxanthine-guanine-xanthine phosphoribosyltransferase (hgxpirt) from2 sulfobolus solfataricus in complex with alpha-3 phosphoribosylpyrophosphoric acid (prpp) and magnesium
97	<a href="#">c2ps3A</a>	Alignment	not modelled	34.9	11	<b>PDB header:</b> metal transport <b>Chain:</b> A; <b>PDB Molecule:</b> high-affinity zinc uptake system protein znua; <b>PDBTitle:</b> structure and metal binding properties of znua, a periplasmic zinc2 transporter from escherichia coli
98	<a href="#">c3hjtB</a>	Alignment	not modelled	31.5	6	<b>PDB header:</b> cell adhesion, transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> lmb; <b>PDBTitle:</b> structure of laminin binding protein (lmb) of streptococcus agalactiae2 a bifunctional protein with adhesin and metal transporting activity
99	<a href="#">c3pc3A</a>	Alignment	not modelled	29.7	13	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> cg1753, isoform a; <b>PDBTitle:</b> full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
100	<a href="#">c5u18A</a>	Alignment	not modelled	29.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> n-3" methyltransferase; <b>PDBTitle:</b> crystal structure of a methyltransferase involved in the biosynthesis2 of gentamicin in complex with the geneticin
101	<a href="#">c4trbA</a>	Alignment	not modelled	29.2	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> purine phosphoribosyltransferase (gpt-1); <b>PDBTitle:</b> sulfobolus solfataricus adenine phosphoribosyltransferase
						<b>PDB header:</b> transferase

102	<a href="#">c4lmaA_</a>	Alignment	not modelled	27.9	11	<b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure analysis of o-acetylserine sulfhydrylase cysk1 from2 microcystis aeruginosa 7806
103	<a href="#">c4oxqB_</a>	Alignment	not modelled	27.2	10	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> manganese abc transporter, periplasmic-binding protein <b>PDBTitle:</b> structure of staphylococcus pseudintermedius metal-binding protein2 sita in complex with zinc
104	<a href="#">c4aecB_</a>	Alignment	not modelled	26.1	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine synthase, mitochondrial; <b>PDBTitle:</b> crystal structure of the arabidopsis thaliana o-acetylserine-(thiol)-2 lyase c
105	<a href="#">c5uyvA_</a>	Alignment	not modelled	25.6	16	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic chelated iron-binding protein yfea; <b>PDBTitle:</b> yfea ancillary sites that do not co-load with site 2