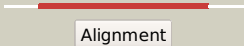

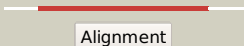

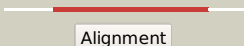







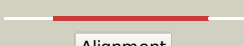











# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD1549\_(fadD11.1)\_1753516\_1754043  
 Date Fri Aug 2 13:30:13 BST 2019  
 Unique Job ID 017af75dd27f9357

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5es8A_</a>	 Alignment		100.0	15	<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
2	<a href="#">c4gr5B_</a>	 Alignment		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
3	<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
4	<a href="#">c5u89A_</a>	 Alignment		100.0	17	<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="#">d1l1cia_</a>	 Alignment		100.0	15	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
6	<a href="#">c4ir7A_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> long chain fatty acid coa ligase fadd10; <b>PDBTitle:</b> crystal structure of mtb fadd10 in complex with dodecanoyl-amp
7	<a href="#">c3r44A_</a>	 Alignment		100.0	28	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acyl coa synthetase fadd13 (fatty-acyl-coa <b>PDBTitle:</b> mycobacterium tuberculosis fatty acyl coa synthetase
8	<a href="#">c5ifiA_</a>	 Alignment		100.0	21	<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
9	<a href="#">c6ijbA_</a>	 Alignment		100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> amp-binding domain protein; <b>PDBTitle:</b> structure of 3-methylmercaptopropionate coa ligase mutant k523a in2 complex with amp and mmpa
10	<a href="#">c3etcB_</a>	 Alignment		100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> amp-binding protein; <b>PDBTitle:</b> 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298
11	<a href="#">c5keiA_</a>	 Alignment		100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-dihydroxybenzoate-amp ligase; <b>PDBTitle:</b> mycobacterium smegmatis mbta apo structure

12	<a href="#">d1amua_</a>	Alignment		100.0	15	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
13	<a href="#">c3t5cA_</a>	Alignment		100.0	28	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> probable chain-fatty-acid-coa ligase fad13; <b>PDBTitle:</b> crystal structure of n-terminal domain of fac13 from mycobacterium2 tuberculosis in different space group c2
14	<a href="#">c4eatB_</a>	Alignment		100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> benzoate-coenzyme a ligase; <b>PDBTitle:</b> crystal structure of a benzoate coenzyme a ligase
15	<a href="#">d1ry2a_</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
16	<a href="#">c4d56A_</a>	Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> apnaa1; <b>PDBTitle:</b> understanding bi-specificity of a-domains
17	<a href="#">c3tsyA_</a>	Alignment		100.0	21	<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
18	<a href="#">c1amuB_</a>	Alignment		100.0	17	<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
19	<a href="#">c6eqoB_</a>	Alignment		99.9	26	<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
20	<a href="#">c3o82B_</a>	Alignment		99.9	15	<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
21	<a href="#">c3wv4B_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> non-ribosomal peptide synthetase; <b>PDBTitle:</b> crystal structure of vinn
22	<a href="#">d1v25a_</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
23	<a href="#">d1mdba_</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
24	<a href="#">d3cw9a1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
25	<a href="#">c5n81B_</a>	Alignment	not modelled	99.9	20	<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
26	<a href="#">d1pg4a_</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
27	<a href="#">c4w8oA_</a>	Alignment	not modelled	99.9	14	<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
28	<a href="#">c5wm7A_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> salicylate-amp ligase; <b>PDBTitle:</b> crystal structure of cahj in complex with amp
29	<a href="#">c2v7hB_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> benzoate-coenzyme a ligase;

29	<a href="#">c2v7bB</a>	Alignment	not modelled	99.9	17	<b>PDBTitle:</b> crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400 <b>PDB header:</b> ligase
30	<a href="#">c3ivrA</a>	Alignment	not modelled	99.9	27	<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
31	<a href="#">c4wd1A</a>	Alignment	not modelled	99.9	24	<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
32	<a href="#">c5e7qB</a>	Alignment	not modelled	99.9	23	<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
33	<a href="#">c3o82A</a>	Alignment	not modelled	99.9	15	<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
34	<a href="#">c3ni2A</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-coumarate:coa ligase; <b>PDBTitle:</b> crystal structures and enzymatic mechanisms of a populus tomentosa 4-2 coumarate:coa ligase
35	<a href="#">c5aplA</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylation domain; <b>PDBTitle:</b> structure of the adenylation domain thr1 involved in the biosynthesis2 of 4-chlorothreonine in streptomyces sp. oh-5093, apo structure
36	<a href="#">c4wv3A</a>	Alignment	not modelled	99.9	24	<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
37	<a href="#">c6h1bA</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid coa ligase; <b>PDBTitle:</b> structure of amide bond synthetase mcba k483a mutant from2 marinactinospora thermotolerans
38	<a href="#">c6abhG</a>	Alignment	not modelled	99.9	12	<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)
39	<a href="#">c3rg2H</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> ligase <b>Chain:</b> H: <b>PDB Molecule:</b> enterobactin synthase component e (ente), 2,3-dihydro-2,3- <b>PDBTitle:</b> structure of a two-domain nrps fusion protein containing the ente2 adenylation domain and entb aryl-carrier protein from enterobactin3 biosynthesis
40	<a href="#">c4dg8A</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pa1221; <b>PDBTitle:</b> structure of pa1221, an nrps protein containing adenylation and pcp2 domains
41	<a href="#">c2d1tA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> luciferin 4-monooxygenase; <b>PDBTitle:</b> crystal structure of the thermostable japanese firefly2 luciferase red-color emission s286n mutant complexed with3 high-energy intermediate analogue
42	<a href="#">c5msdA</a>	Alignment	not modelled	99.9	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
43	<a href="#">c3l8cA</a>	Alignment	not modelled	99.9	14	<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
44	<a href="#">c4r0mA</a>	Alignment	not modelled	99.9	13	<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
45	<a href="#">c5ie2A</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> oxalate--coa ligase; <b>PDBTitle:</b> crystal structure of a plant enzyme
46	<a href="#">c5jipB</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nonribosomal peptide synthase; <b>PDBTitle:</b> crystal structure of cmis6
47	<a href="#">c3dhvA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> ligase <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
48	<a href="#">c4dg9A</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> ligase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> pa1221; <b>PDBTitle:</b> structure of holo-pa1221, an nrps protein containing adenylation and2 pcp domains bound to vinylsulfonamide inhibitor
49	<a href="#">c6akdA</a>	Alignment	not modelled	99.9	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
50	<a href="#">c3qyaA</a>	Alignment	not modelled	99.9	16	<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
51	<a href="#">c3g7sA</a>	Alignment	not modelled	99.9	12	<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
52	<a href="#">c5buqA</a>	Alignment	not modelled	99.9	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
53	<a href="#">c3vngA</a>	Alignment	not modelled	99.9	24	<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

54	<a href="#">c6ac3B_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> luminescent protein <b>Chain:</b> B: <b>PDB Molecule:</b> red-bioluminescence eliciting luciferase; <b>PDBTitle:</b> structure of a natural red emitting luciferase from phrixothrix hirtus2 (p3121 crystal form)
55	<a href="#">c5mstA_</a>	Alignment	not modelled	99.9	18	<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) from2 segniliparus rugosus in complex with amp and a co-purified carboxylic3 acid
56	<a href="#">c4oxiA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> enterobactin synthetase component f-related protein; <b>PDBTitle:</b> crystal structure of vibrio cholerae adenylation domain alme in2 complex with glycy-adenosine-5'-phosphate
57	<a href="#">c5jqjB_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> amp-dependent synthetase and ligase; <b>PDBTitle:</b> crystal structure of idn1
58	<a href="#">c3eynB_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coenzyme a synthetase acsm2a; <b>PDBTitle:</b> crystal structure of human acyl-coa synthetase medium-chain2 family member 2a (l64p mutation) in a complex with coa
59	<a href="#">c3gqwB_</a>	Alignment	not modelled	99.9	15	<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
60	<a href="#">c3iteB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> sidn siderophore synthetase; <b>PDBTitle:</b> the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
61	<a href="#">c3kxwA_</a>	Alignment	not modelled	99.9	16	<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
62	<a href="#">c5jipC_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> nonribosomal peptide synthase; <b>PDBTitle:</b> crystal structure of cmis6
63	<a href="#">c3e7wA_</a>	Alignment	not modelled	99.9	16	<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
64	<a href="#">c5x8gA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-succinylbenzoate--coa ligase; <b>PDBTitle:</b> binary complex structure of a double mutant i454ra456k of o-2 succinylbenzoate coa synthetase (mene) from bacillus subtilis bound3 with its product analogue osb-ncoa at 1.90 angstrom
65	<a href="#">c5ja2A_</a>	Alignment	not modelled	99.9	18	<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
66	<a href="#">c5mssA_</a>	Alignment	not modelled	99.9	17	<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
67	<a href="#">c2vsqA_</a>	Alignment	not modelled	99.9	18	<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
68	<a href="#">c6ozvA_</a>	Alignment	not modelled	99.9	24	<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
69	<a href="#">c5ey8D_</a>	Alignment	not modelled	99.9	22	<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
70	<a href="#">c4fuqD_</a>	Alignment	not modelled	99.9	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
71	<a href="#">c6p1jA_</a>	Alignment	not modelled	99.9	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
72	<a href="#">c5gxdA_</a>	Alignment	not modelled	99.9	19	<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 dfi2 12
73	<a href="#">c5oe3C_</a>	Alignment	not modelled	99.9	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)
74	<a href="#">c6n8eA_</a>	Alignment	not modelled	99.9	21	<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
75	<a href="#">c5burB_</a>	Alignment	not modelled	99.9	21	<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
76	<a href="#">c5c5hA_</a>	Alignment	not modelled	99.9	23	<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
77	<a href="#">c4r0mB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> mcgy protein; <b>PDBTitle:</b> structure of mcgy a-pcp complexed with phenylalanyl-

						adenylate
78	<a href="#">c4lqcA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> bile acid-coenzyme a ligase; <b>PDBTitle:</b> crystal structure of a bile acid-coenzyme a ligase (baib) from2 clostridium scindens (vpi 12708) at 2.19 a resolution
79	<a href="#">c5u2aA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> amp-dependent synthetase and ligase; <b>PDBTitle:</b> crystal structure of brucella canis acyl-coa synthetase
80	<a href="#">c3ip1B</a>	Alignment	not modelled	99.9	15	<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
81	<a href="#">c3e53A</a>	Alignment	not modelled	99.9	21	<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
82	<a href="#">c4zxiA</a>	Alignment	not modelled	99.9	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
83	<a href="#">c4zxiA</a>	Alignment	not modelled	99.9	20	<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
84	<a href="#">c3nyrA</a>	Alignment	not modelled	99.9	16	<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
85	<a href="#">c3qovD</a>	Alignment	not modelled	96.6	14	<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
86	<a href="#">c2y27B</a>	Alignment	not modelled	94.9	19	<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="#">c2y4oA</a>	Alignment	not modelled	92.1	15	<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
88	<a href="#">c3hguB</a>	Alignment	not modelled	64.4	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> ehpf; <b>PDBTitle:</b> structure of phenazine antibiotic biosynthesis protein
89	<a href="#">c4k2bA</a>	Alignment	not modelled	59.7	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ntd biosynthesis operon protein ntda; <b>PDBTitle:</b> crystal structure of ntda from bacillus subtilis in complex with the2 internal aldimine
90	<a href="#">d2ayia1</a>	Alignment	not modelled	58.9	19	<b>Fold:</b> Thermophilic metalloprotease-like <b>Superfamily:</b> Thermophilic metalloprotease-like <b>Family:</b> Thermophilic metalloprotease (M29)
91	<a href="#">c4z1oB</a>	Alignment	not modelled	57.8	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosyltransferase; <b>PDBTitle:</b> hypoxanthine-guanine-xanthine phosphoribosyltransferase (hgxpvt) from2 sulfobolus solfataricus in complex with alpha-3 phosphoribosylpyrophosphoric acid (prpp) and magnesium
92	<a href="#">c4trbA</a>	Alignment	not modelled	56.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine phosphoribosyltransferase (gpt-1); <b>PDBTitle:</b> sulfobolus solfataricus adenine phosphoribosyltransferase
93	<a href="#">c3smaD</a>	Alignment	not modelled	52.9	27	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> frbf; <b>PDBTitle:</b> a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
94	<a href="#">c2zy3A</a>	Alignment	not modelled	48.7	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate beta-decarboxylase; <b>PDBTitle:</b> dodecameric l-aspartate beta-decarboxylase
95	<a href="#">c4icqB</a>	Alignment	not modelled	48.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> aminopeptidase peps; <b>PDBTitle:</b> structural basis for substrate recognition and reaction mechanism of2 bacterial aminopeptidase peps
96	<a href="#">c5ht0B</a>	Alignment	not modelled	45.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside acetyltransferase hmb0005; <b>PDBTitle:</b> crystal structure of an antibiotic_nat family aminoglycoside2 acetyltransferase hmb0038 from an uncultured soil metagenomic sample3 in complex with coenzyme a
97	<a href="#">c1l9xA</a>	Alignment	not modelled	44.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyl hydrolase; <b>PDBTitle:</b> structure of gamma-glutamyl hydrolase
98	<a href="#">d1l9xa</a>	Alignment	not modelled	44.9	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
99	<a href="#">d1nula</a>	Alignment	not modelled	42.6	17	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
100	<a href="#">c5vogA</a>	Alignment	not modelled	41.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of a hypothetical protein from neisseria gonorrhoeae2 with bound pppp
101	<a href="#">c6mb6A</a>	Alignment	not modelled	39.9	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aac(3)-iiib protein; <b>PDBTitle:</b> aac-iiib binary with coash
102	<a href="#">c4h1hB</a>	Alignment	not modelled	39.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lmo1638 protein; <b>PDBTitle:</b> crystal structure of mccf homolog from listeria monocytogenes egd-e



103	<a href="#">c5f1yA_</a>	Alignment	not modelled	37.7	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mccc family protein; <b>PDBTitle:</b> crystal structure of ba3275, the member of s66 family of serine2 peptidases
104	<a href="#">d1a9xa4</a>	Alignment	not modelled	37.7	19	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
105	<a href="#">d1e3ja2</a>	Alignment	not modelled	37.5	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
106	<a href="#">c3tlgB_</a>	Alignment	not modelled	37.4	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mcclf; <b>PDBTitle:</b> microcin c7 self immunity protein mcclf in the inactive mutant apo2 state
107	<a href="#">d1jvba2</a>	Alignment	not modelled	34.9	9	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
108	<a href="#">c4e5sC_</a>	Alignment	not modelled	33.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> mcclike protein (ba_5613); <b>PDBTitle:</b> crystal structure of mcclike protein (ba_5613) from bacillus2 anthracis str. ames
109	<a href="#">c3e4fB_</a>	Alignment	not modelled	33.7	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside n3-acetyltransferase; <b>PDBTitle:</b> crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
110	<a href="#">d2nyga1</a>	Alignment	not modelled	32.8	18	<b>Fold:</b> TTHA0583/YokD-like <b>Superfamily:</b> TTHA0583/YokD-like <b>Family:</b> Aminoglycoside 3-N-acetyltransferase-like
111	<a href="#">d1pl8a2</a>	Alignment	not modelled	32.0	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
112	<a href="#">d1ja1a1</a>	Alignment	not modelled	31.7	19	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> NADPH-cytochrome p450 reductase FAD-binding domain-like
113	<a href="#">c2zy4F_</a>	Alignment	not modelled	31.6	16	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> l-aspartate beta-decarboxylase; <b>PDBTitle:</b> dodecameric l-aspartate beta-decarboxylase
114	<a href="#">c2jkbB_</a>	Alignment	not modelled	30.8	3	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypoxanthine-guanine phosphoribosyltransferase; <b>PDBTitle:</b> saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'-3 monophosphate) (orthorhombic crystal form)
115	<a href="#">c2dkjB_</a>	Alignment	not modelled	30.6	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of t.th.hb8 serine hydroxymethyltransferase
116	<a href="#">c3hjtB_</a>	Alignment	not modelled	30.5	10	<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
117	<a href="#">d1piwa2</a>	Alignment	not modelled	30.4	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
118	<a href="#">c6bc3A_</a>	Alignment	not modelled	30.0	25	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> aac 3-vi protein; <b>PDBTitle:</b> cryo x-ray structure of sisomicin bound aac-via
119	<a href="#">c5uyvA_</a>	Alignment	not modelled	29.8	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
120	<a href="#">c1pzmB_</a>	Alignment	not modelled	29.6	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypoxanthine-guanine phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp