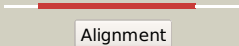



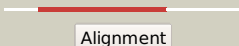

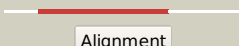

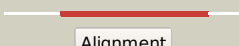

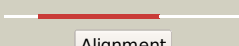

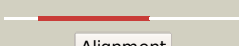










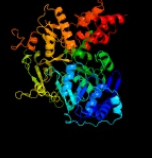

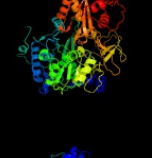
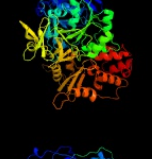
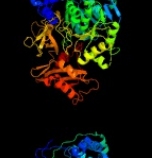
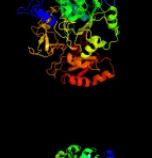

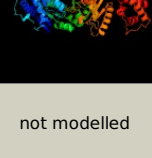


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2380c_(mbtE)_2662077_2667125
Date	Mon Aug 5 13:25:53 BST 2019
Unique Job ID	7b0c56b413b914a6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6n8eA_</a>	 Alignment		100.0	24	<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
2	<a href="#">c5ja2A_</a>	 Alignment		100.0	26	<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
3	<a href="#">c2vsqA_</a>	 Alignment		100.0	25	<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
4	<a href="#">c4zxiA_</a>	 Alignment		100.0	25	<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
5	<a href="#">c5u89A_</a>	 Alignment		100.0	37	<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
6	<a href="#">c4zxiA_</a>	 Alignment		100.0	28	<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
7	<a href="#">c6p1jA_</a>	 Alignment		100.0	33	<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
8	<a href="#">c6ozvA_</a>	 Alignment		100.0	33	<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
9	<a href="#">c5es8A_</a>	 Alignment		100.0	30	<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
10	<a href="#">c6eqoB_</a>	 Alignment		100.0	17	<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 adenylyate ester
11	<a href="#">c5wmmA_</a>	 Alignment		100.0	26	<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="#">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
13	<a href="#">c5mssA</a>	Alignment		100.0	23	<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
14	<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
15	<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 dfi2 12
16	<a href="#">c4dg9A</a>	Alignment		100.0	27	<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 and 2 pcp domains bound to vinylsulfonamide inhibitor
17	<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
18	<a href="#">d1ry2a</a>	Alignment		100.0	21	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
19	<a href="#">c3rg2H</a>	Alignment		100.0	22	<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
20	<a href="#">c4r0mA</a>	Alignment		100.0	20	<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
21	<a href="#">c5msdA</a>	Alignment	not modelled	100.0	24	<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) from 2 nocardia iowensis in complex with amp and benzoic acid
22	<a href="#">c3tsyA</a>	Alignment	not modelled	100.0	19	<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
23	<a href="#">c3e7wA</a>	Alignment	not modelled	100.0	27	<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 of 2 non-ribosomal peptide synthetase (nrps) adenylation domains
24	<a href="#">c5mstA</a>	Alignment	not modelled	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 domain of carboxylic acid reductase (car) from 2 segniliparus rugosus in complex with amp and a co-purified carboxylic acid
25	<a href="#">c3vngA</a>	Alignment	not modelled	100.0	32	<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 from 2 streptomyces
26	<a href="#">c2jgpA</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrocidine synthetase 3; <b>PDBTitle:</b> structure of the tycc5-6 pcp-c bidomain of the tyrocidine synthetase2 tycc
27	<a href="#">d3cw9a1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like <b>PDB header:</b> ligase

28	<a href="#">c4gr5B_</a>	Alignment	not modelled	100.0	31	<b>Chain:</b> B: <b>PDB Molecule:</b> non-ribosomal peptide synthetase; <b>PDBTitle:</b> crystal structure of slgn1deltaasub in complex with ampcpp
29	<a href="#">c5x8gA_</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> 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
30	<a href="#">d1mdba_</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
31	<a href="#">c5ie2A_</a>	Alignment	not modelled	100.0	22	<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
32	<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
33	<a href="#">c3etcB_</a>	Alignment	not modelled	100.0	20	<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
34	<a href="#">c4dg8A_</a>	Alignment	not modelled	100.0	25	<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
35	<a href="#">c5ey8D_</a>	Alignment	not modelled	100.0	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
36	<a href="#">d1amua_</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
37	<a href="#">c4eatB_</a>	Alignment	not modelled	100.0	24	<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
38	<a href="#">c1amuB_</a>	Alignment	not modelled	100.0	32	<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
39	<a href="#">c3ni2A_</a>	Alignment	not modelled	100.0	22	<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
40	<a href="#">c5wm7A_</a>	Alignment	not modelled	100.0	25	<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
41	<a href="#">c3iteB_</a>	Alignment	not modelled	100.0	29	<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 peptide synthetase
42	<a href="#">c3kxwA_</a>	Alignment	not modelled	100.0	19	<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
43	<a href="#">c5aplA_</a>	Alignment	not modelled	100.0	34	<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
44	<a href="#">c4oxiA_</a>	Alignment	not modelled	100.0	20	<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
45	<a href="#">c6h1bA_</a>	Alignment	not modelled	100.0	23	<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
46	<a href="#">c3gqwB_</a>	Alignment	not modelled	100.0	20	<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
47	<a href="#">c4ir7A_</a>	Alignment	not modelled	100.0	22	<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
48	<a href="#">c3r44A_</a>	Alignment	not modelled	100.0	22	<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
49	<a href="#">c4d56A_</a>	Alignment	not modelled	100.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> apnaa1; <b>PDBTitle:</b> understanding bi-specificity of a-domains
50	<a href="#">c5u2aA_</a>	Alignment	not modelled	100.0	23	<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
51	<a href="#">c4r0mB_</a>	Alignment	not modelled	100.0	18	<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
52	<a href="#">c3eynB_</a>	Alignment	not modelled	100.0	21	<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
53	<a href="#">c5keiA_</a>	Alianment	not modelled	100.0	22	<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
54	<a href="#">c5jqbB</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> amp-dependent synthetase and ligase; <b>PDBTitle:</b> crystal structure of idn11
55	<a href="#">c6ac3B</a>	Alignment	not modelled	100.0	19	<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)
56	<a href="#">c2v7bB</a>	Alignment	not modelled	100.0	21	<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
57	<a href="#">c6ijbA</a>	Alignment	not modelled	100.0	18	<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
58	<a href="#">c2d1tA</a>	Alignment	not modelled	100.0	19	<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
59	<a href="#">c3dhvA</a>	Alignment	not modelled	100.0	27	<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
60	<a href="#">c4fuqD</a>	Alignment	not modelled	100.0	21	<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 rhodospseudomonas palustris
61	<a href="#">c5e7qB</a>	Alignment	not modelled	100.0	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
62	<a href="#">c3l8cA</a>	Alignment	not modelled	100.0	24	<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
63	<a href="#">c6akdA</a>	Alignment	not modelled	100.0	28	<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
64	<a href="#">c5buqA</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> unliganded form of o-succinylbenzoate coenzyme a synthetase (mene)2 from bacillus subtilis, solved at 1.98 angstroms
65	<a href="#">d1v25a</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
66	<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
67	<a href="#">c3nyrA</a>	Alignment	not modelled	100.0	26	<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
68	<a href="#">c3g7sA</a>	Alignment	not modelled	100.0	19	<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
69	<a href="#">d1l1cia</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
70	<a href="#">c5t81A</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> epob; <b>PDBTitle:</b> rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium celluloseum
71	<a href="#">c5c5hA</a>	Alignment	not modelled	100.0	20	<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
72	<a href="#">c4tx3B</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide synthetase, module 7; <b>PDBTitle:</b> complex of the x-domain and oxyb from teicoplanin biosynthesis
73	<a href="#">c6m7lB</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative non-ribosomal peptide synthetase; <b>PDBTitle:</b> complex of oxa with the x-domain from gpa biosynthesis
74	<a href="#">c6cgoB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> condensation domain protein; <b>PDBTitle:</b> molecular basis for condensation domain-mediated chain release from2 the enacyloxin polyketide synthase
75	<a href="#">c5jipB</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nonribosomal peptide synthase; <b>PDBTitle:</b> crystal structure of cmis6
76	<a href="#">c5n81B</a>	Alignment	not modelled	100.0	33	<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="#">c6ad3A</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> lovastatin nonaketide synthase moka; <b>PDBTitle:</b> structural characterization of the condensation domain from monacolin2 k polyketide synthase moka
78	<a href="#">c5t3eA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> bacillamide synthetase heterocyclization domain; <b>PDBTitle:</b> crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain. <b>PDB header:</b> transferase

79	<a href="#">c6aefB_</a>	Alignment	not modelled	100.0	14	<b>Chain:</b> B: <b>PDB Molecule:</b> polyketide synthase associated protein papa2; <b>PDBTitle:</b> papa2 acyl transferase
80	<a href="#">c4znmB_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> c-domain type ii peptide synthetase; <b>PDBTitle:</b> crystal structure of sgcc5 protein from streptomyces globisporus (apo2 form)
81	<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
82	<a href="#">c4jn3B_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> cda peptide synthetase i; <b>PDBTitle:</b> crystal structures of the first condensation domain of the cda2 synthetase
83	<a href="#">c3o82B_</a>	Alignment	not modelled	100.0	21	<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
84	<a href="#">c5m6pB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrocidine synthase 2; <b>PDBTitle:</b> crystal structure of the epimerization domain from module 3 of2 tyrocidine synthetase b, tycb3(e)
85	<a href="#">c2xhgA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrocidine synthetase a; <b>PDBTitle:</b> crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis
86	<a href="#">c4lqcA_</a>	Alignment	not modelled	100.0	18	<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
87	<a href="#">c1l5aA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> amide synthase; <b>PDBTitle:</b> crystal structure of vibh, an nrps condensation enzyme
88	<a href="#">c3wv4B_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> non-ribosomal peptide synthetase; <b>PDBTitle:</b> crystal structure of vinn
89	<a href="#">c3o82A_</a>	Alignment	not modelled	100.0	21	<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
90	<a href="#">c3qyaA_</a>	Alignment	not modelled	100.0	20	<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
91	<a href="#">c3ivrA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase <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 rhodopseudomonas palustris cga009
92	<a href="#">c5burB_</a>	Alignment	not modelled	100.0	19	<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
93	<a href="#">c3e53A_</a>	Alignment	not modelled	100.0	20	<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
94	<a href="#">c5oe3C_</a>	Alignment	not modelled	100.0	19	<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)
95	<a href="#">c5dijA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tqaa; <b>PDBTitle:</b> the crystal structure of ct
96	<a href="#">c5jipC_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> nonribosomal peptide synthase; <b>PDBTitle:</b> crystal structure of cmis6
97	<a href="#">c3t5cA_</a>	Alignment	not modelled	100.0	23	<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
98	<a href="#">c6abhG_</a>	Alignment	not modelled	100.0	19	<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)
99	<a href="#">c4hvmC_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> tlmii; <b>PDBTitle:</b> crystal structure of tallysomycin biosynthesis protein tlmii
100	<a href="#">c2y4oA_</a>	Alignment	not modelled	100.0	16	<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
101	<a href="#">c2y27B_</a>	Alignment	not modelled	100.0	18	<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
102	<a href="#">c4gs5A_</a>	Alignment	not modelled	100.0	21	<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
103	<a href="#">c3fotA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 15-o-acetyltransferase; <b>PDBTitle:</b> structural and functional characterization of tri3 trichothecene 15-o-2 acetyltransferase from fusarium

						sporotrichioides
104	<a href="#">c3qovD</a>	Alignment	not modelled	100.0	17	<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
105	<a href="#">c1q9jA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase associated protein 5; <b>PDBTitle:</b> structure of polyketide synthase associated protein 5 from2 mycobacterium tuberculosis
106	<a href="#">c6chjB</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> diacylglycerol o-acyltransferase; <b>PDBTitle:</b> wax ester synthase/diacylglycerol acyltransferase from marinobacter2 aquaeolei vt8
107	<a href="#">d1l5aa2</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
108	<a href="#">c3hguB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> ehpf; <b>PDBTitle:</b> structure of phenazine antibiotic biosynthesis protein
109	<a href="#">d1l5aa1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
110	<a href="#">c6dd2A</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable hydroxycinnamoyl transferase; <b>PDBTitle:</b> crystal structure of selaginella moellendorffii hct
111	<a href="#">c4g0bA</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxycinnamoyl-coa shikimate/quinate <b>PDBTitle:</b> structure of native hct from coffea canephora
112	<a href="#">d1q9ja1</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
113	<a href="#">d1q9ja2</a>	Alignment	not modelled	99.9	10	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
114	<a href="#">c2bghA</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> vinorine synthase; <b>PDBTitle:</b> crystal structure of vinorine synthase
115	<a href="#">c2e1uA</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl transferase; <b>PDBTitle:</b> crystal structure of dendranthema morifolium dmat
116	<a href="#">c2roqA</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> enterobactin synthetase component f; <b>PDBTitle:</b> solution structure of the thiolation-thioesterase di-domain2 of enterobactin synthetase component f
117	<a href="#">c5msvB</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioester reductase domain-containing protein; <b>PDBTitle:</b> structure of the phosphopantetheine modified pcp-r didomain of2 carboxylic acid reductase (car) in complex with nadp
118	<a href="#">c5u3hA</a>	Alignment	not modelled	99.6	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> hmwp2 nonribosomal peptide synthetase; <b>PDBTitle:</b> solution structure of apo pcp1 from yersiniabactin synthetase
119	<a href="#">c2cq8A</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 10-formyltetrahydrofolate dehydrogenase; <b>PDBTitle:</b> solution structure of rsgi ruh-033, a pp-binding domain of2 10-ftfhdh from human cdna
120	<a href="#">c2mr7A</a>	Alignment	not modelled	99.6	35	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-ribosomal peptide synthetase; <b>PDBTitle:</b> apo structure of the peptidyl carrier protein domain 7 of the2 teicoplanin producing non-ribosomal peptide synthetase