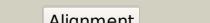
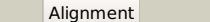
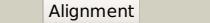
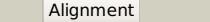
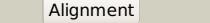
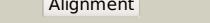
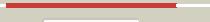


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD1521_(fadD25)_1712308_1714059
Date	Fri Aug 2 13:30:10 BST 2019
Unique Job ID	f0ec825ff83ce21f

Detailed template information

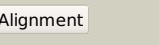
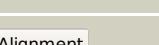
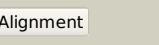
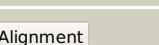
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6egoB_			100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coenzyme a synthetase; <b>PDBTitle:</b> tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nadp+ and phosphomethylphosphonic acid adenylate ester
2	c5es8A_			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	c6p1jA_			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	c5u89A_			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	c5gxdA_			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
6	d1pg4a_			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	c5ifiA_			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	c5msdA_			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) from nocardia iowensis in complex with amp and benzoic acid
9	d1ry2a_			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	c5ja2A_			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	c5wmma_			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="#">c2vsqA</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) from2 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="#">c4zxjA</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 of 2 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="#">c3vnqA</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 from 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
29	<a href="#">c3tsyA</a>	Alignment	not modelled	100.0	20	<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
30	<a href="#">c5ie2A</a>	Alignment	not modelled	100.0	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
31	<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 <i>populus tomentosa</i> 4-2 coumarate:coa ligase
32	<a href="#">c4dg9A</a>	Alignment	not modelled	100.0	17	<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
33	<a href="#">c5x8gA</a>	Alignment	not modelled	100.0	23	<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 <i>bacillus subtilis</i> bound3 with its product analogue osb-ncoa at 1.90 angstrom
34	<a href="#">c4eatB</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 structure of a benzoate coenzyme a ligase
35	<a href="#">c4oxiA</a>	Alignment	not modelled	100.0	16	<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 <i>vibrio cholerae</i> adenylation domain alme in2 complex with glycyl-adenosine-5'-phosphate
36	<a href="#">c5wm7A</a>	Alignment	not modelled	100.0	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
37	<a href="#">c4dg8A</a>	Alignment	not modelled	100.0	18	<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
38	<a href="#">c6ac3B</a>	Alignment	not modelled	100.0	17	<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 <i>phrixothrix hirtus2</i> (p3121 crystal form)
39	<a href="#">c3iteB</a>	Alignment	not modelled	100.0	15	<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
40	<a href="#">c4ir7A</a>	Alignment	not modelled	100.0	21	<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
41	<a href="#">c2d1tA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> luciferin 4-monoxygenase; <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="#">c3etcB</a>	Alignment	not modelled	100.0	17	<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 methanoscarcina2 acetivorans containing a link between lys256 and cys298
43	<a href="#">c3eynB</a>	Alignment	not modelled	100.0	18	<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
44	<a href="#">c6ijbA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> amp-binding domain protein; <b>PDBTitle:</b> structure of 3-methylmercaptoacetone coa ligase mutant k523a in2 complex with amp and mmpa
45	<a href="#">c5aplA</a>	Alignment	not modelled	100.0	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 <i>streptomyces</i> sp. oh-5093, apo structure
46	<a href="#">c3rg2H</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> H: <b>PDB Molecule:</b> enterobactin synthetase 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
47	<a href="#">c3r44A</a>	Alignment	not modelled	100.0	18	<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
48	<a href="#">c5u2aA</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 <i>brucella canis</i> acyl-coa synthetase
49	<a href="#">c5keiA</a>	Alignment	not modelled	100.0	21	<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
50	<a href="#">c4d56A</a>	Alignment	not modelled	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
51	<a href="#">c6h1bA</a>	Alignment	not modelled	100.0	21	<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 <i>marinactinospora thermotolerans</i>
52	<a href="#">c5jjqB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> amp-dependent synthetase and ligase; <b>PDBTitle:</b> crystal structure of idnl1
						<b>PDB header:</b> ligase

53	<a href="#">c3dhvA</a>	Alignment	not modelled	100.0	19	<b>Chain: A: 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: 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: A: 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: D: 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: 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: A: 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: 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="#">d1lcia</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: A: 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: A: 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: A: 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: A: 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: 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: 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: A: 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: A: 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: A: PDB Molecule:</b> luciferase-like enymeamp-coa-ligase; <b>PDBTitle:</b> structure of the luciferase-like enzyme from the nonluminescent2 zophobas morio mealworm
72	<a href="#">c5jjpB</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain: B: PDB Molecule:</b> nonribosomal peptide synthetase; <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: A: 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: 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: A: 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: 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: PDB Molecule:</b> non-ribosomal peptide synthetase; <b>PDBTitle:</b> crystal structure of vinn
78	<a href="#">c4lgaA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain: A: PDB Molecule:</b> bile acid-coenzyme a ligase;

78	<a href="#">c4ygaA</a>	Alignment	not modelled	100.0	19	<b>PDBTitle:</b> crystal structure of a bile acid-coenzyme a ligase (baib) from <i>clostridium scindens</i> (vpi 12708) at 2.19 a resolution <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 from <i>rhodopseudomonas palustris</i> cga009
79	<a href="#">c3ivrA</a>	Alignment	not modelled	100.0	22	<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 with 2 anthraniloyl-amp (crystal form 1)
80	<a href="#">c5oe3C</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> G: <b>PDB Molecule:</b> red-bioluminescence eliciting luciferase; <b>PDBTitle:</b> structure of a natural red emitting luciferase from <i>phrixothrix hirtus</i> 2 (p1 crystal form)
81	<a href="#">c6abhbG</a>	Alignment	not modelled	100.0	16	<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 <i>mycobacterium</i> 2 tuberculosis in different space group c2
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 <i>mycobacterium</i> 2 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> crystal structure of o-succinylbenzoate coenzyme a synthetase (mene) from <i>bacillus</i> 2 subtilis, in complex with atp and magnesium ion
84	<a href="#">c5jjpC</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> nonribosomal peptide synthetase; <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 <i>burkholderia</i> 2 <i>ceocepacia</i>
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-ds2 ligase ii-like protein from <i>dyadobacter fermentans</i> dsm 18053
88	<a href="#">c3gqvD</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) from <i>bacteroides thetaiotaomicron</i> 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 <i>bacteroides vulgatus</i> 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 <i>arabidopsis</i> 2 <i>thaliana</i>
92	<a href="#">c4ep1A</a>	Alignment	not modelled	98.2	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> jasmmonic acid-amido synthetase jar1; <b>PDBTitle:</b> crystal structure of <i>arabidopsis thaliana</i> gh3.11 (jar1) in complex2 with ja-ile
93	<a href="#">c4b2qB</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 synthetase from <i>vitis</i> 2 <i>vinifera</i> 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 (hxgrpx) from <i>sulfolobus solfataricus</i> in complex with alpha-3 phosphoribosylpyrophoric 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 znu; <b>PDBTitle:</b> structure and metal binding properties of znu, a periplasmic zinc2 transporter from <i>escherichia coli</i>
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> lm; <b>PDBTitle:</b> structure of laminin binding protein (lmb) of <i>streptococcus agalactiae</i> 2 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 <i>drosophila</i> 2 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> <i>sulfolobus solfataricus</i> adenine phosphoribosyltransferase

102	<a href="#">c4lmaA_</a>		Alignment	not modelled	27.9	11	<b>Chain: A: 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: 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: 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: A: PDB Molecule:</b> periplasmic chelated iron-binding protein yfea; <b>PDBTitle:</b> yfea ancillary sites that do not co-load with site 2