



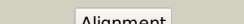
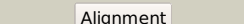
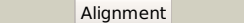
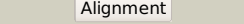
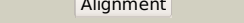
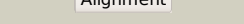
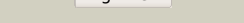











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1185c_(fadD21)_1325782_1327518
Date	Wed Jul 31 22:05:27 BST 2019
Unique Job ID	ef7372f2fae33e71

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6eqoB_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coenzyme a synthetase; <b>PDBTitle:</b> tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nadp+ and phosphomethylphosphonic acid adenylate ester
2	<a href="#">c5u89A_</a>	 Alignment		100.0	22	<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
3	<a href="#">c5es8A_</a>	 Alignment		100.0	21	<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
4	<a href="#">c5gxdA_</a>	 Alignment		100.0	17	<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
5	<a href="#">c6p1jA_</a>	 Alignment		100.0	24	<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
6	<a href="#">d1pg4a_</a>	 Alignment		100.0	17	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
7	<a href="#">c3kxwA_</a>	 Alignment		100.0	32	<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
8	<a href="#">c5ja2A_</a>	 Alignment		100.0	20	<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
9	<a href="#">c5msdA_</a>	 Alignment		100.0	19	<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
10	<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
11	<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

12	<a href="#">c2vsqA_</a>	Alignment		100.0	22	<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
13	<a href="#">d1ry2a_</a>	Alignment		100.0	19	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
14	<a href="#">c5wmmA_</a>	Alignment		100.0	22	<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
15	<a href="#">c4wd1A_</a>	Alignment		100.0	17	<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
16	<a href="#">c5mstA_</a>	Alignment		100.0	16	<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="#">c3gqwB_</a>	Alignment		100.0	27	<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
18	<a href="#">c4r0mB_</a>	Alignment		100.0	20	<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
19	<a href="#">c5mssA_</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-pcp didomain of carboxylic acid reductase (car)2 from segniliparus rugosus in complex with amp
20	<a href="#">c4zxiA_</a>	Alignment		100.0	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
21	<a href="#">c4zxiA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyrocidine synthetase 3; <b>PDBTitle:</b> crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine
22	<a href="#">c3e7wA_</a>	Alignment	not modelled	100.0	21	<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
23	<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
24	<a href="#">c4wv3A_</a>	Alignment	not modelled	100.0	17	<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
25	<a href="#">c3tsyA_</a>	Alignment	not modelled	100.0	18	<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
26	<a href="#">c3vngA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> nrps adenylation protein cytc1; <b>PDBTitle:</b> co-crystal structure of nrps adenylation protein cytc1 with atp from2 streptomyces
27	<a href="#">c5ie2A_</a>	Alignment	not modelled	100.0	20	<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
28	<a href="#">d1mdba_</a>	Alianment	not modelled	100.0	16	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like

					<b>Family:</b> Acetyl-CoA synthetase-like
29	<a href="#">d3cw9a1</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
30	<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
31	<a href="#">c4eatB</a>	Alignment	not modelled	100.0	20 <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
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 and2 pcp domains bound to vinylsulfonamide inhibitor
33	<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
34	<a href="#">c5wm7A</a>	Alignment	not modelled	100.0	18 <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
35	<a href="#">c5aplA</a>	Alignment	not modelled	100.0	20 <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="#">c3eynB</a>	Alignment	not modelled	100.0	17 <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
37	<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 vibrio cholerae adenylation domain alme in2 complex with glycyi-adenosine-5'-phosphate
38	<a href="#">c3rg2H</a>	Alignment	not modelled	100.0	14 <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
39	<a href="#">c6ac3B</a>	Alignment	not modelled	100.0	18 <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)
40	<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-methylmercaptopropionate coa ligase mutant k523a in2 complex with amp and mmpa
41	<a href="#">c4dg8A</a>	Alignment	not modelled	100.0	17 <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
42	<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
43	<a href="#">c3etcB</a>	Alignment	not modelled	100.0	15 <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
44	<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
45	<a href="#">c4ir7A</a>	Alignment	not modelled	100.0	19 <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
46	<a href="#">c5keiA</a>	Alignment	not modelled	100.0	18 <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
47	<a href="#">c5u2aA</a>	Alignment	not modelled	100.0	16 <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
48	<a href="#">c2d1tA</a>	Alignment	not modelled	100.0	18 <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
49	<a href="#">c6h1bA</a>	Alignment	not modelled	100.0	18 <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
50	<a href="#">d1amua</a>	Alignment	not modelled	100.0	16 <b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
51	<a href="#">c6ozvA</a>	Alignment	not modelled	100.0	25 <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
52	<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

53	<a href="#">c2v7bB</a>	Alignment	not modelled	100.0	18	<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
54	<a href="#">c3dhvA</a>	Alignment	not modelled	100.0	20	<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
55	<a href="#">c1amuB</a>	Alignment	not modelled	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
56	<a href="#">c5e7qB</a>	Alignment	not modelled	100.0	17	<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
57	<a href="#">c4fuqD</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> malonyl coa synthetase; <b>PDBTitle:</b> crystal structure of apo matb from rhodopseudomonas palustris
58	<a href="#">c5jjqB</a>	Alignment	not modelled	100.0	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 idn11
59	<a href="#">c3l8cA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--poly(phosphoribitol) ligase subunit 1; <b>PDBTitle:</b> structure of probable d-alanine--poly(phosphoribitol) ligase subunit-12 from streptococcus pyogenes
60	<a href="#">c6akdA</a>	Alignment	not modelled	100.0	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 idn17
61	<a href="#">d1lcia</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
62	<a href="#">c3g7sA</a>	Alignment	not modelled	100.0	16	<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
63	<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
64	<a href="#">c3nyrA</a>	Alignment	not modelled	100.0	21	<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
65	<a href="#">c5buqA</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> unliganded form of o-succinylbenzoate coenzyme a synthetase (mene)2 from bacillus subtilis, solved at 1.98 angstroms
66	<a href="#">c4gr5B</a>	Alignment	not modelled	100.0	22	<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
67	<a href="#">c3iplB</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> crystal structure of o-succinylbenzoic acid-coa ligase from2 staphylococcus aureus subsp. aureus mu50
68	<a href="#">c3e53A</a>	Alignment	not modelled	100.0	58	<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
69	<a href="#">c5c5hA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-succinylbenzoate--coa ligase; <b>PDBTitle:</b> r195k e. coli mene with bound osb-ams
70	<a href="#">c4w8oA</a>	Alignment	not modelled	100.0	18	<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
71	<a href="#">c5jipB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nonribosomal peptide synthase; <b>PDBTitle:</b> crystal structure of cmis6
72	<a href="#">c3qyaA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> luciferase; <b>PDBTitle:</b> crystal structure of a red-emitter mutant of lampyris turkestanicus2 luciferase
73	<a href="#">c3o82B</a>	Alignment	not modelled	100.0	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
74	<a href="#">c5n81B</a>	Alignment	not modelled	100.0	19	<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
75	<a href="#">c4lqcA</a>	Alignment	not modelled	100.0	15	<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
76	<a href="#">c3o82A</a>	Alignment	not modelled	100.0	17	<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
77	<a href="#">c3wv4B</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> non-ribosomal peptide synthetase; <b>PDBTitle:</b> crystal structure of vinn
78	<a href="#">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;

78	<a href="#">c3vra</a>	Alignment	not modelled	100.0	23	<b>PDBTitle:</b> crystal structure of putative long-chain-fatty-acid coa ligase from2 rhodospseudomonas palustris cga009 <b>PDB header:</b> ligase
79	<a href="#">c5oe3C</a>	Alignment	not modelled	100.0	20	<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)
80	<a href="#">c5burB</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> 2-succinylbenzoate--coa ligase; <b>PDBTitle:</b> o-succinylbenzoate coenzyme a synthetase (mene) from bacillus2 subtilis, in complex with atp and magnesium ion
81	<a href="#">c3t5cA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> probable chain-fatty-acid-coa ligase fadd13; <b>PDBTitle:</b> crystal structure of n-terminal domain of facl13 from mycobacterium2 tuberculosis in different space group c2
82	<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)
83	<a href="#">c5jipC</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> nonribosomal peptide synthase; <b>PDBTitle:</b> crystal structure of cmis6
84	<a href="#">c2y4oA</a>	Alignment	not modelled	100.0	17	<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
85	<a href="#">c3qovD</a>	Alignment	not modelled	100.0	15	<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	100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> phenylacetate-coenzyme a ligase; <b>PDBTitle:</b> crystal structure of paak1 in complex with atp from burkholderia2 cenocepacia
87	<a href="#">c4gs5A</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> acyl-coa synthetase (amp-forming)/amp-acid ligase ii-like <b>PDBTitle:</b> the crystal structure of acyl-coa synthetase (amp-forming)/amp-acid2 ligase ii-like protein from dyadobacter fermentans dsm 18053
88	<a href="#">c3hguB</a>	Alignment	not modelled	99.9	14	<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="#">c3laxA</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> phenylacetate-coenzyme a ligase; <b>PDBTitle:</b> the crystal structure of a domain of phenylacetate-coenzyme2 a ligase from bacteroides vulgatus atcc 8482
90	<a href="#">c5kodA</a>	Alignment	not modelled	98.8	12	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> indole-3-acetic acid-amido synthetase gh3.5; <b>PDBTitle:</b> crystal structure of gh3.5 acyl acid amido synthetase from arabidopsis2 thaliana
91	<a href="#">c4b2gB</a>	Alignment	not modelled	98.6	11	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> gh3-1 auxin conjugating enzyme; <b>PDBTitle:</b> crystal structure of an indole-3-acetic acid amido synthase from vitis2 vinifera involved in auxin homeostasis
92	<a href="#">c4eplA</a>	Alignment	not modelled	98.5	12	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> jasmonic acid-amido synthetase jar1; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana gh3.11 (jar1) in complex2 with ja-ile
93	<a href="#">c6avhA</a>	Alignment	not modelled	97.2	13	<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
94	<a href="#">c4ewvB</a>	Alignment	not modelled	96.4	12	<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="#">d2aya1</a>	Alignment	not modelled	67.8	12	<b>Fold:</b> Thermophilic metalloprotease-like <b>Superfamily:</b> Thermophilic metalloprotease-like <b>Family:</b> Thermophilic metalloprotease (M29)
96	<a href="#">c5f1yA</a>	Alignment	not modelled	54.3	22	<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
97	<a href="#">d1zja1</a>	Alignment	not modelled	48.4	10	<b>Fold:</b> Thermophilic metalloprotease-like <b>Superfamily:</b> Thermophilic metalloprotease-like <b>Family:</b> Thermophilic metalloprotease (M29)
98	<a href="#">c4je5C</a>	Alignment	not modelled	46.2	21	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> aromatic/aminoadipate aminotransferase 1; <b>PDBTitle:</b> crystal structure of the aromatic aminotransferase aro8, a putative2 alpha-aminoadipate aminotransferase in saccharomyces cerevisiae
99	<a href="#">c3vrhA</a>	Alignment	not modelled	45.1	13	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein ph0300; <b>PDBTitle:</b> crystal structure of ph0300
100	<a href="#">c5ghaC</a>	Alignment	not modelled	41.5	17	<b>PDB header:</b> transferase/transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> sulfur transferase ttua; <b>PDBTitle:</b> sulfur transferase ttua in complex with sulfur carrier ttub
101	<a href="#">c4icqB</a>	Alignment	not modelled	40.9	12	<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
102	<a href="#">c4oxqB</a>	Alignment	not modelled	38.0	10	<b>PDB header:</b> metal binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> manganese abc transporter, periplasmic-binding protein <b>PDBTitle:</b> structure of staphylococcus pseudintermedius metal-

						binding protein2 sita in complex with zinc
103	<a href="#">d1k92a1</a>	Alignment	not modelled	33.7	26	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
104	<a href="#">c5uyvA</a>	Alignment	not modelled	33.4	13	<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
105	<a href="#">d1xvla1</a>	Alignment	not modelled	33.3	11	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> TroA-like
106	<a href="#">c2jkzB</a>	Alignment	not modelled	32.0	9	<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)
107	<a href="#">c4z1oB</a>	Alignment	not modelled	32.0	9	<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
108	<a href="#">c3hjtB</a>	Alignment	not modelled	31.5	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
109	<a href="#">c2ps3A</a>	Alignment	not modelled	30.9	10	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> high-affinity zinc uptake system protein znua; <b>PDBTitle:</b> structure and metal binding properties of znua, a periplasmic zinc2 transporter from escherichia coli
110	<a href="#">d1pl8a2</a>	Alignment	not modelled	30.9	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
111	<a href="#">c3d6kB</a>	Alignment	not modelled	30.6	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative aminotransferase; <b>PDBTitle:</b> the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
112	<a href="#">c3bcxA</a>	Alignment	not modelled	26.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; <b>PDBTitle:</b> e1 dehydrase
113	<a href="#">c4xrvB</a>	Alignment	not modelled	26.7	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic solute binding protein; <b>PDBTitle:</b> structure of a zn abc transporter substrate binding protein from2 paracoccus denitrificans
114	<a href="#">d1ja1a1</a>	Alignment	not modelled	25.6	15	<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
115	<a href="#">c6hnuA</a>	Alignment	not modelled	24.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aromatic amino acid aminotransferase i; <b>PDBTitle:</b> crystal structure of the aminotransferase aro8 from c. albicans with2 ligands
116	<a href="#">d1f20a1</a>	Alignment	not modelled	22.5	11	<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
117	<a href="#">c3tlgB</a>	Alignment	not modelled	22.5	8	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mccf; <b>PDBTitle:</b> microcin c7 self immunity protein mccf in the inactive mutant apo2 state
118	<a href="#">c4k2bA</a>	Alignment	not modelled	21.9	12	<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
119	<a href="#">c3pplB</a>	Alignment	not modelled	21.7	7	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of an aspartate transaminase (ncgI0237, cgl0240)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.25 a3 resolution
120	<a href="#">c4j5uB</a>	Alignment	not modelled	21.6	7	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> x-ray crystal structure of a serine hydroxymethyltransferase with2 covalently bound plp from rickettsia rickettsii str. sheila smith