



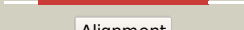

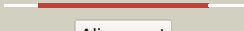









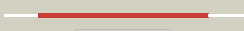







# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD2187\_(fadD15)\_2448168\_2449970  
 Date Mon Aug 5 13:25:31 BST 2019  
 Unique Job ID b9c8def0b95c04a7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5msdA_</a>	 Alignment		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) from2 nocardia iowensis in complex with amp and benzoic acid
2	<a href="#">c5mstA_</a>	 Alignment		100.0	22	<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
3	<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
4	<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
5	<a href="#">c5gxdA_</a>	 Alignment		100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> amp-dependent synthetase and ligase; <b>PDBTitle:</b> structure of acryloyl-coa lyase prpe from dinoroseobacter shibae df12 12
6	<a href="#">c5ifiA_</a>	 Alignment		100.0	19	<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
7	<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
8	<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
9	<a href="#">c6p1iA_</a>	 Alignment		100.0	22	<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
10	<a href="#">c4wd1A_</a>	 Alignment		100.0	23	<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
11	<a href="#">d1pg4a_</a>	 Alignment		100.0	18	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like

12	<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
13	<a href="#">c5ja2A_</a>	Alignment		100.0	19	<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
14	<a href="#">c6n8eA_</a>	Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> holo-obif1; <b>PDBTitle:</b> crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
15	<a href="#">c2vsqA_</a>	Alignment		100.0	24	<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="#">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
17	<a href="#">d1mdba_</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
18	<a href="#">c5ie2A_</a>	Alignment		100.0	23	<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
19	<a href="#">c4zxiA_</a>	Alignment		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
20	<a href="#">d3cw9a1</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
21	<a href="#">c4wv3A_</a>	Alignment	not modelled	100.0	21	<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
22	<a href="#">c3e7wA_</a>	Alignment	not modelled	100.0	19	<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="#">c4eatB_</a>	Alignment	not modelled	100.0	23	<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
24	<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
25	<a href="#">c3vnqA_</a>	Alignment	not modelled	100.0	23	<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
26	<a href="#">c4zxiA_</a>	Alignment	not modelled	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
27	<a href="#">c5x8gA_</a>	Alignment	not modelled	100.0	25	<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
						<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> amp-binding protein;

28	<a href="#">c3etcB_</a>	Alignment	not modelled	100.0	21	<b>PDBTitle:</b> 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298 <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
29	<a href="#">c3gqwB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein 4-coumarate--coa ligase 1, resveratrol <b>PDBTitle:</b> 4-coumaroyl-coa ligase::stilbene synthase fusion protein
30	<a href="#">c3tsyA_</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
31	<a href="#">c3r44A_</a>	Alignment	not modelled	100.0	24	<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
32	<a href="#">c5wm7A_</a>	Alignment	not modelled	100.0	24	<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
33	<a href="#">c6ijbA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-coumarate:coa ligase; <b>PDBTitle:</b> crystal structures and enzymatic mechanisms of a populus tomentosa 4-2 coumarate:coa ligase
34	<a href="#">c3ni2A_</a>	Alignment	not modelled	100.0	27	<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
35	<a href="#">c5ey8D_</a>	Alignment	not modelled	100.0	22	<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
36	<a href="#">c3kxwA_</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
37	<a href="#">c2d1tA_</a>	Alignment	not modelled	100.0	27	<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)
38	<a href="#">c6ac3B_</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 marinactinospora thermotolerans
39	<a href="#">c6h1bA_</a>	Alignment	not modelled	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
40	<a href="#">c3rg2H_</a>	Alignment	not modelled	100.0	18	<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="#">c4ir7A_</a>	Alignment	not modelled	100.0	23	<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
42	<a href="#">c4dg9A_</a>	Alignment	not modelled	100.0	19	<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
43	<a href="#">c5aplA_</a>	Alignment	not modelled	100.0	21	<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
44	<a href="#">c5u2aA_</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
45	<a href="#">c5keiA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> apnaa1; <b>PDBTitle:</b> understanding bi-specificity of a-domains
46	<a href="#">c4d56A_</a>	Alignment	not modelled	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
47	<a href="#">c4r0mB_</a>	Alignment	not modelled	100.0	21	<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
48	<a href="#">c5e7qB_</a>	Alignment	not modelled	100.0	19	<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
49	<a href="#">c3iteB_</a>	Alignment	not modelled	100.0	17	<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
50	<a href="#">c2v7bB_</a>	Alignment	not modelled	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
51	<a href="#">c4r0mA_</a>	Alignment	not modelled	100.0	19	<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
52	<a href="#">c4dg8A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase

53	<a href="#">c4oxiA_</a>	Alignment	not modelled	100.0	16	<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
54	<a href="#">d1amua_</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
55	<a href="#">c5jqbB_</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 idn11
56	<a href="#">c4fuqD_</a>	Alignment	not modelled	100.0	25	<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
57	<a href="#">d1v25a_</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Acetyl-CoA synthetase-like <b>Superfamily:</b> Acetyl-CoA synthetase-like <b>Family:</b> Acetyl-CoA synthetase-like
58	<a href="#">d1lcia_</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
59	<a href="#">c6akdA_</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 idn17
60	<a href="#">c1amuB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> peptide synthetase <b>Chain:</b> B: <b>PDB Molecule:</b> gramicidin synthetase 1; <b>PDBTitle:</b> phenylalanine activating domain of gramicidin synthetase 12 in a complex with amp and phenylalanine
61	<a href="#">c5buqA_</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> unliganded form of o-succinylbenzoate coenzyme a synthetase (mene)2 from bacillus subtilis, solved at 1.98 angstroms
62	<a href="#">c3l8cA_</a>	Alignment	not modelled	100.0	19	<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="#">c3dhvA_</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; <b>PDBTitle:</b> crystal structure of delta protein in complex with d-alanine2 adenylate
64	<a href="#">c3g7sA_</a>	Alignment	not modelled	100.0	21	<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
65	<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
66	<a href="#">c5c5hA_</a>	Alignment	not modelled	100.0	22	<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
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="#">c6ozvA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> txo1; <b>PDBTitle:</b> the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo1 serine module in3 complex with amp
69	<a href="#">c4gr5B_</a>	Alignment	not modelled	100.0	24	<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
70	<a href="#">c4w8oA_</a>	Alignment	not modelled	100.0	23	<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="#">c3o82B_</a>	Alignment	not modelled	100.0	16	<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
72	<a href="#">c5jipB_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nonribosomal peptide synthase; <b>PDBTitle:</b> crystal structure of cmis6
73	<a href="#">c3o82A_</a>	Alignment	not modelled	100.0	16	<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
74	<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
75	<a href="#">c3wv4B_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> non-ribosomal peptide synthetase; <b>PDBTitle:</b> crystal structure of vinn
76	<a href="#">c3ivrA_</a>	Alignment	not modelled	100.0	26	<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
77	<a href="#">c5oe3C_</a>	Alignment	not modelled	100.0	23	<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)
						<b>PDB header:</b> ligase

78	<a href="#">c4lqcA</a>	Alignment	not modelled	100.0	19	<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) from <i>clostridium scindens</i> (vpi 12708) at 2.19 a resolution
79	<a href="#">c3t5cA</a>	Alignment	not modelled	100.0	27	<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 fac13 from <i>mycobacterium tuberculosis</i> in different space group c2
80	<a href="#">c5n81B</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrocidine synthase 1; <b>PDBTitle:</b> crystal structure of an engineered tyca variant in complex with an o-2 propargyl-beta-tyr-amp analog
81	<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 <i>bacillus subtilis</i> , in complex with atp and magnesium ion
82	<a href="#">c3e53A</a>	Alignment	not modelled	100.0	22	<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 <i>mycobacterium tuberculosis</i>
83	<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 <i>phrixothrix hirtus2</i> (p1 crystal form)
84	<a href="#">c5jipC</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> nonribosomal peptide synthase; <b>PDBTitle:</b> crystal structure of cmis6
85	<a href="#">c4gs5A</a>	Alignment	not modelled	100.0	20	<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 <i>dyadobacter fermentans dsm 18053</i>
86	<a href="#">c2y4oA</a>	Alignment	not modelled	100.0	18	<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
87	<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 <i>burkholderia2 cenocepacia</i>
88	<a href="#">c3qovD</a>	Alignment	not modelled	100.0	11	<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>2 bacteroides thetaiotaomicron vpi-5482</i> at 2.20 a resolution
89	<a href="#">c3hguB</a>	Alignment	not modelled	99.7	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
90	<a href="#">c3laxA</a>	Alignment	not modelled	99.4	11	<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 atcc 8482</i>
91	<a href="#">c5kodA</a>	Alignment	not modelled	97.4	15	<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>arabidopsis2 thaliana</i>
92	<a href="#">c6avhA</a>	Alignment	not modelled	95.9	20	<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
93	<a href="#">c4b2gB</a>	Alignment	not modelled	95.2	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> gh3-1 auxin conjugating enzyme; <b>PDBTitle:</b> crystal structure of an indole-3-acetic acid amido synthase from <i>vitis2 vinifera</i> involved in auxin homeostasis
94	<a href="#">c4eplA</a>	Alignment	not modelled	94.5	16	<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
95	<a href="#">c4ewvB</a>	Alignment	not modelled	93.5	17	<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
96	<a href="#">d2ayia1</a>	Alignment	not modelled	82.6	16	<b>Fold:</b> Thermophilic metalloprotease-like <b>Superfamily:</b> Thermophilic metalloprotease-like <b>Family:</b> Thermophilic metalloprotease (M29)
97	<a href="#">c3isIA</a>	Alignment	not modelled	82.3	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine catabolism protein pucg; <b>PDBTitle:</b> crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from <i>bacillus subtilis</i>
98	<a href="#">d1piwa2</a>	Alignment	not modelled	75.1	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
99	<a href="#">d1pl8a2</a>	Alignment	not modelled	70.4	20	<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
100	<a href="#">c6mb6A</a>	Alignment	not modelled	68.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aac(3)-iiib protein; <b>PDBTitle:</b> aac-iiib binary with coash
101	<a href="#">d1kola2</a>	Alignment	not modelled	65.9	18	<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
102	<a href="#">c3smaD</a>	Alignment	not modelled	65.2	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> frbf; <b>PDBTitle:</b> a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf <b>PDB header:</b> transferase

103	<a href="#">c5ht0B_</a>	Alignment	not modelled	64.6	16	<b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside acetyltransferase hmb0005; <b>PDBTitle:</b> crystal structure of an antibiotic_nat family aminoglycoside2 acetyltransferase hmb0038 from an uncultured soil metagenomic sample3 in complex with coenzyme a
104	<a href="#">c4k2bA_</a>	Alignment	not modelled	62.0	30	<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
105	<a href="#">c3ippA_</a>	Alignment	not modelled	60.7	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thiosulfate sulfurtransferase ynje; <b>PDBTitle:</b> crystal structure of sulfur-free ynje
106	<a href="#">d2nyga1</a>	Alignment	not modelled	60.5	20	<b>Fold:</b> TTHA0583/YokD-like <b>Superfamily:</b> TTHA0583/YokD-like <b>Family:</b> Aminoglycoside 3-N-acetyltransferase-like
107	<a href="#">c5w70B_</a>	Alignment	not modelled	57.4	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> l-glutamine:2-deoxy-scylo-inosose aminotransferase; <b>PDBTitle:</b> x-ray structure of rbmb from streptomyces ribosidificus
108	<a href="#">d1z7wa1</a>	Alignment	not modelled	56.8	14	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
109	<a href="#">c6bc3A_</a>	Alignment	not modelled	55.5	19	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> aac 3-vi protein; <b>PDBTitle:</b> cryo x-ray structure of sisomicin bound aac-via
110	<a href="#">c6mn5A_</a>	Alignment	not modelled	55.3	26	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside n(3)-acetyltransferase, aac(3)-iva; <b>PDBTitle:</b> crystal structure of aminoglycoside acetyltransferase aac(3)-iva,2 h154a mutant, in complex with gentamicin c1a
111	<a href="#">d1d1ta2</a>	Alignment	not modelled	55.3	8	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
112	<a href="#">d1iz0a2</a>	Alignment	not modelled	54.5	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
113	<a href="#">d1p0fa2</a>	Alignment	not modelled	54.0	7	<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
114	<a href="#">c5u18A_</a>	Alignment	not modelled	52.9	24	<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
115	<a href="#">c1uarA_</a>	Alignment	not modelled	52.2	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhodanese; <b>PDBTitle:</b> crystal structure of rhodanese from thermus thermophilus hb8
116	<a href="#">c3e4fB_</a>	Alignment	not modelled	51.4	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside n3-acetyltransferase; <b>PDBTitle:</b> crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
117	<a href="#">c3olhA_</a>	Alignment	not modelled	51.3	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-mercaptopyruvate sulfurtransferase; <b>PDBTitle:</b> human 3-mercaptopyruvate sulfurtransferase
118	<a href="#">c4lmaA_</a>	Alignment	not modelled	50.9	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure analysis of o-acetylserine sulfhydrylase cysk1 from2 microcystis aeruginosa 7806
119	<a href="#">d1e3ia2</a>	Alignment	not modelled	46.9	5	<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
120	<a href="#">c6h98A_</a>	Alignment	not modelled	44.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfurtransferase; <b>PDBTitle:</b> native crystal structure of anaerobic ergothioneine biosynthesis2 enzyme from chlorobium limicola.