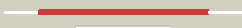



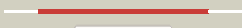


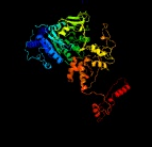
















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2948c_(fadD22)_3297847_3299964
Date	Thu Aug 8 16:20:10 BST 2019
Unique Job ID	c75c8489a25c31c0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5es8A_	 Alignment		100.0	22	PDB header: ligase Chain: A: PDB Molecule: linear gramicidin synthetase subunit a; PDBTitle: crystal structure of the initiation module of lgra in the thiolation2 state
2	c5ja2A_	 Alignment		100.0	26	PDB header: ligase Chain: A: PDB Molecule: enterobactin synthase component f; PDBTitle: entf, a terminal nonribosomal peptide synthetase module bound to the2 non-native mbth-like protein pa2412
3	c2vsqA_	 Alignment		100.0	23	PDB header: ligase Chain: A: PDB Molecule: surfactin synthetase subunit 3; PDBTitle: structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module
4	c5u89A_	 Alignment		100.0	24	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: amino acid adenylation domain protein; PDBTitle: crystal structure of a cross-module fragment from the dimodular nrps2 dhbf
5	c6n8eA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: holo-obif1; PDBTitle: crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
6	c4zxiA_	 Alignment		100.0	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: tyrocidine synthetase 3; PDBTitle: crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine
7	c6eqoB_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: acetyl-coenzyme a synthetase; PDBTitle: tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nadp+ and phosphomethylphosphonic acid adenylyate ester
8	c4zxiA_	 Alignment		100.0	25	PDB header: biosynthetic protein Chain: A: PDB Molecule: enterobactin synthase component f; PDBTitle: crystal structure of holo-entf a nonribosomal peptide synthetase in2 the thioester-forming conformation
9	c5mssA_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: thioester reductase domain-containing protein; PDBTitle: structure of the a-pcp didomain of carboxylic acid reductase (car)2 from segniliparus rugosus in complex with amp
10	c5wmmA_	 Alignment		100.0	25	PDB header: biosynthetic protein Chain: A: PDB Molecule: nrps; PDBTitle: crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios
11	c6p1jA_	 Alignment		100.0	26	PDB header: biosynthetic protein Chain: A: PDB Molecule: txo2; PDBTitle: the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo2 serine module

12	c4dg9A_	Alignment		100.0	22	PDB header: ligase/inhibitor Chain: A: PDB Molecule: pa1221; PDBTitle: structure of holo-pa1221, an nrps protein containing adenylation and2 pcp domains bound to vinylsulfonamide inhibitor
13	c5gxdA_	Alignment		100.0	22	PDB header: lyase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: structure of acryloyl-coa lyase prpe from dinoroseobacter shibae dfl2 12
14	c3rg2H_	Alignment		100.0	23	PDB header: ligase Chain: H: PDB Molecule: enterobactin synthase component e (ente), 2,3-dihydro-2,3- PDBTitle: structure of a two-domain nrps fusion protein containing the ente2 adenylation domain and entb aryl-carrier protein from enterobactin3 biosynthesis
15	d1pg4a_	Alignment		100.0	22	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
16	c4wd1A_	Alignment		100.0	22	PDB header: ligase Chain: A: PDB Molecule: acetoacetate-coa ligase; PDBTitle: acetoacetyl-coa synthetase from streptomyces lividans
17	c5ifiA_	Alignment		100.0	22	PDB header: ligase Chain: A: PDB Molecule: acetyl-coenzyme a synthetase; PDBTitle: crystal structure of acetyl-coa synthetase in complex with adenosine-2 5'-propylphosphate from cryptococcus neoformans h99
18	c4r0mA_	Alignment		100.0	19	PDB header: ligase Chain: A: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
19	d1ry2a_	Alignment		100.0	23	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
20	c5msdA_	Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: carboxylic acid reductase; PDBTitle: structure of the a domain of carboxylic acid reductase (car) from2 nocardia iowensis in complex with amp and benzoic acid
21	c3tsyA_	Alignment	not modelled	100.0	21	PDB header: ligase, transferase Chain: A: PDB Molecule: fusion protein 4-coumarate--coa ligase 1, resveratrol PDBTitle: 4-coumaroyl-coa ligase::stilbene synthase fusion protein
22	c5mstA_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: thioester reductase domain-containing protein; PDBTitle: structure of the a domain of carboxylic acid reductase (car) from2 segniliparus rugosus in complex with amp and a co-purified carboxylic3 acid
23	c3e7wA_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: d-alanine--poly(phosphoribitol) ligase subunit 1; PDBTitle: crystal structure of dlta: implications for the reaction mechanism of2 non-ribosomal peptide synthetase (nrps) adenylation domains
24	d3cw9a1	Alignment	not modelled	100.0	22	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
25	c3vngA_	Alignment	not modelled	100.0	24	PDB header: ligase Chain: A: PDB Molecule: nrps adenylation protein cytc1; PDBTitle: co-crystal structure of nrps adenylation protein cytc1 with atp from2 streptomyces
26	c4wv3A_	Alignment	not modelled	100.0	26	PDB header: ligase/ligase inhibitor Chain: A: PDB Molecule: anthranilate-coa ligase; PDBTitle: crystal structure of the anthranilate coa ligase auaeii in complex2 with anthranoyl-amp
27	c5ie2A_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: oxalate--coa ligase; PDBTitle: crystal structure of a plant enzyme
						PDB header: ligase

28	c5x8gA_	Alignment	not modelled	100.0	25	Chain: A: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: 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
29	d1mdba_	Alignment	not modelled	100.0	24	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
30	c4eatB_	Alignment	not modelled	100.0	31	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structure of a benzoate coenzyme a ligase
31	c3etcB_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: B: PDB Molecule: amp-binding protein; PDBTitle: 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298
32	c6ozvA_	Alignment	not modelled	100.0	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: txo1; PDBTitle: the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo1 serine module in3 complex with amp
33	c4dg8A_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: pa1221; PDBTitle: structure of pa1221, an nrps protein containing adenylation and pcp2 domains
34	c3ni2A_	Alignment	not modelled	100.0	25	PDB header: ligase Chain: A: PDB Molecule: 4-coumarate:coa ligase; PDBTitle: crystal structures and enzymatic mechanisms of a populus tomentosa 4-2 coumarate:coa ligase
35	c5u2aA_	Alignment	not modelled	100.0	26	PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of brucella canis acyl-coa synthetase
36	c3gqwB_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: B: PDB Molecule: fatty acid amp ligase; PDBTitle: crystal structure of a fatty acid amp ligase from e. coli with an acyl2 adenylate product bound
37	c5wm7A_	Alignment	not modelled	100.0	27	PDB header: ligase Chain: A: PDB Molecule: salicylate-amp ligase; PDBTitle: crystal structure of cahj in complex with amp
38	c5ey8D_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: D: PDB Molecule: acyl-coa synthase; PDBTitle: structure of fadd32 from mycobacterium smegmatis complexed to ampc20
39	c3kxwA_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: saframycin mx1 synthetase b; PDBTitle: the crystal structure of fatty acid amp ligase from legionella2 pneumophila
40	c2v7bB_	Alignment	not modelled	100.0	30	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
41	c6ijbA_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: amp-binding domain protein; PDBTitle: structure of 3-methylmercaptopropionate coa ligase mutant k523a in2 complex with amp and mmpa
42	c3iteB_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: B: PDB Molecule: sidn siderophore synthetase; PDBTitle: the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
43	c3eynB_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: B: PDB Molecule: acyl-coenzyme a synthetase acsm2a; PDBTitle: crystal structure of human acyl-coa synthetase medium-chain2 family member 2a (l64p mutation) in a complex with coa
44	c4r0mB_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
45	c5aplA_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A: PDB Molecule: adenylation domain; PDBTitle: structure of the adenylation domain thr1 involved in the biosynthesis2 of 4-chlorothreonine in streptomyces sp. oh-5093, apo structure
46	c4ir7A_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: long chain fatty acid coa ligase fadd10; PDBTitle: crystal structure of mtb fadd10 in complex with dodecanoyl-amp
47	d1amua_	Alignment	not modelled	100.0	22	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
48	c6h1bA_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: fatty acid coa ligase; PDBTitle: structure of amide bond synthetase mcba k483a mutant from2 marinactinospora thermotolerans
49	c4fuqD_	Alignment	not modelled	100.0	25	PDB header: ligase Chain: D: PDB Molecule: malonyl coa synthetase; PDBTitle: crystal structure of apo matb from rhodopseudomonas palustris
50	c2d1tA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: luciferin 4-monooxygenase; PDBTitle: crystal structure of the thermostable japanese firefly2 luciferase red-color emission s286n mutant complexed with3 high-energy intermediate analogue
51	c6ac3B_	Alignment	not modelled	100.0	20	PDB header: luminescent protein Chain: B: PDB Molecule: red-bioluminescence eliciting luciferase; PDBTitle: structure of a natural red emitting luciferase from phrixothrix hirtus2 (p3121 crystal form)
52	c3r44A_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: fatty acyl coa synthetase fadd13 (fatty-acyl-coa PDBTitle: mycobacterium tuberculosis fatty acyl coa synthetase

53	c5keiA	Alignment	not modelled	100.0	24	PDB header: ligase Chain: A: PDB Molecule: 2,3-dihydroxybenzoate-amp ligase; PDBTitle: mycobacterium smegmatis mbta apo structure
54	c4d56A	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: apnaa1; PDBTitle: understanding bi-specificity of a-domains
55	c4oxiA	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: enterobactin synthetase component f-related protein; PDBTitle: crystal structure of vibrio cholerae adenylation domain alme in2 complex with glycyL-adenosine-5'-phosphate
56	c1amuB	Alignment	not modelled	100.0	20	PDB header: peptide synthetase Chain: B: PDB Molecule: gramicidin synthetase 1; PDBTitle: phenylalanine activating domain of gramicidin synthetase 12 in a complex with amp and phenylalanine
57	c5jjqB	Alignment	not modelled	100.0	23	PDB header: ligase Chain: B: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn11
58	c5e7qB	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: acyl-coa synthetase; PDBTitle: acyl-coa synthetase ptma2 from streptomyces platensis
59	c3l8cA	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: d-alanine--poly(phosphoribitol) ligase subunit 1; PDBTitle: structure of probable d-alanine--poly(phosphoribitol) ligase subunit-12 from streptococcus pyogenes
60	c3dhvA	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: d-alanine-poly(phosphoribitol) ligase; PDBTitle: crystal structure of dltA protein in complex with d-alanine2 adenylate
61	c4gr5B	Alignment	not modelled	100.0	23	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of slgn1deltaasub in complex with ampcpp
62	c3nyrA	Alignment	not modelled	100.0	25	PDB header: ligase Chain: A: PDB Molecule: malonyl-coa ligase; PDBTitle: malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
63	c6akdA	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn17
64	c3iplB	Alignment	not modelled	100.0	21	PDB header: ligase Chain: B: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: crystal structure of o-succinylbenzoic acid-coa ligase from2 staphylococcus aureus subsp. aureus mu50
65	d1v25a	Alignment	not modelled	100.0	23	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
66	c5buqA	Alignment	not modelled	100.0	24	PDB header: ligase Chain: A: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: unliganded form of o-succinylbenzoate coenzyme a synthetase (mene)2 from bacillus subtilis, solved at 1.98 angstroms
67	d1lcia	Alignment	not modelled	100.0	18	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
68	c3g7sA	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: long-chain-fatty-acid--coa ligase (fadd-1); PDBTitle: crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus
69	c5c5hA	Alignment	not modelled	100.0	25	PDB header: ligase Chain: A: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: r195k e. coli mene with bound osb-ams
70	c4w8oA	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: luciferase-like enzymeamp-coa-ligase; PDBTitle: structure of the luciferase-like enzyme from the nonluminescent2 zophobas morio mealworm
71	c4lqcA	Alignment	not modelled	100.0	15	PDB header: ligase Chain: A: PDB Molecule: bile acid-coenzyme a ligase; PDBTitle: crystal structure of a bile acid-coenzyme a ligase (baib) from2 clostridium scindens (vpi 12708) at 2.19 a resolution
72	c3o82B	Alignment	not modelled	100.0	19	PDB header: ligase Chain: B: PDB Molecule: peptide arylation enzyme; PDBTitle: structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
73	c5jipB	Alignment	not modelled	100.0	23	PDB header: ligase Chain: B: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
74	c3o82A	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: peptide arylation enzyme; PDBTitle: structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
75	c3qyaA	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: luciferase; PDBTitle: crystal structure of a red-emitter mutant of lampyris turkestanicus2 luciferase
76	c5n81B	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: tyrocidine synthase 1; PDBTitle: crystal structure of an engineered tyca variant in complex with an o-2 propargyl-beta-tyr-amp analog
77	c5oe3C	Alignment	not modelled	100.0	31	PDB header: ligase Chain: C: PDB Molecule: anthranilate--coa ligase; PDBTitle: crystal structure of the n-terminal domain of pqsa in complex with2 anthraniloyl-amp (crystal form 1)
78	c3wv4B	Alignment	not modelled	100.0	22	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase;

						PDBTitle: crystal structure of vinn
79	c3ivrA_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: putative long-chain-fatty-acid coa ligase; PDBTitle: crystal structure of putative long-chain-fatty-acid coa ligase from <i>rhodospseudomonas palustris</i> cga009
80	c5burB_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: B: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: o-succinylbenzoate coenzyme a synthetase (mene) from <i>bacillus2 subtilis</i> , in complex with atp and magnesium ion
81	c3t5cA_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: probable chain-fatty-acid-coa ligase fadd13; PDBTitle: crystal structure of n-terminal domain of facl13 from <i>mycobacterium2 tuberculosis</i> in different space group c2
82	c6abhG_	Alignment	not modelled	100.0	18	PDB header: luminescent protein Chain: G: PDB Molecule: red-bioluminescence eliciting luciferase; PDBTitle: structure of a natural red emitting luciferase from <i>phrixothrix hirtus2</i> (p1 crystal form)
83	c3e53A_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: fatty-acid-coa ligase fadd28; PDBTitle: crystal structure of n-terminal domain of a fatty acyl amp2 ligase faal28 from <i>mycobacterium tuberculosis</i>
84	c5jipC_	Alignment	not modelled	100.0	24	PDB header: ligase Chain: C: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
85	c2y4oA_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak2 in complex with phenylacetyl adenylate
86	c4gs5A_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: acyl-coa synthetase (amp-forming)/amp-acid ligase ii-like PDBTitle: the crystal structure of acyl-coa synthetase (amp-forming)/amp-acid2 ligase ii-like protein from <i>dyadobacter fermentans dsm 18053</i>
87	c2y27B_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak1 in complex with atp from <i>burkholderia2 cenocepacia</i>
88	c3qovD_	Alignment	not modelled	100.0	15	PDB header: ligase Chain: D: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of a hypothetical acyl-coa ligase (bt_0428) from <i>bacteroides thetaiotaomicron vpi-5482</i> at 2.20 a resolution
89	c3hguB_	Alignment	not modelled	100.0	14	PDB header: biosynthetic protein Chain: B: PDB Molecule: ehpf; PDBTitle: structure of phenazine antibiotic biosynthesis protein
90	c2jgpA_	Alignment	not modelled	99.8	15	PDB header: ligase Chain: A: PDB Molecule: tyrocidine synthetase 3; PDBTitle: structure of the tycc5-6 pcp-c bidomain of the tyrocidine synthetase2 tycc
91	c5u3hA_	Alignment	not modelled	99.7	16	PDB header: ligase Chain: A: PDB Molecule: hmwp2 nonribosomal peptide synthetase; PDBTitle: solution structure of apo pcp1 from <i>yersiniabactin synthetase</i>
92	c5msvB_	Alignment	not modelled	99.7	24	PDB header: oxidoreductase Chain: B: PDB Molecule: thioester reductase domain-containing protein; PDBTitle: structure of the phosphopantetheine modified pcp-r didomain of 2 carboxylic acid reductase (car) in complex with nadp
93	c2roqA_	Alignment	not modelled	99.6	15	PDB header: transferase Chain: A: PDB Molecule: enterobactin synthetase component f; PDBTitle: solution structure of the thiolation-thioesterase di-domain2 of enterobactin synthetase component f
94	c2cq8A_	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 10-formyltetrahydrofolate dehydrogenase; PDBTitle: solution structure of rsgi ruh-033, a pp-binding domain of 2 10-fthfdh from human cdna
95	c6h0jA_	Alignment	not modelled	99.5	30	PDB header: protein binding Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: a1-type acp domain from module 5 of mlsa1
96	c2mr7A_	Alignment	not modelled	99.5	28	PDB header: biosynthetic protein Chain: A: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: apo structure of the peptidyl carrier protein domain 7 of the 2 teicoplanin producing non-ribosomal peptide synthetase
97	c2ju2A_	Alignment	not modelled	99.5	44	PDB header: transferase Chain: A: PDB Molecule: erythronolide synthase; PDBTitle: minimized mean solution structure of the acyl carrier2 protein domain from module 2 of 6-deoxyerythronolide b3 synthase (debs)
98	c5mtiA_	Alignment	not modelled	99.5	21	PDB header: transport protein Chain: A: PDB Molecule: phosphopantetheine-binding protein; PDBTitle: bamb_5917 acyl-carrier protein
99	c5hvcA_	Alignment	not modelled	99.5	34	PDB header: transferase Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: solution structure of the apo state of the acyl carrier protein from the mlsa2 subunit of the mycolactone polyketide synthase
100	c4pxhF_	Alignment	not modelled	99.5	22	PDB header: oxidoreductase/protein binding Chain: F: PDB Molecule: peptide synthetase; PDBTitle: structure of p450sky (cyp163b3), a cytochrome p450 from <i>skyllamycin2</i> biosynthesis in complex with a peptidyl carrier protein domain
101	c3laxA_	Alignment	not modelled	99.5	15	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: the crystal structure of a domain of phenylacetate-coenzyme2 a ligase from <i>bacteroides vulgatus atcc 8482</i>
102	d2gdwa1	Alignment	not modelled	99.4	22	Fold: Acyl carrier protein-like Superfamily: ACP-like

						Family: Peptidyl carrier domain
103	c2liuA_	Alignment	not modelled	99.4	17	PDB header: transferase Chain: A: PDB Molecule: cura; PDBTitle: nmr structure of holo-acpi domain from cura module from lynngbya2 majuscula
104	c5kodA_	Alignment	not modelled	99.4	12	PDB header: ligase Chain: A: PDB Molecule: indole-3-acetic acid-amido synthetase gh3.5; PDBTitle: crystal structure of gh3.5 acyl acid amido synthetase from arabidopsis2 thaliana
105	c4i4dA_	Alignment	not modelled	99.4	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: peptide synthetase nrps type ii-pcp; PDBTitle: structure of blmi, a type-ii acyl-carrier-protein from streptomyces2 verticillus involved in bleomycin biosynthesis
106	c2l22A_	Alignment	not modelled	99.4	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: mupirocin didomain acyl carrier protein; PDBTitle: mupirocin didomain acp
107	c2n98A_	Alignment	not modelled	99.4	20	PDB header: transport protein Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: solution structure of acyl carrier protein lipid from actinoplanes2 friuliensis
108	c2mf4A_	Alignment	not modelled	99.4	17	PDB header: transferase Chain: A: PDB Molecule: hybrid polyketide synthase-non ribosomal peptide PDBTitle: 1h, 13c, 15n chemical shift assignments of streptomyces virginiae vira2 acp5a
109	c4hkgB_	Alignment	not modelled	99.4	29	PDB header: phosphopantetheine binding protein Chain: B: PDB Molecule: phosphopantetheine attachment site family protein; PDBTitle: crystal structure of free-standing peptidyl carrier protein from2 uncharacterized acinetobacter baumannii secondary metabolic pathway
110	c4ca3A_	Alignment	not modelled	99.3	20	PDB header: ribosomal protein Chain: A: PDB Molecule: hybrid polyketide synthase-non ribosomal peptide PDBTitle: solution structure of streptomyces virginiae vira acp5b
111	c5ejdK_	Alignment	not modelled	99.3	13	PDB header: biosynthetic protein Chain: K: PDB Molecule: tqaa; PDBTitle: the crystal structure of holo t3ct
112	c6c4qA_	Alignment	not modelled	99.3	22	PDB header: transport protein Chain: A: PDB Molecule: polyketide synthase pks13; PDBTitle: 1.16 angstrom resolution crystal structure of acyl carrier protein2 domain (residues 1-100) of polyketide synthase pks13 from3 mycobacterium tuberculosis
113	c2fq1A_	Alignment	not modelled	99.3	19	PDB header: hydrolase Chain: A: PDB Molecule: isochorismatase; PDBTitle: crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
114	c2afdA_	Alignment	not modelled	99.3	20	PDB header: ligand binding protein Chain: A: PDB Molecule: protein asl1650; PDBTitle: solution structure of asl1650, an acyl carrier protein from anaena2 sp. pcc 7120 with a variant phosphopantetheinylation-site sequence
115	c5zk4D_	Alignment	not modelled	99.3	27	PDB header: transferase Chain: D: PDB Molecule: disa protein; PDBTitle: the structure of dszs acyltransferase with carrier protein
116	c5kp8B_	Alignment	not modelled	99.2	16	PDB header: transferase Chain: B: PDB Molecule: curb; PDBTitle: crystal structure of the curacin biosynthetic pathway hmg synthase in2 complex with acetyl donor-acp
117	d1or5a_	Alignment	not modelled	99.2	22	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
118	d1klpa_	Alignment	not modelled	99.2	10	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
119	d1nq4a_	Alignment	not modelled	99.2	21	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
120	c2n6yA_	Alignment	not modelled	99.2	11	PDB header: ligase Chain: A: PDB Molecule: hmpw2 nonribosomal peptide synthetase; PDBTitle: solution structure of holo arcp from yersiniabactin synthetase