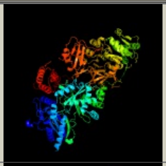
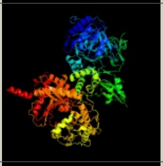
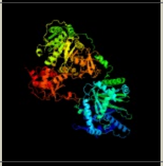
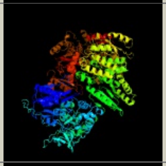
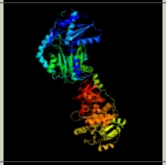
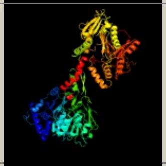
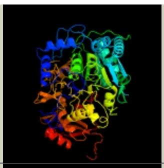
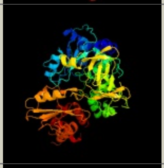
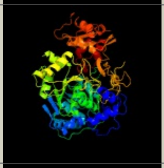
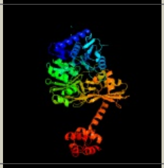
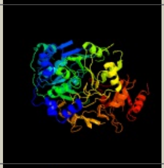
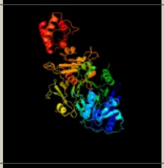
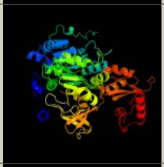
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0101_(nrp)_109998_117536
Date	Tue Jul 23 14:50:14 BST 2019
Unique Job ID	f717650e271bf63c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vsqA_	Alignment		100.0	29	**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
2	c5ja2A_	Alignment		100.0	19	**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	c4zxiA_	Alignment		100.0	29	**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
4	c5u89A_	Alignment		100.0	32	**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	c4zxjA_	Alignment		100.0	27	**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
6	c6p1jA_	Alignment		100.0	40	**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
7	c6eqoB_	Alignment		100.0	15	**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 adenylate ester
8	c5es8A_	Alignment		100.0	28	**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
9	c6ozvA_	Alignment		100.0	39	**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
10	c5wmmA_	Alignment		100.0	17	**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	c5mssA_	Alignment		100.0	17	**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

12	c5ifiA_	Alignment		100.0	16	**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
13	c4dg9A_	Alignment		100.0	28	**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
14	d1pg4a_	Alignment		100.0	18	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
15	c4wd1A_	Alignment		100.0	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetoacetate-coa ligase; **PDBTitle:** acetoacetyl-coa synthetase from streptomyces lividans
16	c3rg2H_	Alignment		100.0	22	**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
17	d1ry2a_	Alignment		100.0	16	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
18	c4r0mA_	Alignment		100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**mcyg protein; **PDBTitle:** structure of mcyg a-pcp complexed with phenylalanyl-adenylate
19	c5gxdA_	Alignment		100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**amp-dependent synthetase and ligase; **PDBTitle:** structure of acryloyl-coa lyase prpe from dinoroseobacter shibae dfl2 12
20	c5msvB_	Alignment		100.0	51	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioester reductase domain-containing protein; **PDBTitle:** structure of the phosphopantetheine modified pcp-r didomain of2 carboxylic acid reductase (car) in complex with nadp
21	c2jgpA_	Alignment	not modelled	100.0	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrocidine synthetase 3; **PDBTitle:** structure of the tycc5-6 pcp-c bidomain of the tyrocidine synthetase2 tycc
22	c5msdA_	Alignment	not modelled	100.0	18	**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
23	c4dqvA_	Alignment	not modelled	100.0	97	**PDB header:**ligase **Chain:** A: **PDB Molecule:**probable peptide synthetase nrp (peptide synthase); **PDBTitle:** crystal structure of reductase (r) domain of non-ribosomal peptide2 synthetase from mycobacterium tuberculosis
24	c3tsyA_	Alignment	not modelled	100.0	14	**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
25	c5msuC_	Alignment	not modelled	100.0	69	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carboxylic acid reductase; **PDBTitle:** structure of the r domain of carboxylic acid reductase (car) from2 mycobacterium marinum in complex with nadp, p21 form
26	c5mstA_	Alignment	not modelled	100.0	19	**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
27	c4gr5B_	Alignment	not modelled	100.0	36	**PDB header:**ligase **Chain:** B: **PDB Molecule:**non-ribosomal peptide synthetase; **PDBTitle:** crystal structure of slgn1deltaasub in complex with ampcpp

28	c3e7wA_	Alignment	not modelled	100.0	25	**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
29	c3vnqA_	Alignment	not modelled	100.0	36	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nrps adenylation protein cytc1; **PDBTitle:** co-crystal structure of nrps adenylation protein cytc1 with atp from2 streptomyces
30	d3cw9a1	Alignment	not modelled	100.0	24	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
31	c5x8gA_	Alignment	not modelled	100.0	23	**PDB header:**ligase **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
32	d1mdba_	Alignment	not modelled	100.0	23	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
33	d1amua_	Alignment	not modelled	100.0	32	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
34	c3ni2A_	Alignment	not modelled	100.0	18	**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	c4dg8A_	Alignment	not modelled	100.0	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pa1221; **PDBTitle:** structure of pa1221, an nrps protein containing adenylation and pcp2 domains
36	c4eatB_	Alignment	not modelled	100.0	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**benzoate-coenzyme a ligase; **PDBTitle:** crystal structure of a benzoate coenzyme a ligase
37	c1amuB_	Alignment	not modelled	100.0	31	**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
38	c3iteB_	Alignment	not modelled	100.0	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**sidn siderophore synthetase; **PDBTitle:** the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
39	c5ie2A_	Alignment	not modelled	100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**oxalate--coa ligase; **PDBTitle:** crystal structure of a plant enzyme
40	c4wv3A_	Alignment	not modelled	100.0	20	**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
41	c5t81A_	Alignment	not modelled	100.0	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**epob; **PDBTitle:** rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum
42	c6h1bA_	Alignment	not modelled	100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**fatty acid coa ligase; **PDBTitle:** structure of amide bond synthetase mcba k483a mutant from2 marinactinospora thermotolerans
43	c3etcB_	Alignment	not modelled	100.0	20	**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
44	c5ey8D_	Alignment	not modelled	100.0	23	**PDB header:**ligase **Chain:** D: **PDB Molecule:**acyl-coa synthase; **PDBTitle:** structure of fadd32 from mycobacterium smegmatis complexed to ampc20
45	c5aplA_	Alignment	not modelled	100.0	35	**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	c3kxwA_	Alignment	not modelled	100.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**saframycin mx1 synthetase b; **PDBTitle:** the crystal structure of fatty acid amp ligase from legionella2 pneumophila
47	c4oxiA_	Alignment	not modelled	100.0	24	**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
48	c5wm7A_	Alignment	not modelled	100.0	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**salicylate-amp ligase; **PDBTitle:** crystal structure of cahj in complex with amp
49	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
50	c4ir7A_	Alignment	not modelled	100.0	20	**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
51	c5jjqB_	Alignment	not modelled	100.0	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**amp-dependent synthetase and ligase; **PDBTitle:** crystal structure of idnl1
52	c5keiA_	Alignment	not modelled	100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**2,3-dihydroxybenzoate-amp ligase; **PDBTitle:** mycobacterium smegmatis mbta apo structure

53	c4d56A_	Alignment	not modelled	100.0	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**apnaa1; **PDBTitle:** understanding bi-specificity of a-domains
54	c5u2aA_	Alignment	not modelled	100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**amp-dependent synthetase and ligase; **PDBTitle:** crystal structure of brucella canis acyl-coa synthetase
55	c6cgoB_	Alignment	not modelled	100.0	21	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**condensation domain protein; **PDBTitle:** molecular basis for condensation domain-mediated chain release from2 the enacyloxin polyketide synthase
56	c3gqwB_	Alignment	not modelled	100.0	18	**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
57	c4tx3B_	Alignment	not modelled	100.0	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide synthetase, module 7; **PDBTitle:** complex of the x-domain and oxyb from teicoplanin biosynthesis
58	c4r0mB_	Alignment	not modelled	100.0	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**mcyg protein; **PDBTitle:** structure of mcyg a-pcp complexed with phenylalanyl-adenylate
59	c6ijbA_	Alignment	not modelled	100.0	19	**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
60	c2v7bB_	Alignment	not modelled	100.0	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**benzoate-coenzyme a ligase; **PDBTitle:** crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
61	c6ac3B_	Alignment	not modelled	100.0	19	**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)
62	c3eynB_	Alignment	not modelled	100.0	20	**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
63	c2d1tA_	Alignment	not modelled	100.0	19	**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
64	c6akdA_	Alignment	not modelled	100.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**amp-dependent synthetase and ligase; **PDBTitle:** crystal structure of idnl7
65	c4fuqD_	Alignment	not modelled	100.0	23	**PDB header:**ligase **Chain:** D: **PDB Molecule:**malonyl coa synthetase; **PDBTitle:** crystal structure of apo matb from rhodopseudomonas palustris
66	c3l8cA_	Alignment	not modelled	100.0	23	**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
67	c5buqA_	Alignment	not modelled	100.0	21	**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
68	c3dhvA_	Alignment	not modelled	100.0	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-poly(phosphoribitol) ligase; **PDBTitle:** crystal structure of dlta protein in complex with d-alanine2 adenylate
69	c5e7qB_	Alignment	not modelled	100.0	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acyl-coa synthetase; **PDBTitle:** acyl-coa synthetase ptma2 from streptomyces platensis
70	c6m7lB_	Alignment	not modelled	100.0	39	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**putative non-ribosomal peptide synthetase; **PDBTitle:** complex of oxya with the x-domain from gpa biosynthesis
71	c3nyrA_	Alignment	not modelled	100.0	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**malonyl-coa ligase; **PDBTitle:** malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
72	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
73	d1v25a_	Alignment	not modelled	100.0	24	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
74	d1lcia_	Alignment	not modelled	100.0	16	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
75	c3g7sA_	Alignment	not modelled	100.0	18	**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
76	c6ad3A_	Alignment	not modelled	100.0	24	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**lovastatin nonaketide synthase moka; **PDBTitle:** structural characterization of the condensation domain from monacolin2 k polyketide synthase moka
77	c6aefB_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyketide synthase associated protein papa2; **PDBTitle:** papa2 acyl transferase
78	c4jn3B	Alignment	not modelled	100.0	23	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**cda peptide synthetase i;

78	[illegible]	Alignment	not modelled	100.0	[illegible]	**PDBTitle:** crystal structures of the first condensation domain of the cda2 synthetase
79	c5c5hA_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**2-succinylbenzoate--coa ligase; **PDBTitle:** r195k e. coli mene with bound osb-ams
80	c5t3eA_	Alignment	not modelled	100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**bacillamide synthetase heterocyclization domain; **PDBTitle:** crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain.
81	c4znmB_	Alignment	not modelled	100.0	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**c-domain type ii peptide synthetase; **PDBTitle:** crystal structure of sgcc5 protein from streptomyces globisporus (apo2 form)
82	c1l5aA_	Alignment	not modelled	100.0	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**amide synthase; **PDBTitle:** crystal structure of vibh, an nrps condensation enzyme
83	c2xhgA_	Alignment	not modelled	100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**tyrocidine synthetase a; **PDBTitle:** crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis
84	c5m6pB_	Alignment	not modelled	100.0	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**tyrocidine synthase 2; **PDBTitle:** crystal structure of the epimerization domain from module 3 of2 tyrocidine synthetase b, tycb3(e)
85	c5jjpB_	Alignment	not modelled	100.0	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nonribosomal peptide synthase; **PDBTitle:** crystal structure of cmis6
86	c5dijA_	Alignment	not modelled	100.0	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**tqaa; **PDBTitle:** the crystal structure of ct
87	c5n81B_	Alignment	not modelled	100.0	30	**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
88	c4w8oA_	Alignment	not modelled	100.0	18	**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
89	c4lgcA_	Alignment	not modelled	100.0	13	**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
90	c3wv4B_	Alignment	not modelled	100.0	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**non-ribosomal peptide synthetase; **PDBTitle:** crystal structure of vinn
91	c4hvmC_	Alignment	not modelled	100.0	20	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**tlmii; **PDBTitle:** crystal structure of tallysomycin biosynthesis protein tlmii
92	c3o82B_	Alignment	not modelled	100.0	22	**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
93	c3qyaA_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**luciferase; **PDBTitle:** crystal structure of a red-emitter mutant of lampyris turkestanicus2 luciferase
94	c5burB_	Alignment	not modelled	100.0	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**2-succinylbenzoate--coa ligase; **PDBTitle:** o-succinylbenzoate coenzyme a synthetase (mene) from bacillus2 subtilis, in complex with atp and magnesium ion
95	c3o82A_	Alignment	not modelled	100.0	22	**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
96	c3ivrA_	Alignment	not modelled	100.0	25	**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 from2 rhodopseudomonas palustris cga009
97	c5jjpC_	Alignment	not modelled	100.0	24	**PDB header:**ligase **Chain:** C: **PDB Molecule:**nonribosomal peptide synthase; **PDBTitle:** crystal structure of cmis6
98	c5oe3C_	Alignment	not modelled	100.0	22	**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)
99	c3e53A_	Alignment	not modelled	100.0	26	**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 mycobacterium tuberculosis
100	c3t5cA_	Alignment	not modelled	100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**probable chain-fatty-acid-coa ligase fadd13; **PDBTitle:** crystal structure of n-terminal domain of facl13 from mycobacterium2 tuberculosis in different space group c2
101	c6abhG_	Alignment	not modelled	100.0	17	**PDB header:**luminescent protein **Chain:** G: **PDB Molecule:**red-bioluminescence eliciting luciferase; **PDBTitle:** structure of a natural red emitting luciferase from phrixothrix hirtus2 (p1 crystal form)
102	c4gs5A_	Alignment	not modelled	100.0	16	**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 dyadobacter fermentans dsm 18053
						PDB header:transferase

103	c3fotA_	Alignment	not modelled	100.0	13	**Chain:** A: **PDB Molecule:**15-o-acetyltransferase; **PDBTitle:** structural and functional characterization of tri3 trichothecene 15-o-2 acetyltransferase from fusarium sporotrichioides
104	c4w4tA_	Alignment	not modelled	100.0	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mxaa; **PDBTitle:** the crystal structure of the terminal r domain from the myxalamid pks-2 nrps biosynthetic pathway
105	c2y4oA_	Alignment	not modelled	100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of paak2 in complex with phenylacetyl adenylate
106	c2y27B_	Alignment	not modelled	100.0	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of paak1 in complex with atp from burkholderia2 cenocepacia
107	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) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
108	c1q9jA_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**polyketide synthase associated protein 5; **PDBTitle:** structure of polyketide synthase associated protein 5 from2 mycobacterium tuberculosis
109	c4f6cA_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ausa reductase domain protein; **PDBTitle:** crystal structure of aureusimine biosynthetic cluster reductase domain
110	c6chjB_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**diacylglycerol o-acyltransferase; **PDBTitle:** wax ester synthase/diacylglycerol acyltransferase from marinobacter2 aquaeolei vt8
111	d1l5aa2	Alignment	not modelled	100.0	13	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
112	c2v6gA_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**progesterone 5-beta-reductase; **PDBTitle:** structure of progesterone 5beta-reductase from digitalis2 lanata in complex with nadp
113	c5df1A_	Alignment	not modelled	100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iridoid synthase; **PDBTitle:** iridoid synthase from catharanthus roseus - ternary complex with nadp+2 and geranic acid
114	c3pvzD_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine 4,6-dehydratase; **PDBTitle:** udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri
115	c1z7eC_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of full length arna
116	c1z45A_	Alignment	not modelled	100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**gal10 bifunctional protein; **PDBTitle:** crystal structure of the gal10 fusion protein galactose2 mutarotase/udp-galactose 4-epimerase from saccharomyces cerevisiae3 complexed with nad, udp-glucose, and galactose
117	c6el3A_	Alignment	not modelled	100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxo-delta(4,5)-steroid 5-beta-reductase; **PDBTitle:** structure of progesterone 5beta-reductase from arabidopsis thaliana in2 complex with nadp
118	c3w1vA_	Alignment	not modelled	100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**capsular polysaccharide synthesis enzyme cap8e; **PDBTitle:** crystal structure of capsular polysaccharide synthesizing enzyme cape2 from staphylococcus aureus in complex with inihibitor
119	d1l5aa1	Alignment	not modelled	100.0	23	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
120	c3hguB_	Alignment	not modelled	100.0	12	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**ehpf; **PDBTitle:** structure of phenazine antibiotic biosynthesis protein