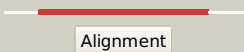

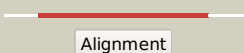
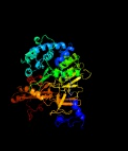
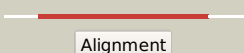
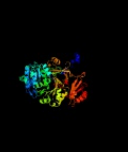
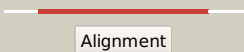

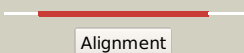

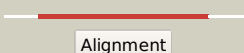

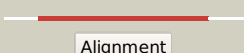





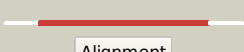

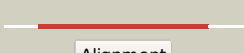



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0551c_(fadD8)_641099_642814
Date	Fri Jul 26 01:50:10 BST 2019
Unique Job ID	7f3086aa2e13b981

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6eqoB_	 Alignment		100.0	21	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
2	c5es8A_	 Alignment		100.0	19	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
3	c6p1jA_	 Alignment		100.0	23	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
4	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
5	c5u89A_	 Alignment		100.0	26	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
6	c5ja2A_	 Alignment		100.0	21	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
7	c5ifiA_	 Alignment		100.0	19	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
8	d1pg4a_	 Alignment		100.0	19	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
9	c2vsqA_	 Alignment		100.0	21	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
10	d1ry2a_	 Alignment		100.0	21	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
11	c5wmmA_	 Alignment		100.0	23	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

12	c4wd1A_	Alignment		100.0	17	PDB header: ligase Chain: A: PDB Molecule: acetoacetate-coa ligase; PDBTitle: acetoacetyl-coa synthetase from streptomyces lividans
13	c4wv3A_	Alignment		100.0	24	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
14	c3e7wA_	Alignment		100.0	18	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
15	d1mdba_	Alignment		100.0	25	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
16	c5msdA_	Alignment		100.0	20	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
17	c5ie2A_	Alignment		100.0	24	PDB header: ligase Chain: A: PDB Molecule: oxalate--coa ligase; PDBTitle: crystal structure of a plant enzyme
18	c4eatB_	Alignment		100.0	22	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structure of a benzoate coenzyme a ligase
19	c4zxiA_	Alignment		100.0	20	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
20	c4zxiA_	Alignment		100.0	21	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
21	c3vngA_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: nrps adenylation protein cytc1; PDBTitle: co-crystal structure of nrps adenylation protein cytc1 with atp from2 streptomyces
22	d3cw9a1	Alignment	not modelled	100.0	22	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
23	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
24	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
25	c6h1bA_	Alignment	not modelled	100.0	30	PDB header: ligase Chain: A: PDB Molecule: fatty acid coa ligase; PDBTitle: structure of amide bond synthetase mcba k483a mutant from2 marinactinospora thermotolerans
26	c5x8gA_	Alignment	not modelled	100.0	28	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
27	c5mssA_	Alignment	not modelled	100.0	19	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 PDB header: ligase

28	c4oxiA_	Alignment	not modelled	100.0	18	Chain: A: PDB Molecule: enterobactin synthetase component f-related protein; PDBTitle: crystal structure of vibrio cholerae adenylation domain alme in2 complex with glycy-adenosine-5'-phosphate
29	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
30	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
31	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
32	c3r44A_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: fatty acyl coa synthetase fadd13 (fatty-acyl-coa PDBTitle: mycobacterium tuberculosis fatty acyl coa synthetase
33	c5u2aA_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of brucella canis acyl-coa synthetase
34	c4ir7A_	Alignment	not modelled	100.0	23	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
35	c6ijbA_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: amp-binding domain protein; PDBTitle: structure of 3-methylmercaptopyruvate coa ligase mutant k523a in2 complex with amp and mmpa
36	c5e7qB_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: B: PDB Molecule: acyl-coa synthetase; PDBTitle: acyl-coa synthetase ptma2 from streptomyces platensis
37	c3rg2H_	Alignment	not modelled	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
38	c4dg8A_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: pa1221; PDBTitle: structure of pa1221, an nrps protein containing adenylation and pcp2 domains
39	c5aplA_	Alignment	not modelled	100.0	21	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
40	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
41	c5keiA_	Alignment	not modelled	100.0	25	PDB header: ligase Chain: A: PDB Molecule: 2,3-dihydroxybenzoate-amp ligase; PDBTitle: mycobacterium smegmatis mbta apo structure
42	d1amua_	Alignment	not modelled	100.0	18	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
43	c1amuB_	Alignment	not modelled	100.0	18	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
44	c2v7bB_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
45	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
46	c6ac3B_	Alignment	not modelled	100.0	24	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)
47	c3tsyA_	Alignment	not modelled	100.0	22	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
48	c2d1tA_	Alignment	not modelled	100.0	23	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
49	c3gqwB_	Alignment	not modelled	100.0	21	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
50	c4dg9A_	Alignment	not modelled	100.0	21	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
51	c3dhvA_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: d-alanine-poly(phosphoribitol) ligase; PDBTitle: crystal structure of dlta protein in complex with d-alanine2 adenylate
52	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
53	c4r0mB_	Alignment	not modelled	100.0	20 PDB header: ligase Chain: B: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
54	d1lcia_	Alignment	not modelled	100.0	20 Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
55	c4r0mA_	Alignment	not modelled	100.0	21 PDB header: ligase Chain: A: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
56	c4d56A_	Alignment	not modelled	100.0	24 PDB header: hydrolase Chain: A: PDB Molecule: apnaa1; PDBTitle: understanding bi-specificity of a-domains
57	c3iteB_	Alignment	not modelled	100.0	18 PDB header: ligase Chain: B: PDB Molecule: sidn siderophore synthetase; PDBTitle: the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
58	c3l8cA_	Alignment	not modelled	100.0	19 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
59	c6akdA_	Alignment	not modelled	100.0	22 PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn17
60	c5jqbB_	Alignment	not modelled	100.0	22 PDB header: ligase Chain: B: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn11
61	c5buqA_	Alignment	not modelled	100.0	26 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
62	d1v25a_	Alignment	not modelled	100.0	25 Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
63	c3iplB_	Alignment	not modelled	100.0	22 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
64	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
65	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
66	c6ozvA_	Alignment	not modelled	100.0	21 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
67	c5c5hA_	Alignment	not modelled	100.0	23 PDB header: ligase Chain: A: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: r195k e. coli mene with bound osb-ams
68	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
69	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
70	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
71	c4w8oA_	Alignment	not modelled	100.0	17 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
72	c3ivrA_	Alignment	not modelled	100.0	24 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
73	c5jpbB_	Alignment	not modelled	100.0	19 PDB header: ligase Chain: B: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
74	c3qyaA_	Alignment	not modelled	100.0	22 PDB header: oxidoreductase Chain: A: PDB Molecule: luciferase; PDBTitle: crystal structure of a red-emitter mutant of lampyris turkestanicus2 luciferase
75	c5n81B_	Alignment	not modelled	100.0	20 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
76	c5oe3C_	Alignment	not modelled	100.0	18 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)
77	c4lqcA_	Alignment	not modelled	100.0	17 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

78	c3wv4B_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of vinn
79	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
80	c5burB_	Alignment	not modelled	100.0	23	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
81	c6abhG_	Alignment	not modelled	100.0	19	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)
82	c5jipC_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: C: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
83	c3e53A_	Alignment	not modelled	100.0	22	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
84	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
85	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 dyadobacter fermentans dsm 18053
86	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
87	c3qovD_	Alignment	not modelled	100.0	16	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
88	c3hguB_	Alignment	not modelled	99.8	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: ehpf; PDBTitle: structure of phenazine antibiotic biosynthesis protein
89	c3laxA_	Alignment	not modelled	99.7	20	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: the crystal structure of a domain of phenylacetate-coenzyme2 a ligase from bacteroides vulgatus atcc 8482
90	c4ep1A_	Alignment	not modelled	98.3	16	PDB header: ligase Chain: A: PDB Molecule: jasmonic acid-amido synthetase jar1; PDBTitle: crystal structure of arabidopsis thaliana gh3.11 (jar1) in complex2 with ja-ile
91	c5kodA_	Alignment	not modelled	98.3	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
92	c4b2gB_	Alignment	not modelled	97.8	11	PDB header: signaling protein Chain: B: PDB Molecule: gh3-1 auxin conjugating enzyme; PDBTitle: crystal structure of an indole-3-acetic acid amido synthase from vitis2 vinifera involved in auxin homeostasis
93	c6avhA_	Alignment	not modelled	97.7	11	PDB header: ligase, plant protein Chain: A: PDB Molecule: gh3.15 acyl acid amido synthetase; PDBTitle: gh3.15 acyl acid amido synthetase
94	c4ewvB_	Alignment	not modelled	96.4	11	PDB header: ligase Chain: B: PDB Molecule: 4-substituted benzoates-glutamate ligase gh3.12; PDBTitle: crystal structure of gh3.12 in complex with ampcpp
95	d2ayia1	Alignment	not modelled	72.7	8	Fold: Thermophilic metalloprotease-like Superfamily: Thermophilic metalloprotease-like Family: Thermophilic metalloprotease (M29)
96	c3smaD_	Alignment	not modelled	65.9	18	PDB header: transferase Chain: D: PDB Molecule: frbf; PDBTitle: a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
97	c6mb6A_	Alignment	not modelled	64.4	20	PDB header: transferase Chain: A: PDB Molecule: aac(3)-iiib protein; PDBTitle: aac-iiib binary with coash
98	c5ht0B_	Alignment	not modelled	62.6	18	PDB header: transferase Chain: B: PDB Molecule: aminoglycoside acetyltransferase hmb0005; PDBTitle: crystal structure of an antibiotic_nat family aminoglycoside2 acetyltransferase hmb0038 from an uncultured soil metagenomic sample3 in complex with coenzyme a
99	c5u18A_	Alignment	not modelled	58.7	26	PDB header: transferase Chain: A: PDB Molecule: n-3" methyltransferase; PDBTitle: crystal structure of a methyltransferase involved in the biosynthesis2 of gentamicin in complex with the geneticin
100	c6bc3A_	Alignment	not modelled	56.8	20	PDB header: transferase/antibiotic Chain: A: PDB Molecule: aac 3-vi protein; PDBTitle: cryo x-ray structure of sisomicin bound aac-via
101	c4k2bA_	Alignment	not modelled	55.9	20	PDB header: transferase Chain: A: PDB Molecule: ntd biosynthesis operon protein ntda; PDBTitle: crystal structure of ntda from bacillus subtilis in complex with the2 internal aldimine
102	d1piwa2	Alignment	not modelled	54.8	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

						Family: Alcohol dehydrogenase-like, C-terminal domain
103	d2nyga1	Alignment	not modelled	53.5	18	Fold: TTHA0583/YokD-like Superfamily: TTHA0583/YokD-like Family: Aminoglycoside 3-N-acetyltransferase-like
104	c3e4fB_	Alignment	not modelled	53.4	16	PDB header: transferase Chain: B: PDB Molecule: aminoglycoside n3-acetyltransferase; PDBTitle: crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
105	c6mn5A_	Alignment	not modelled	52.2	22	PDB header: transferase/antibiotic Chain: A: PDB Molecule: aminoglycoside n(3)-acetyltransferase, aac(3)-iva; PDBTitle: crystal structure of aminoglycoside acetyltransferase aac(3)-iva,2 h154a mutant, in complex with gentamicin c1a
106	c2jwB_	Alignment	not modelled	50.4	12	PDB header: membrane protein Chain: B: PDB Molecule: protein tolR; PDBTitle: solution structure of periplasmic domain of tolR from h.2 influenzae with saxs data
107	d1kola2	Alignment	not modelled	49.5	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
108	c3ippA_	Alignment	not modelled	46.0	10	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase ynje; PDBTitle: crystal structure of sulfur-free ynje
109	c6raoI_	Alignment	not modelled	45.5	14	PDB header: virus like particle Chain: I: PDB Molecule: afp11; PDBTitle: cryo-em structure of the anti-feeding prophage (afp) baseplate, 6-fold2 symmetrised
110	c3u5rG_	Alignment	not modelled	45.1	18	PDB header: structural genomics, unknown function Chain: G: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein smc02350 from2 sinorhizobium meliloti 1021
111	c4z1oB_	Alignment	not modelled	44.1	13	PDB header: transferase Chain: B: PDB Molecule: phosphoribosyltransferase; PDBTitle: hypoxanthine-guanine-xanthine phosphoribosyltransferase (hgxpRT) from2 sulfolobus solfataricus in complex with alpha-3 phosphoribosylpyrophosphoric acid (prpp) and magnesium
112	c1uarA_	Alignment	not modelled	40.7	10	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: crystal structure of rhodanese from thermus thermophilus hb8
113	d1udxa3	Alignment	not modelled	37.6	20	Fold: Obg GTP-binding protein C-terminal domain Superfamily: Obg GTP-binding protein C-terminal domain Family: Obg GTP-binding protein C-terminal domain
114	c3bcxA_	Alignment	not modelled	37.2	12	PDB header: transferase Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; PDBTitle: e1 dehydrase
115	c5by4A_	Alignment	not modelled	36.8	14	PDB header: protein transport Chain: A: PDB Molecule: protein tolR; PDBTitle: structure and function of the escherichia coli tol-pal stator protein2 tolR
116	d1rjwa2	Alignment	not modelled	36.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
117	c2ywiA_	Alignment	not modelled	34.3	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein; PDBTitle: crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
118	c3eegB_	Alignment	not modelled	34.1	9	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
119	c2cw6B_	Alignment	not modelled	33.7	15	PDB header: lyase Chain: B: PDB Molecule: hydroxymethylglutaryl-coa lyase, mitochondrial; PDBTitle: crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
120	c3olhA_	Alignment	not modelled	33.0	5	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: human 3-mercaptopyruvate sulfurtransferase