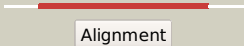

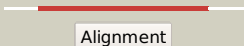

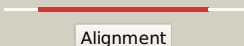







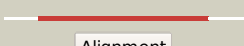




















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1013_(pks16)_1131629_1133263
Date	Wed Jul 31 22:05:08 BST 2019
Unique Job ID	b9f68106191b584c

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 nadt+ and phosphomethylphosphonic acid adenylate ester
2	c5gxdA_	 Alignment		100.0	19	PDB header: lyase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: structure of acryloyl-coa lyase prpe from dinoroseobacter shibae dfl2 12
3	c6p1jA_	 Alignment		100.0	20	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	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
5	d1pg4a_	 Alignment		100.0	18	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
6	c5ifiA_	 Alignment		100.0	18	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
7	c5wmmA_	 Alignment		100.0	22	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
8	c4wd1A_	 Alignment		100.0	19	PDB header: ligase Chain: A: PDB Molecule: acetoacetate-coa ligase; PDBTitle: acetoacetyl-coa synthetase from streptomyces lividans
9	c5u89A_	 Alignment		100.0	23	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
10	d1ry2a_	 Alignment		100.0	19	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
11	c5ja2A_	 Alignment		100.0	20	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

12	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
13	c3gqwB_	Alignment		100.0	28	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
14	c6n8eA_	Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: holo-obif1; PDBTitle: crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
15	c5msdA_	Alignment		100.0	17	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
16	c3e7wA_	Alignment		100.0	17	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
17	c4wv3A_	Alignment		100.0	18	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
18	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
19	d3cw9a1	Alignment		100.0	21	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
20	c3kxwA_	Alignment		100.0	24	PDB header: ligase Chain: A: PDB Molecule: saframycin mx1 synthetase b; PDBTitle: the crystal structure of fatty acid amp ligase from legionella2 pneumophila
21	c4zxiA_	Alignment	not modelled	100.0	20	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
22	c5mstA_	Alignment	not modelled	100.0	17	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	c4r0mB_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: B: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
24	c5ey8D_	Alignment	not modelled	100.0	27	PDB header: ligase Chain: D: PDB Molecule: acyl-coa synthase; PDBTitle: structure of fadd32 from mycobacterium smegmatis complexed to ampc20
25	c5ie2A_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: oxalate--coa ligase; PDBTitle: crystal structure of a plant enzyme
26	c5mssA_	Alignment	not modelled	100.0	20	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
27	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
						PDB header: ligase

28	c4eatB_	Alignment	not modelled	100.0	20	Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structure of a benzoate coenzyme a ligase
29	c5x8gA_	Alignment	not modelled	100.0	21	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
30	d1mdba_	Alignment	not modelled	100.0	20	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
31	c5u2aA_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of brucella canis acyl-coa synthetase
32	c5wm7A_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: salicylate-amp ligase; PDBTitle: crystal structure of cahj in complex with amp
33	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
34	c3etcB_	Alignment	not modelled	100.0	17	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
35	c4r0mA_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
36	c3ni2A_	Alignment	not modelled	100.0	22	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
37	c3rg2H_	Alignment	not modelled	100.0	20	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	c3eynB_	Alignment	not modelled	100.0	18	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
39	c6h1bA_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: fatty acid coa ligase; PDBTitle: structure of amide bond synthetase mcba k483a mutant from2 marinactinospora thermotolerans
40	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
41	c6ijbA_	Alignment	not modelled	100.0	16	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	c4dg8A_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: pa1221; PDBTitle: structure of pa1221, an nrps protein containing adenylation and pcp2 domains
43	c3r44A_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: fatty acyl coa synthetase fadd13 (fatty-acyl-coa PDBTitle: mycobacterium tuberculosis fatty acyl coa synthetase
44	c5aplA_	Alignment	not modelled	100.0	22	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
45	c2v7bB_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
46	c4dg9A_	Alignment	not modelled	100.0	18	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
47	c5keiA_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: 2,3-dihydroxybenzoate-amp ligase; PDBTitle: mycobacterium smegmatis mbta apo structure
48	c4fuqD_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: D: PDB Molecule: malonyl coa synthetase; PDBTitle: crystal structure of apo matb from rhodopseudomonas palustris
49	c4oxiA_	Alignment	not modelled	100.0	16	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 glycyI-adenosine-5'-phosphate
50	c3iteB_	Alignment	not modelled	100.0	14	PDB header: ligase Chain: B: PDB Molecule: sidn siderophore synthetase; PDBTitle: the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
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	d1amua_	Alignment	not modelled	100.0	17	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like

53	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
54	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
55	c4d56A	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: apnaa1; PDBTitle: understanding bi-specificity of a-domains
56	c5e7qB	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B; PDB Molecule: acyl-coa synthetase; PDBTitle: acyl-coa synthetase ptma2 from streptomyces platensis
57	c1amuB	Alignment	not modelled	100.0	15	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
58	d1v25a	Alignment	not modelled	100.0	23	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
59	c5jjqB	Alignment	not modelled	100.0	20	PDB header: ligase Chain: B; PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn11
60	d1l1cia	Alignment	not modelled	100.0	18	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
61	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
62	c6ozvA	Alignment	not modelled	100.0	19	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
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	c3ip1B	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	c5buqA	Alignment	not modelled	100.0	19	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
66	c3g7sA	Alignment	not modelled	100.0	22	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
67	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
68	c4gr5B	Alignment	not modelled	100.0	24	PDB header: ligase Chain: B; PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of slgn1deltaasub in complex with ampcpp
69	c5c5hA	Alignment	not modelled	100.0	20	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	19	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	c5jipB	Alignment	not modelled	100.0	20	PDB header: ligase Chain: B; PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
72	c3o82B	Alignment	not modelled	100.0	20	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	c3o82A	Alignment	not modelled	100.0	20	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
74	c4lqcA	Alignment	not modelled	100.0	16	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
75	c3qyaA	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A; PDB Molecule: luciferase; PDBTitle: crystal structure of a red-emitter mutant of lampyris turkestanicus2 luciferase
76	c5oe3C	Alignment	not modelled	100.0	23	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	c3wv4B	Alignment	not modelled	100.0	19	PDB header: ligase Chain: B; PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of vinn
						PDB header: ligase

78	c3ivrA	Alignment	not modelled	100.0	20	Chain: A: PDB Molecule: putative long-chain-fatty-acid coa ligase; PDBTitle: crystal structure of putative long-chain-fatty-acid coa ligase from2 rhodospseudomonas palustris cga009
79	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
80	c3t5cA	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: probable chain-fatty-acid-coa ligase fadd13; PDBTitle: crystal structure of n-terminal domain of fac13 from mycobacterium2 tuberculosis in different space group c2
81	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
82	c3e53A	Alignment	not modelled	100.0	24	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
83	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 phrixothrix hirtus2 (p1 crystal form)
84	c5jipC	Alignment	not modelled	100.0	20	PDB header: ligase Chain: C: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
85	c2y4oA	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak2 in complex with phenylacetyl adenylate
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	17	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	c4gs5A	Alignment	not modelled	100.0	18	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
89	c3hguB	Alignment	not modelled	99.9	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: ehpf; PDBTitle: structure of phenazine antibiotic biosynthesis protein
90	c3laxA	Alignment	not modelled	99.7	18	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
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	c4eplA	Alignment	not modelled	98.1	11	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
93	c4b2gB	Alignment	not modelled	97.5	8	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
94	c6avhA	Alignment	not modelled	97.2	15	PDB header: ligase, plant protein Chain: A: PDB Molecule: gh3.15 acyl acid amido synthetase; PDBTitle: gh3.15 acyl acid amido synthetase
95	c4ewvB	Alignment	not modelled	95.6	11	PDB header: ligase Chain: B: PDB Molecule: 4-substituted benzoates-glutamate ligase gh3.12; PDBTitle: crystal structure of gh3.12 in complex with amcpp
96	d2ayia1	Alignment	not modelled	74.6	14	Fold: Thermophilic metalloprotease-like Superfamily: Thermophilic metalloprotease-like Family: Thermophilic metalloprotease (M29)
97	d1pl8a2	Alignment	not modelled	63.8	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
98	c4k2bA	Alignment	not modelled	54.2	26	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
99	d1piwa2	Alignment	not modelled	51.5	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
100	c3smaD	Alignment	not modelled	49.8	32	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
101	c4z1oB	Alignment	not modelled	49.7	19	PDB header: transferase Chain: B: PDB Molecule: phosphoribosyltransferase; PDBTitle: hypoxanthine-guanine-xanthine phosphoribosyltransferase (hgxpvt) from2 sulfobolus solfataricus in complex with alpha-3 phosphoribosylpyrophosphoric acid (prpp) and magnesium
102	c4trbA	Alignment	not modelled	46.8	19	PDB header: transferase Chain: A: PDB Molecule: purine phosphoribosyltransferase (gpt-1);

						PDBTitle: sulfolobus solfataricus adenine phosphoribosyltransferase
103	c6bc3A_	Alignment	not modelled	43.7	20	PDB header: transferase/antibiotic Chain: A: PDB Molecule: aac 3-vi protein; PDBTitle: cryo x-ray structure of sisomicin bound aac-via
104	c5vogA_	Alignment	not modelled	40.8	19	PDB header: transferase Chain: A: PDB Molecule: putative phosphoribosyltransferase; PDBTitle: crystal structure of a hypothetical protein from neisseria gonorrhoeae2 with bound pppp
105	d1kola2	Alignment	not modelled	38.5	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
106	c6mn5A_	Alignment	not modelled	37.2	30	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
107	c5ht0B_	Alignment	not modelled	37.1	30	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
108	c3e4fB_	Alignment	not modelled	36.7	18	PDB header: transferase Chain: B: PDB Molecule: aminoglycoside n3-acetyltransferase; PDBTitle: crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
109	d2nyga1	Alignment	not modelled	36.4	20	Fold: TTHA0583/YokD-like Superfamily: TTHA0583/YokD-like Family: Aminoglycoside 3-N-acetyltransferase-like
110	c6mb6A_	Alignment	not modelled	33.5	26	PDB header: transferase Chain: A: PDB Molecule: aac(3)-iiib protein; PDBTitle: aac-iiib binary with coash
111	d1f06a2	Alignment	not modelled	32.8	23	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
112	c5w70B_	Alignment	not modelled	32.3	20	PDB header: transferase Chain: B: PDB Molecule: l- glutamine:2-deoxy-scylo-inosose aminotransferase; PDBTitle: x-ray structure of rbmb from streptomyces ribosidificus
113	c3ippA_	Alignment	not modelled	31.1	17	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase ynje; PDBTitle: crystal structure of sulfur-free ynje
114	c1uarA_	Alignment	not modelled	29.5	8	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: crystal structure of rhodanese from thermus thermophilus hb8
115	d1z7wa1	Alignment	not modelled	29.0	10	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
116	c3mlcC_	Alignment	not modelled	28.5	19	PDB header: isomerase Chain: C: PDB Molecule: fg41 malonate semialdehyde decarboxylase; PDBTitle: crystal structure of fg41msad inactivated by 3-chloropropiolate
117	c3bcxA_	Alignment	not modelled	26.5	12	PDB header: transferase Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; PDBTitle: e1 dehydrase
118	c5u18A_	Alignment	not modelled	26.3	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
119	c6raoI_	Alignment	not modelled	26.2	10	PDB header: virus like particle Chain: I: PDB Molecule: afp11; PDBTitle: cryo-em structure of the anti-feeding prophage (afp) baseplate, 6-fold2 symmetrised
120	d1zjca1	Alignment	not modelled	26.2	16	Fold: Thermophilic metalloprotease-like Superfamily: Thermophilic metalloprotease-like Family: Thermophilic metalloprotease (M29)