














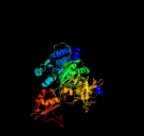

















Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1925_(fadD31)_2177094_2178956
 Date Fri Aug 2 13:30:54 BST 2019
 Unique Job ID 4f85f2aac894e28c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6eqoB_	 Alignment		100.0	19	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	c5ey8D_	 Alignment		100.0	44	PDB header: ligase Chain: D: PDB Molecule: acyl-coa synthase; PDBTitle: structure of fadd32 from mycobacterium smegmatis complexed to ampc20
3	c5es8A_	 Alignment		100.0	24	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
4	c6p1jA_	 Alignment		100.0	25	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
5	c5gxdA_	 Alignment		100.0	17	PDB header: lyase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: structure of acryloyl-coa lyase prpe from dinoroseobacter shibae df12 12
6	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
7	c5u89A_	 Alignment		100.0	22	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
8	c5ja2A_	 Alignment		100.0	22	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
9	d1pg4a_	 Alignment		100.0	18	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
10	d1ry2a_	 Alignment		100.0	19	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	18	PDB header: ligase Chain: A: PDB Molecule: acetoacetate-coa ligase; PDBTitle: acetoacetyl-coa synthetase from streptomyces lividans
13	c2vsqA_	Alignment		100.0	19	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
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	21	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	c3kxwA_	Alignment		100.0	29	PDB header: ligase Chain: A: PDB Molecule: saframycin mx1 synthetase b; PDBTitle: the crystal structure of fatty acid amp ligase from legionella2 pneumophila
17	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
18	c5mstA_	Alignment		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
19	c4zxiA_	Alignment		100.0	22	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
20	c3gqwB_	Alignment		100.0	30	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
21	c3tsyA_	Alignment	not modelled	100.0	23	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	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
23	c4zxiA_	Alignment	not modelled	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
24	c4r0mB_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: B: PDB Molecule: mcgy protein; PDBTitle: structure of mcgy a-pcp complexed with phenylalanyl-adenylate
25	c4r0mA_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: mcgy protein; PDBTitle: structure of mcgy a-pcp complexed with phenylalanyl-adenylate
26	c5ie2A_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: oxalate--coa ligase; PDBTitle: crystal structure of a plant enzyme
27	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
28	c4wv3A_	Alignment	not modelled	100.0	21	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
29	d3cw9a1	Alignment	not modelled	100.0	21 Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
30	d1mdba_	Alignment	not modelled	100.0	19 Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
31	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
32	c4eatB_	Alignment	not modelled	100.0	22 PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structure of a benzoate coenzyme a ligase
33	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
34	c3etcB_	Alignment	not modelled	100.0	13 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	c5wm7A_	Alignment	not modelled	100.0	21 PDB header: ligase Chain: A: PDB Molecule: salicylate-amp ligase; PDBTitle: crystal structure of cahj in complex with amp
36	c5x8gA_	Alignment	not modelled	100.0	22 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
37	c3eynB_	Alignment	not modelled	100.0	15 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
38	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 glycy-adenosine-5'-phosphate
39	c3r44A_	Alignment	not modelled	100.0	22 PDB header: ligase Chain: A: PDB Molecule: fatty acyl coa synthetase fadd13 (fatty-acyl-coa PDBTitle: mycobacterium tuberculosis fatty acyl coa synthetase
40	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
41	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)
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	c6ijbA_	Alignment	not modelled	100.0	17 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
44	c3rg2H_	Alignment	not modelled	100.0	16 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
45	c3iteB_	Alignment	not modelled	100.0	16 PDB header: ligase Chain: B: PDB Molecule: sidn siderophore synthetase; PDBTitle: the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
46	c4ir7A_	Alignment	not modelled	100.0	18 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	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
48	c2d1tA_	Alignment	not modelled	100.0	18 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	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
50	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
51	d1amua_	Alignment	not modelled	100.0	19 Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
52	c5keiA_	Alignment	not modelled	100.0	21 PDB header: ligase Chain: A: PDB Molecule: 2,3-dihydroxybenzoate-amp ligase; PDBTitle: mycobacterium smegmatis mbta apo structure
					PDB header: hydrolase

53	c4d56A_	Alignment	not modelled	100.0	21	Chain: A: PDB Molecule: apnaa1; PDBTitle: understanding bi-specificity of a-domains
54	c6ozvA_	Alignment	not modelled	100.0	24	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
55	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
56	c5jjqB_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: B: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn11
57	d1v25a_	Alignment	not modelled	100.0	19	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
58	c5e7qB_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: acyl-coa synthetase; PDBTitle: acyl-coa synthetase ptma2 from streptomyces platensis
59	c6akdA_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn17
60	c3dhvA_	Alignment	not modelled	100.0	20	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	c4fuqD_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: D: PDB Molecule: malonyl coa synthetase; PDBTitle: crystal structure of apo matb from rhodopseudomonas palustris
62	c3g7sA_	Alignment	not modelled	100.0	20	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
63	d1lcia_	Alignment	not modelled	100.0	16	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
64	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
65	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
66	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
67	c3nyrA_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: malonyl-coa ligase; PDBTitle: malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
68	c3iplB_	Alignment	not modelled	100.0	19	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
69	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
70	c5jipB_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: B: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
71	c5c5hA_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: r195k e. coli mene with bound osb-ams
72	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
73	c3e53A_	Alignment	not modelled	100.0	34	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
74	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
75	c5n81B_	Alignment	not modelled	100.0	21	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	c3wv4B_	Alignment	not modelled	100.0	24	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of vinn
77	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
78	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
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 from2 rhodospseudomonas palustris cga009
80	c5oe3C_	Alignment	not modelled	100.0	20	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)
81	c3t5cA_	Alignment	not modelled	100.0	23	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
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 phrixothrix hirtus2 (p1 crystal form)
83	c5burB_	Alignment	not modelled	100.0	22	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
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	22	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	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
87	c2y27B_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: B: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak1 in complex with atp from burkholderia2 cenocepacia
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) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
89	c3hguB_	Alignment	not modelled	99.9	16	PDB header: biosynthetic protein Chain: B: PDB Molecule: ehpf; PDBTitle: structure of phenazine antibiotic biosynthesis protein
90	c3laxA_	Alignment	not modelled	99.6	13	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	99.1	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	98.7	15	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	98.4	14	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	98.1	11	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	96.6	18	PDB header: ligase Chain: B: PDB Molecule: 4-substituted benzoates-glutamate ligase gh3.12; PDBTitle: crystal structure of gh3.12 in complex with ampcpp
96	c5f1yA_	Alignment	not modelled	68.1	30	PDB header: hydrolase Chain: A: PDB Molecule: mccc family protein; PDBTitle: crystal structure of ba3275, the member of s66 family of serine2 peptidases
97	c4je5C_	Alignment	not modelled	58.2	18	PDB header: transferase Chain: C: PDB Molecule: aromatic/aminoadipate aminotransferase 1; PDBTitle: crystal structure of the aromatic aminotransferase aro8, a putative2 alpha-aminoadipate aminotransferase in saccharomyces cerevisiae
98	c4j5uB_	Alignment	not modelled	57.3	13	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: x-ray crystal structure of a serine hydroxymethyltransferase with2 covalently bound plp from rickettsia rickettsii str. sheila smith
99	d2ayia1	Alignment	not modelled	51.0	22	Fold: Thermophilic metalloprotease-like Superfamily: Thermophilic metalloprotease-like Family: Thermophilic metalloprotease (M29)
100	c2dkjB_	Alignment	not modelled	40.4	13	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.hb8 serine hydroxymethyltransferase
101	c5dlcC_	Alignment	not modelled	38.9	16	PDB header: transferase Chain: C: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: x-ray crystal structure of a pyridoxine 5-prime-phosphate synthase2 from pseudomonas aeruginosa
102	c1c4kA_	Alignment	not modelled	38.4	17	PDB header: lyase Chain: A: PDB Molecule: protein (ornithine decarboxylase); PDBTitle: ornithine decarboxylase mutant (gly121tyr)

103	c3g23A_	Alignment	not modelled	34.1	20	PDB header: hydrolase Chain: A: PDB Molecule: ld-carboxypeptidase a; PDBTitle: crystal structure of a ld-carboxypeptidase a (saro_1426) from2 novosphingobium aromaticivorans dsm at 1.89 a resolution
104	c3d6kB_	Alignment	not modelled	33.7	13	PDB header: transferase Chain: B: PDB Molecule: putative aminotransferase; PDBTitle: the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
105	c3tlgB_	Alignment	not modelled	32.5	13	PDB header: hydrolase Chain: B: PDB Molecule: mccf; PDBTitle: microcin c7 self immunity protein mccf in the inactive mutant apo2 state
106	c6hnuA_	Alignment	not modelled	31.5	19	PDB header: transferase Chain: A: PDB Molecule: aromatic amino acid aminotransferase i; PDBTitle: crystal structure of the aminotransferase aro8 from c. albicans with2 ligands
107	c6raoI_	Alignment	not modelled	29.3	9	PDB header: virus like particle Chain: I: PDB Molecule: afp11; PDBTitle: cryo-em structure of the anti-feeding prophage (afp) baseplate, 6-fold2 symmetrised
108	c4e5sC_	Alignment	not modelled	28.8	22	PDB header: hydrolase Chain: C: PDB Molecule: mccflike protein (ba_5613); PDBTitle: crystal structure of mccflike protein (ba_5613) from bacillus2 anthracis str. ames
109	c4wxFC_	Alignment	not modelled	28.8	13	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of l-serine hydroxymethyltransferase in complex with2 glycine
110	d1ja1a1	Alignment	not modelled	28.5	23	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: NADPH-cytochrome p450 reductase FAD-binding domain-like
111	c4oxqB_	Alignment	not modelled	25.9	11	PDB header: metal binding protein Chain: B: PDB Molecule: manganese abc transporter, periplasmic-binding protein PDBTitle: structure of staphylococcus pseudintermedius metal-binding protein2 sita in complex with zinc
112	c3gjzB_	Alignment	not modelled	25.8	17	PDB header: immune system Chain: B: PDB Molecule: microcin immunity protein mccf; PDBTitle: crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
113	d1vjoa_	Alignment	not modelled	25.6	24	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
114	c3hjtB_	Alignment	not modelled	24.9	7	PDB header: cell adhesion, transport protein Chain: B: PDB Molecule: lmb; PDBTitle: structure of laminin binding protein (lmb) of streptococcus agalactiae2 a bifunctional protein with adhesin and metal transporting activity
115	d1pl8a2	Alignment	not modelled	23.9	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
116	c3n75E_	Alignment	not modelled	21.8	10	PDB header: lyase Chain: E: PDB Molecule: lysine decarboxylase, inducible; PDBTitle: x-ray crystal structure of the escherichia coli inducible lysine2 decarboxylase ldci
117	c4h1hB_	Alignment	not modelled	21.7	23	PDB header: hydrolase Chain: B: PDB Molecule: lmo1638 protein; PDBTitle: crystal structure of mccf homolog from listeria monocytogenes egd-e
118	d1f20a1	Alignment	not modelled	21.1	19	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: NADPH-cytochrome p450 reductase FAD-binding domain-like