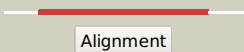

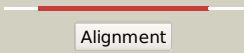



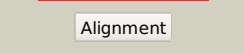



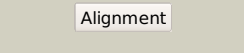

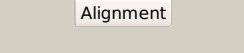



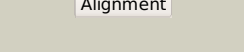

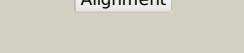

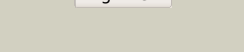

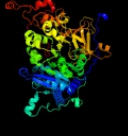

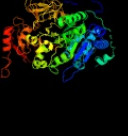








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2950c_(fadD29)_3300606_3302465
Date	Thu Aug 8 16:20:11 BST 2019
Unique Job ID	484180bff4b7048a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6eqoB_			100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: acetyl-coenzyme a synthetase; PDBTitle: tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nadp+ and phosphomethylphosphonic acid adenylate ester
2	c5gxdA_			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
3	c5es8A_			100.0	21	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_			100.0	24	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	c5u89A_			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
6	d1pg4a_			100.0	17	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
7	c5wmmA_			100.0	24	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	c5ja2A_			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
9	c5ey8D_			100.0	35	PDB header: ligase Chain: D: PDB Molecule: acyl-coa synthase; PDBTitle: structure of fadd32 from mycobacterium smegmatis complexed to ampc20
10	c5ifiA_			100.0	17	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
11	c5msdA_			100.0	19	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

12	c6n8eA_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: holo-obif1; PDBTitle: crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
13	c2vsqA_	Alignment		100.0	23	PDB header: ligase Chain: A: PDB Molecule: surfactin synthetase subunit 3; PDBTitle: structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module
14	d1ry2a_	Alignment		100.0	18	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
15	c4wd1A_	Alignment		100.0	15	PDB header: ligase Chain: A: PDB Molecule: acetoacetate-coa ligase; PDBTitle: acetoacetyl-coa synthetase from streptomyces lividans
16	c3kxwA_	Alignment		100.0	33	PDB header: ligase Chain: A: PDB Molecule: saframycin mx1 synthetase b; PDBTitle: the crystal structure of fatty acid amp ligase from legionella2 pneumophila
17	c5mstA_	Alignment		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
18	c4r0mB_	Alignment		100.0	25	PDB header: ligase Chain: B: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
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	c5mssA_	Alignment		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
21	c3gqwB_	Alignment	not modelled	100.0	29	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
22	c4zxiA_	Alignment	not modelled	100.0	19	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
23	c3tsyA_	Alignment	not modelled	100.0	19	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
24	c3e7wA_	Alignment	not modelled	100.0	22	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
25	c4r0mA_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
26	c5ie2A_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: oxalate--coa ligase; PDBTitle: crystal structure of a plant enzyme
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
28	d3cw9a1	Alianment	not modelled	100.0	20	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like

						Family: Acetyl-CoA synthetase-like
29	d1mdba_	Alignment	not modelled	100.0	18	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
30	c4wv3A_	Alignment	not modelled	100.0	19	PDB header: ligase/inhibitor Chain: A: PDB Molecule: anthranilate-coa ligase; PDBTitle: crystal structure of the anthranilate coa ligase auaeii in complex2 with anthranoyl-amp
31	c4eatB_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structure of a benzoate coenzyme a ligase
32	c5x8gA_	Alignment	not modelled	100.0	24	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
33	c3etcB_	Alignment	not modelled	100.0	16	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
34	c3ni2A_	Alignment	not modelled	100.0	21	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	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
36	c3eynB_	Alignment	not modelled	100.0	17	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
37	c5wm7A_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: salicylate-amp ligase; PDBTitle: crystal structure of cahj in complex with amp
38	c3rg2H_	Alignment	not modelled	100.0	15	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
39	c6ozvA_	Alignment	not modelled	100.0	25	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
40	c5u2aA_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of brucella canis acyl-coa synthetase
41	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
42	c3iteB_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: B: PDB Molecule: sidn siderophore synthetase; PDBTitle: the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
43	c5aplA_	Alignment	not modelled	100.0	23	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
44	c6ac3B_	Alignment	not modelled	100.0	18	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)
45	c4oxiA_	Alignment	not modelled	100.0	15	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
46	c3r44A_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: fatty acyl coa synthetase fadd13 (fatty-acyl-coa PDBTitle: mycobacterium tuberculosis fatty acyl coa synthetase
47	c6ijbA_	Alignment	not modelled	100.0	14	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
48	c2d1tA_	Alignment	not modelled	100.0	21	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	c6h1bA_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: fatty acid coa ligase; PDBTitle: structure of amide bond synthetase mcba k483a mutant from2 marinactinospora thermotolerans
50	c4d56A_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: apnaa1; PDBTitle: understanding bi-specificity of a-domains
51	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
52	c6akdA_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn17

53	d1amua_	Alignment	not modelled	100.0	17	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
54	c5keiA_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: 2,3-dihydroxybenzoate-amp ligase; PDBTitle: mycobacterium smegmatis mbta apo structure
55	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
56	c5e7qB_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: acyl-coa synthetase; PDBTitle: acyl-coa synthetase ptma2 from streptomyces platensis
57	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
58	d1v25a_	Alignment	not modelled	100.0	20	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
59	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
60	c5jjqB_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: B: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn11
61	c3g7sA_	Alignment	not modelled	100.0	19	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
62	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
63	c4gr5B_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of slgn1deltaasub in complex with ampcpp
64	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
65	d1l1cia_	Alignment	not modelled	100.0	17	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
66	c5buqA_	Alignment	not modelled	100.0	23	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	c3e53A_	Alignment	not modelled	100.0	54	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
69	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
70	c4w8oA_	Alignment	not modelled	100.0	20	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	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
72	c5jipB_	Alignment	not modelled	100.0	24	PDB header: ligase Chain: B: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
73	c3o82B_	Alignment	not modelled	100.0	18	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
74	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
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	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
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	c3wv4B_	Alianment	not modelled	100.0	22	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase;

						PDBTitle: crystal structure of vinn
79	c3ivrA_	Alignment	not modelled	100.0	22	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	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 fac13 from mycobacterium2 tuberculosis in different space group c2
81	c5oe3C_	Alignment	not modelled	100.0	19	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)
82	c5burB_	Alignment	not modelled	100.0	26	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
83	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)
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	19	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	17	PDB header: ligase Chain: B: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak1 in complex with atp from burkholderia2 cenocepacia
87	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
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	100.0	12	PDB header: biosynthetic protein Chain: B: PDB Molecule: ehpf; PDBTitle: structure of phenazine antibiotic biosynthesis protein
90	c3laxA_	Alignment	not modelled	99.6	15	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: the crystal structure of a domain of phenylacetate-coenzyme2 a ligase from bacteroides vulgatus atcc 8482
91	c5kodA_	Alignment	not modelled	99.4	9	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	99.3	14	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	99.0	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
94	c6avhA_	Alignment	not modelled	98.2	14	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	98.2	13	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	c6hnuA_	Alignment	not modelled	65.0	21	PDB header: transferase Chain: A: PDB Molecule: aromatic amino acid aminotransferase i; PDBTitle: crystal structure of the aminotransferase aro8 from c. albicans with2 ligands
97	c4j5uB_	Alignment	not modelled	60.1	9	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
98	c4je5C_	Alignment	not modelled	58.5	19	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
99	c2dkjB_	Alignment	not modelled	40.2	12	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.hb8 serine hydroxymethyltransferase
100	d1kl1a_	Alignment	not modelled	38.2	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
101	c4wxfC_	Alignment	not modelled	34.7	11	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of l-serine hydroxymethyltransferase in complex with2 glycine
102	d1nula_	Alignment	not modelled	33.8	20	Fold: PRTase-like Superfamily: PRTase-like

						Family: Phosphoribosyltransferases (PRTases)
103	c6raoI_	Alignment	not modelled	32.3	12	PDB header: virus like particle Chain: I; PDB Molecule: afp11; PDBTitle: cryo-em structure of the anti-feeding prophage (afp) baseplate, 6-fold2 symmetrised
104	c4z1oB_	Alignment	not modelled	31.2	11	PDB header: transferase Chain: B; PDB Molecule: phosphoribosyltransferase; PDBTitle: hypoxanthine-guanine-xanthine phosphoribosyltransferase (hgxprt) from2 sulfobolus solfataricus in complex with alpha-3 phosphoribosylpyrophosphoric acid (prpp) and magnesium
105	d2ayia1	Alignment	not modelled	31.0	17	Fold: Thermophilic metalloprotease-like Superfamily: Thermophilic metalloprotease-like Family: Thermophilic metalloprotease (M29)
106	c3h7fB_	Alignment	not modelled	30.7	14	PDB header: transferase Chain: B; PDB Molecule: serine hydroxymethyltransferase 1; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis
107	d1ejia_	Alignment	not modelled	30.2	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
108	d1uj4a2	Alignment	not modelled	28.8	19	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
109	c2ypdB_	Alignment	not modelled	27.7	21	PDB header: oxidoreductase Chain: B; PDB Molecule: probable jmc domain-containing histone demethylation prot PDBTitle: crystal structure of the jumonji domain of human jumonji domain2 containing 1c protein
110	c5vogA_	Alignment	not modelled	27.0	19	PDB header: transferase Chain: A; PDB Molecule: putative phosphoribosyltransferase; PDBTitle: crystal structure of a hypothetical protein from neisseria gonorrhoeae2 with bound pggpp
111	c3d6kB_	Alignment	not modelled	26.7	13	PDB header: transferase Chain: B; PDB Molecule: putative aminotransferase; PDBTitle: the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
112	c4trbA_	Alignment	not modelled	25.8	17	PDB header: transferase Chain: A; PDB Molecule: purine phosphoribosyltransferase (gpt-1); PDBTitle: sulfobolus solfataricus adenine phosphoribosyltransferase
113	c4bhel_	Alignment	not modelled	22.0	15	PDB header: transferase Chain: I; PDB Molecule: serine hydroxymethyltransferase; PDBTitle: methanococcus jannaschii serine hydroxymethyl-transferase2 in complex with plp
114	c5f1yA_	Alignment	not modelled	21.9	32	PDB header: hydrolase Chain: A; PDB Molecule: mccc family protein; PDBTitle: crystal structure of ba3275, the member of s66 family of serine2 peptidases