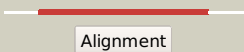

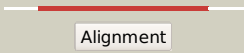

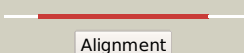

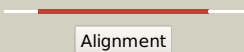











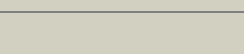





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3826_(fadD23)_4299990_4301744
Date	Fri Aug 9 18:20:53 BST 2019
Unique Job ID	67b8d7eaf65196e4

Detailed template information


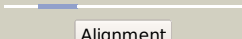
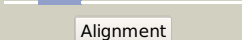
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6eqoB_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: acetyl-coenzyme a synthetase; PDBTitle: tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nadp+ and phosphomethylphosphonic acid adenylate ester
2	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
3	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
4	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 dfi2 12
5	c5es8A_	 Alignment		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
6	d1pg4a_	 Alignment		100.0	19	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
7	c5u89A_	 Alignment		100.0	20	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	c5msdA_	 Alignment		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
9	c3kxwA_	 Alignment		100.0	32	PDB header: ligase Chain: A: PDB Molecule: saframycin mx1 synthetase b; PDBTitle: the crystal structure of fatty acid amp ligase from legionella2 pneumophila
10	c5ey8D_	 Alignment		100.0	35	PDB header: ligase Chain: D: PDB Molecule: acyl-coa synthase; PDBTitle: structure of fadd32 from mycobacterium smegmatis complexed to ampc20
11	c5mstA_	 Alignment		100.0	18	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

12	c5wmmA_	Alignment		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
13	d1ry2a_	Alignment		100.0	19	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
14	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
15	c4wd1A_	Alignment		100.0	16	PDB header: ligase Chain: A; PDB Molecule: acetoacetate-coa ligase; PDBTitle: acetoacetyl-coa synthetase from streptomyces lividans
16	c6n8eA_	Alignment		100.0	22	PDB header: hydrolase Chain: A; PDB Molecule: holo-obif1; PDBTitle: crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
17	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
18	c3gqwB_	Alignment		100.0	25	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
19	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
20	c4r0mB_	Alignment		100.0	23	PDB header: ligase Chain: B; PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
21	c3e7wA_	Alignment	not modelled	100.0	21	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
22	c4zxiA_	Alignment	not modelled	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
23	c4zxiA_	Alignment	not modelled	100.0	22	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	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
25	c4wv3A_	Alignment	not modelled	100.0	17	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
26	d3cw9a1	Alignment	not modelled	100.0	20	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
27	c3tsyA_	Alignment	not modelled	100.0	20	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
28	c5ie2A_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A; PDB Molecule: oxalate--coa ligase; PDBTitle: crystal structure of a plant enzyme

29	c3vngA_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: nrps adenylation protein cytc1; PDBTitle: co-crystal structure of nrps adenylation protein cytc1 with atp from2 streptomyces
30	d1mdba_	Alignment	not modelled	100.0	17	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	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
34	c5wm7A_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: salicylate-amp ligase; PDBTitle: crystal structure of cahj in complex with amp
35	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 glycyI-adenosine-5'-phosphate
36	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
37	c3eynB_	Alignment	not modelled	100.0	16	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	c5aplA_	Alignment	not modelled	100.0	20	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
39	c6ijbA_	Alignment	not modelled	100.0	14	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
40	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
41	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)
42	c4ir7A_	Alignment	not modelled	100.0	17	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
43	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
44	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
45	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
46	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
47	c3r44A_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: fatty acyl coa synthetase fadd13 (fatty-acyl-coa PDBTitle: mycobacterium tuberculosis fatty acyl coa synthetase
48	c5u2aA_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of brucella canis acyl-coa synthetase
49	c2d1tA_	Alignment	not modelled	100.0	17	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
50	c6akdA_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: amp-dependent synthetase and ligase; PDBTitle: crystal structure of idn17
51	d1lamua_	Alignment	not modelled	100.0	15	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
52	c5keiA_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: 2,3-dihydroxybenzoate-amp ligase; PDBTitle: mycobacterium smegmatis mbta apo structure
53	c2v7bB_	Alignment	not modelled	100.0	16	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase;

53	c2v7bb	Alignment	not modelled	100.0	10	PDBTitle: crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
54	c4d56A	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: apnaa1; PDBTitle: understanding bi-specificity of a-domains
55	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
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	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
58	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
59	c4fuqD	Alignment	not modelled	100.0	20	PDB header: ligase Chain: D; PDB Molecule: malonyl coa synthetase; PDBTitle: crystal structure of apo matb from rhodopseudomonas palustris
60	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
61	c3l8cA	Alignment	not modelled	100.0	17	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	d1l1cia	Alignment	not modelled	100.0	20	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
63	d1v25a	Alignment	not modelled	100.0	19	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
64	c3nyrA	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A; PDB Molecule: malonyl-coa ligase; PDBTitle: malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
65	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
66	c3g7sA	Alignment	not modelled	100.0	17	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	c3e53A	Alignment	not modelled	100.0	61	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
68	c4gr5B	Alignment	not modelled	100.0	21	PDB header: ligase Chain: B; PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of slgn1deltaasub in complex with ampcpp
69	c3ip1B	Alignment	not modelled	100.0	18	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	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
71	c4w8oA	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A; PDB Molecule: luciferase-like enzymeamp-coa-ligase; PDBTitle: structure of the luciferase-like enzyme from the nonluminescent2 zophobas morio mealworm
72	c5jipB	Alignment	not modelled	100.0	23	PDB header: ligase Chain: B; PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
73	c3qyaA	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A; PDB Molecule: luciferase; PDBTitle: crystal structure of a red-emitter mutant of lampyris turkestanicus2 luciferase
74	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
75	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
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	18	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	c3ivrA	Alignment	not modelled	100.0	20	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
79	c4lqcA	Alignment	not modelled	100.0	18	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
80	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)
81	c3t5cA	Alignment	not modelled	100.0	18	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	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
83	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)
84	c5jipC	Alignment	not modelled	100.0	19	PDB header: ligase Chain: C: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
85	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
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	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
88	c4gs5A	Alignment	not modelled	100.0	21	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	99.6	21	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	98.9	14	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	98.5	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
93	c4eplA	Alignment	not modelled	98.4	13	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
94	c6avhA	Alignment	not modelled	97.7	17	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	96.8	12	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	52.3	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
97	c4je5C	Alignment	not modelled	44.1	21	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	c4z1oB	Alignment	not modelled	38.7	9	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
99	c4trbA	Alignment	not modelled	31.3	20	PDB header: transferase Chain: A: PDB Molecule: purine phosphoribosyltransferase (gpt-1); PDBTitle: sulfobolus solfataricus adenine phosphoribosyltransferase
100	c5ghrA	Alignment	not modelled	30.5	14	PDB header: dna binding protein/replication Chain: A: PDB Molecule: ssdna-specific exonuclease; PDBTitle: dna replication protein
101	d1nula	Alignment	not modelled	28.2	14	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
102	c5vogA	Alignment	not modelled	27.6	17	PDB header: transferase Chain: A: PDB Molecule: putative phosphoribosyltransferase; PDBTitle: crystal structure of a hypothetical protein from neisseria

					gonorrhoeae2 with bound pppp
103	d1hska2	 Alignment	not modelled	25.7	15 Fold: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain Superfamily: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain Family: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain PDB header: metal transport
104	c2ps3A_	 Alignment	not modelled	25.3	12 Chain: A: PDB Molecule: high-affinity zinc uptake system protein znua; PDBTitle: structure and metal binding properties of znua, a periplasmic zinc2 transporter from escherichia coli PDB header: metal binding protein
105	c4oxqB_	 Alignment	not modelled	23.6	10 Chain: B: PDB Molecule: manganese abc transporter, periplasmic-binding protein PDBTitle: structure of staphylococcus pseudintermedius metal-binding protein2 sita in complex with zinc