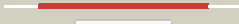



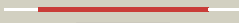




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2786c_(ribF)_3093915_3094910
Date	Wed Aug 7 12:50:44 BST 2019
Unique Job ID	48c645c7bc0cf262

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2x0kB_	 Alignment		100.0	45	PDB header: transferase Chain: B; PDB Molecule: riboflavin biosynthesis protein ribf; PDBTitle: crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
2	c3op1A_	 Alignment		100.0	33	PDB header: transferase Chain: A; PDB Molecule: macrolide-efflux protein; PDBTitle: crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
3	c1t6zB_	 Alignment		100.0	34	PDB header: transferase Chain: B; PDB Molecule: riboflavin kinase/fmn adenylyltransferase; PDBTitle: crystal structure of riboflavin bound tm379
4	d1nb9a_	 Alignment		100.0	34	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: ATP-dependent riboflavin kinase-like
5	d1n08a_	 Alignment		100.0	30	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: ATP-dependent riboflavin kinase-like
6	c3bnwA_	 Alignment		100.0	34	PDB header: transferase Chain: A; PDB Molecule: riboflavin kinase, putative; PDBTitle: crystal structure of riboflavin kinase from trypanosoma brucei
7	d1mrza1	 Alignment		100.0	35	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: ATP-dependent riboflavin kinase-like
8	d1mrza2	 Alignment		100.0	33	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Adenylyltransferase
9	c5xf2B_	 Alignment		99.9	22	PDB header: transferase Chain: B; PDB Molecule: putative cytidyltransferase; PDBTitle: crystal structure of semet-hldc from burkholderia pseudomallei
10	c3guzB_	 Alignment		99.9	18	PDB header: ligase Chain: B; PDB Molecule: pantothenate synthetase; PDBTitle: structural and substrate-binding studies of pantothenate2 synthenate (ps)provide insights into homotropic inhibition3 by pantoate in ps's
11	c5x3dA_	 Alignment		99.9	18	PDB header: transferase Chain: A; PDB Molecule: phosphoenolpyruvate phosphomutase; PDBTitle: crystal structure of hep-cmp-bound form of cytidyltransferase2 (cytase) domain of fom1 from streptomyces wedmorensis

12	c4zcsE	Alignment		99.8	17	PDB header: transferase Chain: E: PDB Molecule: choline-phosphate cytidyltransferase; PDBTitle: crystal structure of the c-terminal catalytic domain of plasmodium2 falciparum ctp:phosphocholine cytidyltransferase in complex with3 cdp-choline
13	c3glvB	Alignment		99.8	19	PDB header: biosynthetic protein Chain: B: PDB Molecule: lipopolysaccharide core biosynthesis protein; PDBTitle: crystal structure of the lipopolysaccharide core biosynthesis protein2 from thermoplasma volcanium gss1
14	d1coza	Alignment		99.7	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Cytidylyltransferase
15	c1lw7A	Alignment		99.7	15	PDB header: transferase Chain: A: PDB Molecule: transcriptional regulator nadr; PDBTitle: nadr protein from haemophilus influenzae
16	c3h05A	Alignment		99.6	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein vpa0413; PDBTitle: the crystal structure of a putative nicotinate-nucleotide2 adenyltransferase from vibrio parahaemolyticus
17	c3uk2B	Alignment		99.6	20	PDB header: ligase Chain: B: PDB Molecule: pantothenate synthetase; PDBTitle: the structure of pantothenate synthetase from burkholderia2 thailandensis
18	d1lw7a1	Alignment		99.6	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenyltransferase
19	d1v8fa	Alignment		99.6	23	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
20	c2h29A	Alignment		99.6	15	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide PDBTitle: crystal structure of nicotinic acid mononucleotide2 adenyltransferase from staphylococcus aureus: product3 bound form 1
21	c3e27B	Alignment	not modelled	99.6	16	PDB header: transferase Chain: B: PDB Molecule: nicotinate (nicotinamide) nucleotide adenyltransferase; PDBTitle: nicotinic acid mononucleotide (namn) adenyltransferase from bacillus2 anthracis: product complex
22	c2ejcA	Alignment	not modelled	99.5	17	PDB header: ligase Chain: A: PDB Molecule: pantoate--beta-alanine ligase; PDBTitle: crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima
23	d1ihoA	Alignment	not modelled	99.5	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
24	c3elbA	Alignment	not modelled	99.5	13	PDB header: transferase Chain: A: PDB Molecule: ethanolamine-phosphate cytidyltransferase; PDBTitle: human ctp: phosphoethanolamine cytidyltransferase in complex with2 cmp
25	c3nv7A	Alignment	not modelled	99.5	16	PDB header: transferase Chain: A: PDB Molecule: phosphopantetheine adenyltransferase; PDBTitle: crystal structure of h.pylori phosphopantetheine adenyltransferase2 mutant i4v/n76y
26	d1qjca	Alignment	not modelled	99.5	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenyltransferase
27	c2b7ID	Alignment	not modelled	99.5	20	PDB header: transferase Chain: D: PDB Molecule: glycerol-3-phosphate cytidyltransferase; PDBTitle: crystal structure of ctp:glycerol-3-phosphate2 cytidyltransferase from staphylococcus aureus
28	c5lltB	Alignment	not modelled	99.5	11	PDB header: transferase Chain: B: PDB Molecule: nicotinate-nucleotide adenyltransferase; PDBTitle: plasmodium falciparum nicotinic acid mononucleotide2 adenyltransferase complexed with naad

29	d1f9aa_	Alignment	not modelled	99.5	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
30	d1kr2a_	Alignment	not modelled	99.5	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
31	c5h16D_	Alignment	not modelled	99.4	23	PDB header: transferase Chain: D: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of the complex of phosphopantetheine2 adenylyltransferase from acinetobacter baumannii with citrate at 2.33 a resolution.
32	c3n8hA_	Alignment	not modelled	99.4	18	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantoate-beta-alanine ligase from francisella2 tularensis
33	c3x1mC_	Alignment	not modelled	99.4	26	PDB header: transferase Chain: C: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of phosphopantetheine adenylyltransferase/ppat from2 pseudomonas aeruginosa with coa
34	c4rpiA_	Alignment	not modelled	99.4	17	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide adenylyltransferase; PDBTitle: crystal structure of nicotinate mononucleotide adenylyltransferase2 from mycobacterium tuberculosis
35	d1nuua_	Alignment	not modelled	99.4	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
36	d1tfua_	Alignment	not modelled	99.4	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
37	c3mxtA_	Alignment	not modelled	99.4	19	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantoate-beta-alanine ligase from campylobacter2 jejuni
38	c3ikzA_	Alignment	not modelled	99.4	22	PDB header: transferase Chain: A: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of phosphopantetheine adenylyltransferase from2 burkholderia pseudomallei
39	c3innB_	Alignment	not modelled	99.4	21	PDB header: ligase Chain: B: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantoate-beta-alanine-ligase in complex2 with atp at low occupancy at 2.1 a resolution
40	d1o6ba_	Alignment	not modelled	99.4	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
41	c3ag5A_	Alignment	not modelled	99.4	18	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantothenate synthetase from staphylococcus2 aureus
42	c5kwvA_	Alignment	not modelled	99.3	19	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of a pantoate-beta-alanine ligase from neisseria2 gonorrhoeae with bound amppnp
43	d1vlha_	Alignment	not modelled	99.3	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
44	d2a84a1	Alignment	not modelled	99.3	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
45	d1ej2a_	Alignment	not modelled	99.3	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
46	c4f3rC_	Alignment	not modelled	99.1	20	PDB header: transferase Chain: C: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: structure of phosphopantetheine adenylyltransferase (cbu_0288) from2 coxiella burnetii
47	c3hl4B_	Alignment	not modelled	99.1	16	PDB header: transferase Chain: B: PDB Molecule: choline-phosphate cytidylyltransferase a; PDBTitle: crystal structure of a mammalian ctp:phosphocholine2 cytidylyltransferase with cdp-choline
48	c3nd5D_	Alignment	not modelled	99.1	20	PDB header: transferase Chain: D: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of phosphopantetheine adenylyltransferase (ppat)2 from enterococcus faecalis
49	d1od6a_	Alignment	not modelled	99.1	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
50	c3f3mA_	Alignment	not modelled	99.0	16	PDB header: transferase Chain: A: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: six crystal structures of two phosphopantetheine adenylyltransferases2 reveal an alternative ligand binding mode and an associated3 structural change
51	c2r5wA_	Alignment	not modelled	99.0	17	PDB header: hydrolase, transferase Chain: A: PDB Molecule: nicotinamide-nucleotide adenylyltransferase; PDBTitle: crystal structure of a bifunctional nm2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
52	c1yunB_	Alignment	not modelled	99.0	19	PDB header: transferase Chain: B: PDB Molecule: probable nicotinate-nucleotide PDBTitle: crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from pseudomonas aeruginosa
53	c2qjoB_	Alignment	not modelled	98.9	13	PDB header: transferase, hydrolase Chain: B: PDB Molecule: bifunctional nm2 adenylyltransferase/nudix hydrolase; PDBTitle: crystal structure of a bifunctional nm2 adenylyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.

54	d1kama_	Alignment	not modelled	98.9	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
55	c5y0tD_	Alignment	not modelled	98.9	24	PDB header: ligase Chain: D: PDB Molecule: thermotoga maritima tmcal; PDBTitle: crystal structure of thermotoga maritima tmcal bound with alpha-thio2 atp(form ii)
56	c6gyeB_	Alignment	not modelled	98.8	20	PDB header: transport protein Chain: B: PDB Molecule: nicotinamide-nucleotide adenylyltransferase nadr family / PDBTitle: crystal structure of nadr protein in complex with nr
57	c5y0nB_	Alignment	not modelled	98.8	19	PDB header: ligase Chain: B: PDB Molecule: upf0348 protein b4417_3650; PDBTitle: crystal structure of bacillus subtilis tmcal bound with atp (semet2 derivative)
58	d1k4ma_	Alignment	not modelled	98.8	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
59	c3gmiA_	Alignment	not modelled	98.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0348 protein mj0951; PDBTitle: crystal structure of a protein of unknown function from2 methanocaldococcus jannaschii
60	c4mvcA_	Alignment	not modelled	98.7	18	PDB header: transferase Chain: A: PDB Molecule: choline-phosphate cytidylyltransferase a; PDBTitle: crystal structure of a mammalian cytidylyltransferase
61	c3do8B_	Alignment	not modelled	98.7	20	PDB header: transferase Chain: B: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: the crystal structure of the protein with unknown function from2 archaeoglobus fulgidus
62	c4wsoA_	Alignment	not modelled	98.7	16	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide adenylyltransferase; PDBTitle: x-ray crystal structure of a nicotinate nucleotide adenylyltransferase2 from burkholderia thailandensis bound to nad
63	d1jhda2	Alignment	not modelled	98.3	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: ATP sulfurylase catalytic domain
64	c2qjfB_	Alignment	not modelled	97.6	17	PDB header: transferase Chain: B: PDB Molecule: bifunctional 3'-phosphoadenosine 5'- PDBTitle: crystal structure of atp-sulfurylase domain of human paps2 synthetase 1
65	c1xnjB_	Alignment	not modelled	97.5	17	PDB header: transferase Chain: B: PDB Molecule: bifunctional 3'-phosphoadenosine 5'- PDBTitle: phosphosulfate PDBTitle: aps complex of human paps synthetase 1
66	d1x6va2	Alignment	not modelled	97.5	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: ATP sulfurylase catalytic domain
67	c1r6xA_	Alignment	not modelled	97.4	17	PDB header: transferase Chain: A: PDB Molecule: atp:sulfate adenylyltransferase; PDBTitle: the crystal structure of a truncated form of yeast atp2 sulfurylase, lacking the c-terminal aps kinase-like domain,3 in complex with sulfate
68	c1xjqA_	Alignment	not modelled	97.3	17	PDB header: transferase Chain: A: PDB Molecule: bifunctional 3'-phosphoadenosine 5'- PDBTitle: phosphosulfate PDBTitle: adp complex of human paps synthetase 1
69	d1g8fa2	Alignment	not modelled	97.3	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: ATP sulfurylase catalytic domain
70	c1jhdA_	Alignment	not modelled	97.1	16	PDB header: transferase Chain: A: PDB Molecule: sulfate adenylyltransferase; PDBTitle: crystal structure of bacterial atp sulfurylase from the2 riftia pachyptila symbiont
71	c1g8gB_	Alignment	not modelled	97.1	20	PDB header: transferase Chain: B: PDB Molecule: sulfate adenylyltransferase; PDBTitle: atp sulfurylase from s. cerevisiae: the binary product complex with2 aps
72	c1m8pB_	Alignment	not modelled	97.0	19	PDB header: transferase Chain: B: PDB Molecule: sulfate adenylyltransferase; PDBTitle: crystal structure of p. chrysogenum atp sulfurylase in the t-state
73	d1v47a2	Alignment	not modelled	97.0	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: ATP sulfurylase catalytic domain
74	d1m8pa2	Alignment	not modelled	96.9	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: ATP sulfurylase catalytic domain
75	c3cr8C_	Alignment	not modelled	96.5	13	PDB header: transferase Chain: C: PDB Molecule: sulfate adenylyltransferase, adenylylsulfate kinase; PDBTitle: hexameric aps kinase from thiobacillus denitrificans
76	c2gksB_	Alignment	not modelled	96.3	15	PDB header: transferase Chain: B: PDB Molecule: bifunctional sat/aps kinase; PDBTitle: crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
77	c4mafH_	Alignment	not modelled	94.1	15	PDB header: transferase Chain: H: PDB Molecule: atp sulfurylase; PDBTitle: soybean atp sulfurylase
78	c1v47B_	Alignment	not modelled	91.1	21	PDB header: transferase Chain: B: PDB Molecule: atp sulfurylase; PDBTitle: crystal structure of atp sulfurylase from thermus2 thermophilus hb8 in complex with aps
79	c3ih5A_	Alignment	not modelled	73.8	12	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: crystal structure of electron transfer flavoprotein alpha-

						subunit from2 bacteroides thetaiotaomicron PDB header: flavoprotein Chain: E: PDB Molecule: caffel-coa reductase-etf complex subunit care; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffel-coa2 reductase reaction
80	c6fahE	Alignment	not modelled	73.0	12	
81	d1lwah2	Alignment	not modelled	72.3	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
82	c4l2iA	Alignment	not modelled	70.7	12	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein alpha subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
83	c5diyB	Alignment	not modelled	58.2	18	PDB header: hydrolase Chain: B: PDB Molecule: hyaluronidase; PDBTitle: thermobaculum terrenum o-glcnae hydrolase mutant - d120n
84	c5h06C	Alignment	not modelled	54.4	13	PDB header: hydrolase Chain: C: PDB Molecule: amyp; PDBTitle: crystal structure of amyp in complex with maltose
85	d1gcya2	Alignment	not modelled	53.8	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
86	d2vbua1	Alignment	not modelled	53.4	15	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: CTP-dependent riboflavin kinase-like
87	c3lx4B	Alignment	not modelled	52.9	20	PDB header: oxidoreductase Chain: B: PDB Molecule: fe-hydrogenase; PDBTitle: stepwise [fe]-hydrogenase h-cluster assembly revealed in the2 structure of hyda(deltaefg)
88	d1hf2a2	Alignment	not modelled	52.7	15	Fold: Cell-division inhibitor MinC, N-terminal domain Superfamily: Cell-division inhibitor MinC, N-terminal domain Family: Cell-division inhibitor MinC, N-terminal domain
89	c5ol2D	Alignment	not modelled	52.3	11	PDB header: flavoprotein Chain: D: PDB Molecule: electron transfer flavoprotein large subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
90	c5mp7C	Alignment	not modelled	51.8	12	PDB header: transferase Chain: C: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosylpyrophosphate synthetase from2 mycobacterium smegmatis
91	d2h85a2	Alignment	not modelled	51.3	19	Fold: EndoU-like Superfamily: EndoU-like Family: Nsp15 C-terminal domain-like
92	c5t3oB	Alignment	not modelled	51.1	19	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphorybosylpyrophosphate synthetase ii2 from thermus thermophilus
93	c4hebA	Alignment	not modelled	51.0	20	PDB header: cell cycle Chain: A: PDB Molecule: septum formation protein maf; PDBTitle: the crystal structure of maf protein of bacillus subtilis
94	c2bdqA	Alignment	not modelled	50.4	18	PDB header: metal transport Chain: A: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of the putative copper homeostasis protein cutc from2 streptococcus agalactiae, northeast structural genomics target sar15.
95	c1dkrB	Alignment	not modelled	50.3	14	PDB header: transferase Chain: B: PDB Molecule: phosphoribosyl pyrophosphate synthetase; PDBTitle: crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
96	d2g2ca1	Alignment	not modelled	50.3	19	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
97	c1ehaA	Alignment	not modelled	48.6	28	PDB header: hydrolase Chain: A: PDB Molecule: glycosyltrehalose trehalohydrolase; PDBTitle: crystal structure of glycosyltrehalose trehalohydrolase from2 sulfolobus solfataricus
98	c1gcyA	Alignment	not modelled	48.1	17	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltotetrahydrolase; PDBTitle: high resolution crystal structure of maltotetraose-forming2 exo-amylase
99	c5un8B	Alignment	not modelled	48.0	13	PDB header: hydrolase Chain: B: PDB Molecule: protein o-glcnae; PDBTitle: crystal structure of human o-glcnae in complex with glycopeptide2 p53
100	d2ozka2	Alignment	not modelled	47.2	24	Fold: EndoU-like Superfamily: EndoU-like Family: Nsp15 C-terminal domain-like
101	c2is8A	Alignment	not modelled	46.9	16	PDB header: structural protein Chain: A: PDB Molecule: molybdopterin biosynthesis enzyme, moab; PDBTitle: crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
102	c3bdkB	Alignment	not modelled	44.6	18	PDB header: lyase Chain: B: PDB Molecule: d-mannonate dehydratase; PDBTitle: crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
103	d1mxga2	Alignment	not modelled	44.3	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
104	d2cbia2	Alignment	not modelled	43.5	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases

				Family:alpha-D-glucuronidase/Hyaluronidase catalytic domain	
105	c5m99A_	Alignment	not modelled	43.3	18 PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: functional characterization and crystal structure of thermostable2 amylase from thermotoga petrophila, reveals high thermostability and3 an archaic form of dimerization
106	c1mwoA_	Alignment	not modelled	42.7	19 PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase; PDBTitle: crystal structure analysis of the hyperthermostable2 pyrococcus woesei alpha-amylase
107	c3kbqA_	Alignment	not modelled	42.7	15 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ta0487; PDBTitle: the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
108	c3focB_	Alignment	not modelled	42.5	12 PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase from giardia lamblia
109	c3clrD_	Alignment	not modelled	41.1	12 PDB header: electron transport Chain: D: PDB Molecule: electron transfer flavoprotein subunit alpha; PDBTitle: crystal structure of the r236a etf mutant from m. methylotrophus
110	c1wpcA_	Alignment	not modelled	40.7	21 PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltohexaosidase; PDBTitle: crystal structure of maltohexaoase-producing amylase complexed with2 pseudo-maltononaose
111	c2j5bA_	Alignment	not modelled	39.7	9 PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: structure of the tyrosyl trna synthetase from acanthamoeba polyphaga2 mimivirus complexed with tyrosinol
112	c2by0A_	Alignment	not modelled	39.7	28 PDB header: hydrolase Chain: A: PDB Molecule: maltooligosyltrehalose trehalohydrolase; PDBTitle: is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
113	d1mkza_	Alignment	not modelled	37.2	15 Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
114	c2qlcC_	Alignment	not modelled	37.1	18 PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein radc homolog; PDBTitle: the crystal structure of dna repair protein radc from chlorobium2 tepidum t1s
115	d2qtia2	Alignment	not modelled	36.8	25 Fold: EndoU-like Superfamily: EndoU-like Family: Nsp15 C-terminal domain-like
116	c4j75B_	Alignment	not modelled	36.6	14 PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of a parasite trna synthetase, product-bound
117	c3hv0A_	Alignment	not modelled	36.6	12 PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase from cryptosporidium parvum
118	c5ykbB_	Alignment	not modelled	35.6	15 PDB header: isomerase Chain: B: PDB Molecule: trehalose synthase; PDBTitle: the n253f mutant structure of trehalose synthase from deinococcus2 radiodurans reveals an open active-site conformation
119	c5zxbB_	Alignment	not modelled	35.0	11 PDB header: hydrolase Chain: B: PDB Molecule: cyclic maltosyl-maltose hydrolase; PDBTitle: cyclic alpha-maltosyl-(1-->6)-maltose hydrolase from arthrobacter2 globiformis, ligand-free form
120	c2g4rB_	Alignment	not modelled	34.3	15 PDB header: biosynthetic protein Chain: B: PDB Molecule: molybdopterin biosynthesis mog protein; PDBTitle: anomalous substructure of moga