



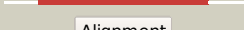

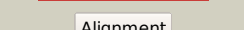

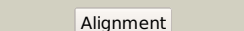



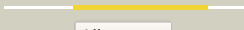

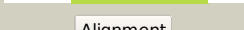

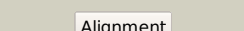

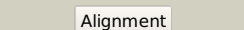
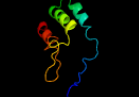


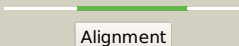

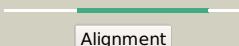

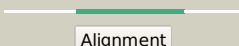

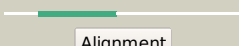
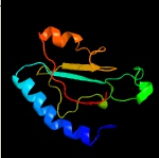
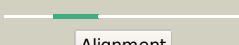

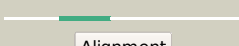

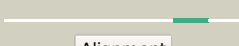






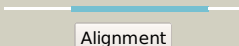
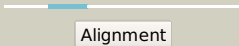
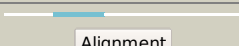
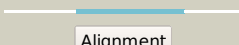
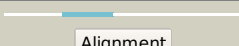
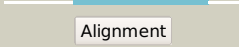



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2172c_(-)_2433639_2434544
Date	Mon Aug 5 13:25:29 BST 2019
Unique Job ID	81711de6f76a1866

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ijdB_</a>	 Alignment		100.0	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> uncharacterized protein cthe_2304 from clostridium thermocellum binds2 two copies of 5-methyl-5,6,7,8-tetrahydrofolic acid
2	<a href="#">c6fnuA_</a>	 Alignment		99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methylenetetrahydrofolate reductase 1; <b>PDBTitle:</b> structure of s. cerevisiae methylenetetrahydrofolate reductase 1,2 catalytic domain
3	<a href="#">d1v93a_</a>	 Alignment		99.8	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FAD-linked oxidoreductase <b>Family:</b> Methylenetetrahydrofolate reductase
4	<a href="#">d1b5ta_</a>	 Alignment		99.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FAD-linked oxidoreductase <b>Family:</b> Methylenetetrahydrofolate reductase
5	<a href="#">c2fmoA_</a>	 Alignment		99.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 5,10-methylenetetrahydrofolate reductase; <b>PDBTitle:</b> ala177val mutant of e. coli methylenetetrahydrofolate2 reductase
6	<a href="#">c6fcxA_</a>	 Alignment		99.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methylenetetrahydrofolate reductase; <b>PDBTitle:</b> structure of human 5,10-methylenetetrahydrofolate reductase (mthfr)
7	<a href="#">c3tr9A_</a>	 Alignment		70.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> structure of a dihydropteroate synthase (folp) in complex with pteroiC2 acid from coxiella burnetii
8	<a href="#">c6cluC_</a>	 Alignment		63.3	21	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> C: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> staphylococcus aureus dihydropteroate synthase (sadhps) f17l e208k2 double mutant structure
9	<a href="#">c4i7vD_</a>	 Alignment		61.5	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> agrobacterium tumefaciens dhdpS with pyruvate
10	<a href="#">c3ug9A_</a>	 Alignment		55.9	26	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> archaeal-type opsin 1, archaeal-type opsin 2; <b>PDBTitle:</b> crystal structure of the closed state of channelrhodopsin
11	<a href="#">c5ks8D_</a>	 Alignment		51.4	16	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate carboxylase subunit beta; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus

12	<a href="#">c3daqB_</a>	 Alignment		51.0	18	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
13	<a href="#">c5ks8F_</a>	 Alignment		49.8	16	<b>PDB header:</b> ligase <b>Chain:</b> F; <b>PDB Molecule:</b> pyruvate carboxylase subunit beta; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from 2 methylacobacillus flagellatus
14	<a href="#">c3lerA_</a>	 Alignment		45.1	20	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
15	<a href="#">c3eefA_</a>	 Alignment		43.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> n-carbamoylsarcosine amidase related protein; <b>PDBTitle:</b> crystal structure of n-carbamoylsarcosine amidase from thermoplasma2 acidophilum
16	<a href="#">c4n7bA_</a>	 Alignment		42.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> lytb; <b>PDBTitle:</b> structure of the e-1-hydroxy-2-methyl-but-2-enyl-4-diphosphate2 reductase from plasmodium falciparum
17	<a href="#">d1to0a_</a>	 Alignment		40.3	17	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> YbeA-like
18	<a href="#">d1pdaa2</a>	 Alignment		40.1	32	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain <b>Family:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
19	<a href="#">d1pjqa3</a>	 Alignment		40.0	26	<b>Fold:</b> Siroheme synthase middle domains-like <b>Superfamily:</b> Siroheme synthase middle domains-like <b>Family:</b> Siroheme synthase middle domains-like
20	<a href="#">d2j0pa1</a>	 Alignment		38.6	21	<b>Fold:</b> Heme iron utilization protein-like <b>Superfamily:</b> Heme iron utilization protein-like <b>Family:</b> HemS/ChuS-like
21	<a href="#">d1gtka2</a>	 Alignment	not modelled	37.7	32	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain <b>Family:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
22	<a href="#">c2nx9B_</a>	 Alignment	not modelled	37.2	16	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> oxaloacetate decarboxylase 2, subunit alpha; <b>PDBTitle:</b> crystal structure of the carboxyltransferase domain of the 2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
23	<a href="#">c3pkrA_</a>	 Alignment	not modelled	36.8	17	<b>PDB header:</b> motor protein <b>Chain:</b> A; <b>PDB Molecule:</b> flagellar motor switch protein; <b>PDBTitle:</b> crystal structure of flig (residue 86-343) from h. pylori
24	<a href="#">d2hq2a1</a>	 Alignment	not modelled	36.4	21	<b>Fold:</b> Heme iron utilization protein-like <b>Superfamily:</b> Heme iron utilization protein-like <b>Family:</b> HemS/ChuS-like
25	<a href="#">c3n2xB_</a>	 Alignment	not modelled	36.1	20	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein yage; <b>PDBTitle:</b> crystal structure of yage, a prophage protein belonging to the 2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
26	<a href="#">c3vndD_</a>	 Alignment	not modelled	34.1	17	<b>PDB header:</b> lyase <b>Chain:</b> D; <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-subunit from the 2 psychrophile shewanella frigidimarina k14-2
27	<a href="#">d1eyea_</a>	 Alignment	not modelled	33.8	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
28	<a href="#">c5k9vA_</a>	 Alignment	not modelled	31.5	16	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> tryptophan synthase alpha chain;

28	<a href="#">c3k2aA</a>	Alignment	not modelled	31.5	10	<b>PDBTitle:</b> crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila <b>PDB header:</b> lyase
29	<a href="#">c3thaB</a>	Alignment	not modelled	29.8	13	<b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> tryptophan synthase subunit alpha from campylobacter jejuni.
30	<a href="#">c5ktlA</a>	Alignment	not modelled	29.0	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate synthase; <b>PDBTitle:</b> dihydrodipicolinate synthase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
31	<a href="#">c2y8vB</a>	Alignment	not modelled	27.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> class iii chitinase, putative; <b>PDBTitle:</b> structure of chitinase, chic, from aspergillus fumigatus.
32	<a href="#">c3la8A</a>	Alignment	not modelled	26.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative purine nucleoside phosphorylase; <b>PDBTitle:</b> the crystal structure of smu.1229 from streptococcus mutans ua159
33	<a href="#">c3ke8A</a>	Alignment	not modelled	25.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; <b>PDBTitle:</b> crystal structure of isph:hmbpp-complex
34	<a href="#">c3urkA</a>	Alignment	not modelled	25.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; <b>PDBTitle:</b> isph in complex with propynyl diphosphate (1061)
35	<a href="#">c5douC</a>	Alignment	not modelled	24.9	14	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> carbamoyl-phosphate synthase [ammonia], mitochondrial; <b>PDBTitle:</b> crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
36	<a href="#">d1t3va</a>	Alignment	not modelled	24.8	9	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Nitrogenase accessory factor-like <b>Family:</b> MTH1175-like
37	<a href="#">c1rr2A</a>	Alignment	not modelled	24.5	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transcarboxylase 5s subunit; <b>PDBTitle:</b> propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
38	<a href="#">c3pl4A</a>	Alignment	not modelled	24.3	16	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar motor switch protein; <b>PDBTitle:</b> crystal structure of flig (residue 116-343) from h. pylori
39	<a href="#">c3eb2A</a>	Alignment	not modelled	23.8	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dihydrodipicolinate synthetase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 2.0a resolution
40	<a href="#">d1tx2a</a>	Alignment	not modelled	22.6	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
41	<a href="#">c1tx2A</a>	Alignment	not modelled	22.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dhps, dihydropteroate synthase; <b>PDBTitle:</b> dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
42	<a href="#">c4imhA</a>	Alignment	not modelled	21.0	26	<b>PDB header:</b> metal transport, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> hemin degrading factor; <b>PDBTitle:</b> crystal structure of cytoplasmic heme binding protein, phus, from2 pseudomonas aeruginosa
43	<a href="#">c3cyvA</a>	Alignment	not modelled	20.7	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uroporphyrinogen decarboxylase from2 shigella flexineri: new insights into its catalytic3 mechanism
44	<a href="#">c6g3uA</a>	Alignment	not modelled	19.6	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate dehydrogenase; <b>PDBTitle:</b> structure of pseudomonas aeruginosa isocitrate dehydrogenase, idh
45	<a href="#">d1bnba</a>	Alignment	not modelled	19.6	50	<b>Fold:</b> Defensin-like <b>Superfamily:</b> Defensin-like <b>Family:</b> Defensin
46	<a href="#">d1ajza</a>	Alignment	not modelled	18.5	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
47	<a href="#">c6cceD</a>	Alignment	not modelled	18.5	26	<b>PDB header:</b> transcription/dna/antibiotic <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> crystal structure of a mycobacterium smegmatis rna polymerase2 transcription initiation complex with inhibitor kanglemycin a
48	<a href="#">c2jmkA</a>	Alignment	not modelled	18.3	38	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ta0956; <b>PDBTitle:</b> solution structure of ta0956
49	<a href="#">c4htgA</a>	Alignment	not modelled	17.5	32	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> porphobilinogen deaminase, chloroplastic; <b>PDBTitle:</b> porphobilinogen deaminase from arabidopsis thaliana
50	<a href="#">c2xucA</a>	Alignment	not modelled	17.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase; <b>PDBTitle:</b> natural product-guided discovery of a fungal chitinase inhibitor
51	<a href="#">c2yxgD</a>	Alignment	not modelled	17.2	9	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase (dapa)
52	<a href="#">c3e96B</a>	Alignment	not modelled	17.1	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
53	<a href="#">c2kb2A</a>	Alignment	not modelled	17.0	12	<b>PDB header:</b> signaling protein, hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> blrp1; <b>PDBTitle:</b> blrp1 bluf
						<b>PDB header:</b> structural genomics, transferase

54	<a href="#">c2huzB</a>	Alignment	not modelled	16.8	12	<b>Chain:</b> B: <b>PDB Molecule:</b> glucosamine 6-phosphate n-acetyltransferase; <b>PDBTitle:</b> crystal structure of gnpnat1
55	<a href="#">d1ta3a</a>	Alignment	not modelled	16.8	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Type II chitinase
56	<a href="#">c3noeA</a>	Alignment	not modelled	16.7	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
57	<a href="#">c2uy2A</a>	Alignment	not modelled	16.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endochitinase; <b>PDBTitle:</b> sccts1_apo crystal structure
58	<a href="#">d1xkya1</a>	Alignment	not modelled	15.7	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
59	<a href="#">c4ijjF</a>	Alignment	not modelled	15.7	39	<b>PDB header:</b> cell cycle <b>Chain:</b> F: <b>PDB Molecule:</b> tubulin tyrosine ligase, ttl; <b>PDBTitle:</b> crystal structure of tubulin-stathmin-ttl-apo complex
60	<a href="#">c2vefB</a>	Alignment	not modelled	15.1	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> dihydropteroate synthase from streptococcus pneumoniae
61	<a href="#">d1o5ka</a>	Alignment	not modelled	15.1	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
62	<a href="#">c6npcB</a>	Alignment	not modelled	15.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> tmpa, 2-trimethylaminoethylphosphonate hydroxylase; <b>PDBTitle:</b> x-ray crystal structure of tmpa, 2-trimethylaminoethylphosphonate2 hydroxylase, with fe, 2og, and 2-trimethylaminoethylphosphonate
63	<a href="#">c4nq1B</a>	Alignment	not modelled	14.7	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate synthase; <b>PDBTitle:</b> legionella pneumophila dihydrodipicolinate synthase with first2 substrate pyruvate bound in the active site
64	<a href="#">c3mcwA</a>	Alignment	not modelled	14.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of a putative hydrolase of the isochorismatase2 family (cv_1320) from chromobacterium violaceum atcc 12472 at 1.06 a3 resolution
65	<a href="#">c4dppB</a>	Alignment	not modelled	14.6	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase 2, chloroplastic; <b>PDBTitle:</b> the structure of dihydrodipicolinate synthase 2 from arabidopsis2 thaliana
66	<a href="#">c4aczB</a>	Alignment	not modelled	14.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endo-alpha-mannosidase; <b>PDBTitle:</b> structure of the gh99 endo-alpha-mannosidase from2 bacteroides thetaiotaomicron
67	<a href="#">c3imkA</a>	Alignment	not modelled	14.5	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative molybdenum carrier protein; <b>PDBTitle:</b> crystal structure of putative molybdenum carrier protein (yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution
68	<a href="#">c2vp8A</a>	Alignment	not modelled	14.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase 2; <b>PDBTitle:</b> structure of mycobacterium tuberculosis rv1207
69	<a href="#">d1us7b</a>	Alignment	not modelled	14.4	19	<b>Fold:</b> Hsp90 co-chaperone CDC37 <b>Superfamily:</b> Hsp90 co-chaperone CDC37 <b>Family:</b> Hsp90 co-chaperone CDC37
70	<a href="#">c1us7B</a>	Alignment	not modelled	14.4	19	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> hsp90 co-chaperone cdc37; <b>PDBTitle:</b> complex of hsp90 and p50
71	<a href="#">d2c1wa1</a>	Alignment	not modelled	14.1	26	<b>Fold:</b> EndoU-like <b>Superfamily:</b> EndoU-like <b>Family:</b> Eukaryotic EndoU ribonuclease
72	<a href="#">d1fft1</a>	Alignment	not modelled	13.7	11	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Periplasmic domain of cytochrome c oxidase subunit II
73	<a href="#">d1itwa</a>	Alignment	not modelled	13.6	23	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Monomeric isocitrate dehydrogenase
74	<a href="#">d3bula2</a>	Alignment	not modelled	13.5	9	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
75	<a href="#">d1l3ka2</a>	Alignment	not modelled	13.0	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
76	<a href="#">c3dnfB</a>	Alignment	not modelled	13.0	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; <b>PDBTitle:</b> structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
77	<a href="#">c3nwrA</a>	Alignment	not modelled	12.6	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> a rubisco-like protein; <b>PDBTitle:</b> crystal structure of a rubisco-like protein from burkholderia fungorum
78	<a href="#">c2y8kA</a>	Alignment	not modelled	12.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate binding family 6; <b>PDBTitle:</b> structure of ctgh5-cbm6, an arabinoxylan-specific xylanase. <b>PDB header:</b> hydrolase

79	<a href="#">c4b16A_</a>	Alignment	not modelled	12.4	16	<b>Chain:</b> A; <b>PDB Molecule:</b> chitinase like lectin; <b>PDBTitle:</b> crystal structure of tamarind chitinase like lectin (tc1l) complexed2 with n-acetyl glucosamine (glcnac)
80	<a href="#">c2h31A_</a>	Alignment	not modelled	12.3	15	<b>PDB header:</b> ligase, lyase <b>Chain:</b> A; <b>PDB Molecule:</b> multifunctional protein ade2; <b>PDBTitle:</b> crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
81	<a href="#">c2hd1A_</a>	Alignment	not modelled	12.2	31	<b>PDB header:</b> cytokine <b>Chain:</b> A; <b>PDB Molecule:</b> small inducible cytokine b14; <b>PDBTitle:</b> solution structure of brak/cxc114
82	<a href="#">d1qopa_</a>	Alignment	not modelled	12.2	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
83	<a href="#">c5dotA_</a>	Alignment	not modelled	12.1	15	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> carbamoyl-phosphate synthase [ammonia], mitochondrial; <b>PDBTitle:</b> crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form
84	<a href="#">d1o13a_</a>	Alignment	not modelled	11.6	9	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Nitrogenase accessory factor-like <b>Family:</b> MTH1175-like
85	<a href="#">c4heoA_</a>	Alignment	not modelled	11.6	32	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> hendra virus phosphoprotein c terminal domain
86	<a href="#">d4croa_</a>	Alignment	not modelled	11.6	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
87	<a href="#">c5ey5A_</a>	Alignment	not modelled	11.6	22	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> lbcats-a; <b>PDBTitle:</b> lbcats
88	<a href="#">c3navB_</a>	Alignment	not modelled	11.4	17	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
89	<a href="#">d1yrxa1</a>	Alignment	not modelled	11.4	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Acylphosphatase/BLUF domain-like <b>Family:</b> BLUF domain
90	<a href="#">c4r33A_</a>	Alignment	not modelled	11.4	13	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> nosl; <b>PDBTitle:</b> x-ray structure of the tryptophan lyase nosl with tryptophan and s-2 adenosyl-l-homocysteine bound
91	<a href="#">d1kr7a_</a>	Alignment	not modelled	11.3	30	<b>Fold:</b> Globin-like <b>Superfamily:</b> Globin-like <b>Family:</b> Nerve tissue mini-hemoglobin (neural globin)
92	<a href="#">c4ja0A_</a>	Alignment	not modelled	11.1	17	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase; <b>PDBTitle:</b> crystal structure of the invertebrate bi-functional purine2 biosynthesis enzyme paics at 2.8 a resolution
93	<a href="#">c6omzA_</a>	Alignment	not modelled	11.0	21	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> crystal structure of dihydropteroate synthase from mycobacterium2 smegmatis with bound 6-hydroxymethylpterin-monophosphate
94	<a href="#">c2ehhE_</a>	Alignment	not modelled	10.8	11	<b>PDB header:</b> lyase <b>Chain:</b> E; <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
95	<a href="#">c5c8j_</a>	Alignment	not modelled	10.5	11	<b>PDB header:</b> membrane protein <b>Chain:</b> J; <b>PDB Molecule:</b> protein mj0480; <b>PDBTitle:</b> a yidc-like protein in the archaeal plasma membrane
96	<a href="#">c2ypnA_</a>	Alignment	not modelled	10.5	32	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> protein (hydroxymethylbilane synthase); <b>PDBTitle:</b> hydroxymethylbilane synthase
97	<a href="#">d2hvma_</a>	Alignment	not modelled	10.5	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Type II chitinase
98	<a href="#">c2pijB_</a>	Alignment	not modelled	10.3	18	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> prophage pfl 6 cro; <b>PDBTitle:</b> structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
99	<a href="#">c2o5iD_</a>	Alignment	not modelled	10.3	23	<b>PDB header:</b> transferase/dna-rna hybrid <b>Chain:</b> D; <b>PDB Molecule:</b> dna-directed rna polymerase beta' chain; <b>PDBTitle:</b> crystal structure of the t. thermophilus rna polymerase elongation2 complex