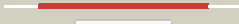



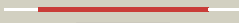












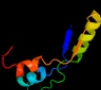

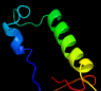



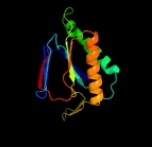
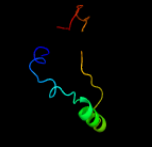
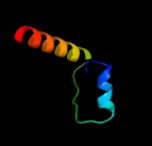

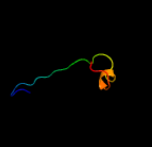
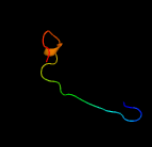
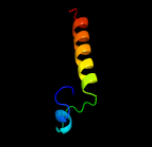



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1897c_(-)_2144458_2144889
Date	Fri Aug 2 13:30:51 BST 2019
Unique Job ID	96c51331362ec5d4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2dboA_	 Alignment		100.0	45	PDB header: hydrolase Chain: A: PDB Molecule: d-tyrosyl-trna(tyr) deacylase; PDBTitle: crystal structure of d-tyr-trna(tyr) deacylase from aquifex aeolicus
2	d1jkea_	 Alignment		100.0	44	Fold: DTD-like Superfamily: DTD-like Family: DTD-like
3	c3ko7E_	 Alignment		100.0	31	PDB header: hydrolase Chain: E: PDB Molecule: d-tyrosyl-trna(tyr) deacylase; PDBTitle: dtd from plasmodium falciparum in complex with d-lysine
4	d1j7ga_	 Alignment		100.0	45	Fold: DTD-like Superfamily: DTD-like Family: DTD-like
5	c2okvC_	 Alignment		100.0	40	PDB header: hydrolase Chain: C: PDB Molecule: probable d-tyrosyl-trna(tyr) deacylase 1; PDBTitle: c-myc dna unwinding element binding protein
6	c5xaqB_	 Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: probable d-tyrosyl-trna(tyr) deacylase 2; PDBTitle: crystal structure of animalia-specific trna deacylase from mus2 musculus
7	d1tc5a_	 Alignment		100.0	24	Fold: DTD-like Superfamily: DTD-like Family: DTD-like
8	c4rrcA_	 Alignment		61.3	18	PDB header: ligase Chain: A: PDB Molecule: probable threonine--trna ligase 2; PDBTitle: n-terminal editing domain of threonyl-trna synthetase from aeropyrum2 pernix with l-thr3aa (snapshot 3)
9	c4lnaA_	 Alignment		57.7	21	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase i from spirosuma2 linguale dsm 74, nysgrc target 029362
10	c2z8nB_	 Alignment		50.2	25	PDB header: lyase Chain: B: PDB Molecule: 27.5 kda virulence protein; PDBTitle: structural basis for the catalytic mechanism of phosphothreonine lyase
11	c2hl2A_	 Alignment		37.2	22	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase; PDBTitle: crystal structure of the editing domain of threonyl-trna2 synthetase from pyrococcus abyssi in complex with an3 analog of seryladenylate

12	c4uc0A_	Alignment		34.9	19	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of a purine nucleoside phosphorylase (psi-nysgrc-2 029736) from agrobacterium vitis
13	c4rrfD_	Alignment		30.7	16	PDB header: ligase Chain: D: PDB Molecule: threonine--trna ligase; PDBTitle: editing domain of threonyl-trna synthetase from methanococcus2 jannaschii with l-ser3aa
14	d1s7ia_	Alignment		29.2	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: DGPF domain (Pfam 04946)
15	c5h3iC_	Alignment		27.7	18	PDB header: lipid binding protein Chain: C: PDB Molecule: putative acyl-coa-binding protein; PDBTitle: crystal structure of oryza sativa acyl-coa-binding protein 2
16	c3i0uA_	Alignment		24.6	23	PDB header: lyase Chain: A: PDB Molecule: phosphothreonine lyase ospf; PDBTitle: structure of the type iii effector/phosphothreonine lyase ospf from2 shigella flexneri
17	d2giab1	Alignment		22.0	20	Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: Guide RNA binding protein gBP
18	c2giaB_	Alignment		22.0	20	PDB header: translation Chain: B: PDB Molecule: mitochondrial rna-binding protein 1; PDBTitle: crystal structures of trypanosoma brucei mrp1/mrp2
19	c5ijmA_	Alignment		20.2	20	PDB header: lipid binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an acyl-coa binding protein (lmjf.17.0620) of2 leishmania major
20	d1ofua2	Alignment		20.2	18	Fold: Bacillus chorismate mutase-like Superfamily: Tubulin C-terminal domain-like Family: Tubulin, C-terminal domain
21	c4zc0A_	Alignment	not modelled	19.4	18	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
22	c4nsnC_	Alignment	not modelled	18.8	20	PDB header: transferase Chain: C: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase from2 porphyromonas gingivalis atcc 33277, nysgrc target 030972,3 orthorhombic symmetry
23	c3pnrB_	Alignment	not modelled	18.5	14	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: pbipc-c; PDBTitle: structure of pbipc-c in complex with falcipain-2
24	d1a9xb2	Alignment	not modelled	18.2	28	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
25	c1ofuB_	Alignment	not modelled	14.7	18	PDB header: bacterial cell division inhibitor Chain: B: PDB Molecule: cell division protein ftsz; PDBTitle: crystal structure of sula:ftsZ from pseudomonas aeruginosa
26	c1k6mA_	Alignment	not modelled	13.9	6	PDB header: transferase, hydrolase Chain: A: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2- PDBTitle: crystal structure of human liver 6-phosphofructo-2-kinase/fructose-2,2 6-bisphosphatase
27	c3epyA_	Alignment	not modelled	13.7	18	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl-coa-binding domain-containing protein 7; PDBTitle: crystal structure of human acyl-coa binding domain 7 complexed with2 palmitoyl-coa
28	c3bh0A_	Alignment	not modelled	11.2	11	PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase;

						PDBTitle: atpase domain of g40p
29	d1rq2a2	Alignment	not modelled	11.0	19	Fold: Bacillus chorismate mutase-like Superfamily: Tubulin C-terminal domain-like Family: Tubulin, C-terminal domain
30	d1o51a_	Alignment	not modelled	10.7	22	Fold: Ferredoxin-like Superfamily: GlnB-like Family: DUF190/COG1993
31	c4zmiA_	Alignment	not modelled	10.0	14	PDB header: dna binding protein Chain: A: PDB Molecule: telomere length regulator taz1; PDBTitle: crystal structure of the helical domain of s. pombe taz1
32	c2wh5A_	Alignment	not modelled	10.0	18	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl-coa-binding domain-containing protein 4; PDBTitle: crystal structure of human acyl-coa binding domain 42 complexed with stearyl-coa
33	c2r6r1_	Alignment	not modelled	10.0	14	PDB header: cell cycle Chain: 1: PDB Molecule: cell division protein ftsz; PDBTitle: aquifex aeolicus ftsz
34	c2lbbA_	Alignment	not modelled	9.7	21	PDB header: protein binding Chain: A: PDB Molecule: acyl coa binding protein; PDBTitle: solution structure of acyl coa binding protein from babesia bovis t2bo
35	c6bbmA_	Alignment	not modelled	9.6	17	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: mechanisms of opening and closing of the bacterial replicative2 helicase: the dnab helicase and lambda p helicase loader complex
36	d1s1ma1	Alignment	not modelled	9.6	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
37	d1tf5a1	Alignment	not modelled	9.6	33	Fold: Pre-protein crosslinking domain of SecA Superfamily: Pre-protein crosslinking domain of SecA Family: Pre-protein crosslinking domain of SecA
38	c1st7A_	Alignment	not modelled	9.5	26	PDB header: transport protein Chain: A: PDB Molecule: acyl-coa-binding protein; PDBTitle: solution structure of acyl coenzyme a binding protein from2 yeast
39	c2m71A_	Alignment	not modelled	8.9	10	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-3; PDBTitle: solution structure of the a c-terminal domain of translation2 initiation factor if-3 from campylobacter jejuni
40	c5he9E_	Alignment	not modelled	8.8	17	PDB header: protein binding Chain: E: PDB Molecule: phage inhibitor protein; PDBTitle: bacterial initiation protein in complex with phage inhibitor protein
41	c5vodD_	Alignment	not modelled	8.6	60	PDB header: viral protein/immune system Chain: D: PDB Molecule: envelope glycoprotein ul130; PDBTitle: crystal structure of hcmv pentamer in complex with neutralizing2 antibody 9i6
42	c3tekA_	Alignment	not modelled	8.5	34	PDB header: dna binding protein Chain: A: PDB Molecule: thermodbp-single stranded dna binding protein; PDBTitle: thermodbp: a non-canonical single-stranded dna binding protein with a2 novel structure and mechanism
43	c4yheB_	Alignment	not modelled	8.1	13	PDB header: hydrolase Chain: B: PDB Molecule: gh5; PDBTitle: native bacteroidetes-affiliated gh5 cellulase linked with a2 polysaccharide utilization locus
44	d1llna_	Alignment	not modelled	8.0	21	Fold: Ribosome inactivating proteins (RIP) Superfamily: Ribosome inactivating proteins (RIP) Family: Plant cytotoxins
45	c4m1eC_	Alignment	not modelled	7.9	22	PDB header: transferase Chain: C: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase i from2 planctomyces limnophilus dsm 3776, nysgrc target 029364.
46	c2q6tB_	Alignment	not modelled	7.7	20	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
47	c4uznA_	Alignment	not modelled	7.6	36	PDB header: hydrolase Chain: A: PDB Molecule: endo-beta-1,4-glucanase (celulase b); PDBTitle: the native structure of the family 46 carbohydrate-binding2 module (cbm46) of endo-beta-1,4-glucanase b (cel5b) from3 bacillus halodurans
48	c1bifA_	Alignment	not modelled	7.6	8	PDB header: bifunctional enzyme Chain: A: PDB Molecule: 6-phosphofructo-2-kinase/ fructose-2,6-bisphosphatase; PDBTitle: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase bifunctional2 enzyme complexed with atp-g-s and phosphate
49	c2copA_	Alignment	not modelled	7.5	18	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl-coenzyme a binding domain containing 6; PDBTitle: solution structure of rsgi ruh-040, an acbp domain from2 human cdna
50	d2j44a2	Alignment	not modelled	7.1	13	Fold: Prealbumin-like Superfamily: Starch-binding domain-like Family: PUD-like
51	d1a79a1	Alignment	not modelled	7.0	29	Fold: Restriction endonuclease-like Superfamily: tRNA-intron endonuclease catalytic domain-like Family: tRNA-intron endonuclease catalytic domain-like
52	d1hb6a_	Alignment	not modelled	7.0	24	Fold: Acyl-CoA binding protein-like Superfamily: Acyl-CoA binding protein Family: Acyl-CoA binding protein
53	d1i96v_	Alignment	not modelled	6.8	12	Fold: IF3-like Superfamily: Translation initiation factor IF3, C-terminal domain Family: Translation initiation factor IF3, C-terminal domain

54	d1j3ba2	Alignment	not modelled	6.8	23	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
55	c3v2uC	Alignment	not modelled	6.7	17	PDB header: transcription Chain: C: PDB Molecule: protein gal3; PDBTitle: crystal structure of the yeast gal regulon complex of the repressor, 2 gal80p, and the transducer, gal3p, with galactose and atp
56	c5j67C	Alignment	not modelled	6.7	31	PDB header: membrane protein Chain: C: PDB Molecule: astrotactin-2; PDBTitle: structure of astrotactin-2, a conserved vertebrate-specific and 2 perforin-like membrane protein involved in neuronal development
57	c2dclB	Alignment	not modelled	6.6	29	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical upf0166 protein ph1503; PDBTitle: structure of ph1503 protein from pyrococcus horikoshii ot3
58	c2v4uA	Alignment	not modelled	6.5	8	PDB header: ligase Chain: A: PDB Molecule: ctp synthase 2; PDBTitle: human ctp synthetase 2 - glutaminase domain in complex with 2 5-oxo-l-norleucine
59	c2q1yB	Alignment	not modelled	6.4	20	PDB header: cell cycle, signaling protein Chain: B: PDB Molecule: cell division protein ftsz; PDBTitle: crystal structure of cell division protein ftsz from mycobacterium 2 tuberculosis in complex with gtp-gamma-s
60	c3h16A	Alignment	not modelled	6.4	27	PDB header: signaling protein Chain: A: PDB Molecule: tir protein; PDBTitle: crystal structure of a bacteria tir domain, pdtir from paracoccus 2 denitrificans
61	d1ii2a2	Alignment	not modelled	6.3	11	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
62	c3flvA	Alignment	not modelled	6.3	18	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl-coa-binding domain-containing protein 5; PDBTitle: the crystal structure of human acyl-coenzyme a binding domain 2 containing 5
63	d2ifea	Alignment	not modelled	6.3	20	Fold: IF3-like Superfamily: Translation initiation factor IF3, C-terminal domain Family: Translation initiation factor IF3, C-terminal domain
64	c3fp5A	Alignment	not modelled	6.2	18	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl-coa binding protein; PDBTitle: crystal structure of acbp from monilophthora perniciosa
65	d1hbka	Alignment	not modelled	6.1	18	Fold: Acyl-CoA binding protein-like Superfamily: Acyl-CoA binding protein Family: Acyl-CoA binding protein
66	c2vawA	Alignment	not modelled	6.1	18	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: ftsz pseudomonas aeruginosa gdp
67	c2pebB	Alignment	not modelled	6.1	27	PDB header: oxidoreductase Chain: B: PDB Molecule: putative dioxygenase; PDBTitle: crystal structure of a putative dioxygenase (npun_f1925) from nostoc 2 punctiforme pcc 73102 at 1.46 a resolution
68	c1a79B	Alignment	not modelled	5.9	29	PDB header: endonuclease Chain: B: PDB Molecule: trna endonuclease; PDBTitle: crystal structure of the trna splicing endonuclease from 2 methanococcus jannaschii
69	d2ftsA1	Alignment	not modelled	5.9	21	Fold: beta-clip Superfamily: MoeA C-terminal domain-like Family: MoeA C-terminal domain-like
70	c5abrB	Alignment	not modelled	5.8	20	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin, 2fe-2s; PDBTitle: structure of fesi protein from azotobacter vinelandii
71	c1keeH	Alignment	not modelled	5.8	28	PDB header: ligase Chain: H: PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate 2 synthetase by the antibiotic acivicin
72	c3icgD	Alignment	not modelled	5.7	18	PDB header: hydrolase Chain: D: PDB Molecule: endoglucanase d; PDBTitle: crystal structure of the catalytic and carbohydrate binding domain of 2 endoglucanase d from clostridium cellulovorans
73	c4zfwA	Alignment	not modelled	5.7	21	PDB header: hydrolase Chain: A: PDB Molecule: rrna n-glycosidase; PDBTitle: structural studies on a non-toxic homologue of type ii rips from 2 momordica charantia (bitter melon) in complex with galactose.
74	c2wjvE	Alignment	not modelled	5.5	31	PDB header: hydrolase Chain: E: PDB Molecule: regulator of nonsense transcripts 2; PDBTitle: crystal structure of the complex between human nonsense 2 mediated decay factors upf1 and upf2
75	c4r11F	Alignment	not modelled	5.5	29	PDB header: cell adhesion/protein binding Chain: F: PDB Molecule: cadherin-related hmr-1; PDBTitle: a conserved phosphorylation switch controls the interaction between 2 cadherin and beta-catenin in vitro and in vivo
76	c5vbaA	Alignment	not modelled	5.5	20	PDB header: chaperone, hydrolase Chain: A: PDB Molecule: lysozyme, esx-1 secretion-associated protein espg1 chimera; PDBTitle: structure of espg1 chaperone from the type vii (esx-1) secretion 2 system determined with the assistance of n-terminal t4 lysozyme 3 fusion
77	c1wuua	Alignment	not modelled	5.5	30	PDB header: transferase Chain: A: PDB Molecule: galactokinase; PDBTitle: crystal structure of human galactokinase complexed with 2 mgampnp and galactose
						PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz;

78	c4e6eA_	Alignment	not modelled	5.4	21	PDBTitle: crystal structure of a putative cell division protein ftsz (tfu_1113)2 from thermobifida fusca yx-er1 at 2.22 a resolution (psi community3 target, van wezel g.p.)
79	c4gfiA_	Alignment	not modelled	5.4	22	PDB header: isomerase Chain: A: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topo-78, an n-terminal 78kda fragment of2 topoisomerase v
80	d1tiga_	Alignment	not modelled	5.4	19	Fold: IF3-like Superfamily: Translation initiation factor IF3, C-terminal domain Family: Translation initiation factor IF3, C-terminal domain
81	c2yadA_	Alignment	not modelled	5.3	20	PDB header: surfactant protein Chain: A: PDB Molecule: surfactant protein c brichos domain; PDBTitle: brichos domain of surfactant protein c precursor protein
82	c3bgwD_	Alignment	not modelled	5.3	12	PDB header: replication Chain: D: PDB Molecule: dnab-like replicative helicase; PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase