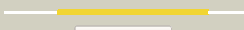


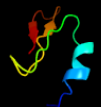



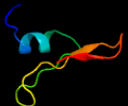





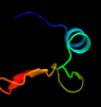

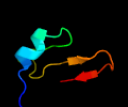



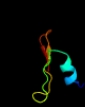

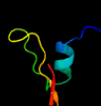

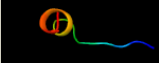
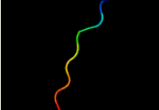

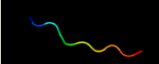

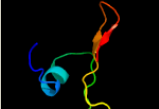
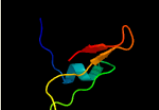



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0692 (-) _791834_792163
Date	Fri Jul 26 01:50:26 BST 2019
Unique Job ID	c816ffd93afa3335

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6jx3B_	 Alignment		72.4	22	PDB header: peptide binding protein Chain: B: PDB Molecule: tfub1; PDBTitle: lasso peptide synthetase b1 complexed with the leader peptide
2	d1aisa1	 Alignment		59.8	24	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
3	d1nh2a1	 Alignment		54.0	16	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
4	d1cdwa1	 Alignment		51.7	13	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
5	d1aisa2	 Alignment		49.6	26	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
6	d1mp9a1	 Alignment		46.4	24	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
7	d1qnaa1	 Alignment		43.9	16	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
8	d1cdwa2	 Alignment		38.0	18	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
9	d1mp9a2	 Alignment		35.9	21	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
10	d1nh2a2	 Alignment		28.6	21	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
11	d1qnaa2	 Alignment		28.6	21	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain

12	c5k83C_	Alignment		19.8	23	PDB header: hydrolase Chain: C: PDB Molecule: apolipoprotein b mrna editing enzyme, catalytic peptide- PDBTitle: crystal structure of a primate apobec3g n-domain, in complex with2 ssdna
13	d2fsja2	Alignment		18.2	43	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ta0583-like
14	c5z3qD_	Alignment		18.1	40	PDB header: viral protein Chain: D: PDB Molecule: pv-2c; PDBTitle: crystal structure of a soluble fragment of poliovirus 2c atpase (2.552 angstrom)
15	c3deeA_	Alignment		17.1	10	PDB header: transcription Chain: A: PDB Molecule: putative regulatory protein; PDBTitle: crystal structure of a putative regulatory protein involved in2 transcription (ngo1945) from neisseria gonorrhoeae fa 1090 at 2.25 a3 resolution
16	c5grbF_	Alignment		15.0	30	PDB header: hydrolase/inhibitor Chain: F: PDB Molecule: ev71 2c atpase; PDBTitle: crystal structure of 2c helicase from enterovirus 71 (ev71) bound with2 atpgammas
17	d2gtin1	Alignment		12.8	45	Fold: Streptavidin-like Superfamily: Extracellular hemoglobin linker subunit, receptor domain Family: Extracellular hemoglobin linker subunit, receptor domain
18	c1mp9B_	Alignment		12.7	21	PDB header: dna binding protein Chain: B: PDB Molecule: tata-binding protein; PDBTitle: tbp from a mesothermophilic archaeon, sulfobolus acidocaldarius
19	c1d3uA_	Alignment		12.5	26	PDB header: gene regulation/dna Chain: A: PDB Molecule: tata-binding protein; PDBTitle: tata-binding protein/transcription factor (ii)b/bre+tata-2 box complex from pyrococcus woesei
20	c2nytB_	Alignment		12.3	14	PDB header: hydrolase Chain: B: PDB Molecule: probable c->u-editing enzyme apobec-2; PDBTitle: the apobec2 crystal structure and functional implications2 for aid
21	d2gtlm1	Alignment	not modelled	12.0	45	Fold: Streptavidin-like Superfamily: Extracellular hemoglobin linker subunit, receptor domain Family: Extracellular hemoglobin linker subunit, receptor domain
22	c1ngmM_	Alignment	not modelled	11.3	16	PDB header: transcription/dna Chain: M: PDB Molecule: transcription initiation factor tfiid; PDBTitle: crystal structure of a yeast brf1-tbp-dna ternary complex
23	c2mzZA_	Alignment	not modelled	11.3	16	PDB header: hydrolase, antiviral protein Chain: A: PDB Molecule: apolipoprotein b mrna-editing enzyme, catalytic PDBTitle: nmr structure of apobec3g ntd variant, sntd
24	d2gtlo1	Alignment	not modelled	11.2	27	Fold: Streptavidin-like Superfamily: Extracellular hemoglobin linker subunit, receptor domain Family: Extracellular hemoglobin linker subunit, receptor domain
25	c2qibA_	Alignment	not modelled	10.7	13	PDB header: transcription Chain: A: PDB Molecule: tetr-family transcriptional regulator; PDBTitle: crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor
26	d1qi9a_	Alignment	not modelled	10.3	26	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Haloperoxidase (bromoperoxidase)
27	c2yMaB_	Alignment	not modelled	9.9	27	PDB header: carbohydrate binding protein Chain: B: PDB Molecule: protein os-9 homolog; PDBTitle: x-ray structure of the yos9 dimerization domain
28	c3vowB_	Alignment	not modelled	9.6	18	PDB header: hydrolase Chain: B: PDB Molecule: probable dna dc->du-editing enzyme apobec-3c; PDBTitle: crystal structure of the human apobec3c having hiv-1 vif-binding2 interface
						PDB header: transferase

29	c5x62A	Alignment	not modelled	9.5	70	Chain: A; PDB Molecule: carnosine n-methyltransferase; PDBTitle: crystal structure of a carnosine n-methyltransferase bound by adohcy
30	c5aj3f	Alignment	not modelled	9.1	34	PDB header: ribosome Chain: F; PDB Molecule: mitoribosomal protein bs6m, mrps6; PDBTitle: structure of the small subunit of the mammalian mitoribosome
31	c5tkmA	Alignment	not modelled	8.9	18	PDB header: hydrolase Chain: A; PDB Molecule: dna dc->du-editing enzyme apobec-3b; PDBTitle: crystal structure of human apobec3b n-terminal domain
32	d1gmua2	Alignment	not modelled	8.3	21	Fold: Ferredoxin-like Superfamily: Urease metallochaperone UreE, C-terminal domain Family: Urease metallochaperone UreE, C-terminal domain
33	d1smpi	Alignment	not modelled	7.5	30	Fold: Streptavidin-like Superfamily: beta-Barrel protease inhibitors Family: Metalloprotease inhibitor
34	c3tcqA	Alignment	not modelled	6.8	25	PDB header: viral protein Chain: A; PDB Molecule: matrix protein vp40; PDBTitle: crystal structure of matrix protein vp40 from ebola virus sudan
35	c6dk4A	Alignment	not modelled	6.7	12	PDB header: metal transport Chain: A; PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of campylobacter jejuni peroxide stress regulator
36	d1w7ab4	Alignment	not modelled	6.4	23	Fold: MutS N-terminal domain-like Superfamily: DNA repair protein MutS, domain I Family: DNA repair protein MutS, domain I
37	d1u3em2	Alignment	not modelled	5.8	25	Fold: DNA-binding domain of intron-encoded endonucleases Superfamily: DNA-binding domain of intron-encoded endonucleases Family: DNA-binding domain of intron-encoded endonucleases
38	c4bs9A	Alignment	not modelled	5.7	12	PDB header: isomerase Chain: A; PDB Molecule: trud; PDBTitle: structure of the heterocyclase trud
39	d2h28a1	Alignment	not modelled	5.7	29	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
40	c4b0aA	Alignment	not modelled	5.5	21	PDB header: transcription Chain: A; PDB Molecule: transcription initiation factor tfiid subunit 1, linker, PDBTitle: the high-resolution structure of ytbp-ytaf1 identifies2 conserved and competing interaction surfaces in3 transcriptional activation
41	d1tm9a	Alignment	not modelled	5.5	89	Fold: Hypothetical protein MG354 Superfamily: Hypothetical protein MG354 Family: Hypothetical protein MG354
42	c2kboA	Alignment	not modelled	5.4	16	PDB header: hydrolase Chain: A; PDB Molecule: dna dc->du-editing enzyme apobec-3g; PDBTitle: structure, interaction, and real-time monitoring of the2 enzymatic reaction of wild type apobec3g
43	c2z8uQ	Alignment	not modelled	5.3	24	PDB header: transcription Chain: Q; PDB Molecule: tata-box-binding protein; PDBTitle: methanococcus jannaschii tbp
44	c5aa6F	Alignment	not modelled	5.3	53	PDB header: oxidoreductase Chain: F; PDB Molecule: vanadium-dependent bromoperoxidase 2; PDBTitle: homohexameric structure of the second vanadate-dependent2 bromoperoxidase (anii) from ascophyllum nodosum
45	d2ea9a1	Alignment	not modelled	5.3	22	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
46	c3ik5A	Alignment	not modelled	5.3	30	PDB header: viral protein/signaling protein Chain: A; PDB Molecule: protein nef; PDBTitle: sivmac239 nef in complex with tcr zeta itam 1 polypeptide (a63-r80)
47	c3nb3C	Alignment	not modelled	5.2	38	PDB header: virus Chain: C; PDB Molecule: outer membrane protein a; PDBTitle: the host outer membrane proteins ompa and ompc are packed at specific2 sites in the shigella phage sf6 virion as structural components