
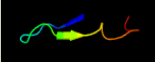
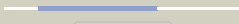
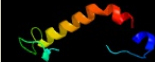








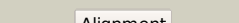
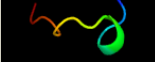





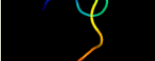




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2309A (-) _2583055_2583342
Date	Mon Aug 5 13:25:45 BST 2019
Unique Job ID	21cc9ade2e8dcb9d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2htja1	 Alignment		56.4	55	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FaeA-like
2	c5mlqA	 Alignment		27.5	19	PDB header: ligase Chain: A: PDB Molecule: cdps; PDBTitle: structure of cdps from nocardia brasiliensis
3	c2v8sV	 Alignment		19.0	33	PDB header: protein transport Chain: V: PDB Molecule: vesicle transport through interaction with PDBTitle: vti1b habc domain - epsinr enth domain complex
4	c3onjA	 Alignment		17.7	50	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain
5	c3uc7E	 Alignment		12.5	57	PDB header: de novo protein Chain: E: PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form
6	c1gk7A	 Alignment		12.4	63	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 1a fragment (1a)
7	c3uc8C	 Alignment		12.3	57	PDB header: de novo protein Chain: C: PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - tetragonal crystal form
8	c3uc7A	 Alignment		12.3	57	PDB header: de novo protein Chain: A: PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form
9	c3uc8B	 Alignment		12.3	57	PDB header: de novo protein Chain: B: PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - tetragonal crystal form
10	c3uc7D	 Alignment		12.3	57	PDB header: de novo protein Chain: D: PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form
11	c2ll5A	 Alignment		12.3	57	PDB header: de novo protein Chain: A: PDB Molecule: cyclo-tc1; PDBTitle: cyclo-tc1 trp-cage

12	c3uc8A_	Alignment		12.3	57	PDB header: de novo protein Chain: A; PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - tetragonal crystal form
13	c3uc7C_	Alignment		12.3	57	PDB header: de novo protein Chain: C; PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form
14	c3uc7F_	Alignment		12.3	57	PDB header: de novo protein Chain: F; PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form
15	c3uc7B_	Alignment		12.3	57	PDB header: de novo protein Chain: B; PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form
16	d1z0pa1	Alignment		12.0	37	Fold: Long alpha-hairpin Superfamily: SPy1572-like Family: SPy1572-like
17	c6ivsA_	Alignment		9.8	19	PDB header: transcription Chain: A; PDB Molecule: anti-sigma-i factor rsg1; PDBTitle: solution structure of the n-terminal domain of the anti-sigma factor2 rsg1 from clostridium thermocellum
18	c4x01D_	Alignment		9.5	64	PDB header: dna binding protein Chain: D; PDB Molecule: dna binding ctp1; PDBTitle: s. pombe ctp1 tetramerization domain
19	d3e9va1	Alignment		8.9	31	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
20	d1ew4a_	Alignment		8.3	60	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
21	d2z15a1	Alignment	not modelled	8.3	34	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
22	d1uhwa_	Alignment	not modelled	8.0	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
23	c5x5IM_	Alignment	not modelled	7.8	56	PDB header: dna binding protein/dna Chain: M; PDB Molecule: ader; PDBTitle: crystal structure of response regulator ader dna binding domain in2 complex with an intercistronic region
24	c3lk2B_	Alignment	not modelled	7.3	50	PDB header: protein binding Chain: B; PDB Molecule: f-actin-capping protein subunit beta isoforms 1 and 2; PDBTitle: crystal structure of capz bound to the uncapping motif from carmil
25	c4akrB_	Alignment	not modelled	7.3	50	PDB header: actin-binding protein Chain: B; PDB Molecule: f-actin-capping protein subunit beta; PDBTitle: crystal structure of the cytoplasmic actin capping protein2 cap32_34 from dictyostelium discoideum
26	c6g8yA_	Alignment	not modelled	7.3	24	PDB header: protein binding Chain: A; PDB Molecule: acetylated cis-golgi protein, involved in er-to-golgi PDBTitle: crystal structures of the single pdz domains from grasp65 and their2 interaction with the golgin gm130
27	c5u8mA_	Alignment	not modelled	7.1	41	PDB header: transcription Chain: A; PDB Molecule: response regulator; PDBTitle: a novel family of redox sensors in the streptococci evolved from two-2 component response regulators
28	d1iznb_	Alignment	not modelled	6.7	50	Fold: Subunits of heterodimeric actin filament capping protein Capz Superfamily: Subunits of heterodimeric actin filament capping protein Capz

						Family: Capz beta-1 subunit
29	c4hs5B_	Alignment	not modelled	6.6	50	PDB header: metal binding protein Chain: B: PDB Molecule: protein cyay; PDBTitle: frataxin from psychromonas ingrahamii as a model to study stability2 modulation within cyay protein family
30	c5oqmh_	Alignment	not modelled	6.6	86	PDB header: transcription Chain: H: PDB Molecule: dna-directed rna polymerases i, ii, and iii subunit rpabc3; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
31	c1kgsA_	Alignment	not modelled	6.5	35	PDB header: dna binding protein Chain: A: PDB Molecule: dna binding response regulator d; PDBTitle: crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
32	c4jpdA_	Alignment	not modelled	6.4	40	PDB header: metal binding protein Chain: A: PDB Molecule: protein cyay; PDBTitle: the structure of cyay from burkholderia cenocepacia
33	c2eg5C_	Alignment	not modelled	6.3	21	PDB header: transferase Chain: C: PDB Molecule: xanthosine methyltransferase; PDBTitle: the structure of xanthosine methyltransferase
34	c2vqzB_	Alignment	not modelled	6.1	37	PDB header: transcription Chain: B: PDB Molecule: polymerase basic protein 2; PDBTitle: structure of the cap-binding domain of influenza virus2 polymerase subunit pb2 with bound m7gtp
35	c2xxsA_	Alignment	not modelled	6.0	75	PDB header: protein binding Chain: A: PDB Molecule: protein mxig; PDBTitle: solution structure of the n-terminal domain of the shigella2 type iii secretion protein mxig
36	c3s4rB_	Alignment	not modelled	6.0	50	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1a/1b fragment with a stabilizing2 mutation
37	d2bsqe1	Alignment	not modelled	5.8	27	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
38	c4di1A_	Alignment	not modelled	5.6	40	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase echa17; PDBTitle: crystal structure of enoyl-coa hydratase echa17 from mycobacterium2 marinum
39	c3qkrC_	Alignment	not modelled	5.6	58	PDB header: replication Chain: C: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: mre11 rad50 binding domain bound to rad50
40	c3qkuC_	Alignment	not modelled	5.5	58	PDB header: replication Chain: C: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: mre11 rad50 binding domain in complex with rad50 and amp-prp
41	d1umha_	Alignment	not modelled	5.5	41	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: F-box associated region, FBA
42	d1gff1_	Alignment	not modelled	5.4	89	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Microviridae-like VP
43	c2msrA_	Alignment	not modelled	5.4	57	PDB header: protein binding Chain: A: PDB Molecule: histone-lysine n-methyltransferase 2a; PDBTitle: solution structure of ledgf/p75 ibd in complex with ml1 peptide (140-2 160)
44	c6fcoB_	Alignment	not modelled	5.4	24	PDB header: transport protein Chain: B: PDB Molecule: mitochondrial frataxin-like protein; PDBTitle: structural and functional characterisation of frataxin (fxn) like2 protein from chaetomium thermophilum
45	d1vqod1	Alignment	not modelled	5.3	38	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5