
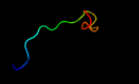
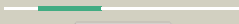






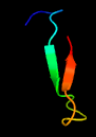


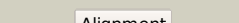
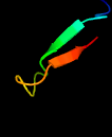



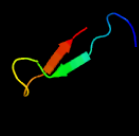


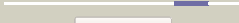






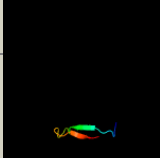
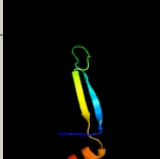
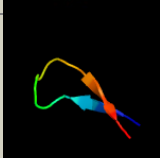
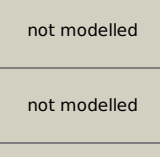


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2698 (-)_3014183_3014668
Date	Wed Aug 7 12:50:35 BST 2019
Unique Job ID	f54f050968901e42

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5b0hB_	 Alignment		56.9	30	PDB header: metal binding protein Chain: B; PDB Molecule: leukocyte cell-derived chemotaxin-2; PDBTitle: crystal structure of human leukocyte cell-derived chemotaxin 2
2	c6hwhX_	 Alignment		49.7	19	PDB header: electron transport Chain: X; PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
3	c1mtpB_	 Alignment		37.4	50	PDB header: structural genomics Chain: B; PDB Molecule: serine proteinase inhibitor (serpin), chain b; PDBTitle: the x-ray crystal structure of a serpin from a thermophilic prokaryote
4	d1wjra_	 Alignment		29.6	47	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
5	d1oi1a2	 Alignment		29.2	9	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
6	c3q0xA_	 Alignment		24.5	7	PDB header: structural protein Chain: A; PDB Molecule: centriole protein; PDBTitle: n-terminal coiled-coil dimer domain of c. reinhardtii sas-6 homolog2 bld12p
7	c1oz3C_	 Alignment		22.2	18	PDB header: transcription Chain: C; PDB Molecule: lethal(3)malignant brain tumor-like protein; PDBTitle: crystal structure of 3-mbt repeats of lethal (3) malignant brain tumor2 (native-i) at 1.85 angstrom
8	c3ut1A_	 Alignment		21.5	14	PDB header: transcription Chain: A; PDB Molecule: lethal(3)malignant brain tumor-like protein 3; PDBTitle: crystal structure of the 3-mbt repeat domain of l3mbt13
9	c3ceyA_	 Alignment		19.4	25	PDB header: transcription regulator Chain: A; PDB Molecule: lethal(3)malignant brain tumor-like 2 protein; PDBTitle: crystal structure of l3mbt12
10	d1px5a1	 Alignment		18.8	55	Fold: PAP/OAS1 substrate-binding domain Superfamily: PAP/OAS1 substrate-binding domain Family: 2'-5'-oligoadenylate synthetase 1, OAS1, second domain
11	c3q0yA_	 Alignment		18.8	8	PDB header: structural protein Chain: A; PDB Molecule: centriole protein; PDBTitle: n-terminal domain of c. reinhardtii sas-6 homolog bld12p

12	c4ckmA	Alignment		15.1	57	PDB header: structural protein Chain: A: PDB Molecule: sas-6; PDBTitle: structure of the n-terminal domain of leishmania sas-6
13	c4cknA	Alignment		15.0	57	PDB header: structural protein Chain: A: PDB Molecule: sas-6; PDBTitle: structure of an n-terminal fragment of leishmania sas-6 containing 2 parts of its coiled coil domain, f257e mutant
14	c3h6zA	Alignment		14.3	10	PDB header: transcription Chain: A: PDB Molecule: polycomb protein sfmbt; PDBTitle: crystal structure of the four mbt repeats of drosophila melanogaster 2 sfmbt in complex with peptide rhr (me)k vlr
15	c1px5A	Alignment		13.9	55	PDB header: transferase Chain: A: PDB Molecule: 2'-5'-oligoadenylate synthetase 1; PDBTitle: crystal structure of the 2'-specific and double-stranded 2 rna-activated interferon-induced antiviral protein 2'-5'-3 oligoadenylate synthetase
16	c2vytA	Alignment		13.8	14	PDB header: transcription Chain: A: PDB Molecule: sex comb on midleg-like protein 2; PDBTitle: the mbt repeats of human scm12 bind to peptides containing mono 2 methylated lysine.
17	c4s3nA	Alignment		13.7	55	PDB header: transferase/rna Chain: A: PDB Molecule: 2'-5'-oligoadenylate synthase 3; PDBTitle: crystal structure of human oas3 domain i in complex with dsrna
18	d1oz2a2	Alignment		13.1	14	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
19	d1ky8a	Alignment		13.0	22	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
20	d1wjjsa	Alignment		12.4	18	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
21	d1oi1a1	Alignment	not modelled	12.2	14	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
22	c6mvtA	Alignment	not modelled	12.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of a bacterial aldh16 complexed with nadh
23	c5tuvB	Alignment	not modelled	12.0	10	PDB header: transcription Chain: B: PDB Molecule: transcription factor e2f5; PDBTitle: crystal structure of the e2f5-dp1-p107 ternary complex
24	c2y3wA	Alignment	not modelled	11.9	29	PDB header: structural protein Chain: A: PDB Molecule: spindle assembly abnormal protein 6 homolog; PDBTitle: n-terminal head domain and beginning of coiled coil domain of danio2 rerio sas-6
25	d1oz2a1	Alignment	not modelled	11.2	24	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
26	c4xq7A	Alignment	not modelled	11.1	45	PDB header: transferase Chain: A: PDB Molecule: 2'-5'-oligoadenylate synthase-like protein; PDBTitle: the crystal structure of the oas-like domain (old) of human oasl
27	c2r58A	Alignment	not modelled	10.9	14	PDB header: transcription Chain: A: PDB Molecule: polycomb protein scm; PDBTitle: crystal structure of the two mbt repeats from sex-comb on midleg (scm)2 in complex with di-methyl lysine
28	d1oz2a3	Alignment	not modelled	10.6	18	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
						PDB header: structural protein

29	c5a17A_	Alignment	not modelled	10.5	14	Chain: A: PDB Molecule: spindle assembly abnormal protein 6 homolog; PDBTitle: n-terminal fragment of drosophila melanogaster sas-6 (f143d),2 dimerised via the coiled-coil domain.
30	d1wjqa_	Alignment	not modelled	10.3	12	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
31	c2djgC_	Alignment	not modelled	10.3	33	PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl-peptidase 1; PDBTitle: re-determination of the native structure of human dipeptidyl peptidase2 i (cathepsin c)
32	c3sk7B_	Alignment	not modelled	9.4	50	PDB header: replication inhibitor Chain: B: PDB Molecule: protein seqa; PDBTitle: crystal structure of v. cholerae seqa
33	c1xdyC_	Alignment	not modelled	9.4	26	PDB header: oxidoreductase Chain: C: PDB Molecule: bacterial sulfite oxidase; PDBTitle: structural and biochemical identification of a novel2 bacterial oxidoreductase, w-containing cofactor
34	c4gfcA_	Alignment	not modelled	9.1	7	PDB header: structural protein Chain: A: PDB Molecule: spindle assembly abnormal protein 6; PDBTitle: n-terminal coiled-coil dimer of c.elegans sas-6, crystal form b
35	c2k2uB_	Alignment	not modelled	9.0	57	PDB header: transcription Chain: B: PDB Molecule: alpha trans-inducing protein; PDBTitle: nmr structure of the complex between tfb1 subunit of tfiih2 and the activation domain of vp16
36	d2ozga1	Alignment	not modelled	8.5	13	Fold: SCP-like Superfamily: SCP-like Family: EF1021 C-terminal domain-like
37	d1imhc2	Alignment	not modelled	8.1	6	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: Rel/Dorsal transcription factors, DNA-binding domain
38	c5tuga_	Alignment	not modelled	8.0	50	PDB header: motor protein Chain: A: PDB Molecule: flagellar biosynthesis protein flag; PDBTitle: archaeum periplasmic stator protein complex flaf and flag from2 sulfobolbus acidocaldarius
39	d1j2jb_	Alignment	not modelled	8.0	33	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
40	d2uyoa1	Alignment	not modelled	7.8	33	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: ML2640-like
41	c6d97B_	Alignment	not modelled	7.3	17	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde dehydrogenase 12; PDBTitle: structure of aldehyde dehydrogenase 12 (aldh12) from zea mays
42	c2n5IA_	Alignment	not modelled	7.2	11	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: regnase-1 c-terminal domain
43	c3fmtF_	Alignment	not modelled	7.1	67	PDB header: replication inhibitor/dna Chain: F: PDB Molecule: protein seqa; PDBTitle: crystal structure of seqa bound to dna
44	c1sz1A_	Alignment	not modelled	7.0	30	PDB header: transferase/rna Chain: A: PDB Molecule: trna nucleotidyltransferase; PDBTitle: mechanism of cca-adding enzymes specificity revealed by crystal2 structures of ternary complexes
45	c2azpA_	Alignment	not modelled	6.8	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa1268; PDBTitle: crystal structure of pa1268 solved by sulfur sad
46	c1nrnR_	Alignment	not modelled	6.6	36	PDB header: serine proteinase/receptor Chain: R: PDB Molecule: receptor based peptide nrs; PDBTitle: crystallographic structures of thrombin complexed with2 thrombin receptor peptides: existence of expected and3 novel binding modes
47	d1r89a1	Alignment	not modelled	6.6	30	Fold: PAP/OAS1 substrate-binding domain Superfamily: PAP/OAS1 substrate-binding domain Family: Archaeal tRNA CCA-adding enzyme substrate-binding domain
48	c1jr3E_	Alignment	not modelled	6.5	37	PDB header: transferase Chain: E: PDB Molecule: dna polymerase iii, delta' subunit; PDBTitle: crystal structure of the processivity clamp loader gamma complex of e.2 coli dna polymerase iii
49	c2jg7G_	Alignment	not modelled	5.7	14	PDB header: oxidoreductase Chain: G: PDB Molecule: antiquitin; PDBTitle: crystal structure of seabream antiquitin and elucidation of2 its substrate specificity
50	c3pyiA_	Alignment	not modelled	5.6	7	PDB header: structural protein Chain: A: PDB Molecule: spindle assembly abnormal protein 6; PDBTitle: structure of the n-terminal domain of c. elegans sas-6
51	c6b9tH_	Alignment	not modelled	5.6	30	PDB header: oxidoreductase Chain: H: PDB Molecule: methylphosphonate synthase; PDBTitle: crystal structure of mpns with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
52	d2j2za2	Alignment	not modelled	5.3	67	Fold: C2 domain-like Superfamily: Periplasmic chaperone C-domain Family: Periplasmic chaperone C-domain
53	c1ciiA_	Alignment	not modelled	5.2	15	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
54	c2x0dA_	Alignment	not modelled	5.1	19	PDB header: transferase Chain: A: PDB Molecule: wsaf; PDBTitle: apo structure of wsaf