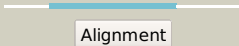

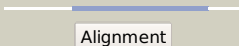



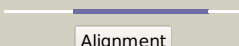
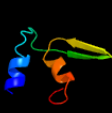
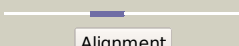

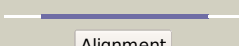
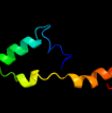
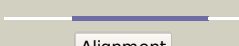

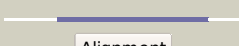








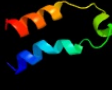
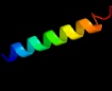


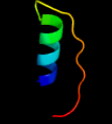





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3196A (-) _3566693_3566893
Date	Thu Aug 8 16:20:39 BST 2019
Unique Job ID	6eb900d4534401e8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6dkmB_	 Alignment		31.9	33	PDB header: de novo protein Chain: B; PDB Molecule: dhd131_b; PDBTitle: dhd131
2	d2juza1	 Alignment		24.9	26	Fold: YejL-like Superfamily: YejL-like Family: YejL-like
3	c3h6pD_	 Alignment		18.1	58	PDB header: structural genomics, unknown function Chain: D; PDB Molecule: esat-6-like protein esxr; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
4	c6c23C_	 Alignment		16.3	23	PDB header: gene regulation Chain: C; PDB Molecule: histone-lysine n-methyltransferase ezh2; PDBTitle: cryo-em structure of prc2 bound to cofactors aebp2 and jarid2 in the2 compact active state
5	c6fc3B_	 Alignment		16.2	60	PDB header: translation Chain: B; PDB Molecule: cap-associated protein caf20; PDBTitle: crystal structure of the eif4e-p20 complex from saccharomyces2 cerevisiae
6	c5ocdD_	 Alignment		16.2	23	PDB header: rna binding protein Chain: D; PDB Molecule: cyclodipeptide synthase; PDBTitle: structure of a cdps from fluoribacter dumoffii
7	d2qtia1	 Alignment		15.2	24	Fold: YejL-like Superfamily: YejL-like Family: YejL-like
8	d2jrxal	 Alignment		13.1	21	Fold: YejL-like Superfamily: YejL-like Family: YejL-like
9	d1jcb2	 Alignment		13.0	37	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Domains B1 and B5 of PheRS-beta, PheT
10	d1k3xa1	 Alignment		12.5	26	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
11	c1h4uA_	 Alignment		11.8	55	PDB header: extracellular matrix protein Chain: A; PDB Molecule: nidogen-1; PDBTitle: domain g2 of mouse nidogen-1

12	d2juwa1	Alignment		11.6	21	Fold: YejL-like Superfamily: YejL-like Family: YejL-like
13	c4cs6A_	Alignment		11.4	30	PDB header: transferase Chain: A; PDB Molecule: aminoglycoside adenylyltransferase; PDBTitle: crystal structure of aada - an aminoglycoside adenylyltransferase
14	c2o35A_	Alignment		10.9	25	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein duf1244; PDBTitle: protein of unknown function (duf1244) from sinorhizobium meliloti
15	d2o35a1	Alignment		10.9	25	Fold: SMc04008-like Superfamily: SMc04008-like Family: SMc04008-like
16	d2jpqa1	Alignment		9.7	17	Fold: YejL-like Superfamily: YejL-like Family: YejL-like
17	c3mstA_	Alignment		9.4	14	PDB header: transport protein Chain: A; PDB Molecule: putative nitrate transport protein; PDBTitle: crystal structure of a putative nitrate transport protein (tvn0104)2 from thermoplasma volcanium at 1.35 a resolution
18	d1qgxa_	Alignment		9.1	21	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
19	c3byaB_	Alignment		9.0	47	PDB header: metal binding protein Chain: B; PDB Molecule: glutamate [nmda] receptor subunit zeta-1 peptide; PDBTitle: structure of a calmodulin complex
20	c2hqwb_	Alignment		8.6	47	PDB header: metal binding protein Chain: B; PDB Molecule: glutamate nmda receptor subunit zeta 1; PDBTitle: crystal structure of ca2+/calmodulin bound to nmda receptor nr1c12 peptide
21	d1k82a1	Alignment	not modelled	8.5	29	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
22	d1ql4a1	Alignment	not modelled	8.1	55	Fold: GFP-like Superfamily: GFP-like Family: Domain G2 of nidogen-1
23	c2opfA_	Alignment	not modelled	7.8	26	PDB header: hydrolase/dna Chain: A; PDB Molecule: endonuclease viii; PDBTitle: crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
24	c2l9mA_	Alignment	not modelled	7.5	24	PDB header: apoptosis inhibitor Chain: A; PDB Molecule: baculoviral iap repeat-containing protein 2; PDBTitle: structure of ciap1 card
25	c2rdcA_	Alignment	not modelled	7.1	40	PDB header: lipid binding protein Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative lipid binding protein (gsu0061) from2 geobacter sulfurreducens pca at 1.80 a resolution
26	c3dd7D_	Alignment	not modelled	7.0	42	PDB header: ribosome inhibitor Chain: D; PDB Molecule: prevent host death protein; PDBTitle: structure of doch66y in complex with the c-terminal domain of phd
27	c3a9fA_	Alignment	not modelled	7.0	23	PDB header: electron transport Chain: A; PDB Molecule: cytochrome c; PDBTitle: crystal structure of the c-terminal domain of cytochrome cz from2 chlorobium tepidum
28	c4jpdA_	Alignment	not modelled	7.0	24	PDB header: metal binding protein Chain: A; PDB Molecule: protein cyay; PDBTitle: the structure of cyay from burkholderia cenocepacia

29	c4yxpA	Alignment	not modelled	6.5	44	PDB header: viral protein Chain: A: PDB Molecule: mrna export factor; PDBTitle: the structure of the folded domain of the signature multifunctional2 protein icp27 from herpes simplex virus-1 reveals an intertwined3 dimer.
30	d2otaa1	Alignment	not modelled	6.3	20	Fold: YejL-like Superfamily: YejL-like Family: YejL-like
31	d2ga5a1	Alignment	not modelled	6.2	24	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
32	c5tcmA	Alignment	not modelled	5.9	29	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: first bromodomain from leishmania donovani ldbpk_091320 complexed with2 bi-2536
33	c3q4hB	Alignment	not modelled	5.9	38	PDB header: metal transport Chain: B: PDB Molecule: low molecular weight protein antigen 7; PDBTitle: crystal structure of the mycobacterium smegmatis esx9 complex2 (msmeg_0620-msmeg_0621)
34	c1xkmA	Alignment	not modelled	5.9	60	PDB header: antibiotic Chain: A: PDB Molecule: distinctin chain a; PDBTitle: nmr structure of antimicrobial peptide distinctin in water
35	c1xkmC	Alignment	not modelled	5.9	60	PDB header: antibiotic Chain: C: PDB Molecule: distinctin chain a; PDBTitle: nmr structure of antimicrobial peptide distinctin in water
36	d1r2za1	Alignment	not modelled	5.6	24	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
37	d1w8ia	Alignment	not modelled	5.6	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
38	d1ayia	Alignment	not modelled	5.5	27	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
39	c2lkiA	Alignment	not modelled	5.4	50	PDB header: cell adhesion Chain: A: PDB Molecule: erythrocyte membrane protein 1 (pfemp1); PDBTitle: structure of the core intracellular domain of pfemp1
40	c6fddC	Alignment	not modelled	5.2	32	PDB header: structural protein Chain: C: PDB Molecule: whirlin; PDBTitle: crystal structure of the hhd2 domain of whirlin
41	c2kmgA	Alignment	not modelled	5.1	50	PDB header: gene regulation Chain: A: PDB Molecule: klca; PDBTitle: the structure of the klca and ardb proteins show a novel2 fold and antirestriction activity against type i dna3 restriction systems in vivo but not in vitro