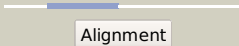


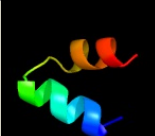
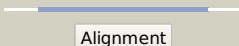
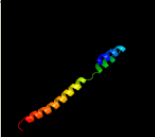
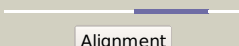
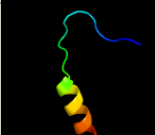
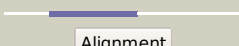
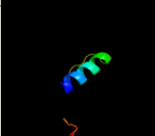
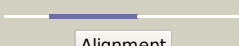



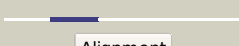






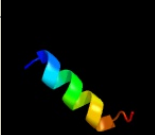
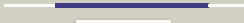
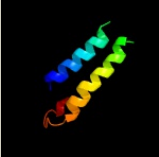
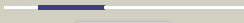



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1893 (-) _2140493_2140711
Date	Fri Aug 2 13:30:51 BST 2019
Unique Job ID	0af244ffabc4018f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5vidL_	 Alignment		26.1	52	PDB header: toxin Chain: I; PDB Molecule: bot.0671.2; PDBTitle: receptor binding domain of bont/b in complex with mini-protein binder2 bot.0671.2
2	c5vidG_	 Alignment		26.1	52	PDB header: toxin Chain: G; PDB Molecule: bot.0671.2; PDBTitle: receptor binding domain of bont/b in complex with mini-protein binder2 bot.0671.2
3	c4uosA_	 Alignment		21.1	17	PDB header: de novo protein Chain: A; PDB Molecule: designed helical bundle; PDBTitle: thermodynamic hyperstability in parametrically designed2 helical bundles
4	c2ejsA_	 Alignment		16.1	25	PDB header: ligase Chain: A; PDB Molecule: autocrine motility factor receptor, isoform 2; PDBTitle: solution structure of ruh-076, a human cue domain
5	c2vxaL_	 Alignment		13.7	29	PDB header: flavoprotein Chain: L; PDB Molecule: dodecin; PDBTitle: h.halophila dodecin in complex with riboflavin
6	c3oqtP_	 Alignment		13.1	18	PDB header: flavoprotein Chain: P; PDB Molecule: rv1498a protein; PDBTitle: crystal structure of rv1498a protein from mycobacterium tuberculosis
7	c4atsA_	 Alignment		8.5	62	PDB header: viral protein Chain: A; PDB Molecule: structural protein orf273; PDBTitle: structure of the orf273 protein from the acidianus two-tailed virus
8	c3onrI_	 Alignment		8.4	44	PDB header: metal binding protein Chain: I; PDB Molecule: protein transport protein sece2; PDBTitle: crystal structure of the calcium chelating immunodominant antigen,2 calcium dodecin (rv0379),from mycobacterium tuberculosis with a novel3 calcium-binding site
9	c2kxhB_	 Alignment		8.3	58	PDB header: protein binding Chain: B; PDB Molecule: peptide of far upstream element-binding protein 1; PDBTitle: solution structure of the first two rrm domains of fir in the complex2 with fbp nbx peptide
10	c6r1eC_	 Alignment		8.2	31	PDB header: flavoprotein Chain: C; PDB Molecule: dodecin; PDBTitle: structure of dodecin from streptomyces coelicolor
11	d2ux9a1	 Alignment		8.1	13	Fold: Dodecin subunit-like Superfamily: Dodecin-like Family: Dodecin-like

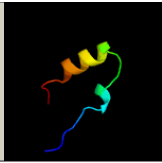
12	d1eq1a_  Alignment		8.0	18 Fold: Apolipoprotein III Superfamily: Apolipoprotein III Family: Apolipoprotein III
13	c2d9sA_  Alignment		6.1	27 PDB header: ligase Chain: A: PDB Molecule: cbl e3 ubiquitin protein ligase; PDB Title: solution structure of rsgi ruh-049, a uba domain from mouse2 cdna

14

[d1luza_](#)



Alignment



6.1

18

Fold:OB-fold

Superfamily:Nucleic acid-binding proteins

Family:Cold shock DNA-binding domain-like