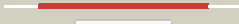
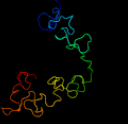

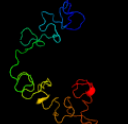
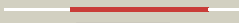
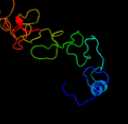

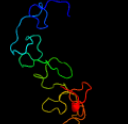

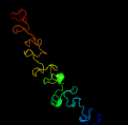



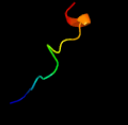

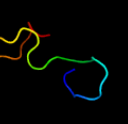

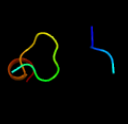






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3906c_(-)_4391275_4391784
Date	Sat Aug 10 22:05:09 BST 2019
Unique Job ID	4f14901a1d88d3f2

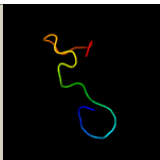
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fbyC_	 Alignment		99.9	26	PDB header: cell adhesion Chain: C; PDB Molecule: cartilage oligomeric matrix protein; PDBTitle: the crystal structure of the signature domain of cartilage oligomeric2 matrix protein.
2	c1yo8A_	 Alignment		99.9	25	PDB header: cell adhesion Chain: A; PDB Molecule: thrombospondin-2; PDBTitle: structure of the c-terminal domain of human thrombospondin-2
3	c1ux6A_	 Alignment		99.8	23	PDB header: cell adhesion Chain: A; PDB Molecule: thrombospondin-1; PDBTitle: structure of a thrombospondin c-terminal fragment reveals a novel2 calcium core in the type 3 repeats
4	d1ux6a2	 Alignment		99.7	25	Fold: TSP type-3 repeat Superfamily: TSP type-3 repeat Family: TSP type-3 repeat
5	c5wtlB_	 Alignment		99.3	25	PDB header: membrane protein Chain: B; PDB Molecule: ompa family protein; PDBTitle: crystal structure of the periplasmic portion of outer membrane protein2 a (ompa) from capnocytophaga gingivalis
6	d1tzoa_	 Alignment		63.8	36	Fold: Anthrax protective antigen Superfamily: Anthrax protective antigen Family: Anthrax protective antigen
7	d1acca_	 Alignment		38.7	29	Fold: Anthrax protective antigen Superfamily: Anthrax protective antigen Family: Anthrax protective antigen
8	d1ohzb_	 Alignment		26.8	42	Fold: Type I dockerin domain Superfamily: Type I dockerin domain Family: Type I dockerin domain
9	c2j42A_	 Alignment		26.5	26	PDB header: toxin Chain: A; PDB Molecule: c2 toxin component-ii; PDBTitle: low quality crystal structure of the transport component c2-2 ii of the c2-toxin from clostridium botulinum
10	c4dh2B_	 Alignment		23.8	31	PDB header: cell adhesion/protein binding Chain: B; PDB Molecule: dockerin type 1; PDBTitle: crystal structure of coh-olpc(cthe_0452)-doc435(cthe_0435) complex: a2 novel type i cohesin-dockerin complex from clostridium thermocellum3 attc 27405
11	c3p0dD_	 Alignment		21.7	42	PDB header: hydrolase Chain: D; PDB Molecule: glycoside hydrolase family 9; PDBTitle: crystal structure of a multimodular ternary protein complex from2 clostridium thermocellum

12	c4uyqB_	Alignment		21.2	42	PDB header: cell adhesion/protein binding Chain: B: PDB Molecule: cellulosomal scaffoldin adaptor protein b; PDBTitle: high resolution structure of the third cohesin scac in complex with2 the scab dockerin with a mutation in the c-terminal helix (in to si)3 from acetivbrio cellulolyticus displaying a type i interaction.
13	c2y3nB_	Alignment		20.1	28	PDB header: structrual protein/hydrolase Chain: B: PDB Molecule: cellulosomal family-48 processive glycoside hydrolase; PDBTitle: type ii cohesin-dockerin domain from bacteroides cellolosolvens
14	c3ul4B_	Alignment		16.2	42	PDB header: cell adhesion/protein binding Chain: B: PDB Molecule: cellulosome enzyme, dockerin type i; PDBTitle: crystal structure of coh-olpa(cthe_3080)-doc918(cthe_0918) complex: a2 novel type i cohesin-dockerin complex from clostridium thermocellum3 attc 27405
15	d1dava_	Alignment		15.9	31	Fold: Type I dockerin domain Superfamily: Type I dockerin domain Family: Type I dockerin domain
16	c5nrmB_	Alignment		15.6	42	PDB header: cell adhesion Chain: B: PDB Molecule: doccel5: type i dockerin repeat domain from a. PDBTitle: crystal structure of the sixth cohesin from acetivbrio2 cellulolyticus' scaffoldin b in complex with cel5 dockerin s51i, l52n3 mutant
17	c5lxvB_	Alignment		15.2	50	PDB header: protein binding Chain: B: PDB Molecule: carbohydrate-binding protein wp_009985128; PDBTitle: crystal structure of ruminococcus flavefaciens scaffoldin c cohesin in2 complex with a dockerin from an uncharacterized cbm-containing3 protein
18	d2cclb1	Alignment		15.1	46	Fold: Type I dockerin domain Superfamily: Type I dockerin domain Family: Type I dockerin domain
19	c2vn5B_	Alignment		11.8	28	PDB header: cell adhesion Chain: B: PDB Molecule: endoglucanase a; PDBTitle: the clostridium cellulolyticum dockerin displays a dual2 binding mode for its cohesin partner

20 [c2b59B](#)

Alignment



10.2

16

PDB header:hydrolase/structural protein
Chain: B: **PDB Molecule:**cellulosomal scaffolding protein a;
PDBTitle: the type ii cohesin dockerin complex