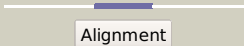

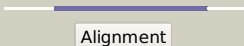

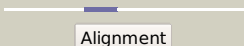



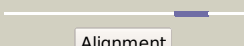

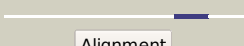

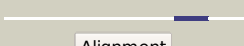
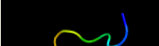









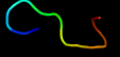
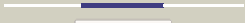
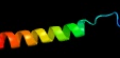


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0476 (-) _566511_566774
Date	Tue Jul 23 14:50:55 BST 2019
Unique Job ID	f563e1ee639451a9

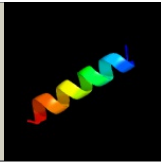
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2n1pA_	 Alignment		18.1	23	PDB header: viral protein Chain: A; PDB Molecule: non-structural protein 5b, ns5b; PDBTitle: structure of the c-terminal membrane domain of hcv ns5b protein
2	c6d79A_	 Alignment		17.4	14	PDB header: transport protein Chain: A; PDB Molecule: sulfate transporter cysz; PDBTitle: structure of cysz, a sulfate permease from pseudomonas fragi
3	d2c4fl3	 Alignment		17.3	44	Fold: GLA-domain Superfamily: GLA-domain Family: GLA-domain
4	d1danl3	 Alignment		15.9	44	Fold: GLA-domain Superfamily: GLA-domain Family: GLA-domain
5	c3ixsF_	 Alignment		13.4	27	PDB header: protein binding Chain: F; PDB Molecule: ring1 and yy1-binding protein; PDBTitle: ring1b c-terminal domain/rybp c-terminal domain complex
6	c2zfdB_	 Alignment		8.0	25	PDB header: signaling protein/transferase Chain: B; PDB Molecule: putative uncharacterized protein t20115_90; PDBTitle: the crystal structure of plant specific calcium binding protein atcbl22 in complex with the regulatory domain of atcplk14
7	c5u89B_	 Alignment		7.4	40	PDB header: hydrolase/inhibitor Chain: B; PDB Molecule: mbth domain protein; PDBTitle: crystal structure of a cross-module fragment from the dimodular nrps2 dhbf
8	c3a0hx_	 Alignment		7.0	28	PDB header: electron transport Chain: X; PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of i-substituted photosystem ii complex
9	c3a0bx_	 Alignment		7.0	28	PDB header: electron transport Chain: X; PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of br-substituted photosystem ii complex
10	c3a0hX_	 Alignment		7.0	28	PDB header: electron transport Chain: X; PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of i-substituted photosystem ii complex
11	c3a0bX_	 Alignment		7.0	28	PDB header: electron transport Chain: X; PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of br-substituted photosystem ii complex

12	d1pjca2	 Alignment		6.7	8 Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: L-alanine dehydrogenase-like
13	c2kncA_	 Alignment		5.9	23 PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib; PDBTitle: platelet integrin alfaIib-beta3 transmembrane-cytoplasmic2 heterocomplex

14 [c1s5lx_](#)

Alignment



5.9

28

PDB header: photosynthesis

Chain: X: **PDB Molecule:** photosystem ii psbx protein;

PDBTitle: architecture of the photosynthetic oxygen evolving center