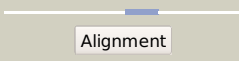
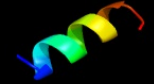
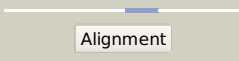

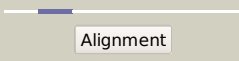
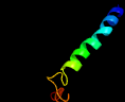
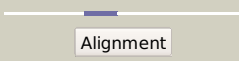
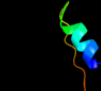
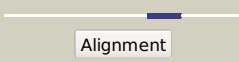

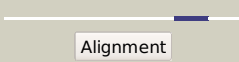
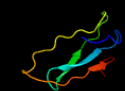
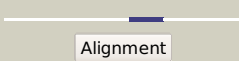
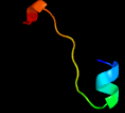
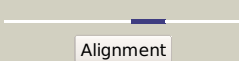



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1797_(-)_2035490_2036710
Date	Fri Aug 2 13:30:40 BST 2019
Unique Job ID	bd05c71bf4d026d5

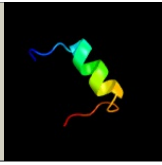
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k42B_	 Alignment		26.4	29	PDB header: signaling protein Chain: B: PDB Molecule: espfu; PDBTitle: solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehec effector
2	c2lnhC_	 Alignment		20.6	29	PDB header: signaling protein/protein binding Chain: C: PDB Molecule: secreted effector protein espf(u); PDBTitle: enterohaemorrhagic e. coli (ehec) exploits a tryptophan switch to2 hijack host f-actin assembly
3	c5yq7L_	 Alignment		17.9	28	PDB header: photosynthesis Chain: L: PDB Molecule: precursor for l subunits of photosynthetic reaction center; PDBTitle: cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii
4	d3etja2	 Alignment		10.4	30	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
5	c3sluB_	 Alignment		8.9	33	PDB header: hydrolase Chain: B: PDB Molecule: m23 peptidase domain protein; PDBTitle: crystal structure of nmb0315
6	c4z29B_	 Alignment		7.8	17	PDB header: signaling protein Chain: B: PDB Molecule: magnetotaxis protein mtxa; PDBTitle: crystal structure of the magnetobacterial protein mtxa c-terminal2 domain
7	d3boea1	 Alignment		6.7	25	Fold: CdCA1 repeat-like Superfamily: CdCA1 repeat-like Family: CdCA1 repeat-like
8	c4pcvB_	 Alignment		6.7	15	PDB header: oxidoreductase Chain: B: PDB Molecule: bdca (yjgi); PDBTitle: the structure of bdca (yjgi) from e. coli

9

[c2daeA](#)

Alignment



5.6

35

PDB header: structural genomics, unknown function

Chain: A: **PDB Molecule:** kiaa0733 protein;

PDBTitle: solution structure of the n-terminal cue domain in the2 human mitogen-activated protein kinase kinase kinase 73 interacting protein 2 (map3k7ip2)