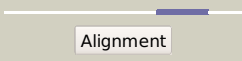

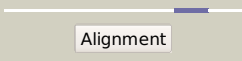
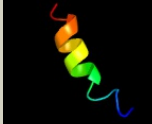
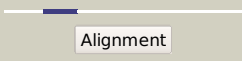

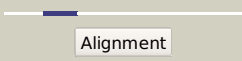
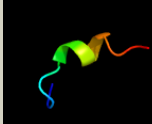
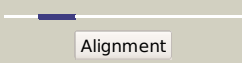
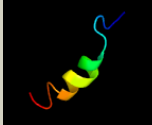
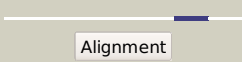
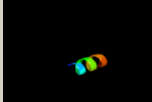
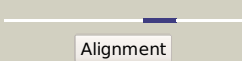
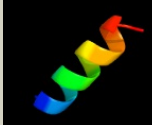
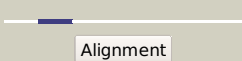

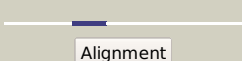

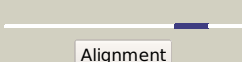
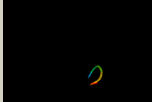
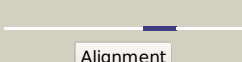

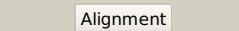



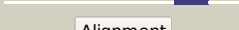



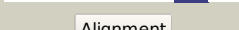

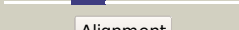
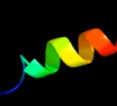




Phyre2

Email	mdejesus@rockefeller.edu
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Date	Tue Jul 23 14:50:47 BST 2019
Unique Job ID	44da144ee4cba295

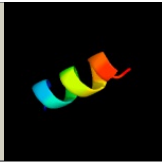
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ijjA_	 Alignment		11.5	13	PDB header: signaling protein Chain: A: PDB Molecule: erbb-2 receptor protein-tyrosine kinase; PDBTitle: solution structure of the neu/erbb-2 membrane spanning2 segment
2	c2lowA_	 Alignment		10.3	28	PDB header: membrane protein Chain: A: PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfip
3	d1n93x_	 Alignment		9.4	36	Fold: P40 nucleoprotein Superfamily: P40 nucleoprotein Family: P40 nucleoprotein
4	c1n93X_	 Alignment		9.4	36	PDB header: viral protein Chain: X: PDB Molecule: p40 nucleoprotein; PDBTitle: crystal structure of the borna disease virus nucleoprotein
5	c2lx0A_	 Alignment		7.9	33	PDB header: membrane protein Chain: A: PDB Molecule: membrane fusion protein p14; PDBTitle: arced helix (arch) nmr structure of the reovirus p14 fusion-associated2 small transmembrane (fast) protein transmembrane domain (tmd) in3 dodecyl phosphocholine (dpc) micelles
6	c5tfyl_	 Alignment		7.4	54	PDB header: cell adhesion Chain: J: PDB Molecule: flagellin; PDBTitle: the archaeal flagellum of methanospirillum hungatei strain jf1.
7	d1g5ta_	 Alignment		6.8	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
8	c5tp6B_	 Alignment		6.7	67	PDB header: oxidoreductase Chain: B: PDB Molecule: nitric oxide synthase, inducible; PDBTitle: solution structure of the cam34 with the inos cam binding domain2 peptide
9	d1ldda_	 Alignment		6.5	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: SCF ubiquitin ligase complex WHB domain
10	d1yt3a2	 Alignment		6.2	57	Fold: SAM domain-like Superfamily: HRDC-like Family: RNase D C-terminal domains
11	d1g64b_	 Alignment		6.2	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)

12	c6b2zS_	 Alignment		5.9	21	PDB header: membrane protein Chain: S; PDB Molecule: atp synthase subunit j, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
13	c6b2zi_	 Alignment		5.9	21	PDB header: membrane protein Chain: I; PDB Molecule: atp synthase subunit c, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
14	c5o4uK_	 Alignment		5.6	46	PDB header: cell adhesion Chain: K; PDB Molecule: flagellin; PDBTitle: the flagellin of pyrococcus furiosus
15	c3n1hA_	 Alignment		5.6	20	PDB header: dna binding protein Chain: A; PDB Molecule: stwwhy2; PDBTitle: crystal structure of stwwhy2
16	c5z1lL_	 Alignment		5.4	38	PDB header: protein fibril Chain: L; PDB Molecule: flagellin; PDBTitle: cryo-em structure of methanoccus maripaludis archaellum
17	c5j6vA_	 Alignment		5.2	21	PDB header: antimicrobial protein Chain: A; PDB Molecule: hylin-d; PDBTitle: nmr structures of hylin-a1 analogs: hylin-d
18	c4oqgF_	 Alignment		5.2	25	PDB header: electron transport Chain: F; PDB Molecule: cytochrome b6-f complex subunit 7; PDBTitle: internal lipid architecture of the hetero-oligomeric cytochrome b6f2 complex

19 [c4h44F_](#)

Alignment



5.2

25

PDB header: photosynthesis
Chain: F; **PDB Molecule:** cytochrome b6-f complex subunit 7;
PDB Title: 2.70 a cytochrome b6f complex structure from nostoc pcc 7120