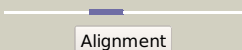
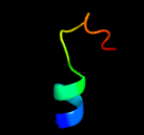
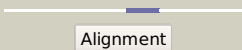
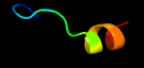
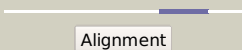

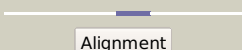



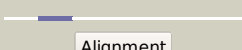

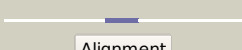

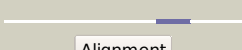

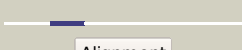

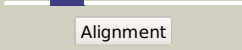





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2656c (-)_2978670_2979062
Date	Wed Aug 7 12:50:30 BST 2019
Unique Job ID	e298af618a9e319c

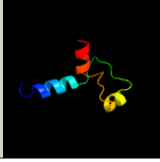
Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2m0nA_	 Alignment		17.0	56	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of a duf3349 annotated protein from mycobacterium2 abscessus, mab_3403c. seattle structural genomics center for3 infectious disease target myaba.17112.a.a2
2	c2jt1A_	 Alignment		15.9	60	PDB header: transcription Chain: A; PDB Molecule: pefi protein; PDBTitle: solution nmr structure of pefi (plasmid-encoded fimbriae regulatory)2 protein from salmonella typhimurium. northeast structural genomics3 target str82
3	c4n3xD_	 Alignment		14.2	28	PDB header: endocytosis Chain: D; PDB Molecule: rab5 gdp/gtp exchange factor; PDBTitle: crystal structure of rabex-5 cc domain
4	c3vzaE_	 Alignment		13.6	36	PDB header: cell cycle Chain: E; PDB Molecule: centromere protein t; PDBTitle: crystal structure of the chicken spc24-spc25 globular domain in2 complex with cenp-t peptide
5	c3vzaF_	 Alignment		13.6	36	PDB header: cell cycle Chain: F; PDB Molecule: centromere protein t; PDBTitle: crystal structure of the chicken spc24-spc25 globular domain in2 complex with cenp-t peptide
6	c2mv6A_	 Alignment		11.6	43	PDB header: membrane protein Chain: A; PDB Molecule: erythropoietin receptor; PDBTitle: solution structure of the transmembrane domain and the juxta-membrane2 domain of the erythropoietin receptor in micelles
7	c2q7rA_	 Alignment		11.1	50	PDB header: hydrolase Chain: A; PDB Molecule: mucosa-associated lymphoid tissue lymphoma translocation PDBTitle: x-ray structure of the death domain of the human mucosa associated2 lymphoid tissue lymphoma translocation protein 1
8	c2jp6A_	 Alignment		10.1	64	PDB header: toxin Chain: A; PDB Molecule: potassium channel toxin alpha-ktx 18.1; PDBTitle: structural and functional characterization of the2 recombinant form of the kv1.3 channel blocker tc32
9	d1ejxc2	 Alignment		8.4	86	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: alpha-subunit of urease, catalytic domain
10	d1e9yb2	 Alignment		8.2	71	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: alpha-subunit of urease, catalytic domain
11	c3gw6F_	 Alignment		6.6	25	PDB header: chaperone Chain: F; PDB Molecule: endo-n-acetylneuraminidase; PDBTitle: intramolecular chaperone

12

[c5e06A](#)

Alignment



6.0

23

PDB header: nuclear protein
Chain: A: **PDB Molecule:** nucleocapsid protein;
PDB Title: structure of sin nombre virus nucleoprotein in long-axis crystal form