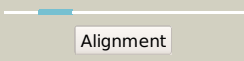

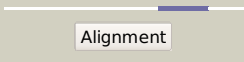
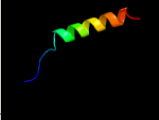
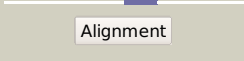

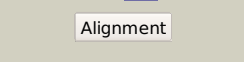

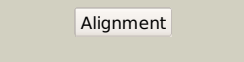
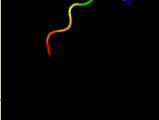
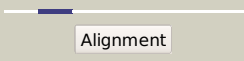

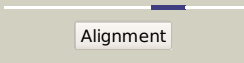

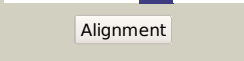

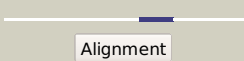
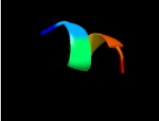
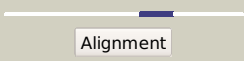

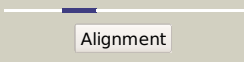



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2273_(-)_2546112_2546441
Date	Mon Aug 5 13:25:41 BST 2019
Unique Job ID	ad82e7b0dacf6e60

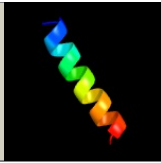
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5kk9A_	 Alignment		32.1	100	PDB header: transport protein Chain: A: PDB Molecule: gap junction beta-1 protein; PDBTitle: connexin 32 g12r n-terminal mutant,
2	c2y94C_	 Alignment		19.9	20	PDB header: transferase Chain: C: PDB Molecule: 5'-amp-activated protein kinase catalytic subunit alpha-1; PDBTitle: structure of an active form of mammalian ampk
3	d2p06a1	 Alignment		10.0	27	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: AF0060-like
4	c2p06A_	 Alignment		10.0	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af_0060; PDBTitle: crystal structure of a predicted coding region af_0060 from2 archaeoglobus fulgidus dsm 4304
5	c3p7jA_	 Alignment		8.1	75	PDB header: transcription Chain: A: PDB Molecule: heterochromatin protein 1; PDBTitle: drosophila hp1a chromo shadow domain
6	d1dz1a_	 Alignment		7.5	63	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
7	c4pzuF_	 Alignment		6.5	42	PDB header: transferase Chain: F: PDB Molecule: uncharacterized protein rv3404c/mt3512; PDBTitle: crystal structure of a putative uncharacterize protein rv3404c and2 likely sugar n-formyltransferase from mycobacterium tuberculosis
8	c3ggzH_	 Alignment		6.3	71	PDB header: protein transport, endocytosis Chain: H: PDB Molecule: vacuolar protein-sorting-associated protein 46; PDBTitle: crystal structure of s.cerevisiae ist1 n-terminal domain in complex2 with did2 mim motif
9	c3ggzE_	 Alignment		6.2	71	PDB header: protein transport, endocytosis Chain: E: PDB Molecule: vacuolar protein-sorting-associated protein 46; PDBTitle: crystal structure of s.cerevisiae ist1 n-terminal domain in complex2 with did2 mim motif
10	c3ggzF_	 Alignment		6.2	71	PDB header: protein transport, endocytosis Chain: F: PDB Molecule: vacuolar protein-sorting-associated protein 46; PDBTitle: crystal structure of s.cerevisiae ist1 n-terminal domain in complex2 with did2 mim motif
11	c6igzM_	 Alignment		6.1	38	PDB header: plant protein Chain: M: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: structure of psi-lhci

12	c5h7pB_	Alignment		6.1	71	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein-sorting-associated protein 46; PDBTitle: nmr structure of the vta1ntd-did2(176-204) complex
13	c3ggzG_	Alignment		6.1	71	PDB header: protein transport, endocytosis Chain: G: PDB Molecule: vacuolar protein-sorting-associated protein 46; PDBTitle: crystal structure of s.cerevisiae ist1 n-terminal domain in complex2 with did2 mim motif
14	d2fmma1	Alignment		6.0	63	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain

15 [c4hr1A_](#)

Alignment



5.9

42

PDB header: unknown function
Chain: A: **PDB Molecule:** putative uncharacterized protein;
PDB Title: structure of pav1-137, a protein from the virus pav1 that infects *pyrococcus abyssi*.