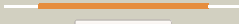

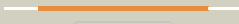
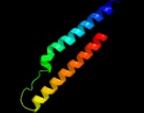

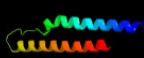



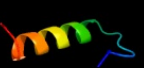






Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3893c_(PE36)_4375940_4376173
 Date Sat Aug 10 22:05:08 BST 2019
 Unique Job ID 07000448301204e8

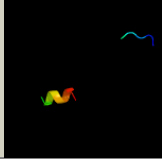
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsA_	 Alignment		86.8	33	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	d2g38a1	 Alignment		85.2	23	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
3	c2g38A_	 Alignment		85.2	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
4	c5kinC_	 Alignment		13.3	41	PDB header: lyase Chain: C: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
5	d1ir1s_	 Alignment		9.7	32	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
6	c2ykaB_	 Alignment		9.0	44	PDB header: rna binding protein/transcription Chain: B: PDB Molecule: 52 kda immediate-early phosphoprotein; PDBTitle: rrm domain of mrna export adaptor ref2-i bound to hvs orf572 peptide
7	c1vw4S_	 Alignment		6.6	50	PDB header: ribosome Chain: S: PDB Molecule: 54s ribosomal protein l24, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit

8

[c4etrA_](#)

Alignment



5.6

29

PDB header: unknown function

Chain: A: **PDB Molecule:** putative uncharacterized protein;

PDBTitle: x-ray structure of pa2169 from pseudomonas aeruginosa