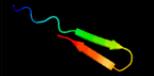
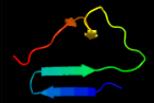
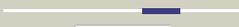
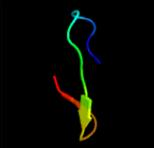


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3655c_(-)_4095179_4095478
Date	Fri Aug 9 18:20:34 BST 2019
Unique Job ID	ff83509b82a54735

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2f2ha1	 Alignment		9.1	20	Fold: Putative glucosidase YicI, C-terminal domain Superfamily: Putative glucosidase YicI, C-terminal domain Family: Putative glucosidase YicI, C-terminal domain
2	c1fctA	 Alignment		8.4	43	PDB header: transit peptide Chain: A: PDB Molecule: ferredoxin chloroplastic transit peptide PDBTitle: nmr structures of ferredoxin chloroplastic transit peptide2 from chlamydomonas reinhardtii promoted by3 trifluoroethanol in aqueous solution
3	c1wqsA	 Alignment		7.7	30	PDB header: hydrolase Chain: A: PDB Molecule: 3c-like protease; PDBTitle: crystal structure of norovirus 3c-like protease
4	c4v194	 Alignment		7.5	0	PDB header: ribosome Chain: 4: PDB Molecule: mitoribosomal protein bl31m, mrpl55; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
5	c1rfoC	 Alignment		6.0	47	PDB header: viral protein Chain: C: PDB Molecule: whisker antigen control protein; PDBTitle: trimeric foldon of the t4 phagehead fibrin
6	c3ld3A	 Alignment		5.7	30	PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic phosphatase from anaplasma2 phagocytophilum at 1.75a resolution

7 [c2m0nA](#)

Alignment



5.6

53

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