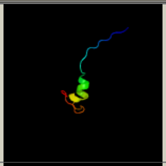
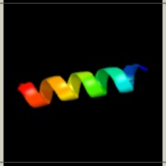
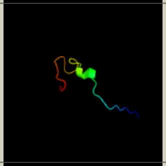
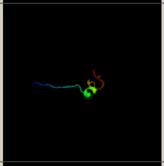
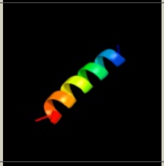
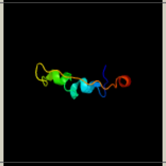
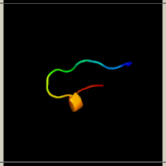
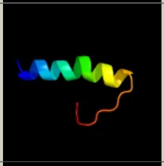
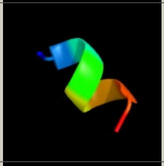
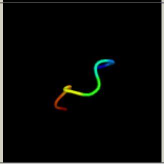
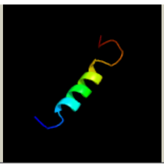
Email	mdejesus@rockefeller.edu
Description	RVBD2806_(-)_3113278_3113469
Date	Wed Aug 7 12:50:47 BST 2019
Unique Job ID	aba10ba9712b8368

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vh4a_	Alignment		12.1	33	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Stabilizer of iron transporter SufD **Family:**Stabilizer of iron transporter SufD
2	c5v8kB_	Alignment		11.3	33	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**proteinsubunit pshx; **PDBTitle:** homodimeric reaction center of h. modesticaldum
3	c4dn7B_	Alignment		8.9	26	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, atp-binding protein; **PDBTitle:** crystal structure of putative abc transporter, atp-binding protein2 from methanosarcina mazei go1
4	c5awfA_	Alignment		8.8	26	**PDB header:**transport protein/protein binding **Chain:** A: **PDB Molecule:**fes cluster assembly protein sufb; **PDBTitle:** crystal structure of sufb-sufc-sufd complex from escherichia coli
5	c5c4yB_	Alignment		8.7	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative transcription regulator lmo0852; **PDBTitle:** crystal structure of putative tetr family transcription factor from2 listeria monocytogenes
6	d1tyza_	Alignment		8.5	25	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
7	c3pntA_	Alignment		7.3	43	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**nad+-glycohydrolase; **PDBTitle:** crystal structure of the streptococcus pyogenes nad+ glycohydrolase2 spn in complex with ifs, the immunity factor for spn
8	d2hkua2	Alignment		5.3	25	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
9	c4ue4B_	Alignment		5.2	75	**PDB header:**translation **Chain:** B: **PDB Molecule:**ftsq signal sequence; **PDBTitle:** structural basis for targeting and elongation arrest of bacillus2 signal recognition particle
10	c2hyiJ_	Alignment		5.2	50	**PDB header:**hydrolase/rna binding protein/rna **Chain:** J: **PDB Molecule:**protein casc3; **PDBTitle:** structure of the human exon junction complex with a trapped2 dead-box helicase bound to rna

11	c6re80_	 Alignment		5.1	36	**PDB header:**proton transport **Chain:** 0: **PDB Molecule:**asa-10: polytomella f-atp synthase associated subunit 10; **PDBTitle:** cryo-em structure of polytomella f-atp synthase, rotary substate 2d,2 composite map