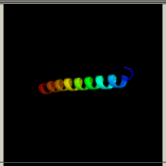
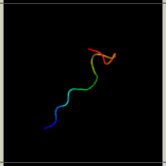
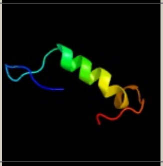
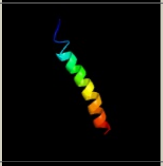
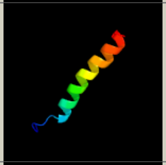
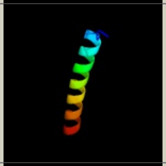
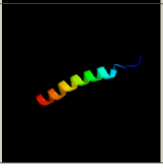
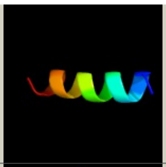
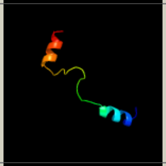
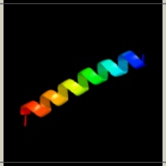
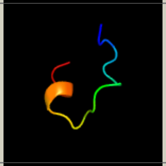
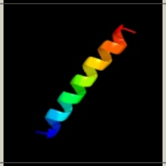
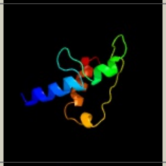
Phyre^2

Email	mdejesus@rockefeller.edu
Description	RVBD0779c_(-)_872675_873295
Date	Fri Jul 26 01:50:36 BST 2019
Unique Job ID	a53b84756140b8c7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4wpyA_	Alignment		28.3	18	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**protein dl-rv1738; **PDBTitle:** racemic crystal structure of rv1738 from mycobacterium tuberculosis2 (form-ii)
2	d1gr0a1	Alignment		27.0	44	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
3	d2fgga1	Alignment		26.3	15	**Fold:**dsRBD-like **Superfamily:**Rv2632c-like **Family:**Rv2632c-like
4	c5ydcA_	Alignment		23.8	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**uncharacterized hth-type transcriptional regulator rv1828; **PDBTitle:** crystal structure of mercury soaked c-terminal domain of rv1828 from2 mycobacterium tuberculosis
5	d2axtm1	Alignment		17.4	8	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein M, PsbM **Family:**PsbM-like
6	c3a0hm_	Alignment		14.3	8	**PDB header:**electron transport **Chain:** M: **PDB Molecule:**photosystem ii reaction center protein m; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
7	d1q90b_	Alignment		11.8	20	**Fold:**Heme-binding four-helical bundle **Superfamily:**Transmembrane di-heme cytochromes **Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
8	c2l35B_	Alignment		11.2	21	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**tyro protein tyrosine kinase-binding protein; **PDBTitle:** structure of the dap12-nkg2c transmembrane heterotrimer
9	c2l34B_	Alignment		11.0	21	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**tyro protein tyrosine kinase-binding protein; **PDBTitle:** structure of the dap12 transmembrane homodimer
10	c4wolA_	Alignment		11.0	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tyro protein tyrosine kinase-binding protein; **PDBTitle:** crystal structure of the dap12 transmembrane domain in lipidic cubic2 phase
11	c2l34A_	Alignment		11.0	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tyro protein tyrosine kinase-binding protein; **PDBTitle:** structure of the dap12 transmembrane homodimer

12	c4h1wB_	Alignment		8.4	25	**PDB header:**hydrolase/hydrolase regulator **Chain:** B: **PDB Molecule:**sarcolipin; **PDBTitle:** e1 structure of the (sr) ca2+-atpase in complex with sarcolipin
13	c3w5aC_	Alignment		8.4	25	**PDB header:**metal transport/membrane protein **Chain:** C: **PDB Molecule:**sarcolipin; **PDBTitle:** crystal structure of the calcium pump and sarcolipin from rabbit fast2 twitch skeletal muscle in the e1.mg2+ state
14	d1vp5a_	Alignment		8.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
15	c1k6nH_	Alignment		7.5	8	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**photosynthetic reaction center h subunit; **PDBTitle:** e(l212)a,d(l213)a double mutant structure of photosynthetic reaction2 center from rhodobacter sphaeroides
16	c4v1aq_	Alignment		6.9	33	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:** **PDBTitle:** structure of the large subunit of the mammalian mitoribosome, part 22 of 2
17	c1eysH_	Alignment		5.9	8	**PDB header:**electron transport **Chain:** H: **PDB Molecule:**photosynthetic reaction center; **PDBTitle:** crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
18	d1nbwa3	Alignment		5.8	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
19	c2i5nH_	Alignment		5.7	33	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**reaction center protein h chain; **PDBTitle:** 1.96 a x-ray structure of photosynthetic reaction center from2 rhodopseudomonas viridis:crystals grown by microfluidic technique
20	c1yybA_	Alignment		5.5	37	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**programmed cell death protein 5; **PDBTitle:** solution structure of 1-26 fragment of human programmed2 cell death 5 protein
21	d1zara1	Alignment	not modelled	5.4	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Rio2 serine protein kinase N-terminal domain