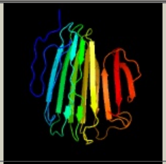
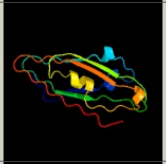
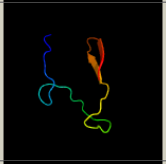
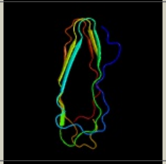
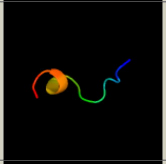
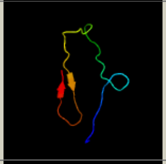
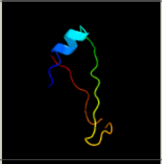
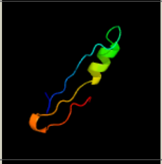
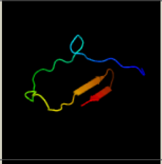
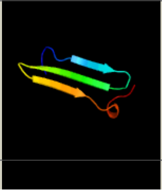
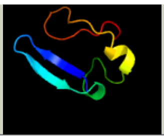
Phyre^2

Email	mdejesus@rockefeller.edu
Description	RVBD1853_(ureD)_2101029_2101655
Date	Fri Aug 2 13:30:46 BST 2019
Unique Job ID	38dbd4172ee0aae9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sf5D_	Alignment		100.0	12	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**urease accessory protein ureh; **PDBTitle:** crystal structure of helicobacter pylori urease accessory protein2 uref/h complex
2	c4dn7B_	Alignment		93.7	16	**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
3	d1vh4a_	Alignment		72.6	14	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Stabilizer of iron transporter SufD **Family:**Stabilizer of iron transporter SufD
4	d1x9la_	Alignment		22.6	20	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**DR1885-like metal-binding protein **Family:**DR1885-like metal-binding protein
5	c5awfA_	Alignment		15.5	6	**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
6	c4zhjA_	Alignment		12.6	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**mg-chelatase subunit chlh; **PDBTitle:** crystal structure of the catalytic subunit of magnesium chelatase
7	c3zk0A_	Alignment		11.0	7	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**sco3965; **PDBTitle:** the crystal structure of a cu(i) metallochaperone from2 streptomyces lividans in its apo form
8	d1js8a2	Alignment		9.2	14	**Fold:**C-terminal domain of mollusc hemocyanin **Superfamily:**C-terminal domain of mollusc hemocyanin **Family:**C-terminal domain of mollusc hemocyanin
9	d1stfi_	Alignment		8.2	14	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Cystatins
10	c2k6zA_	Alignment		8.0	11	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha1943; **PDBTitle:** solution structures of copper loaded form pcua (trans2 conformation of the peptide bond involving the nitrogen of3 p14)
11	d1t6la1	Alignment		5.9	8	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor

12	c2x8nA_	Alignment		5.2	9	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**cv0863; **PDBTitle:** solution nmr structure of uncharacterized protein cv0863 from2 chromobacterium violaceum. northeast structural genomics target3 (nesg) target cvt3. ocsp target cv0863.