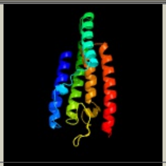
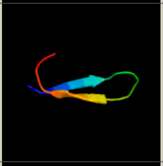
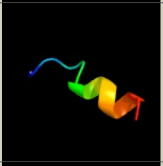
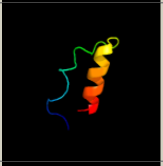
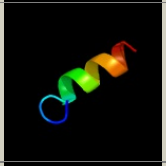
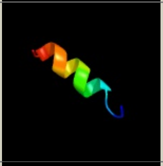
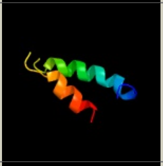
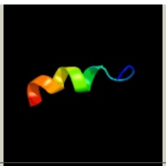
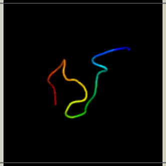
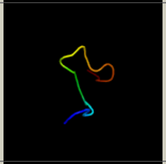
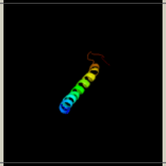
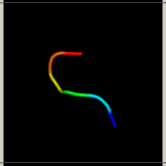
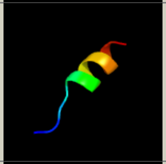
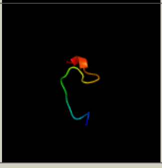
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1139c_(-)_1266490_1266990
Date	Wed Jul 31 22:05:22 BST 2019
Unique Job ID	f8c71828c767fe83

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5v7pA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-s-isoprenylcysteine o-methyltransferase; **PDBTitle:** atomic structure of the eukaryotic intramembrane ras methyltransferase2 icmt (isoprenylcysteine carboxyl methyltransferase), in complex with3 a monobody
2	c4a2nB_	Alignment		99.9	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**isoprenylcysteine carboxyl methyltransferase; **PDBTitle:** crystal structure of ma-icmt
3	c4quvB_	Alignment		99.6	14	**PDB header:**oxidoreductase, membrane protein **Chain:** B: **PDB Molecule:**delta(14)-sterol reductase; **PDBTitle:** structure of an integral membrane delta(14)-sterol reductase
4	d1s7ia_	Alignment		33.2	17	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**DGPF domain (Pfam 04946)
5	c1p58F_	Alignment		28.3	31	**PDB header:**virus **Chain:** F: **PDB Molecule:**envelope protein m; **PDBTitle:** complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
6	c1p58E_	Alignment		27.3	19	**PDB header:**virus **Chain:** E: **PDB Molecule:**envelope protein m; **PDBTitle:** complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
7	c3j2pD_	Alignment		18.8	27	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**small envelope protein m; **PDBTitle:** cryoem structure of dengue virus envelope protein heterotetramer
8	c5wsnD_	Alignment		14.8	29	**PDB header:**virus **Chain:** D: **PDB Molecule:**m protein; **PDBTitle:** structure of japanese encephalitis virus
9	c5ht7A_	Alignment		12.4	37	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a transition-metal-ion-binding betagamma-2 crystallin from methanosaeta thermophila
10	c4b03D_	Alignment		11.4	19	**PDB header:**virus **Chain:** D: **PDB Molecule:**dengue virus 1 prm protein; **PDBTitle:** 6a electron cryomicroscopy structure of immature dengue virus serotype2 1
11	c4cbfB_	Alignment		10.7	13	**PDB header:**virus **Chain:** B: **PDB Molecule:**m protein; **PDBTitle:** near-atomic resolution cryo-em structure of dengue serotype 4 virus

12	c5ireD_	Alignment		10.7	20	**PDB header:**virus **Chain:** D: **PDB Molecule:**m protein; **PDBTitle:** the cryo-em structure of zika virus
13	c6epzA_	Alignment		10.5	26	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic alpha-galactoside-binding protein; **PDBTitle:** structure of the periplasmic binding protein melb (atu4661) in complex2 with melibiose from agrobacterium fabrum c58
14	d1e7la1	Alignment		8.4	50	**Fold:**LEM/SAP HeH motif **Superfamily:**Recombination endonuclease VII, C-terminal and dimerization domains **Family:**Recombination endonuclease VII, C-terminal and dimerization domains
15	c2wokA_	Alignment		8.0	35	**PDB header:**peptide binding protein/peptide **Chain:** A: **PDB Molecule:**clavulanic acid biosynthesis oligopeptide binding protein **PDBTitle:** clavulanic acid biosynthesis oligopeptide binding protein 2 complexed2 with bradykinin
16	c2kncA_	Alignment		7.4	9	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
17	d1rgoa2	Alignment		7.0	67	**Fold:**CCCH zinc finger **Superfamily:**CCCH zinc finger **Family:**CCCH zinc finger
18	d1hsta_	Alignment		6.5	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5
19	c2rqpA_	Alignment		6.3	23	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**heterochromatin protein 1-binding protein 3; **PDBTitle:** the solution structure of heterochromatin protein 1-binding2 protein 74 histone h1 like domain
20	c4fajA_	Alignment		6.3	15	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**prgz; **PDBTitle:** structure and mode of peptide binding of pheromone receptor prgz
21	c2d5wA_	Alignment	not modelled	5.8	39	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**peptide abc transporter, peptide-binding protein; **PDBTitle:** the crystal structure of oligopeptide binding protein from thermus2 thermophilus hb8 complexed with pentapeptide
22	c3j00Z_	Alignment	not modelled	5.5	15	**PDB header:**ribosome/ribosomal protein **Chain:** Z: **PDB Molecule:**cell division protein ftsq; **PDBTitle:** structure of the ribosome-secye complex in the membrane environment
23	d1yqaa1	Alignment	not modelled	5.5	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5
24	c2kb1A_	Alignment	not modelled	5.3	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**wsk3; **PDBTitle:** nmr studies of a channel protein without membrane:2 structure and dynamics of water-solubilized kcsa
25	c2xp1A_	Alignment	not modelled	5.3	38	**PDB header:**transcription **Chain:** A: **PDB Molecule:**spt6; **PDBTitle:** structure of the tandem sh2 domains from antonospora locustae2 transcription elongation factor spt6