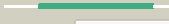
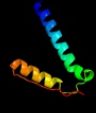
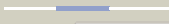








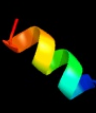

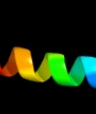

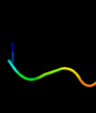



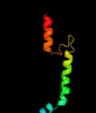



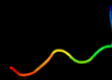
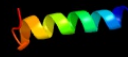



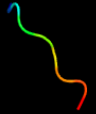




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3126c_(-)_3491805_3492119
Date	Thu Aug 8 16:20:31 BST 2019
Unique Job ID	bb400b3ecec59672

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2fb5a1</a>	 Alignment		48.2	21	<b>Fold:</b> Yojj-like <b>Superfamily:</b> Yojj-like <b>Family:</b> Yojj-like
2	<a href="#">c3brvB_</a>	 Alignment		23.2	38	<b>PDB header:</b> transferase/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nf-kappa-b essential modulator; <b>PDBTitle:</b> nemo/ikkb association domain structure
3	<a href="#">c3msvB_</a>	 Alignment		14.5	16	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> nuclear import adaptor, nro1; <b>PDBTitle:</b> the hypoxic regulator of sterol synthesis nro1 is a nuclear import2 adaptor
4	<a href="#">c1yodB_</a>	 Alignment		10.8	50	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> water-solublized phospholamban; <b>PDBTitle:</b> crystal structure of a water soluble analog of phospholamban
5	<a href="#">c1yodA_</a>	 Alignment		9.9	50	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> water-solublized phospholamban; <b>PDBTitle:</b> crystal structure of a water soluble analog of phospholamban
6	<a href="#">c3qtmB_</a>	 Alignment		9.9	25	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein c4b3.07; <b>PDBTitle:</b> structure of s. pombe nuclear import adaptor nro1 (space group p21)
7	<a href="#">c3jqhA_</a>	 Alignment		9.5	53	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> c-type lectin domain family 4 member m; <b>PDBTitle:</b> structure of the neck region of the glycan-binding receptor dc-signr
8	<a href="#">c5iy3A_</a>	 Alignment		9.1	44	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> zika virus non-structural protein ns1
9	<a href="#">c5yxaC_</a>	 Alignment		8.7	30	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> non-structural protein 1; <b>PDBTitle:</b> crystal structure of the c-terminal fragment of ns1 protein from2 yellow fever virus
10	<a href="#">c6rdf7_</a>	 Alignment		8.7	26	<b>PDB header:</b> proton transport <b>Chain:</b> 7: <b>PDB Molecule:</b> mitochondrial atp synthase associated protein asa7; <b>PDBTitle:</b> cryoem structure of polytomella f-atp synthase, primary rotary state2 3, monomer-masked refinement
11	<a href="#">c4o6cB_</a>	 Alignment		8.1	45	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> ns1; <b>PDBTitle:</b> west nile virus non-structural protein 1 (ns1) form 2 crystal

12	<a href="#">d1zpsa1</a>	Alignment		8.0	37	<b>Fold:</b> HisI-like <b>Superfamily:</b> HisI-like <b>Family:</b> HisI-like
13	<a href="#">c5k6kB_</a>	Alignment		7.5	44	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> zika virus protein; <b>PDBTitle:</b> zika virus non-structural protein 1 (ns1)
14	<a href="#">d2db7a1</a>	Alignment		7.3	36	<b>Fold:</b> Orange domain-like <b>Superfamily:</b> Orange domain-like <b>Family:</b> Hairy Orange domain
15	<a href="#">c2lqA_</a>	Alignment		7.3	50	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> coiled-coil-helix-coiled-coil-helix domain-containing <b>PDBTitle:</b> solution structure of chch5
16	<a href="#">d1v54i_</a>	Alignment		6.2	16	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit VIc <b>Family:</b> Mitochondrial cytochrome c oxidase subunit VIc
17	<a href="#">d1dnpa1</a>	Alignment		6.0	27	<b>Fold:</b> Cryptochrome/photolyase FAD-binding domain <b>Superfamily:</b> Cryptochrome/photolyase FAD-binding domain <b>Family:</b> Cryptochrome/photolyase FAD-binding domain
18	<a href="#">c4o6bA_</a>	Alignment		6.0	56	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural protein 1; <b>PDBTitle:</b> dengue type2 virus non-structural protein 1 (ns1) form 1 crystal
19	<a href="#">c2n2uA_</a>	Alignment		5.8	100	<b>PDB header:</b> unknown function, structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> or358; <b>PDBTitle:</b> solution nmr structure of de novo designed ferredoxin fold protein2 sfr3, northeast structural genomics consortium (nesg) target or358
20	<a href="#">c5yylC_</a>	Alignment		5.6	56	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> apisimin; <b>PDBTitle:</b> structure of major royal jelly protein 1 oligomer
21	<a href="#">d1j75a_</a>	Alignment	not modelled	5.4	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Z-DNA binding domain