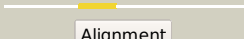
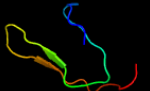
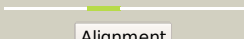


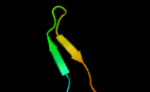






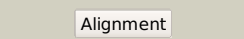
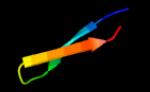
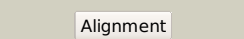

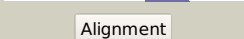
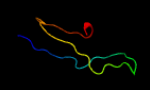
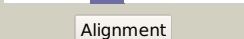

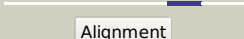
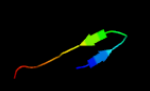


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2046_(lpl)_2291277_2291933
 Date Mon Aug 5 13:25:15 BST 2019
 Unique Job ID 6361f08b3389482b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4b03D_	 Alignment		70.2	31	PDB header: virus Chain: D: PDB Molecule: dengue virus 1 prm protein; PDBTitle: 6a electron cryomicroscopy structure of immature dengue virus serotype2 1
2	c3c6rE_	 Alignment		61.3	18	PDB header: virus Chain: E: PDB Molecule: peptide pr; PDBTitle: low ph immature dengue virus
3	c3c6eC_	 Alignment		61.2	18	PDB header: viral protein Chain: C: PDB Molecule: prm; PDBTitle: crystal structure of the precursor membrane protein-envelope protein2 heterodimer from the dengue 2 virus at neutral ph
4	c3ixxE_	 Alignment		56.1	18	PDB header: virus Chain: E: PDB Molecule: peptide pr; PDBTitle: the pseudo-atomic structure of west nile immature virus in complex2 with fab fragments of the anti-fusion loop antibody e53
5	c4edqA_	 Alignment		23.7	24	PDB header: transport protein/contractile protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,myosin-binding protein PDBTitle: mbp-fusion protein of myosin-binding protein c residues 149-269
6	c6rdu9_	 Alignment		23.6	30	PDB header: proton transport Chain: 9: PDB Molecule: asa-9: polytomella f-atp synthase associated subunit 9; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 monomer-masked refinement
7	d2nt0a1	 Alignment		17.6	25	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: Composite domain of glycosyl hydrolase families 5, 30, 39 and 51
8	c3uotB_	 Alignment		12.0	22	PDB header: cell cycle Chain: B: PDB Molecule: mediator of dna damage checkpoint protein 1; PDBTitle: crystal structure of mdc1 fha domain in complex with a phosphorylated2 peptide from the mdc1 n-terminus
9	c5o60W_	 Alignment		10.9	12	PDB header: ribosome Chain: W: PDB Molecule: 50s ribosomal protein l25; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
10	c5umwA_	 Alignment		10.1	39	PDB header: tiancimycin-binding protein Chain: A: PDB Molecule: glyoxalase/bleomycin resistance protein/dioxygenase; PDBTitle: crystal structure of tnms2, an antibiotic binding protein from2 streptomyces sp. cb03234
11	d2ea9a1	 Alignment		9.1	27	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like

12	d1feua_	Alignment		8.9	21	Fold: Ribosomal protein L25-like Superfamily: Ribosomal protein L25-like Family: Ribosomal protein L25-like
13	d2h28a1	Alignment		8.2	20	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
14	c4lqbA_	Alignment		8.1	11	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein kfla3161
15	d2inwa1	Alignment		7.6	27	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
16	c6ou9A_	Alignment		7.5	19	PDB header: virus like particle Chain: A: PDB Molecule: major capsid protein; PDBTitle: asymmetric focused reconstruction of human norovirus gi.7 houston2 strain vip asymmetric unit in t=3 symmetry
17	c2kieA_	Alignment		6.8	18	PDB header: hydrolase Chain: A: PDB Molecule: inositol polyphosphate 5-phosphatase ocr1-1; PDBTitle: a ph domain within ocr1 bridges clathrin mediated membrane2 trafficking to phosphoinositide metabolis
18	c6nggB_	Alignment		6.3	50	PDB header: immune system Chain: B: PDB Molecule: cd160 antigen; PDBTitle: crystal structure of human cd160 v58m mutant
19	c2be1A_	Alignment		6.1	16	PDB header: transcription Chain: A: PDB Molecule: serine/threonine-protein kinase/endoribonuclease ire1; PDBTitle: structure of the compact luminal domain of yeast ire1
20	c2ml7A_	Alignment		5.7	35	PDB header: unknown function Chain: A: PDB Molecule: specific abundant protein 3; PDBTitle: ginsentides: characterization, structure and application of a new2 class of highly stable cystine knot peptides in ginseng
21	c4hc5A_	Alignment	not modelled	5.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxalase/bleomycin resistance protein/dioxygenase; PDBTitle: crystal structure of member of glyoxalase/bleomycin resistance2 protein/dioxygenase superfamily from sphaerobacter thermophilus dsm3 20745
22	c3mwdA_	Alignment	not modelled	5.4	7	PDB header: transferase Chain: A: PDB Molecule: atp-citrate synthase; PDBTitle: truncated human atp-citrate lyase with citrate bound
23	c5f3jD_	Alignment	not modelled	5.4	8	PDB header: immune system Chain: D: PDB Molecule: antibody 2d10 single chain variable fragment; PDBTitle: crystal structure of dbp in complex with inhibitory monoclonal2 antibody 2d10
24	c5jxpA_	Alignment	not modelled	5.3	19	PDB header: hydrolase Chain: A: PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDBTitle: crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation