
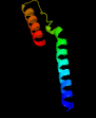




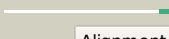

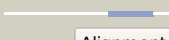










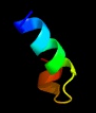


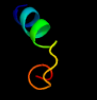
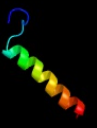


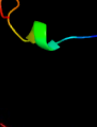

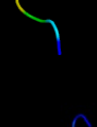

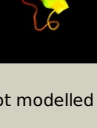


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3652_(PE_PGRS60)_4093811_4094125
 Date Fri Aug 9 18:20:34 BST 2019
 Unique Job ID ab8ae3d8df7a9cfb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g38A_	 Alignment		99.8	35	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
2	d2g38a1	 Alignment		99.8	35	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
3	c5xfsA_	 Alignment		99.8	45	PDB header: protein transport Chain: A; PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis
4	c2knpA_	 Alignment		41.5	56	PDB header: unknown function Chain: A; PDB Molecule: mcccc-1; PDBTitle: isolation and characterization of peptides from momordica2 cochinchinensis seeds.
5	c4uvkA_	 Alignment		21.0	19	PDB header: cell cycle Chain: A; PDB Molecule: zyro0d15994p; PDBTitle: cohesin subunit scc3 from z. rouxii, 88-1035
6	c2kukA_	 Alignment		15.8	67	PDB header: antiviral protein Chain: A; PDB Molecule: leaf cyclotide 2; PDBTitle: solution structure of vhl-2
7	d1v29a_	 Alignment		15.8	58	Fold: Nitrile hydratase alpha chain Superfamily: Nitrile hydratase alpha chain Family: Nitrile hydratase alpha chain
8	c5sxpG_	 Alignment		15.5	78	PDB header: signaling protein/ligase Chain: G; PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: structural basis for the interaction between itch prr and beta-pix
9	d1w1oa2	 Alignment		14.9	24	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
10	c4pjwA_	 Alignment		14.9	29	PDB header: cell cycle Chain: A; PDB Molecule: cohesin subunit sa-2; PDBTitle: crystal structure of human stromal antigen 2 (sa2) in complex with2 sister chromatid cohesion protein 1 (scc1), with bound mes
11	c1wlpA_	 Alignment		13.2	78	PDB header: oxidoreductase/signaling protein Chain: A; PDB Molecule: cytochrome b-245 light chain; PDBTitle: solution structure of the p22phox-p47phox complex

12	c6h8qA_	Alignment		13.0	19	PDB header: cell cycle Chain: A; PDB Molecule: cohesin subunit scc3; PDBTitle: structural basis for scc3-dependent cohesin recruitment to chromatin
13	c3gvmA_	Alignment		11.2	22	PDB header: viral protein Chain: A; PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
14	c6o58H_	Alignment		10.8	33	PDB header: transport protein Chain: H; PDB Molecule: essential mcu regulator, mitochondrial; PDBTitle: human mcu-emre complex, dimer of channel
15	c6o58P_	Alignment		10.8	33	PDB header: transport protein Chain: P; PDB Molecule: essential mcu regulator, mitochondrial; PDBTitle: human mcu-emre complex, dimer of channel
16	c5yixB_	Alignment		10.6	38	PDB header: dna binding protein Chain: B; PDB Molecule: cell cycle regulatory protein gcrA; PDBTitle: caulobacter crescentus gcrA sigma-interacting domain (sid) in complex2 with domain 2 of sigma 70
17	d1f0la3	Alignment		10.6	33	Fold: Toxins' membrane translocation domains Superfamily: Diphtheria toxin, middle domain Family: Diphtheria toxin, middle domain
18	c2mn1A_	Alignment		9.5	50	PDB header: unknown function Chain: A; PDB Molecule: kalata b1[w23ww]; PDBTitle: solution structure of kalata b1[w23ww]
19	d1w0ba_	Alignment		9.5	40	Fold: Spectrin repeat-like Superfamily: Alpha-hemoglobin stabilizing protein AHSP Family: Alpha-hemoglobin stabilizing protein AHSP
20	d1mx3a2	Alignment		9.4	31	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
21	d1eaic_	Alignment	not modelled	9.1	50	Fold: Serine protease inhibitors Superfamily: Serine protease inhibitors Family: ATI-like
22	d1z8ua1	Alignment	not modelled	9.0	42	Fold: Spectrin repeat-like Superfamily: Alpha-hemoglobin stabilizing protein AHSP Family: Alpha-hemoglobin stabilizing protein AHSP
23	c5jhoA_	Alignment	not modelled	8.3	13	PDB header: transport protein Chain: A; PDB Molecule: electroneutral sodium bicarbonate exchanger 1; PDBTitle: crystal structure of the regulatory domain of the sodium driven2 chloride bicarbonate exchanger.
24	c4lwsB_	Alignment	not modelled	6.3	11	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
25	c3bboG_	Alignment	not modelled	5.6	40	PDB header: ribosome Chain: G; PDB Molecule: ribosomal protein l4; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome