
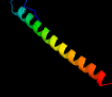

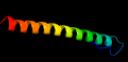

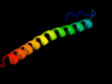

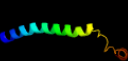



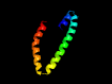


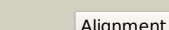
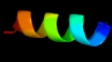





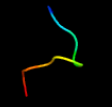

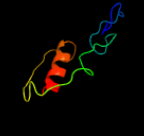


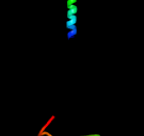
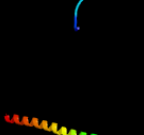

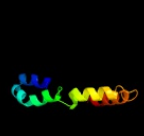
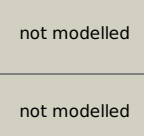


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0335c_(PE6)_399535_400050
 Date Tue Jul 23 14:50:40 BST 2019
 Unique Job ID 208508567af050c3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g38A_	 Alignment		99.8	31	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	31	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
3	c5xfsA_	 Alignment		99.8	40	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	d1wa8a1	 Alignment		43.1	12	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
5	d1lghb_	 Alignment		31.7	33	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
6	c3dghB_	 Alignment		23.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: toluene 4-monoxygenase hydroxylase beta subunit; PDBTitle: crystal structure of toluene 4-monoxygenase hydroxylase
7	c3onjA_	 Alignment		21.6	17	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain
8	c1wrgA_	 Alignment		21.3	33	PDB header: membrane protein Chain: A: PDB Molecule: light-harvesting protein b-880, beta chain; PDBTitle: light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum
9	c2fsuA_	 Alignment		18.2	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein phnH; PDBTitle: crystal structure of the phnH protein from escherichia coli
10	d2fsua1	 Alignment		18.2	25	Fold: PLP-dependent transferase-like Superfamily: PhnH-like Family: PhnH-like
11	c2di2A_	 Alignment		15.4	55	PDB header: metal binding protein Chain: A: PDB Molecule: nucleocapsid protein p7; PDBTitle: nmr structure of the hiv-2 nucleocapsid protein

12	d2incb1	Alignment		14.9	14	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
13	c5jydA	Alignment		14.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a putative short chain dehydrogenase from2 burkholderia cenocepacia
14	c6et5u	Alignment		13.1	33	PDB header: photosynthesis Chain: U: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
15	c4rglA	Alignment		12.5	21	PDB header: dna binding protein Chain: A: PDB Molecule: filamentation induced by camp protein fic; PDBTitle: crystal structure of a fic family protein (dde_2494) from2 desulfovibrio desulfuricans g20 at 2.70 a resolution
16	c2w0cR	Alignment		12.5	29	PDB header: virus Chain: R: PDB Molecule: protein p3; PDBTitle: x-ray structure of the entire lipid-containing bacteriophage pm2
17	c1nc8A	Alignment		12.2	55	PDB header: viral protein Chain: A: PDB Molecule: nucleocapsid protein; PDBTitle: high-resolution solution nmr structure of the minimal2 active domain of the human immunodeficiency virus type-23 nucleocapsid protein, 15 structures
18	c4wj2A	Alignment		10.5	15	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
19	c3sriB	Alignment		10.0	57	PDB header: cell invasion Chain: B: PDB Molecule: rhoptry neck protein 2; PDBTitle: crystal structure of plasmodium falciparum ama1 in complex with a 29aa2 pfron2 peptide
20	c2inpD	Alignment		9.9	10	PDB header: oxidoreductase Chain: D: PDB Molecule: phenol hydroxylase component phI; PDBTitle: structure of the phenol hydroxylase-regulatory protein2 complex
21	c5fztB	Alignment	not modelled	8.6	40	PDB header: structural protein Chain: B: PDB Molecule: rho gtpase-activating protein 7; PDBTitle: the crystal structure of r7r8 in complex with a dlc12 fragment.
22	d1gija2	Alignment	not modelled	7.4	60	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
23	c4j2ID	Alignment	not modelled	6.9	33	PDB header: transcription regulator Chain: D: PDB Molecule: protein capicua homolog; PDBTitle: crystal structure of axh domain complexed with capicua
24	c4j2IC	Alignment	not modelled	6.9	33	PDB header: transcription regulator Chain: C: PDB Molecule: protein capicua homolog; PDBTitle: crystal structure of axh domain complexed with capicua
25	c3zwbB	Alignment	not modelled	6.9	57	PDB header: immune system Chain: B: PDB Molecule: rhoptry neck protein 2; PDBTitle: crystal structure of plasmodium falciparum ama1 in complex with a2 39aa pfron2 peptide
26	c2q1kA	Alignment	not modelled	6.3	38	PDB header: chaperone Chain: A: PDB Molecule: asce; PDBTitle: cyrstal structure of asce from aeromonas hydrophilla
27	d1v7ba2	Alignment	not modelled	6.0	17	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
28	d1h9fa	Alignment	not modelled	5.9	60	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain