
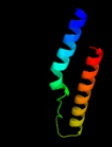

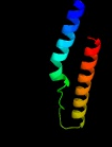

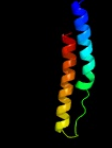

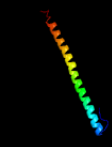



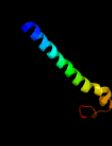

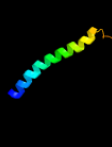



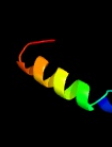

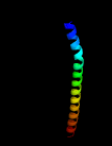




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3872_(PE35)_4350923_4351222
 Date Sat Aug 10 22:05:05 BST 2019
 Unique Job ID 67e16d599860d5e1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g38A_	 Alignment		95.4	24	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		95.4	24	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
3	c5xfsA_	 Alignment		95.1	31	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	c4wj2A_	 Alignment		91.9	17	PDB header: unknown function Chain: A; PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
5	c2r18A_	 Alignment		32.6	25	PDB header: viral protein Chain: A; PDB Molecule: capsid assembly protein vp3; PDBTitle: structural insights into the multifunctional protein vp3 of birnaviruses
6	d1wa8b1	 Alignment		31.2	12	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
7	d1wa8a1	 Alignment		30.4	15	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
8	c3hgkE_	 Alignment		22.0	22	PDB header: transferase Chain: E; PDB Molecule: effector protein hopab2; PDBTitle: crystal structure of effect protein avrptob complexed with2 kinase pto
9	c3sviA_	 Alignment		22.0	19	PDB header: signaling protein Chain: A; PDB Molecule: type iii effector hopab2; PDBTitle: structure of the pto-binding domain of hoppmal generated by limited2 thermolysin digestion
10	c3zbhC_	 Alignment		18.6	18	PDB header: unknown function Chain: C; PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
11	c2kg7B_	 Alignment		16.2	7	PDB header: unknown function Chain: B; PDB Molecule: esat-6-like protein eshx; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288

12	d1jnsa_	Alignment		12.9	20	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
13	d2pv2a1	Alignment		11.9	25	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
14	c1zk6A_	Alignment		10.9	40	PDB header: isomerase Chain: A; PDB Molecule: foldase protein prsa; PDBTitle: nmr solution structure of b. subtilis prsa ppiase
15	c3gpkA_	Alignment		9.8	33	PDB header: isomerase Chain: A; PDB Molecule: ppic-type peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of ppic-type peptidyl-prolyl cis-trans isomerase2 domain at 1.55a resolution.
16	c2l53B_	Alignment		9.4	71	PDB header: ca-binding protein/proton transport Chain: B; PDB Molecule: voltage-gated sodium channel type v alpha isoform b PDBTitle: solution nmr structure of apo-calmodulin in complex with the iq motif2 of human cardiac sodium channel nav1.5
17	c3gvmA_	Alignment		8.9	16	PDB header: viral protein Chain: A; PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
18	d1m5ya3	Alignment		8.4	13	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
19	c1wrgA_	Alignment		7.8	18	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
20	c2jzvA_	Alignment		7.7	13	PDB header: isomerase Chain: A; PDB Molecule: foldase protein prsa; PDBTitle: solution structure of s. aureus prsa-ppiase
21	c4e40A_	Alignment	not modelled	7.6	19	PDB header: transport protein Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: the haptoglobin-hemoglobin receptor of trypanosoma congolense
22	d1ecfa1	Alignment	not modelled	7.3	27	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
23	d1gph11	Alignment	not modelled	7.2	45	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
24	d1eq3a_	Alignment	not modelled	6.9	33	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
25	d1nera_	Alignment	not modelled	6.7	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
26	c6et5u_	Alignment	not modelled	6.6	32	PDB header: photosynthesis Chain: U; PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
27	c2rqsa_	Alignment	not modelled	6.5	33	PDB header: isomerase Chain: A; PDB Molecule: parvulin-like peptidyl-prolyl isomerase; PDBTitle: 3d structure of pin from the psychrophilic archeon cenarchaeum2 symbiosum (cspin)
28	d1wd5a_	Alignment	not modelled	6.4	22	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
						Fold: Light-harvesting complex subunits

29	d1lghb_	Alignment	not modelled	6.3	36	Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
30	c1y66D_	Alignment	not modelled	5.9	39	PDB header: de novo protein Chain: D: PDB Molecule: engrailed homeodomain; PDBTitle: dioxane contributes to the altered conformation and2 oligomerization state of a designed engrailed homeodomain3 variant
31	d1dc1a_	Alignment	not modelled	5.6	58	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease BsobI
32	c2vs0B_	Alignment	not modelled	5.4	17	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
33	d1lkpa1	Alignment	not modelled	5.3	54	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Exotoxin A, N-terminal domain
34	d1jo5a_	Alignment	not modelled	5.3	23	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
35	c2kgjA_	Alignment	not modelled	5.1	20	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase d; PDBTitle: solution structure of parvulin domain of ppid from e.coli