

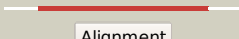
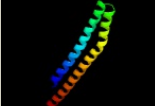
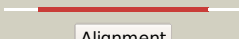
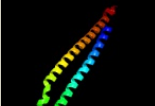

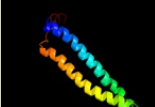




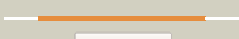
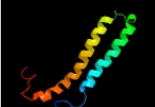
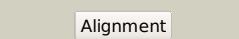

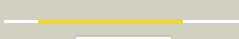

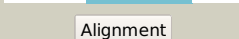
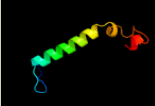
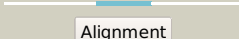
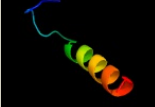

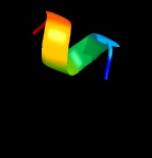




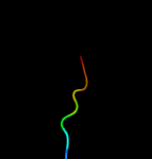
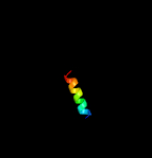
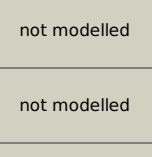


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2798c_(-)_3107321_3107647
Date	Wed Aug 7 12:50:46 BST 2019
Unique Job ID	08ff409470253561

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gvmA_	 Alignment		97.1	14	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
2	c3zbhC_	 Alignment		97.1	16	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
3	c4lwsA_	 Alignment		97.0	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
4	d1wa8a1	 Alignment		97.0	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
5	c2vs0B_	 Alignment		95.9	8	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
6	c4iogD_	 Alignment		94.6	12	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
7	c2kg7B_	 Alignment		86.4	14	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
8	d1wa8b1	 Alignment		83.7	14	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
9	c4lwsB_	 Alignment		77.4	14	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
10	d2fefa1	 Alignment		36.8	27	Fold: Bromodomain-like Superfamily: PA2201 N-terminal domain-like Family: PA2201 N-terminal domain-like
11	c6icZ_	 Alignment		32.9	23	PDB header: splicing Chain: X: PDB Molecule: prkr-interacting protein 1; PDBTitle: cryo-em structure of a human post-catalytic spliceosome (p complex) at 2.3 angstrom

12	d1vcta1	Alignment		19.2	14	Fold: Spectrin repeat-like Superfamily: PhoU-like Family: PhoU-like
13	c5ua4B_	Alignment		16.7	71	PDB header: apoptosis Chain: B: PDB Molecule: bh3-interacting domain death agonist; PDBTitle: crystal structure of a179l:bid bh3 complex
14	d1xl7a2	Alignment		16.1	25	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
15	c2i0mA_	Alignment		12.5	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phosphate transport system protein phou; PDBTitle: crystal structure of the phosphate transport system regulatory protein2 phou from streptococcus pneumoniae
16	c4q25B_	Alignment		10.7	53	PDB header: unknown function Chain: B: PDB Molecule: phosphate-specific transport system accessory protein phou PDBTitle: crystal structure of phou from pseudomonas aeruginosa
17	c3cjhK_	Alignment		10.5	40	PDB header: protein transport Chain: K: PDB Molecule: mitochondrial import inner membrane translocase subunit PDBTitle: tim8-tim13 complex
18	c3nk4C_	Alignment		8.5	78	PDB header: cell adhesion Chain: C: PDB Molecule: zona pellucida 3; PDBTitle: crystal structure of full-length sperm receptor zp3 at 2.0 a2 resolution
19	c3nk3C_	Alignment		8.4	78	PDB header: cell adhesion Chain: C: PDB Molecule: zona pellucida 3; PDBTitle: crystal structure of full-length sperm receptor zp3 at 2.6 a2 resolution
20	d1sumb_	Alignment		8.3	24	Fold: Spectrin repeat-like Superfamily: PhoU-like Family: PhoU-like
21	d1ndba2	Alignment	not modelled	6.8	25	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
22	c4akfA_	Alignment	not modelled	6.7	55	PDB header: transferase Chain: A: PDB Molecule: vipd; PDBTitle: crystal structure of vipd from legionella pneumophila
23	c4zigB_	Alignment	not modelled	6.4	62	PDB header: apoptosis Chain: B: PDB Molecule: bh3-interacting domain death agonist; PDBTitle: crystal structure of core/latch dimer of bax in complex with2 bidbh3mini
24	c1zy3B_	Alignment	not modelled	6.3	67	PDB header: apoptosis Chain: B: PDB Molecule: bh3-peptide from bh3 interacting domain death PDBTitle: structural model of complex of bcl-w protein with bid bh3-2 peptide
25	c2n39A_	Alignment	not modelled	6.3	41	PDB header: dna binding protein Chain: A: PDB Molecule: chromodomain-helicase-dna-binding protein 1; PDBTitle: nmr solution structure of a c-terminal domain of the chromodomain2 helicase dna-binding protein 1
26	d1t72a_	Alignment	not modelled	5.8	53	Fold: Spectrin repeat-like Superfamily: PhoU-like Family: PhoU-like
27	d1t1ua2	Alignment	not modelled	5.5	25	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
28	c2xf5C_	Alignment	not modelled	5.4	67	PDB header: viral protein Chain: C: PDB Molecule: gp23.1; PDBTitle: crystal structure of bacillus subtilis spp1 phage gp23.1, a putative2 chaperone.

