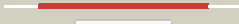




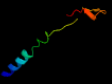

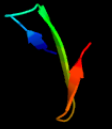



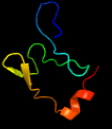
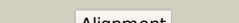






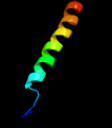
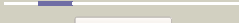

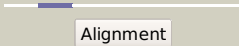




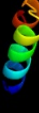
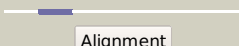



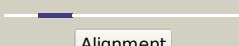

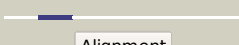
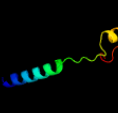

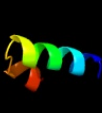


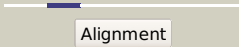




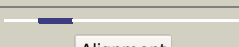


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3450c_(-)_3871263_3872675
Date	Fri Aug 9 18:20:12 BST 2019
Unique Job ID	392df3a290c7bbb7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4kk7A_</a>	 Alignment		100.0	30	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> esx-1 secretion system protein eccb1; <b>PDBTitle:</b> structure of eccb1 from the type vii (esx-1) secretion system of2 mycobacterium tuberculosis.
2	<a href="#">c5cyuA_</a>	 Alignment		100.0	33	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> conserved membrane protein; <b>PDBTitle:</b> structure of the soluble domain of eccb1 from the mycobacterium2 smegmatis esx-1 secretion system.
3	<a href="#">c6navl_</a>	 Alignment		38.1	15	<b>PDB header:</b> structural protein <b>Chain:</b> I; <b>PDB Molecule:</b> m9ud72; <b>PDBTitle:</b> cryo-em reconstruction of sulfolobus islandicus ial14/1 pilus
4	<a href="#">d2fb5a1</a>	 Alignment		33.0	14	<b>Fold:</b> Yojj-like <b>Superfamily:</b> Yojj-like <b>Family:</b> Yojj-like
5	<a href="#">d2i5nh1</a>	 Alignment		30.5	11	<b>Fold:</b> PRC-barrel domain <b>Superfamily:</b> PRC-barrel domain <b>Family:</b> Photosynthetic reaction centre, H-chain, cytoplasmic domain
6	<a href="#">c1k6nH_</a>	 Alignment		29.4	13	<b>PDB header:</b> photosynthesis <b>Chain:</b> H; <b>PDB Molecule:</b> photosynthetic reaction center h subunit; <b>PDBTitle:</b> e(l212)a,d(l213)a double mutant structure of photosynthetic reaction2 center from rhodobacter sphaeroides
7	<a href="#">c2i5nH_</a>	 Alignment		24.3	11	<b>PDB header:</b> photosynthesis <b>Chain:</b> H; <b>PDB Molecule:</b> reaction center protein h chain; <b>PDBTitle:</b> 1.96 a x-ray structure of photosynthetic reaction center from2 rhodopseudomonas viridis:crystals grown by microfluidic technique
8	<a href="#">c5xefA_</a>	 Alignment		20.0	14	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> flagellar protein flis; <b>PDBTitle:</b> crystal structure of flagellar chaperone from bacteria
9	<a href="#">d1rzhh1</a>	 Alignment		16.1	13	<b>Fold:</b> PRC-barrel domain <b>Superfamily:</b> PRC-barrel domain <b>Family:</b> Photosynthetic reaction centre, H-chain, cytoplasmic domain
10	<a href="#">c2k9yB_</a>	 Alignment		15.8	13	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> epha2 dimeric structure in the lipidic bicelle at ph 5.0
11	<a href="#">c2k9yA_</a>	 Alignment		15.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> epha2 dimeric structure in the lipidic bicelle at ph 5.0

12	<a href="#">c1vh6A_</a>	 Alignment		14.7	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar protein flis; <b>PDBTitle:</b> crystal structure of a flagellar protein
13	<a href="#">d1vh6a_</a>	 Alignment		14.7	24	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Flagellar export chaperone FliS <b>Family:</b> Flagellar export chaperone FliS
14	<a href="#">c3k1iA_</a>	 Alignment		13.8	14	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar protein; <b>PDBTitle:</b> crystal strcture of flis-hp1076 complex in h. pylori
15	<a href="#">c2ciua_</a>	 Alignment		11.2	22	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> import inner membrane translocase subunit tim21 <b>PDBTitle:</b> structure of the ims domain of the mitochondrial import2 protein tim21 from s. cerevisiae
16	<a href="#">c6f0kA_</a>	 Alignment		11.1	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c family protein; <b>PDBTitle:</b> alternative complex iii
17	<a href="#">c6cfwE_</a>	 Alignment		9.4	35	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> mbh subunit; <b>PDBTitle:</b> cryoem structure of a respiratory membrane-bound hydrogenase
18	<a href="#">c2wmma_</a>	 Alignment		8.6	9	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> chromosome partition protein mukb; <b>PDBTitle:</b> crystal structure of the hinge domain of mukb
19	<a href="#">c6ch3B_</a>	 Alignment		8.3	32	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> flagellar secretion chaperone flis,flagellin; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of flha and flis-flic2 complex
20	<a href="#">d1y7ma1</a>	 Alignment		7.3	11	<b>Fold:</b> L,D-transpeptidase catalytic domain-like <b>Superfamily:</b> L,D-transpeptidase catalytic domain-like <b>Family:</b> L,D-transpeptidase catalytic domain-like
21	<a href="#">c2lf3A_</a>	 Alignment	not modelled	6.5	56	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> effector protein hopab3; <b>PDBTitle:</b> solution nmr structure of hopmal_281_385 from pseudomonas syringae2 pv. maculicola str. e54326, midwest center for structural genomics3 target apc40104.5 and northeast structural genomics consortium target4 pst2a
22	<a href="#">c3c1za_</a>	 Alignment	not modelled	6.5	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna integrity scanning protein disa; <b>PDBTitle:</b> structure of the ligand-free form of a bacterial dna damage sensor2 protein
23	<a href="#">c2mhgA_</a>	 Alignment	not modelled	6.2	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr structure of protein np_254181.1 from pseudomonas aeruginosa pa01
24	<a href="#">c3hshA_</a>	 Alignment	not modelled	6.0	24	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> collagen alpha-1(xviii) chain; <b>PDBTitle:</b> crystal structure of human collagen xviii trimerization domain2 (tetragonal crystal form)
25	<a href="#">d2zjru1</a>	 Alignment	not modelled	5.8	24	<b>Fold:</b> L28p-like <b>Superfamily:</b> L28p-like <b>Family:</b> Ribosomal protein L28
26	<a href="#">c6gyyB_</a>	 Alignment	not modelled	5.7	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> diadenylate cyclase; <b>PDBTitle:</b> crystal structure of daca from staphylococcus aureus, n166c/t172c2 double mutant