


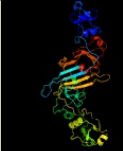

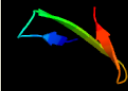

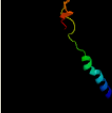



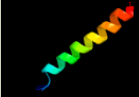
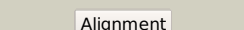

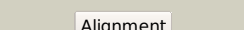


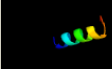

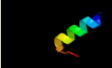

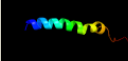
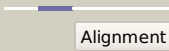

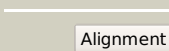
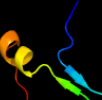
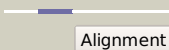
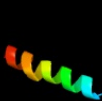
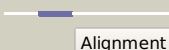
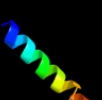
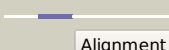



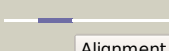

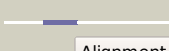
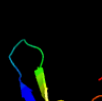


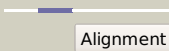
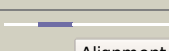
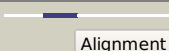


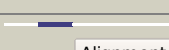

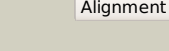






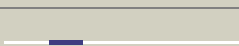
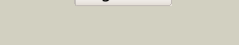
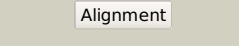
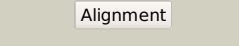
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1782_(-)_2017747_2019267
Date	Fri Aug 2 13:30:39 BST 2019
Unique Job ID	f149d89865bd2d03

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4kk7A_	 Alignment		100.0	33	PDB header: protein transport Chain: A; PDB Molecule: esx-1 secretion system protein eccb1; PDBTitle: structure of eccb1 from the type vii (esx-1) secretion system of <i>Mycobacterium tuberculosis</i> .
2	c5cyuA_	 Alignment		100.0	33	PDB header: membrane protein Chain: A; PDB Molecule: conserved membrane protein; PDBTitle: structure of the soluble domain of eccb1 from the <i>Mycobacterium smegmatis</i> esx-1 secretion system.
3	d2fb5a1	 Alignment		43.6	14	Fold: Yojj-like Superfamily: Yojj-like Family: Yojj-like
4	c6navl_	 Alignment		33.8	26	PDB header: structural protein Chain: I; PDB Molecule: m9ud72; PDBTitle: cryo-em reconstruction of <i>Sulfolobus islandicus</i> Ial14/1 pilus
5	c5xefA_	 Alignment		20.0	9	PDB header: chaperone Chain: A; PDB Molecule: flagellar protein flis; PDBTitle: crystal structure of flagellar chaperone from bacteria
6	c2k9yB_	 Alignment		19.5	27	PDB header: transferase Chain: B; PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at pH 5.0
7	c2k9yA_	 Alignment		19.5	27	PDB header: transferase Chain: A; PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at pH 5.0
8	c2l92A_	 Alignment		16.0	27	PDB header: dna binding protein Chain: A; PDB Molecule: histone family protein nucleoid-structuring protein h-ns; PDBTitle: solution structure of the c-terminal domain of h-ns like protein bv3f
9	c1vh6A_	 Alignment		14.5	23	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: flagellar protein flis; PDBTitle: crystal structure of a flagellar protein
10	d1vh6a_	 Alignment		14.5	23	Fold: Four-helical up-and-down bundle Superfamily: Flagellar export chaperone FliS Family: Flagellar export chaperone FliS
11	c6f0kA_	 Alignment		14.2	19	PDB header: membrane protein Chain: A; PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii

12	c3k1iA_	 Alignment		14.0	9	PDB header: chaperone Chain: A: PDB Molecule: flagellar protein; PDBTitle: crystal strcture of flis-hp1076 complex in h. pylori
13	c2ixsB_	 Alignment		13.9	19	PDB header: hydrolase Chain: B: PDB Molecule: sdai restriction endonuclease; PDBTitle: structure of sdai restriction endonuclease
14	c6hrbD_	 Alignment		13.6	26	PDB header: membrane protein Chain: D: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: cryo-em structure of the kdpfabc complex in an e2 inward-facing state2 (state 2)
15	c5mrwH_	 Alignment		13.6	26	PDB header: hydrolase Chain: H: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex
16	c6hraD_	 Alignment		13.6	26	PDB header: membrane protein Chain: D: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: cryo-em structure of the kdpfabc complex in an e1 outward-facing state2 (state 1)
17	c5mrwL_	 Alignment		13.6	26	PDB header: hydrolase Chain: L: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex
18	c5mrwD_	 Alignment		13.6	26	PDB header: hydrolase Chain: D: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex
19	c2ciua_	 Alignment		12.9	22	PDB header: protein transport Chain: A: PDB Molecule: import inner membrane translocase subunit tim21 PDBTitle: structure of the ims domain of the mitochondrial import2 protein tim21 from s. cerevisiae
20	c3c1za_	 Alignment		11.1	13	PDB header: dna binding protein Chain: A: PDB Molecule: dna integrity scanning protein disa; PDBTitle: structure of the ligand-free form of a bacterial dna damage sensor2 protein
21	c2levA_	 Alignment	not modelled	10.9	45	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ler; PDBTitle: structure of the dna complex of the c-terminal domain of ler
22	c3hshA_	 Alignment	not modelled	10.7	21	PDB header: protein binding Chain: A: PDB Molecule: collagen alpha-1(xviii) chain; PDBTitle: crystal structure of human collagen xviii trimerization domain2 (tetragonal crystal form)
23	c6gyyB_	 Alignment	not modelled	9.6	17	PDB header: transferase Chain: B: PDB Molecule: diadenylate cyclase; PDBTitle: crystal structure of daca from staphylococcus aureus, n166c/t172c2 double mutant
24	c6cfwE_	 Alignment	not modelled	9.6	18	PDB header: membrane protein Chain: E: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
25	d1y7ma1	 Alignment	not modelled	8.8	15	Fold: L,D-transpeptidase catalytic domain-like Superfamily: L,D-transpeptidase catalytic domain-like Family: L,D-transpeptidase catalytic domain-like
26	d1hnra_	 Alignment	not modelled	8.7	20	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
27	c2jr1A_	 Alignment	not modelled	8.3	27	PDB header: dna binding protein Chain: A: PDB Molecule: virulence regulator; PDBTitle: solution structure of the dna binding domain of a nucleoid-associated2 protein, h-ns, from the phytopathogen xylella fastidiosa.
28	c3n3fb_	 Alignment	not modelled	8.2	24	PDB header: protein binding Chain: B: PDB Molecule: collagen alpha-1(xv) chain; PDBTitle: crystal structure of the human collagen xv trimerization domain: a2 potent trimerizing unit common to multiplexin collagens

29	c6ch3B_	 Alignment	not modelled	8.1	27	PDB header: structural protein Chain: B: PDB Molecule: flagellar secretion chaperone flis,flagellin; PDBTitle: crystal structure of the cytoplasmic domain of flha and flis-flic2 complex
30	d2zjru1	 Alignment	not modelled	7.9	21	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L28
31	d2nn6g2	 Alignment	not modelled	6.9	25	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
32	c2i02B_	 Alignment	not modelled	6.1	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein bt2368 from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr375
33	c2lf3A_	 Alignment	not modelled	6.0	56	PDB header: signaling protein Chain: A: PDB Molecule: effector protein hopab3; PDBTitle: solution nmr structure of hoppmal_281_385 from pseudomonas syringae2 pv. maculicola str. es4326, midwest center for structural genomics3 target apc40104.5 and northeast structural genomics consortium target4 pst2a
34	c5zjiO_	 Alignment	not modelled	6.0	28	PDB header: membrane protein Chain: O: PDB Molecule: 16kda membrane protein; PDBTitle: structure of photosystem i supercomplex with light-harvesting2 complexes i and ii
35	d1vqou1	 Alignment	not modelled	5.1	12	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Ribosomal protein L24e
36	c3ccjU_	 Alignment	not modelled	5.1	12	PDB header: ribosome Chain: U: PDB Molecule: 50s ribosomal protein l24e; PDBTitle: structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation c2534u