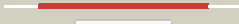




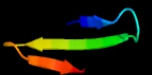

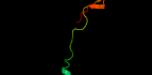


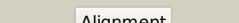

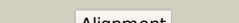


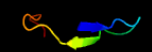



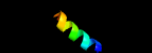
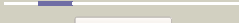

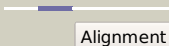

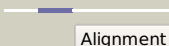
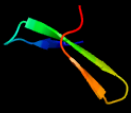




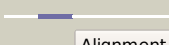
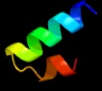
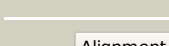

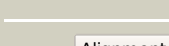
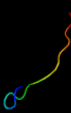
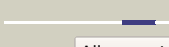



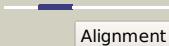
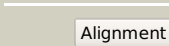
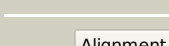


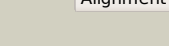


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3869_(-)_4345217_4346659
Date	Sat Aug 10 22:05:05 BST 2019
Unique Job ID	148ed51281011ebe

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4kk7A_	 Alignment		100.0	100	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 of2 mycobacterium tuberculosis.
2	c5cyuA_	 Alignment		100.0	63	PDB header: membrane protein Chain: A: PDB Molecule: conserved membrane protein; PDBTitle: structure of the soluble domain of eccb1 from the mycobacterium2 smegmatis esx-1 secretion system.
3	d2fb5a1	 Alignment		54.3	24	Fold: Yojj-like Superfamily: Yojj-like Family: Yojj-like
4	c6navl_	 Alignment		44.0	20	PDB header: structural protein Chain: I: PDB Molecule: m9ud72; PDBTitle: cryo-em reconstruction of sulfolobus islandicus la14/1 pilus
5	c2k9yB_	 Alignment		23.0	23	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
6	c2k9yA_	 Alignment		23.0	23	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
7	c5xefA_	 Alignment		22.6	14	PDB header: chaperone Chain: A: PDB Molecule: flagellar protein flis; PDBTitle: crystal structure of flagellar chaperone from bacteria
8	c2ciuA_	 Alignment		17.6	35	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
9	d1vh6a_	 Alignment		17.3	27	Fold: Four-helical up-and-down bundle Superfamily: Flagellar export chaperone Flis Family: Flagellar export chaperone Flis
10	c1vh6A_	 Alignment		17.3	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: flagellar protein flis; PDBTitle: crystal structure of a flagellar protein
11	c3c1zA_	 Alignment		17.0	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

12	c3k1iA_	 Alignment		16.4	23	PDB header: chaperone Chain: A: PDB Molecule: flagellar protein; PDBTitle: crystal strcture of flis-hp1076 complex in h. pylori
13	c6gyyB_	 Alignment		15.8	17	PDB header: transferase Chain: B: PDB Molecule: diadenylate cyclase; PDBTitle: crystal structure of daca from staphylococcus aureus, n166c/t172c2 double mutant
14	c6f0kA_	 Alignment		13.4	17	PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
15	c6cfwE_	 Alignment		12.6	35	PDB header: membrane protein Chain: E: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
16	c6ch3B_	 Alignment		10.1	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-flhc2 complex
17	c2ixsB_	 Alignment		10.1	17	PDB header: hydrolase Chain: B: PDB Molecule: sdai restriction endonuclease; PDBTitle: structure of sdai restriction endonuclease
18	d2nn6g2	 Alignment		9.9	27	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
19	c2mhgA_	 Alignment		9.5	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of protein np_254181.1 from pseudomonas aeruginosa pa01
20	d1y7ma1	 Alignment		9.0	11	Fold: L,D-transpeptidase catalytic domain-like Superfamily: L,D-transpeptidase catalytic domain-like Family: L,D-transpeptidase catalytic domain-like
21	c4rv7C_	 Alignment	not modelled	9.0	10	PDB header: transferase Chain: C: PDB Molecule: diadenylate cyclase; PDBTitle: characterization of an essential diadenylate cyclase
22	c2dn5A_	 Alignment	not modelled	7.8	32	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-057, a gtf2i domain in human2 cdna
23	c2dzqA_	 Alignment	not modelled	7.8	27	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-066, a gtf2i domain in human2 cdna
24	c3vwbA_	 Alignment	not modelled	7.6	27	PDB header: transcription/dna Chain: A: PDB Molecule: virulence regulon transcriptional activator virb; PDBTitle: crystal structure of virb core domain (se-met derivative) complexed2 with the cis-acting site (5-bru modifications) upstream icsb promoter
25	c2l02B_	 Alignment	not modelled	7.5	6	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
26	c6hraD_	 Alignment	not modelled	7.4	25	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) PDB header: membrane protein Chain: D: PDB Molecule: potassium-transporting atpase kdpf

27	c6hrbD_	Alignment	not modelled	7.4	25	subunit; PDBTitle: cryo-em structure of the kdpfabc complex in an e2 inward-facing state2 (state 2) PDB header: hydrolase Chain: H: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex
28	c5mrwH_	Alignment	not modelled	7.4	25	PDB header: hydrolase Chain: D: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex
29	c5mrwD_	Alignment	not modelled	7.4	25	PDB header: hydrolase Chain: L: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex
30	c5mrwL_	Alignment	not modelled	7.4	25	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
31	c2lf3A_	Alignment	not modelled	7.4	56	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna
32	c2d99A_	Alignment	not modelled	7.4	23	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: Photosynthetic reaction centre, H-chain, cytoplasmic domain
33	d2i5nh1	Alignment	not modelled	7.3	28	Fold: GTF2I-like repeat Superfamily: GTF2I-like repeat Family: GTF2I-like repeat
34	d1q60a_	Alignment	not modelled	7.2	18	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i; PDBTitle: solution structure of rsgi ruh-069, a gtf2i domain in human2 cdna
35	c2ed2A_	Alignment	not modelled	7.2	18	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L28
36	d2zjr1	Alignment	not modelled	7.2	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)
37	c3hshA_	Alignment	not modelled	7.1	15	PDB header: transcription Chain: A: PDB Molecule: transcription factor gtf2ird2 beta; PDBTitle: solution structure of rsgi ruh-068, a gtf2i domain in human2 cdna
38	c2e31A_	Alignment	not modelled	7.0	23	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i; PDBTitle: solution structure of rsgi ruh-071, a gtf2i domain in human2 cdna
39	c2ejeA_	Alignment	not modelled	6.7	14	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i; PDBTitle: solution structure of rsgi ruh-060, a gtf2i domain in human2 cdna
40	c2dn4A_	Alignment	not modelled	6.5	18	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib; PDBTitle: platelet integrin alfa1iib-beta3 transmembrane-cytoplasmic2 heterocomplex
41	c2kncA_	Alignment	not modelled	6.2	13	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
42	c3n3fB_	Alignment	not modelled	5.7	3	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-067, a gtf2i domain in human2 cdna
43	c2dztA_	Alignment	not modelled	5.6	18	PDB header: antibiotic Chain: A: PDB Molecule: penaeidin-3a; PDBTitle: solution structure of the [t8a]-penaeidin-3
44	c1ueoA_	Alignment	not modelled	5.2	40	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Ribosomal protein L24e
45	d1vqou1	Alignment	not modelled	5.2	18	PDB header: ribosome Chain: U: PDB Molecule: 50s ribosomal protein l24e; PDBTitle: structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation c2534u
46	c3ccjU_	Alignment	not modelled	5.2	18	