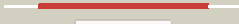
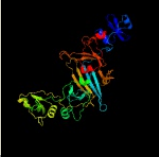

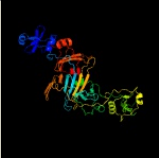

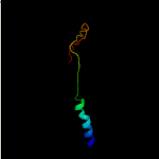



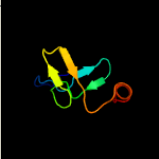

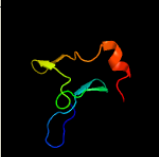

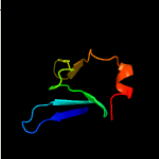

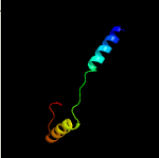



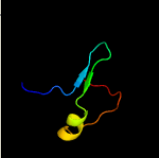


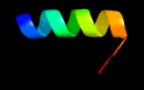
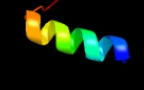


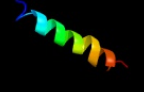

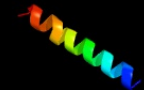
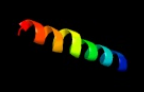
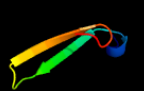


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3895c_(-)_4380631_4382118
Date	Sat Aug 10 22:05:08 BST 2019
Unique Job ID	aa83ac4352c1228b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4kk7A_	 Alignment		100.0	35	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	35	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	c6navl_	 Alignment		42.8	18	PDB header: structural protein Chain: I; PDB Molecule: m9ud72; PDBTitle: cryo-em reconstruction of sulfolobus islandicus la14/1 pilus
4	d2fb5a1	 Alignment		36.8	19	Fold: Yojj-like Superfamily: Yojj-like Family: Yojj-like
5	c1k6nH_	 Alignment		30.3	22	PDB header: photosynthesis Chain: H; PDB Molecule: photosynthetic reaction center h subunit; PDBTitle: e(l212)a,d(l213)a double mutant structure of photosynthetic reaction2 center from rhodobacter sphaeroides
6	d2i5nh1	 Alignment		30.3	20	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: Photosynthetic reaction centre, H-chain, cytoplasmic domain
7	c2i5nH_	 Alignment		23.6	19	PDB header: photosynthesis Chain: H; PDB Molecule: reaction center protein h chain; PDBTitle: 1.96 a x-ray structure of photosynthetic reaction center from2 rhodopseudomonas viridis:crystals grown by microfluidic technique
8	c2wmma_	 Alignment		21.1	16	PDB header: cell cycle Chain: A; PDB Molecule: chromosome partition protein mukb; PDBTitle: crystal structure of the hinge domain of mukb
9	d1rzhh1	 Alignment		18.5	22	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: Photosynthetic reaction centre, H-chain, cytoplasmic domain
10	c2ixsB_	 Alignment		17.4	11	PDB header: hydrolase Chain: B; PDB Molecule: sdai restriction endonuclease; PDBTitle: structure of sdai restriction endonuclease
11	c5xefA_	 Alignment		16.9	5	PDB header: chaperone Chain: A; PDB Molecule: flagellar protein flis; PDBTitle: crystal structure of flagellar chaperone from bacteria

12	d1vh6a_	Alignment		14.3	19	Fold: Four-helical up-and-down bundle Superfamily: Flagellar export chaperone FliS Family: Flagellar export chaperone FliS
13	c1vh6A_	Alignment		14.3	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: flagellar protein flis; PDBTitle: crystal structure of a flagellar protein
14	c3k1iA_	Alignment		13.3	10	PDB header: chaperone Chain: A: PDB Molecule: flagellar protein; PDBTitle: crystal strcture of flis-hp1076 complex in h. pylori
15	c5mrwL_	Alignment		12.7	13	PDB header: hydrolase Chain: L: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex
16	c6hrbD_	Alignment		12.7	13	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)
17	c5mrwD_	Alignment		12.7	13	PDB header: hydrolase Chain: D: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex
18	c5mrwH_	Alignment		12.7	13	PDB header: hydrolase Chain: H: PDB Molecule: potassium-transporting atpase kdpf subunit; PDBTitle: structure of the kdpfabc complex
19	c6hraD_	Alignment		12.7	13	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)
20	d1y7ma1	Alignment		12.1	15	Fold: L,D-transpeptidase catalytic domain-like Superfamily: L,D-transpeptidase catalytic domain-like Family: L,D-transpeptidase catalytic domain-like
21	c2ciua_	Alignment	not modelled	10.5	26	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
22	d2f23a2	Alignment	not modelled	10.0	45	Fold: FKBP-like Superfamily: FKBP-like Family: GreA transcript cleavage factor, C-terminal domain
23	c2lf3A_	Alignment	not modelled	9.2	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
24	c3c1zA_	Alignment	not modelled	9.1	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
25	c3hshA_	Alignment	not modelled	9.0	18	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)
26	c6cfwE_	Alignment	not modelled	8.9	11	PDB header: membrane protein Chain: E: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
27	c6ch3B_	Alignment	not modelled	8.1	23	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
						PDB header: transferase

28	c6gyyB_	Alignment	not modelled	7.6	21	Chain: B; PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of daca from staphylococcus aureus, n166c/t172c2 double mutant
29	c3n3fB_	Alignment	not modelled	7.6	21	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
30	c2i02B_	Alignment	not modelled	7.6	12	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
31	d1vqou1	Alignment	not modelled	7.3	18	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Ribosomal protein L24e
32	c3ccjU_	Alignment	not modelled	7.3	18	PDB header: ribosome Chain: U; PDB Molecule: 50s ribosomal protein l24e; PDBTitle: structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation c2534u
33	c3bmbB_	Alignment	not modelled	7.1	29	PDB header: rna binding protein Chain: B; PDB Molecule: regulator of nucleoside diphosphate kinase; PDBTitle: crystal structure of a new rna polymerase interacting2 protein
34	c6f0kA_	Alignment	not modelled	7.0	18	PDB header: membrane protein Chain: A; PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
35	d1ixsa_	Alignment	not modelled	6.6	30	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
36	c2p4vA_	Alignment	not modelled	6.0	27	PDB header: transcription Chain: A; PDB Molecule: transcription elongation factor greb; PDBTitle: crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
37	d2zjr1	Alignment	not modelled	5.9	20	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L28
38	d2b3ga1	Alignment	not modelled	5.9	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
39	c2kncA_	Alignment	not modelled	5.9	17	PDB header: cell adhesion Chain: A; PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
40	c2a7oA_	Alignment	not modelled	5.8	15	PDB header: transcription Chain: A; PDB Molecule: huntingtin interacting protein b; PDBTitle: solution structure of the hset2/hypb sri domain
41	c2k9yA_	Alignment	not modelled	5.7	3	PDB header: transferase Chain: A; PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
42	c2k9yB_	Alignment	not modelled	5.7	3	PDB header: transferase Chain: B; PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
43	c4jonA_	Alignment	not modelled	5.5	35	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: centrosomal protein of 170 kda; PDBTitle: crystal structure of a centrosomal protein 170kda, transcript variant2 beta (cep170) from homo sapiens at 2.15 a resolution (psi community3 target, sundstrom)
44	c5dn6P_	Alignment	not modelled	5.5	18	PDB header: hydrolase Chain: P; PDB Molecule: atp synthase f0 subcomplex c subunit; PDBTitle: atp synthase from paracoccus denitrificans
45	d2etna2	Alignment	not modelled	5.3	42	Fold: FKBP-like Superfamily: FKBP-like Family: GreA transcript cleavage factor, C-terminal domain
46	c2mhgA_	Alignment	not modelled	5.2	18	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of protein np_254181.1 from pseudomonas aeruginosa pa01
47	c2o35A_	Alignment	not modelled	5.1	26	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein duf1244; PDBTitle: protein of unknown function (duf1244) from sinorhizobium melliloti
48	d2o35a1	Alignment	not modelled	5.1	26	Fold: SMc04008-like Superfamily: SMc04008-like Family: SMc04008-like
49	c2etnA_	Alignment	not modelled	5.1	42	PDB header: transcription Chain: A; PDB Molecule: anti-cleavage anti-grea transcription factor PDBTitle: crystal structure of thermus aquaticus gfh1
50	c2zkru_	Alignment	not modelled	5.0	35	PDB header: ribosomal protein/rna Chain: U; PDB Molecule: rna expansion segment es41; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map