










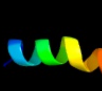



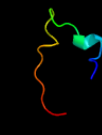

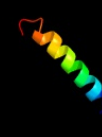





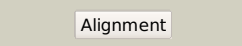
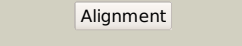
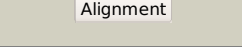
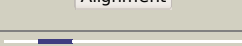
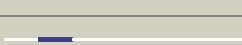




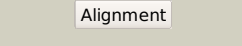
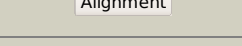
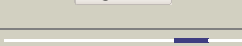

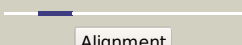
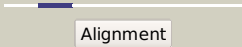


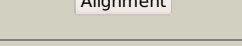
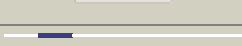
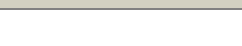




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1254 (-) _1401664_1402815
Date	Wed Jul 31 22:05:34 BST 2019
Unique Job ID	60eeb9ac125ca5b5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bbo2_	 Alignment		16.9	36	PDB header: ribosome Chain: 2: PDB Molecule: ribosomal protein l32; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
2	c2wwbB_	 Alignment		12.6	28	PDB header: ribosome Chain: B: PDB Molecule: protein transport protein sec61 subunit gamma; PDBTitle: cryo-em structure of the mammalian sec61 complex bound to the actively2 translating wheat germ 80s ribosome
3	c4gn0D_	 Alignment		12.0	7	PDB header: signaling protein Chain: D: PDB Molecule: hamp domain of af1503; PDBTitle: de novo phasing of a hamp-complex using an improved arcimboldo method
4	c1ujlA_	 Alignment		9.1	25	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h PDBTitle: solution structure of the herg k+ channel s5-p2 extracellular linker
5	c5jefA_	 Alignment		9.1	3	PDB header: transferase Chain: A: PDB Molecule: nitrate/nitrite sensor protein narq; PDBTitle: fragment of nitrate/nitrite sensor histidine kinase narq (wt) in2 asymmetric holo state
6	d1rhzb_	 Alignment		8.7	28	Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit
7	c2m6iC_	 Alignment		7.5	15	PDB header: membrane protein Chain: C: PDB Molecule: full-length transmembrane domains of human glycine receptor PDBTitle: putative pentameric open-channel structure of full-length2 transmembrane domains of human glycine receptor alpha1 subunit
8	d1yc611	 Alignment		6.7	35	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Bromoviridae-like VP
9	d1ijdb_	 Alignment		6.5	17	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
10	d3bz6a2	 Alignment		6.4	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PSPTO2686-like
11	d1m5wa_	 Alignment		6.3	23	Fold: TIM beta/alpha-barrel Superfamily: Pyridoxine 5'-phosphate synthase Family: Pyridoxine 5'-phosphate synthase

29	c3j1rC_	 Alignment	not modelled	6.2	24	PDB header: cell adhesion, structural protein Chain: C: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
30	c3j1rJ_	 Alignment	not modelled	6.2	24	PDB header: cell adhesion, structural protein Chain: J: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
31	c3j1rA_	 Alignment	not modelled	6.2	24	PDB header: cell adhesion, structural protein Chain: A: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
32	c3j1rO_	 Alignment	not modelled	6.2	24	PDB header: cell adhesion, structural protein Chain: O: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
33	c5muuC_	 Alignment	not modelled	6.1	28	PDB header: virus Chain: C: PDB Molecule: packaging enzyme p4; PDBTitle: dsrna bacteriophage phi6 nucleocapsid
34	d1nkzb_	 Alignment	not modelled	6.0	23	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
35	c3p4hA_	 Alignment	not modelled	6.0	28	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna ligase, n-terminal domain protein; PDBTitle: structures of archaeal members of the ligd 3'-phosphoesterase dna2 repair enzyme superfamily
36	c5dlcC_	 Alignment	not modelled	5.9	23	PDB header: transferase Chain: C: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: x-ray crystal structure of a pyridoxine 5-prime-phosphate synthase2 from pseudomonas aeruginosa
37	c6dmxH_	 Alignment	not modelled	5.8	20	PDB header: transcription Chain: H: PDB Molecule: transcriptional activator myb; PDBTitle: hbz56 in complex with kix and c-myb
38	c6dnqA_	 Alignment	not modelled	5.7	20	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator myb; PDBTitle: hbz77 in complex with kix and c-myb
39	c1vryA_	 Alignment	not modelled	5.7	23	PDB header: membrane protein Chain: A: PDB Molecule: glycine receptor alpha-1 chain; PDBTitle: second and third transmembrane domains of the alpha-12 subunit of human glycine receptor
40	c2d1kC_	 Alignment	not modelled	5.7	33	PDB header: structural protein Chain: C: PDB Molecule: metastasis suppressor protein 1; PDBTitle: ternary complex of the wh2 domain of mim with actin-dnase i
41	c6hk5A_	 Alignment	not modelled	5.6	31	PDB header: metal binding protein Chain: A: PDB Molecule: cooj; PDBTitle: x-ray structure of a truncated mutant of the metallochaperone cooj2 with a high-affinity nickel-binding site
42	d1iq8a4	 Alignment	not modelled	5.5	14	Fold: Cystatin-like Superfamily: Pre-PUA domain Family: Archaeosine tRNA-guanine transglycosylase, C2 domain
43	c6b2zf_	 Alignment	not modelled	5.5	19	PDB header: membrane protein Chain: F: PDB Molecule: atp synthase subunit c, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
44	c6ijoG_	 Alignment	not modelled	5.4	16	PDB header: photosynthesis Chain: G: PDB Molecule: psag; PDBTitle: photosystem i of chlamydomonas reinhardtii
45	c4l67B_	 Alignment	not modelled	5.3	22	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase pak 4; PDBTitle: crystal structure of catalytic domain of pak4
46	c3oruA_	 Alignment	not modelled	5.2	21	PDB header: metal binding protein Chain: A: PDB Molecule: duf1989 family protein; PDBTitle: crystal structure of a duf1989 family protein (tm1040_0329) from2 silicibacter sp. tm1040 at 1.11 a resolution
47	c3p43A_	 Alignment	not modelled	5.2	26	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure and activities of archaeal members of the ligd 3'2 phosphoesterase dna repair enzyme superfamily
48	c3m3nW_	 Alignment	not modelled	5.2	38	PDB header: structural protein Chain: W: PDB Molecule: neural wiskott-aldrich syndrome protein; PDBTitle: structure of a longitudinal actin dimer assembled by tandem w domains
49	d1cmxa_	 Alignment	not modelled	5.2	16	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Ubiquitin carboxyl-terminal hydrolase UCH-L
50	c3n9dA_	 Alignment	not modelled	5.1	19	PDB header: ligase Chain: A: PDB Molecule: probable atp-dependent dna ligase; PDBTitle: monoclinic structure of p. aeruginosa ligd phosphoesterase domain
51	c3utmC_	 Alignment	not modelled	5.0	19	PDB header: transferase/signaling protein Chain: C: PDB Molecule: axin-1; PDBTitle: crystal structure of a mouse tankyrase-axin complex
52	d2bbvc_	 Alignment	not modelled	5.0	8	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Nodaviridae-like VP