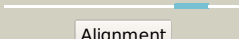

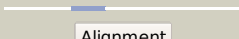

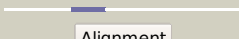






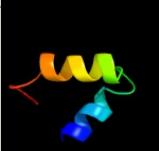

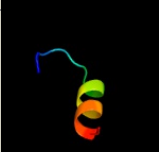







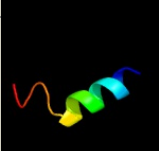
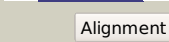

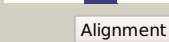
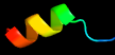
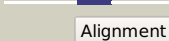

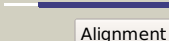

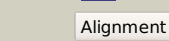

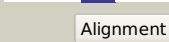

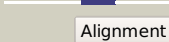

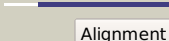




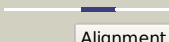
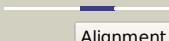



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2208_cobS_2472501_2473250
Date	Mon Aug 5 13:25:33 BST 2019
Unique Job ID	ac5064bbf28fc0b3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1m0fB_	 Alignment		31.9	50	PDB header: virus Chain: B; PDB Molecule: scaffolding protein b; PDBTitle: structural studies of bacteriophage alpha3 assembly, cryo-electron2 microscopy
2	c2v1sD_	 Alignment		24.0	24	PDB header: oxidoreductase Chain: D; PDB Molecule: mitochondrial import receptor subunit tom20 homolog; PDBTitle: crystal structure of rat tom20-aldh presequence complex
3	d1om2a_	 Alignment		16.8	24	Fold: Open three-helical up-and-down bundle Superfamily: Mitochondrial import receptor subunit Tom20 Family: Mitochondrial import receptor subunit Tom20
4	d1pvgal	 Alignment		16.1	30	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: DNA gyrase/MutL, second domain
5	d2d6fc1	 Alignment		13.1	36	Fold: GatB/YqeY motif Superfamily: GatB/YqeY motif Family: GatB/GatE C-terminal domain-like
6	c5z7cA_	 Alignment		11.1	30	PDB header: metal binding protein Chain: A; PDB Molecule: 3'3'-cgamp-specific phosphodiesterase 3; PDBTitle: crystal structure of cyclic gmp-amp specific phosphodiesterases in2 v.cholerae (v-cgap3)
7	d1otfa_	 Alignment		10.3	6	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
8	d1kja1	 Alignment		9.9	20	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: DNA gyrase/MutL, second domain
9	d1s16a1	 Alignment		9.6	30	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: DNA gyrase/MutL, second domain
10	d1e1a1	 Alignment		9.5	30	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: DNA gyrase/MutL, second domain
11	c5k8zB_	 Alignment		9.3	6	PDB header: oxidoreductase Chain: B; PDB Molecule: chlorite dismutase; PDBTitle: crystal structure of dimeric chlorite dismutase from cyanothecae sp.2 pcc7425 (ph 8.5)

12	c6bd4A_	 Alignment		8.3	14	PDB header: membrane protein Chain: A: PDB Molecule: frizzled-4/rubredoxin chimeric protein; PDBTitle: crystal structure of human apo-frizzled4 receptor
13	d1ckqa_	 Alignment		8.3	20	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease EcoRI
14	c4r8zB_	 Alignment		7.5	21	PDB header: hydrolase Chain: B: PDB Molecule: cyclic di-gmp phosphodiesterase; PDBTitle: crystal structure of pa4781 hd-gyp domain from pseudomonas aeruginosa2 at 2.2a resolution showing a bi-metallic ni ion center
15	c5d92B_	 Alignment		7.4	17	PDB header: membrane protein Chain: B: PDB Molecule: af2299 protein,phosphatidylinositol synthase; PDBTitle: structure of a phosphatidylinositolphosphate (pip) synthase from2 renibacterium salmoninarum
16	c4fazB_	 Alignment		7.3	19	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate isomerase protein; PDBTitle: kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylbium petroleiphilum
17	d1bjpa_	 Alignment		6.9	6	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
18	c3ry0A_	 Alignment		6.5	25	PDB header: isomerase Chain: A: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
19	c4o6mA_	 Alignment		6.0	13	PDB header: transferase Chain: A: PDB Molecule: af2299, a cdp-alcohol phosphotransferase; PDBTitle: structure of af2299, a cdp-alcohol phosphotransferase (cmp-bound)
20	c4ef4B_	 Alignment		5.9	5	PDB header: immune system Chain: B: PDB Molecule: transmembrane protein 173; PDBTitle: crystal structure of sting ctd complex with c-di-gmp
21	c2llwA_	 Alignment	not modelled	5.9	21	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein sti1; PDBTitle: solution structure of the yeast sti1 dp2 domain
22	c4fdxB_	 Alignment	not modelled	5.7	6	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonase tautomerase isozyme; PDBTitle: kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylbium petroleiphilum
23	d1aqaa_	 Alignment	not modelled	5.4	16	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
24	c2op8A_	 Alignment	not modelled	5.4	0	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase ywhb; PDBTitle: crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase