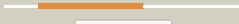
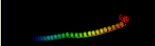
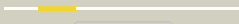
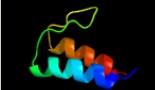

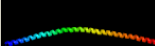



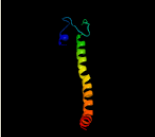

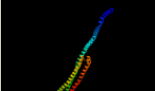



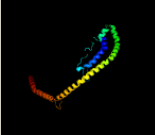

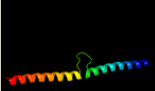

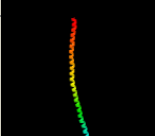

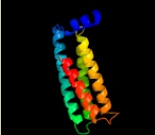


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2927c_(-)_3241232_3241969
Date	Thu Aug 8 16:20:08 BST 2019
Unique Job ID	4038dbbed9792523

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fkip_	 Alignment		83.0	12	PDB header: membrane protein Chain: P: PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
2	c5uyoA_	 Alignment		77.0	11	PDB header: de novo protein Chain: A: PDB Molecule: heeh_rd4_0097; PDBTitle: solution nmr structure of the de novo mini protein heeh_rd4_0097
3	c6fkib_	 Alignment		71.2	9	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit beta, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
4	c2a01B_	 Alignment		55.4	12	PDB header: lipid transport Chain: B: PDB Molecule: apolipoprotein a-i; PDBTitle: crystal structure of lipid-free human apolipoprotein a-i
5	c6nrc6_	 Alignment		54.5	11	PDB header: chaperone Chain: 6: PDB Molecule: prefoldin subunit 6; PDBTitle: htric-hpfd class3
6	c3s84B_	 Alignment		52.9	10	PDB header: transport protein Chain: B: PDB Molecule: apolipoprotein a-iv; PDBTitle: dimeric apo-a-iv
7	c2kk7A_	 Alignment		50.2	36	PDB header: hydrolase Chain: A: PDB Molecule: v-type atp synthase subunit e; PDBTitle: nmr solution structure of the n terminal domain of subunit e2 (e1-52) of a1ao atp synthase from methanocaldococcus3 jannaschii
8	c3r2pA_	 Alignment		45.9	11	PDB header: lipid transport Chain: A: PDB Molecule: apolipoprotein a-i; PDBTitle: 2.2 angstrom crystal structure of c terminal truncated human2 apolipoprotein a-i reveals the assembly of hdl by dimerization.
9	d1l2pa_	 Alignment		34.9	28	Fold: Single transmembrane helix Superfamily: F1F0 ATP synthase subunit B, membrane domain Family: F1F0 ATP synthase subunit B, membrane domain
10	c5t4oJ_	 Alignment		34.5	16	PDB header: hydrolase Chain: J: PDB Molecule: atp synthase subunit b; PDBTitle: autoinhibited e. coli atp synthase state 1
11	c1y4cA_	 Alignment		30.0	12	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp

12	c3iuoA_	Alignment		27.6	19	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent dna helicase recq; PDBTitle: the crystal structure of the c-terminal domain of the atp-dependent2 dna helicase recq from porphyromonas gingivalis to 1.6a
13	c1av1B_	Alignment		18.6	13	PDB header: lipid transport Chain: B; PDB Molecule: apolipoprotein a-i; PDBTitle: crystal structure of human apolipoprotein a-i
14	c5t58B_	Alignment		17.0	16	PDB header: cell cycle Chain: B; PDB Molecule: klla0e05809p; PDBTitle: structure of the mind complex shows a regulatory focus of yeast2 kinetochore assembly
15	c5ww1N_	Alignment		16.4	9	PDB header: cell cycle Chain: N; PDB Molecule: kinetochore protein nnf1; PDBTitle: crystal structure of the schizogenesis pombe kinetochore mis12c2 subcomplex
16	c5ic9C_	Alignment		13.7	14	PDB header: structural protein Chain: C; PDB Molecule: putative uncharacterized protein; PDBTitle: structure of the ctd complex of utp12 and utp13
17	c6nr92_	Alignment		12.9	23	PDB header: chaperone Chain: 2; PDB Molecule: prefoldin subunit 2; PDBTitle: htric-hpfd class5
18	c2y44A_	Alignment		10.1	16	PDB header: membrane protein Chain: A; PDB Molecule: glutamic acid/alanine-rich protein; PDBTitle: crystal structure of garp from trypanosoma congolense
19	c6nr84_	Alignment		10.0	14	PDB header: chaperone Chain: 4; PDB Molecule: prefoldin subunit 4; PDBTitle: htric-hpfd class6
20	c5an5J_	Alignment		9.4	17	PDB header: cell cycle Chain: J; PDB Molecule: cell cycle protein gpsb; PDBTitle: b. subtilis gpsb c-terminal domain
21	c2zdiA_	Alignment	not modelled	9.0	9	PDB header: chaperone Chain: A; PDB Molecule: prefoldin subunit beta; PDBTitle: crystal structure of prefoldin from pyrococcus horikoshii2 ot3
22	c5lskB_	Alignment	not modelled	6.4	16	PDB header: cell cycle Chain: B; PDB Molecule: polyamine-modulated factor 1; PDBTitle: crystal structure of the human kinetochore mis12-cenp-c complex
23	d2hkja2	Alignment	not modelled	6.1	14	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: DNA gyrase/MutL, second domain
24	c5ew5C_	Alignment	not modelled	5.9	12	PDB header: hydrolase Chain: C; PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
25	c2luhB_	Alignment	not modelled	5.6	13	PDB header: protein transport, endocytosis Chain: B; PDB Molecule: vacuolar protein-sorting-associated protein 60; PDBTitle: nmr structure of the vta1-vps60 complex
26	c2n1dA_	Alignment	not modelled	5.3	14	PDB header: protein binding Chain: A; PDB Molecule: mrg/morf4l-binding protein; PDBTitle: solution structure of the mrg15-mrgbp complex
27	c1mkmA_	Alignment	not modelled	5.3	14	PDB header: transcription Chain: A; PDB Molecule: iclr transcriptional regulator; PDBTitle: crystal structure of the thermotoga maritima iclr