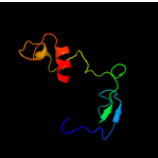

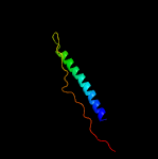
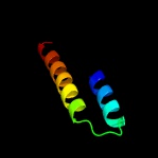
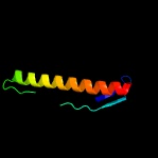
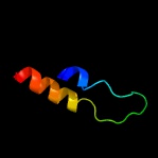
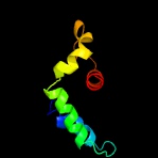

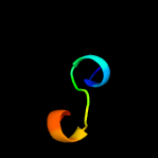


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0614 (-) _709359_710351
Date	Fri Jul 26 01:50:17 BST 2019
Unique Job ID	33c4f0cb70df78dc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6h9cb_	Alignment		25.8	40	PDB header: virus Chain: B: PDB Molecule: vp4; PDBTitle: cryo-em structure of archaeal extremophilic internal membrane-2 containing haloarcula californiae icosahedral virus 1 (hciv-1) at3 3.74 angstroms resolution.
2	c3lf4A_	Alignment		19.3	32	PDB header: fluorescent protein Chain: A: PDB Molecule: fluorescent timer precursor blue102; PDBTitle: crystal structure of fluorescent timer precursor blue102
3	c4hhsA_	Alignment		19.2	43	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-dioxygenase; PDBTitle: crystal structure of fatty acid alpha-dioxygenase (arabidopsis2 thaliana)
4	c2a56A_	Alignment		18.7	32	PDB header: luminescent protein Chain: A: PDB Molecule: gfp-like non-fluorescent chromoprotein fp595 chain 1; PDBTitle: fluorescent protein asfp595, a143s, on-state, 5min irradiation
5	c6h9cA_	Alignment		17.2	31	PDB header: virus Chain: A: PDB Molecule: vp4; PDBTitle: cryo-em structure of archaeal extremophilic internal membrane-2 containing haloarcula californiae icosahedral virus 1 (hciv-1) at3 3.74 angstroms resolution.
6	c6cfzG_	Alignment		17.0	31	PDB header: nuclear protein Chain: G: PDB Molecule: hsk3; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
7	c4o5pB_	Alignment		15.1	50	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from pseudomonas2 aeruginosa
8	c3ktcB_	Alignment		14.9	13	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
9	c2a7yA_	Alignment		14.9	37	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rv2302/mt2359; PDBTitle: solution structure of the conserved hypothetical protein2 rv2302 from the bacterium mycobacterium tuberculosis
10	d2a7ya1	Alignment		14.9	37	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Rv2302-like
11	c4u39N_	Alignment		14.7	54	PDB header: cell cycle Chain: N: PDB Molecule: cell division factor; PDBTitle: crystal structure of ftsz:mciz complex from bacillus subtilis

12	c2de0X_	Alignment		14.7	26	PDB header: transferase Chain: X: PDB Molecule: alpha-(1,6)-fucosyltransferase; PDBTitle: crystal structure of human alpha 1,6-fucosyltransferase, fut8
13	c2bpa3_	Alignment		13.9	62	PDB header: virus/dna Chain: 3: PDB Molecule: protein (subunit of bacteriophage phix174); PDBTitle: atomic structure of single-stranded dna bacteriophage2 phix174 and its functional implications
14	c4wjzA_	Alignment		11.7	18	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
15	c2rpaA_	Alignment		11.3	21	PDB header: hydrolase Chain: A: PDB Molecule: katanin p60 atpase-containing subunit a1; PDBTitle: the solution structure of n-terminal domain of microtubule severing2 enzyme
16	c4kwyB_	Alignment		9.8	14	PDB header: transport protein Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative lipoprotein (cc_3750) from caulobacter2 crescentus cb15 at 2.40 a resolution
17	c3lphD_	Alignment		9.2	47	PDB header: viral protein Chain: D: PDB Molecule: protein rev; PDBTitle: crystal structure of the hiv-1 rev dimer
18	d1ey1a_	Alignment		8.2	13	Fold: NusB-like Superfamily: NusB-like Family: Antitermination factor NusB
19	c6eb0A_	Alignment		7.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxyphenylacetate 3-monooxygenase, oxygenase subunit; PDBTitle: structure of 4-hydroxyphenylacetate 3-monooxygenase (hpab), oxygenase2 component from escherichia coli
20	c4u39L_	Alignment		7.8	54	PDB header: cell cycle Chain: L: PDB Molecule: cell division factor; PDBTitle: crystal structure of ftsz:mciz complex from bacillus subtilis
21	d1jyra_	Alignment	not modelled	7.6	44	Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: HTLV-II matrix protein
22	c4u39J_	Alignment	not modelled	7.4	54	PDB header: cell cycle Chain: J: PDB Molecule: cell division factor; PDBTitle: crystal structure of ftsz:mciz complex from bacillus subtilis
23	c3pvdA_	Alignment	not modelled	6.8	22	PDB header: viral protein Chain: A: PDB Molecule: capsid; PDBTitle: crystal structure of p domain dimer of norovirus va207 complexed with2 3'-sialyl-lewis x tetrasaccharide
24	c3mzIH_	Alignment	not modelled	6.8	23	PDB header: protein transport Chain: H: PDB Molecule: protein transport protein sec31; PDBTitle: sec13/sec31 edge element, loop deletion mutant
25	c3djaA_	Alignment	not modelled	6.8	21	PDB header: transferase Chain: A: PDB Molecule: protein ct_858; PDBTitle: crystal structure of cpaf solved with mad
26	c4oo2D_	Alignment	not modelled	6.7	30	PDB header: oxidoreductase Chain: D: PDB Molecule: chlorophenol-4-monooxygenase; PDBTitle: streptomyces globisporus c-1027 fad dependent (s)-3-chloro-beta-2 tyrosine-s-gcc2 c-5 hydroxylase sgcc apo form
27	d1n26a1	Alignment	not modelled	6.6	78	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
28	c2vwaE_	Alignment	not modelled	6.3	46	PDB header: unknown function Chain: E: PDB Molecule: putative uncharacterized protein p13_0012; PDBTitle: crystal structure of a sporozoite protein essential for2 liver stage development of malaria parasite

29	c2pm7A_	Alignment	not modelled	6.2	21	PDB header: protein transport Chain: A: PDB Molecule: protein transport protein sec31; PDBTitle: crystal structure of yeast sec13/31 edge element of the copii2 vesicular coat, selenomethionine version
30	c3i38C_	Alignment	not modelled	5.8	18	PDB header: chaperone Chain: C: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
31	c3i38E_	Alignment	not modelled	5.8	18	PDB header: chaperone Chain: E: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
32	c1vdbA_	Alignment	not modelled	5.7	44	PDB header: transcription Chain: A: PDB Molecule: fibroin-modulator-binding-protein-1; PDBTitle: nmr structure of fmbp-1 tandem repeat 1 in 30%(v/v) tfe2 solution
33	c1vd7A_	Alignment	not modelled	5.7	44	PDB header: transcription Chain: A: PDB Molecule: fibroin-modulator-binding-protein-1; PDBTitle: solution structure of fmbp-1 tandem repeat 1
34	d1dj3a_	Alignment	not modelled	5.5	70	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
35	d1p9ba_	Alignment	not modelled	5.5	60	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
36	c6f46A_	Alignment	not modelled	5.5	47	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-like protein 1; PDBTitle: structure of the transmembrane helix of bclxl in phospholipid2 nanodiscs
37	c4adjB_	Alignment	not modelled	5.5	45	PDB header: viral protein Chain: B: PDB Molecule: e1 envelope glycoprotein; PDBTitle: crystal structure of the rubella virus glycoprotein e1 in its2 post-fusion form crystallized in presence of 1mm of calcium acetate
38	c2k42B_	Alignment	not modelled	5.4	35	PDB header: signaling protein Chain: B: PDB Molecule: espfu; PDBTitle: solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehc effector
39	c4wxmD_	Alignment	not modelled	5.4	21	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator fleq; PDBTitle: fleq rec domain from pseudomonas aeruginosa pao1
40	d1iwea_	Alignment	not modelled	5.1	60	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like