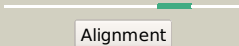
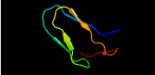

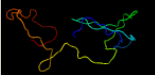

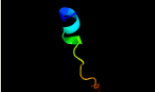

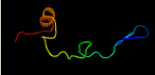
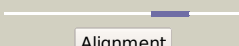

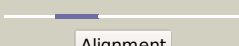

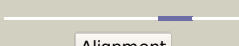
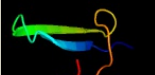
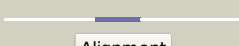


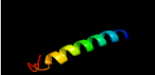

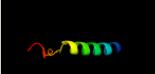









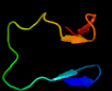
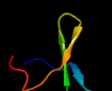


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3835_(-)_4309225_4310574
Date	Fri Aug 9 18:20:54 BST 2019
Unique Job ID	fc509db59989699d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5klcA_	 Alignment		47.8	33	PDB header: sugar binding protein Chain: A; PDB Molecule: carbohydrate binding module e1; PDBTitle: structure of cbm_e1, a novel carbohydrate-binding module found by2 sugar cane soil metagenome
2	c4nl6C_	 Alignment		28.9	13	PDB header: splicing Chain: C; PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
3	c4a1sE_	 Alignment		26.9	44	PDB header: cell cycle Chain: E; PDB Molecule: re60102p; PDBTitle: crystallographic structure of the pins:insc complex
4	c3lybC_	 Alignment		23.6	23	PDB header: hydrolase Chain: C; PDB Molecule: putative endoribonuclease; PDBTitle: structure of putative endoribonuclease(kp1_3112) from klebsiella2 pneumoniae
5	c3gjbA_	 Alignment		17.9	9	PDB header: biosynthetic protein Chain: A; PDB Molecule: cytc3; PDBTitle: cytc3 with fe(ii) and alpha-ketoglutarate
6	c4pmkA_	 Alignment		17.8	30	PDB header: plant protein Chain: A; PDB Molecule: kiwellin; PDBTitle: crystal structure of kiwellin
7	c2lcdA_	 Alignment		15.6	19	PDB header: transcription Chain: A; PDB Molecule: at-rich interactive domain-containing protein 4a; PDBTitle: solution structure of rbbp1 tudor domain
8	c5jqvA_	 Alignment		13.7	18	PDB header: oxidoreductase Chain: A; PDB Molecule: aspartyl/asparaginyl beta-hydroxylase; PDBTitle: aspartyl/asparaginyl beta-hydroxylase (asph)oxygenase and tpr domains2 in complex with manganese, n-oxalylglycine and factor x substrate3 peptide fragment(39mer-4ser)
9	c2momC_	 Alignment		13.6	30	PDB header: membrane protein Chain: C; PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
10	c2momB_	 Alignment		12.4	30	PDB header: membrane protein Chain: B; PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
11	c4d0kC_	 Alignment		10.3	15	PDB header: gene regulation Chain: C; PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit PDBTitle: complex of chaetomium thermophilum pan2 (wd40-cs1) with pan3 (c-term)

12	c4a1aM_	Alignment		10.3	11	PDB header: ribosome Chain: M; PDB Molecule: 60s ribosomal protein l5; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
13	d2fsqa1	Alignment		9.9	36	Fold: LigT-like Superfamily: LigT-like Family: Atu0111-like
14	d1zxqa2	Alignment		9.6	50	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: l set domains
15	d1s6la2	Alignment		9.4	20	Fold: NosL/MerB-like Superfamily: NosL/MerB-like Family: MerB-like
16	c5iwzA_	Alignment		9.3	27	PDB header: cell cycle Chain: A; PDB Molecule: synaptonemal complex protein 2; PDBTitle: synaptonemal complex protein
17	c5ue8B_	Alignment		9.0	55	PDB header: exocytosis Chain: B; PDB Molecule: protein unc-13 homolog a; PDBTitle: the crystal structure of munc13-1 c1c2mun domain
18	c4dzoA_	Alignment		8.8	17	PDB header: cell cycle Chain: A; PDB Molecule: mitotic spindle assembly checkpoint protein mad1; PDBTitle: structure of human mad1 c-terminal domain reveals its involvement in2 kinetochore targeting
19	d1wyka_	Alignment		8.4	19	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
20	d1e8qa_	Alignment		8.2	21	Fold: Cellulose docking domain, docking Superfamily: Cellulose docking domain, docking Family: Cellulose docking domain, docking
21	d1ep5a_	Alignment	not modelled	8.2	22	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
22	c3hqxA_	Alignment	not modelled	8.0	22	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: upf0345 protein aciad0356; PDBTitle: crystal structure of protein of unknown function (duf1255,pf06865)2 from acinetobacter sp. adp1
23	c1kxfA_	Alignment	not modelled	7.9	19	PDB header: viral protein Chain: A; PDB Molecule: sindbis virus capsid protein; PDBTitle: sindbis virus capsid, (wild-type) residues 1-264, tetragonal crystal2 form (form ii)
24	c2yewG_	Alignment	not modelled	7.7	25	PDB header: virus Chain: G; PDB Molecule: capsid protein; PDBTitle: modeling barmah forest virus structural proteins
25	c1t0pB_	Alignment	not modelled	7.7	50	PDB header: immune system Chain: B; PDB Molecule: intercellular adhesion molecule-3; PDBTitle: structural basis of icam recognition by integrin alphahbeta2 revealed2 in the complex structure of binding domains of icam-3 and alphabeta23 at 1.65 a
26	d1vcpa_	Alignment	not modelled	7.7	25	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
27	c4f5cF_	Alignment	not modelled	7.5	20	PDB header: hydrolase/viral protein Chain: F; PDB Molecule: prcv spike protein; PDBTitle: crystal structure of the spike receptor binding domain of a porcine2 respiratory coronavirus in complex with the pig aminopeptidase n3 ectodomain
28	c2n4pA_	Alignment	not modelled	7.4	19	PDB header: dna binding protein Chain: A; PDB Molecule: tar dna-binding protein 43; PDBTitle: solution structure of the n-terminal domain of tdp-43
						PDB header: oxidoreductase

29	c2q49B_	Alignment	not modelled	6.7	21	Chain: B; PDB Molecule: probable n-acetyl-gamma-glutamyl-phosphate reductase; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at2g19940
30	c5mrgA_	Alignment	not modelled	6.6	19	PDB header: dna binding protein Chain: A; PDB Molecule: star dna-binding protein 43; PDBTitle: solution structure of tdp-43 (residues 1-102)
31	c3d2hA_	Alignment	not modelled	6.5	24	PDB header: oxidoreductase Chain: A; PDB Molecule: berberine bridge-forming enzyme; PDBTitle: structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form
32	c2m6oA_	Alignment	not modelled	6.0	43	PDB header: transcription Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: the actinobacterial transcription factor rbpa binds to the principal2 sigma subunit of rna polymerase
33	c5mdxx_	Alignment	not modelled	5.9	30	PDB header: photosynthesis Chain: X; PDB Molecule: photosystem ii reaction center protein x; PDBTitle: cryo-em structure of the psii supercomplex from arabidopsis thaliana
34	c5mdxX_	Alignment	not modelled	5.9	30	PDB header: photosynthesis Chain: X; PDB Molecule: photosystem ii reaction center protein x; PDBTitle: cryo-em structure of the psii supercomplex from arabidopsis thaliana
35	c6mx7C_	Alignment	not modelled	5.9	22	PDB header: virus Chain: C; PDB Molecule: capsid; PDBTitle: cryoem structure of chimeric eastern equine encephalitis virus:2 genome-binding capsid n-terminal domain
36	c3j3bD_	Alignment	not modelled	5.9	17	PDB header: ribosome Chain: D; PDB Molecule: 60s ribosomal protein l5; PDBTitle: structure of the human 60s ribosomal proteins
37	c2miiA_	Alignment	not modelled	5.4	21	PDB header: protein binding Chain: A; PDB Molecule: penicillin-binding protein activator lpob; PDBTitle: nmr structure of e. coli lpob
38	c4c8hC_	Alignment	not modelled	5.1	23	PDB header: dna replication Chain: C; PDB Molecule: ctf4; PDBTitle: crystal structure of the c-terminal region of yeast ctf4,2 selenomethionine protein.
39	c6d6vF_	Alignment	not modelled	5.0	38	PDB header: replication Chain: F; PDB Molecule: telomerase holoenzyme teb heterotrimer teb3 subunit; PDBTitle: cryoem structure of tetrahymena telomerase with telomeric dna at 4.82 angstrom resolution
40	c3jcux_	Alignment	not modelled	5.0	35	PDB header: membrane protein Chain: X; PDB Molecule: photosystem ii reaction center x protein; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution