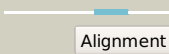


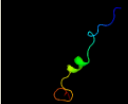
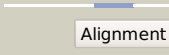
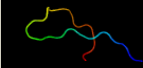
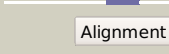
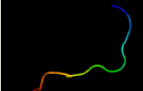

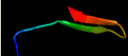
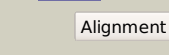
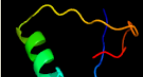

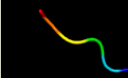


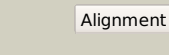
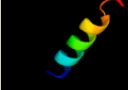
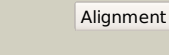
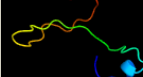
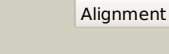



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2137c_(-)_2396910_2397323
Date	Mon Aug 5 13:25:25 BST 2019
Unique Job ID	da934759ec47e69f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ujqA_	 Alignment		35.6	73	PDB header: antimicrobial protein Chain: A: PDB Molecule: bacteriocin; PDBTitle: nmr solution structure of the two-component bacteriocin cbnxy
2	c1ngmB_	 Alignment		30.8	23	PDB header: transcription/dna Chain: B: PDB Molecule: transcription factor iiib brf1 subunit; PDBTitle: crystal structure of a yeast brf1-tbp-dna ternary complex
3	c3j9eD_	 Alignment		20.3	29	PDB header: viral protein Chain: D: PDB Molecule: vp5; PDBTitle: atomic structure of a non-enveloped virus reveals ph sensors for a2 coordinated process of cell entry
4	c6eacC_	 Alignment		13.4	38	PDB header: transferase Chain: C: PDB Molecule: selo; PDBTitle: pseudomonas syringae selo
5	c2m7oA_	 Alignment		13.1	44	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein np_346341.1 from streptococcus pneumoniae
6	d1c4qa_	 Alignment		12.6	23	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
7	c2hj1A_	 Alignment		11.8	83	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae
8	d2hj1a1	 Alignment		11.8	83	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoadD/ThiS Family: HI0395-like
9	c1syqB_	 Alignment		10.1	44	PDB header: cell adhesion Chain: B: PDB Molecule: talin 1; PDBTitle: human vinculin head domain vh1, residues 1-258, in complex with human2 talin's vinculin binding site 1, residues 607-636
10	c1x31D_	 Alignment		9.0	22	PDB header: oxidoreductase Chain: D: PDB Molecule: sarcosine oxidase delta subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
11	c4hecB_	 Alignment		8.7	29	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium tuberculosis

12	d1r4pb_		Alignment		8.6	26	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
13	d1o12a1		Alignment		8.4	31	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA
14	c3cmuA_		Alignment		8.2	49	PDB header: recombination/dna Chain: A: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the recassdna/dsdna2 structures
15	c1dmfF_		Alignment		8.0	60	PDB header: dna binding protein/transferase Chain: F: PDB Molecule: dna polymerase; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol
16	c1dmfH_		Alignment		8.0	60	PDB header: dna binding protein/transferase Chain: H: PDB Molecule: dna polymerase; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol
17	c1dmfB_		Alignment		7.8	60	PDB header: dna binding protein/transferase Chain: B: PDB Molecule: dna polymerase; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol
18	c1dmfD_		Alignment		7.8	60	PDB header: dna binding protein/transferase Chain: D: PDB Molecule: dna polymerase; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol
19	c2ltrA_		Alignment		7.2	22	PDB header: rna binding protein Chain: A: PDB Molecule: protein rde-4; PDBTitle: solution structure of rde-4(32-136)
20	d2ns1b1		Alignment		6.7	32	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
21	c5tvfF_		Alignment	not modelled	6.5	28	PDB header: lyase Chain: F: PDB Molecule: s-adenosylmethionine decarboxylase proenzyme-like, PDBTitle: crystal structure of trypanosoma brucei adometdc/prozyme heterodimer2 in complex with inhibitor cgp 40215
22	d1ov9a_		Alignment	not modelled	6.4	43	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
23	d1dqza_		Alignment	not modelled	6.4	29	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
24	c6a7vU_		Alignment	not modelled	6.2	40	PDB header: toxin/antitoxin Chain: U: PDB Molecule: antitoxin vapb11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
25	c4l1nA_		Alignment	not modelled	6.2	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved lipoprotein, putative; PDBTitle: crystal structure of a putative conserved lipoprotein (nt01cx_1156)2 from clostridium novyi nt at 2.70 a resolution
26	d1f0na_		Alignment	not modelled	6.1	31	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
27	c3b4qA_		Alignment	not modelled	6.0	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a conserved protein domain (unknown2 function) from corynebacterium diphtheriae
28	c3j60L_		Alignment	not modelled	6.0	54	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s8e; PDBTitle: localization of the small subunit ribosomal proteins into a

					5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
29	c1irrA_	Alignment	not modelled	6.0	40 PDB header: cytokine Chain: A: PDB Molecule: paralytic peptide; PDBTitle: solution structure of paralytic peptide of the silkworm,2 bombyx mori
30	c2djca_	Alignment	not modelled	5.9	40 PDB header: cytokine Chain: A: PDB Molecule: growth-blocking peptide; PDBTitle: solution structure of growth-blocking peptide of the2 tobacco cutworm, spodoptera litura
31	d2bosa_	Alignment	not modelled	5.6	22 Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
32	c1t01B_	Alignment	not modelled	5.6	44 PDB header: cell adhesion, structural protein Chain: B: PDB Molecule: talain 1; PDBTitle: vinculin complexed with the vbs1 helix from talin
33	c1v28A_	Alignment	not modelled	5.4	40 PDB header: toxin Chain: A: PDB Molecule: paralytic peptide; PDBTitle: solution structure of paralytic peptide of the wild2 silkmoth, antheraea yamamai
34	c2k5jB_	Alignment	not modelled	5.4	37 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
35	c2rd5D_	Alignment	not modelled	5.4	26 PDB header: protein binding Chain: D: PDB Molecule: pii protein; PDBTitle: structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
36	d2qmma1	Alignment	not modelled	5.4	28 Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF1056-like
37	c3wzhA_	Alignment	not modelled	5.4	22 PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein af_1864; PDBTitle: crystal structure of afcsx3
38	c3ncpD_	Alignment	not modelled	5.3	32 PDB header: signaling protein Chain: D: PDB Molecule: nitrogen regulatory protein p-ii (glnb-2); PDBTitle: glnk2 from archaeoglobus fulgidus
39	c3bzqa_	Alignment	not modelled	5.3	26 PDB header: signaling protein/transcription Chain: A: PDB Molecule: nitrogen regulatory protein p-ii; PDBTitle: high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis