

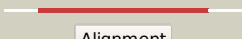













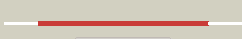







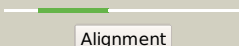

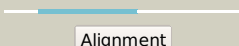

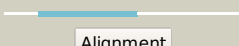

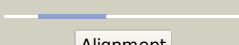

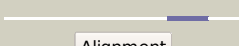
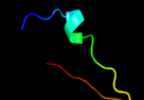

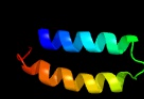





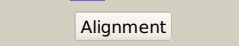

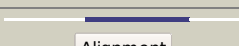

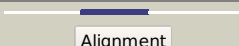

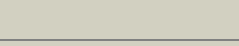


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0718_(rpsH)_812979_813377
Date	Fri Jul 26 01:50:29 BST 2019
Unique Job ID	cb23cc96e80fd9aa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o5jH_	 Alignment		100.0	96	PDB header: ribosome Chain: H: PDB Molecule: 30s ribosomal protein s8; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
2	c3rf2A_	 Alignment		100.0	43	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s8; PDBTitle: crystal structure of 30s ribosomal protein s8 from aquifex aeolicus
3	d1i94h_	 Alignment		100.0	49	Fold: Ribosomal protein S8 Superfamily: Ribosomal protein S8 Family: Ribosomal protein S8
4	d1i6ua_	 Alignment		100.0	25	Fold: Ribosomal protein S8 Superfamily: Ribosomal protein S8 Family: Ribosomal protein S8
5	d1seia_	 Alignment		100.0	57	Fold: Ribosomal protein S8 Superfamily: Ribosomal protein S8 Family: Ribosomal protein S8
6	d1an7a_	 Alignment		100.0	50	Fold: Ribosomal protein S8 Superfamily: Ribosomal protein S8 Family: Ribosomal protein S8
7	c3bbnH_	 Alignment		100.0	41	PDB header: ribosome Chain: H: PDB Molecule: ribosomal protein s8; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
8	c1s1hH_	 Alignment		100.0	26	PDB header: ribosome Chain: H: PDB Molecule: 40s ribosomal protein s22; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
9	d2gy9h1	 Alignment		100.0	48	Fold: Ribosomal protein S8 Superfamily: Ribosomal protein S8 Family: Ribosomal protein S8
10	c5xxuW_	 Alignment		100.0	26	PDB header: ribosome Chain: W: PDB Molecule: ribosomal protein us8; PDBTitle: small subunit of toxoplasma gondii ribosome
11	c2xznH_	 Alignment		100.0	24	PDB header: ribosome Chain: H: PDB Molecule: ribosomal protein s8 containing protein; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2

12	c5xyiW_	 Alignment		100.0	24	PDB header: ribosome Chain: W; PDB Molecule: ribosomal protein s15a; PDBTitle: small subunit of trichomonas vaginalis ribosome
13	c4e4rA_	 Alignment		50.8	23	PDB header: transferase Chain: A; PDB Molecule: phosphate acetyltransferase; PDBTitle: eutd phosphotransacetylase from staphylococcus aureus
14	c2zqeA_	 Alignment		33.5	18	PDB header: dna binding protein Chain: A; PDB Molecule: mutS2 protein; PDBTitle: crystal structure of the smr domain of thermus thermophilus mutS2
15	c4ochA_	 Alignment		30.2	15	PDB header: hydrolase Chain: A; PDB Molecule: endonuclease mutS2; PDBTitle: apo structure of smr domain of mutS2 from deinococcus radiodurans
16	c2k19A_	 Alignment		21.1	16	PDB header: antimicrobial protein Chain: A; PDB Molecule: putative piscicolin 126 immunity protein; PDBTitle: nmr solution structure of pisi
17	c4gl6B_	 Alignment		18.4	35	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf5037 family protein (rumgna_01148) from2 ruminococcus gnavus atcc 29149 at 2.55 a resolution
18	c2zrrA_	 Alignment		18.3	16	PDB header: antimicrobial protein Chain: A; PDB Molecule: mundticin ks immunity protein; PDBTitle: crystal structure of an immunity protein that contributes2 to the self-protection of bacteriocin-producing3 enterococcus mundtii 15-1a
19	d1a6sa_	 Alignment		15.1	24	Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: GAG polyprotein M-domain
20	d1khia2	 Alignment		11.0	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
21	c3qd7X_	 Alignment	not modelled	10.8	14	PDB header: hydrolase Chain: X; PDB Molecule: uncharacterized protein ydal; PDBTitle: crystal structure of ydal, a stand-alone small mutS-related protein2 from escherichia coli
22	d2hgca1	 Alignment	not modelled	10.7	39	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: YjcQ-like
23	c2hgca_	 Alignment	not modelled	10.7	39	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: yjcq protein; PDBTitle: solution nmr structure of the yjcq protein from bacillus2 subtilis. northeast structural genomics target sr346.
24	c4l5gA_	 Alignment	not modelled	9.5	17	PDB header: transcription Chain: A; PDB Molecule: card; PDBTitle: crystal structure of thermus thermophilus card
25	d1zhva2	 Alignment	not modelled	8.8	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: Atu0741-like
26	c6hq9A_	 Alignment	not modelled	8.3	16	PDB header: hydrolase Chain: A; PDB Molecule: dna excision repair protein ercc-6-like 2; PDBTitle: crystal structure of the tudor domain of human ercc6-l2
27	c3mioA_	 Alignment	not modelled	8.1	15	PDB header: lyase Chain: A; PDB Molecule: 3,4-dihydroxy-2-butanone 4-phosphate synthase; PDBTitle: crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00
28	c2qlvF_	 Alignment	not modelled	7.1	15	PDB header: transferase/protein binding Chain: F; PDB Molecule: nuclear protein snf4; PDBTitle: crystal structure of the heterotrimer core of the s. cerevisiae ampk2 homolog snf1

29	c2lwjA_	Alignment	not modelled	7.0	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, card family; PDBTitle: nmr solution structure myxococcus xanthus cdn1
30	d1vm0a_	Alignment	not modelled	6.5	22	Fold: IF3-like Superfamily: AlbA-like Family: Hypothetical protein At2g34160
31	c5j8jA_	Alignment	not modelled	6.5	18	PDB header: hydrolase Chain: A: PDB Molecule: histone deacetylase hda1; PDBTitle: a histone deacetylase from saccharomyces cerevisiae
32	c2e1nA_	Alignment	not modelled	6.4	16	PDB header: circadian clock protein Chain: A: PDB Molecule: pex; PDBTitle: crystal structure of the cyanobacterium circadian clock modifier pex
33	c4n7vB_	Alignment	not modelled	6.0	8	PDB header: cell cycle Chain: B: PDB Molecule: serine/threonine-protein kinase plk4; PDBTitle: crystal structure of human plk4 cryptic polo box (cpb) in complex with2 a cep152 n-terminal fragment
34	d2esha1	Alignment	not modelled	5.9	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PadR-like
35	c5cefA_	Alignment	not modelled	5.5	29	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: cystal structure of aspartate semialdehyde dehydrogenase from2 cryptococcus neoformans
36	c5z08A_	Alignment	not modelled	5.3	11	PDB header: cell cycle Chain: A: PDB Molecule: cenp-i; PDBTitle: the crystal structure of kinetochore subunits cenp-h/i/k triple2 complex
37	c4iivB_	Alignment	not modelled	5.2	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lmo1499 protein; PDBTitle: 2.6 angstrom crystal structure of putative yceg-like protein lmo14992 from listeria monocytogenes
38	c4ayaA_	Alignment	not modelled	5.1	18	PDB header: cell cycle Chain: A: PDB Molecule: dna-binding protein inhibitor id-2; PDBTitle: crystal structure of id2 hlh homodimer at 2.1a resolution