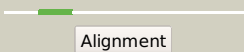

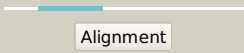


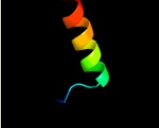
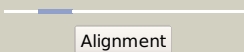
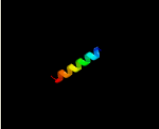
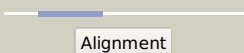
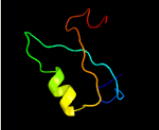
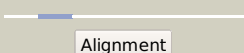

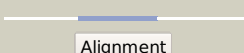

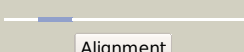

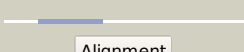
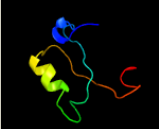
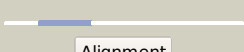

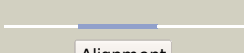



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3122_(-)_3488086_3488556
Date	Thu Aug 8 16:20:30 BST 2019
Unique Job ID	0713da0f4a77c6e3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4k1kA_	 Alignment		56.2	50	PDB header: unknown function Chain: A; PDB Molecule: phage-related protein duf2815; PDBTitle: phage-related protein duf2815 from enterococcus faecalis
2	d1pdaa1	 Alignment		32.8	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
3	c2p38A_	 Alignment		32.4	30	PDB header: biosynthetic protein Chain: A; PDB Molecule: protein involved in ribosomal biogenesis; PDBTitle: crystal structure of pyrococcus abyssi protein homologue of2 saccharomyces cerevisiae nip7p
4	c5gnaB_	 Alignment		28.6	14	PDB header: gene regulation Chain: B; PDB Molecule: flagellar hook-associated protein 2; PDBTitle: crystal structure of flagellin assembly related protein
5	c2ypnA_	 Alignment		28.3	20	PDB header: transferase Chain: A; PDB Molecule: protein (hydroxymethylbilane synthase); PDBTitle: hydroxymethylbilane synthase
6	c4jg2A_	 Alignment		25.8	63	PDB header: unknown function Chain: A; PDB Molecule: phage-related protein; PDBTitle: structure of phage-related protein from bacillus cereus atcc 10987
7	c5npaA_	 Alignment		24.3	15	PDB header: rna binding protein Chain: A; PDB Molecule: loquacious; PDBTitle: solution structure of drosophila melanogaster loquacious dsrbd2
8	c4auvC_	 Alignment		24.3	28	PDB header: apoptosis Chain: C; PDB Molecule: breast cancer metastasis suppressor 1; PDBTitle: crystal structure of the brms1 n-terminal region
9	c4mlqA_	 Alignment		24.0	24	PDB header: transferase Chain: A; PDB Molecule: porphobilinogen deaminase; PDBTitle: crystal structure of bacillus megaterium porphobilinogen deaminase
10	c4htgA_	 Alignment		23.6	26	PDB header: transferase/transferase inhibitor Chain: A; PDB Molecule: porphobilinogen deaminase, chloroplastic; PDBTitle: porphobilinogen deaminase from arabidopsis thaliana
11	c3adiA_	 Alignment		23.4	13	PDB header: gene regulation Chain: A; PDB Molecule: f21m12.9 protein; PDBTitle: structure of arabidopsis hyl1 and its molecular implications for mirna2 processing

12	c3eq1A_			22.9	29	PDB header: transferase Chain: A; PDB Molecule: porphobilinogen deaminase; PDBTitle: the crystal structure of human porphobilinogen deaminase at 2.8a resolution
13	c3b4nB_			20.0	13	PDB header: lyase Chain: B; PDB Molecule: endo-pectate lyase; PDBTitle: crystal structure analysis of pectate lyase peli from2 erwinia chrysanthemi
14	c2xe4A_			19.2	22	PDB header: hydrolase/inhibitor Chain: A; PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major
15	d1g5ga1			18.3	43	Fold: Head and neck region of the ectodomain of NDV fusion glycoprotein Superfamily: Head and neck region of the ectodomain of NDV fusion glycoprotein Family: Head and neck region of the ectodomain of NDV fusion glycoprotein
16	c2h9xA_			17.5	32	PDB header: toxin Chain: A; PDB Molecule: toxin cgna; PDBTitle: nmr structure for the cgna toxin from the sea anemone2 condylactis gigantea
17	d1stua_			16.6	19	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
18	c3mawB_			15.9	43	PDB header: viral protein Chain: B; PDB Molecule: fusion glycoprotein f0; PDBTitle: structure of the newcastle disease virus f protein in the post-fusion2 conformation
19	c3cvfA_			15.7	35	PDB header: signaling protein Chain: A; PDB Molecule: homer protein homolog 3; PDBTitle: crystal structure of the carboxy terminus of homer3
20	c1g5gA_			15.5	43	PDB header: viral protein Chain: A; PDB Molecule: fusion protein; PDBTitle: fragment of fusion protein from newcastle disease virus
21	c3ci9B_		not modelled	14.9	27	PDB header: transcription Chain: B; PDB Molecule: heat shock factor-binding protein 1; PDBTitle: crystal structure of the human hsbp1
22	c2l33A_		not modelled	13.0	16	PDB header: transcription regulator Chain: A; PDB Molecule: interleukin enhancer-binding factor 3; PDBTitle: solution nmr structure of drbm 2 domain of interleukin enhancer-2 binding factor 3 from homo sapiens, northeast structural genomics3 consortium target hr4527e
23	c2mdrA_		not modelled	12.2	17	PDB header: hydrolase Chain: A; PDB Molecule: double-stranded rna-specific adenosine deaminase; PDBTitle: solution structure of the third double-stranded rna-binding domain2 (dsrbd3) of human adenosine-deaminase adar1
24	c6grvA_		not modelled	12.2	55	PDB header: metal binding protein Chain: A; PDB Molecule: metallothionein; PDBTitle: cadmium(ii) form of full-length metallothionein from pseudomonas2 fluorescens q2-87 (pflq2 mt)
25	c4faoL_		not modelled	12.0	45	PDB header: signaling protein/signaling protein Chain: L; PDB Molecule: activin receptor type-2b; PDBTitle: specificity and structure of a high affinity activin-like 1 (alk1)2 signaling complex
26	c3u1nC_		not modelled	11.7	30	PDB header: hydrolase Chain: C; PDB Molecule: sam domain and hd domain-containing protein 1; PDBTitle: structure of the catalytic core of human samhd1
27	d2dmya1		not modelled	11.1	12	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
28	c2dshB_		not modelled	10.9	25	PDB header: hydrolase, dna binding protein Chain: B; PDB Molecule: deoxyguanosinetriphosphate triphosphohydrolase, putative;

28	c2uqb_	Alignment	not modelled	10.9	29	PDBTitle: crystal structure of dntp triphosphohydrolase from thermus2 thermophilus hb8, which is homologous to dgtp triphosphohydrolase
29	d1zkea1	Alignment	not modelled	10.7	37	Fold: ROP-like Superfamily: HP1531-like Family: HP1531-like
30	c2lrsA_	Alignment	not modelled	10.5	25	PDB header: hydrolase Chain: A: PDB Molecule: endoribonuclease dicer homolog 1; PDBTitle: the second dsrbd domain from a. thaliana dicer-like 1
31	d2h62d1	Alignment	not modelled	10.2	45	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Extracellular domain of cell surface receptors
32	d1dv0a_	Alignment	not modelled	10.1	30	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
33	d2b7va1	Alignment	not modelled	10.0	15	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
34	c4bzbB_	Alignment	not modelled	9.7	39	PDB header: hydrolase Chain: B: PDB Molecule: deoxynucleoside triphosphate triphosphohydrolase samhd1; PDBTitle: crystal structure of the tetrameric dgtp-bound samhd12 mutant catalytic core
35	c4yfmA_	Alignment	not modelled	9.5	13	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: class a beta-lactamase from mycobacterium abscessus
36	c2ah6B_	Alignment	not modelled	9.2	14	PDB header: transferase Chain: B: PDB Molecule: bh1595, unknown conserved protein; PDBTitle: crystal structure of a putative cobalamin adenosyltransferase (bh1595)2 from bacillus halodurans c-125 at 1.60 a resolution
37	d2b7ta1	Alignment	not modelled	9.0	16	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
38	c5npgA_	Alignment	not modelled	8.9	19	PDB header: rna binding protein Chain: A: PDB Molecule: loquacious, isoform f; PDBTitle: solution structure of drosophila melanogaster loquacious dsrbd1
39	d1oqa2	Alignment	not modelled	8.7	30	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
40	c2m6oA_	Alignment	not modelled	8.3	19	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the actinobacterial transcription factor rbpa binds to the principal2 sigma subunit of rna polymerase
41	c6em5l_	Alignment	not modelled	8.2	47	PDB header: ribosome Chain: L: PDB Molecule: 60s ribosomal protein l13-a; PDBTitle: state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
42	c6brhA_	Alignment	not modelled	8.2	38	PDB header: hydrolase Chain: A: PDB Molecule: deoxynucleoside triphosphate triphosphohydrolase samhd1; PDBTitle: the sam domain of mouse samhd1 is critical for its activation and2 regulation
43	d1nlwe_	Alignment	not modelled	8.1	19	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
44	c6htuA_	Alignment	not modelled	8.1	22	PDB header: rna binding protein Chain: A: PDB Molecule: double-stranded rna-binding protein staufen homolog 1; PDBTitle: structure of hstau1 dsrbd3-4 in complex with arf1 rna
45	d1uhza_	Alignment	not modelled	8.0	15	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
46	d2v3za1	Alignment	not modelled	7.9	29	Fold: Ribonuclease H-like motif Superfamily: Creatinase/prolidase N-terminal domain Family: Creatinase/prolidase N-terminal domain
47	c2pgsA_	Alignment	not modelled	7.7	25	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyguanosinetriphosphate triphosphohydrolase; PDBTitle: crystal structure of a putative deoxyguanosinetriphosphate2 triphosphohydrolase from pseudomonas syringae pv. phaseolicola 1448a
48	d1a0aa_	Alignment	not modelled	7.7	24	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
49	c6as4C_	Alignment	not modelled	7.3	47	PDB header: viral protein Chain: C: PDB Molecule: nhis acre1 anti-crispr protein; PDBTitle: structure of a phage anti-crispr protein
50	c5fcmB_	Alignment	not modelled	7.3	33	PDB header: cell cycle Chain: B: PDB Molecule: basal body protein; PDBTitle: crbld10-n 1-70
51	c2mz8A_	Alignment	not modelled	7.2	31	PDB header: transcription regulator Chain: A: PDB Molecule: sigma factor-binding protein crl; PDBTitle: solution nmr structure of salmonella typhimurium transcriptional2 regulator protein crl
52	c2ahpB_	Alignment	not modelled	7.1	40	PDB header: de novo protein Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4 leucine zipper, mutation of lys15 to epsilon-azido-lys
53	d1e4qa_	Alignment	not modelled	7.0	33	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin

54	c3rpiA	Alignment	not modelled	7.0	28	PDB header: transcription regulator Chain: A: PDB Molecule: curlin genes transcriptional regulator; PDBTitle: structure of a curlin genes transcriptional regulator protein from2 proteus mirabilis hi4320.
55	d2heka1	Alignment	not modelled	7.0	25	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
56	d2dula1	Alignment	not modelled	7.0	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TRM1-like
57	c3cveC	Alignment	not modelled	7.0	29	PDB header: signaling protein Chain: C: PDB Molecule: homer protein homolog 1; PDBTitle: crystal structure of the carboxy terminus of homer1
58	c2ahpA	Alignment	not modelled	6.9	40	PDB header: de novo protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4 leucine zipper, mutation of lys15 to epsilon-azido-lys
59	c3cg5A	Alignment	not modelled	6.8	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of the covalent adduct formed between tb2 b-lactamase and clavulanate
60	c5ao4D	Alignment	not modelled	6.7	38	PDB header: hydrolase Chain: D: PDB Molecule: deoxynucleoside triphosphate triphosphohydrolase samhd1; PDBTitle: crystal structure of in vitro phosphorylated human samhd1 (amino acid2 residues 115-626) bound to gtp
61	c1vq0A	Alignment	not modelled	6.6	31	PDB header: chaperone Chain: A: PDB Molecule: 33 kda chaperonin; PDBTitle: crystal structure of 33 kda chaperonin (heat shock protein 33 homolog)2 (hsp33) (tm1394) from thermotoga maritima at 2.20 a resolution
62	c3pltB	Alignment	not modelled	6.6	21	PDB header: structural protein Chain: B: PDB Molecule: sphingolipid long chain base-responsive protein lsp1; PDBTitle: crystal structure of lsp1 from saccharomyces cerevisiae
63	c4dbgB	Alignment	not modelled	6.4	16	PDB header: ligase Chain: B: PDB Molecule: ring finger protein 31; PDBTitle: crystal structure of hoil-1-ubl complexed with a hoip-uba derivative
64	c4eo1A	Alignment	not modelled	6.4	78	PDB header: viral protein Chain: A: PDB Molecule: attachment protein g3p; PDBTitle: crystal structure of the tola binding domain from the filamentous2 phage ike
65	d1an2a	Alignment	not modelled	6.3	19	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
66	d1btea	Alignment	not modelled	6.2	45	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Extracellular domain of cell surface receptors
67	c5cwsL	Alignment	not modelled	6.2	59	PDB header: protein transport Chain: L: PDB Molecule: nucleoporin nic96; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
68	c5cwsF	Alignment	not modelled	6.2	59	PDB header: protein transport Chain: F: PDB Molecule: nucleoporin nic96; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
69	c1zhcA	Alignment	not modelled	6.1	9	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein hp1242; PDBTitle: solution structure of hp1242 from helicobacter pylori
70	c2x9aA	Alignment	not modelled	6.1	33	PDB header: viral protein Chain: A: PDB Molecule: attachment protein g3p; PDBTitle: crystal structure of g3p from phage if1 in complex with its2 coreceptor, the c-terminal domain of tola
71	c3kowH	Alignment	not modelled	6.1	43	PDB header: metal binding protein Chain: H: PDB Molecule: d-ornithine aminomutase s component; PDBTitle: crystal structure of ornithine 4,5 aminomutase backsoaked complex
72	c2o6ia	Alignment	not modelled	6.1	33	PDB header: hydrolase Chain: A: PDB Molecule: hd domain protein; PDBTitle: structure of an enterococcus faecalis hd domain phosphohydrolase
73	d2o6ia1	Alignment	not modelled	6.1	33	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
74	c4a18A	Alignment	not modelled	6.0	46	PDB header: ribosome Chain: A: PDB Molecule: ribosomal protein l37; PDBTitle: t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1
75	c5gnjl	Alignment	not modelled	6.0	24	PDB header: dna binding protein/dna Chain: I: PDB Molecule: transcription factor myc2; PDBTitle: structure of a transcription factor and dna complex
76	d1pm4a	Alignment	not modelled	6.0	57	Fold: Superantigen (mitogen) Ypm Superfamily: Superantigen (mitogen) Ypm Family: Superantigen (mitogen) Ypm
77	c5dv7C	Alignment	not modelled	6.0	16	PDB header: rna binding protein Chain: C: PDB Molecule: interleukin enhancer-binding factor 3; PDBTitle: crystal structure of nf90 tandem dsrbds with dsrna
78	c3bg2A	Alignment	not modelled	5.9	17	PDB header: hydrolase Chain: A: PDB Molecule: dgtp triphosphohydrolase; PDBTitle: crystal structure of deoxyguanosinetriphosphate triphosphohydrolase2 from flavobacterium sp. med217 PDB header: lyase

79	c4u49B_	Alignment	not modelled	5.9	29	Chain: B: PDB Molecule: pectate lyase; PDBTitle: crystal structure of pectate lyase pel3 from pectobacterium2 carotovorum with two monomers in the a.u
80	c3adlA_	Alignment	not modelled	5.7	19	PDB header: gene regulation/rna Chain: A: PDB Molecule: risc-loading complex subunit tarbp2; PDBTitle: structure of trbp2 and its molecule implications for mirna processing
81	c3nrxB_	Alignment	not modelled	5.7	22	PDB header: protein binding Chain: B: PDB Molecule: protein regulator of cytokinesis 1; PDBTitle: insights into anti-parallel microtubule crosslinking by prc1, a2 conserved non-motor microtubule binding protein
82	c4bp9A_	Alignment	not modelled	5.6	16	PDB header: hydrolase Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form
83	c6exnD_	Alignment	not modelled	5.5	29	PDB header: splicing Chain: D: PDB Molecule: pre-mrna-splicing factor cwc16; PDBTitle: post-catalytic p complex spliceosome with 3' splice site docked
84	d2nuga2	Alignment	not modelled	5.5	19	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
85	c2g2dA_	Alignment	not modelled	5.4	17	PDB header: transferase Chain: A: PDB Molecule: atp:cobalamin adenosyltransferase; PDBTitle: crystal structure of a putative pduo-type atp:cobalamin2 adenosyltransferase from mycobacterium tuberculosis
86	c3ra3B_	Alignment	not modelled	5.4	41	PDB header: de novo protein Chain: B: PDB Molecule: p2f; PDBTitle: crystal structure of a section of a de novo design gigadalton protein2 fibre
87	d1di2a_	Alignment	not modelled	5.2	25	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
88	d2sh1a_	Alignment	not modelled	5.2	23	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
89	d1rtya_	Alignment	not modelled	5.1	18	Fold: Ferritin-like Superfamily: Cobalamin adenosyltransferase-like Family: Cobalamin adenosyltransferase
90	c5fjaA_	Alignment	not modelled	5.1	43	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase iii subunit rpc1; PDBTitle: cryo-em structure of yeast rna polymerase iii at 4.7 a
91	c6j05B_	Alignment	not modelled	5.1	18	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator arsr; PDBTitle: structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression