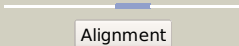





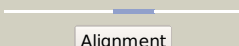
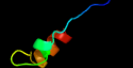
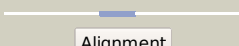

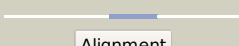
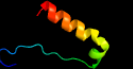
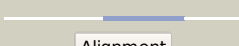
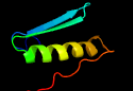





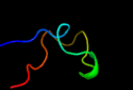

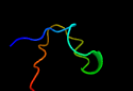


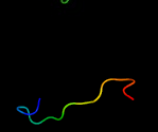


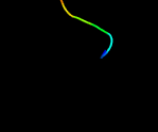





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3258c_(-)_3638808_3639299
Date	Thu Aug 8 16:20:46 BST 2019
Unique Job ID	84273db5fcd5d40e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kysB_	 Alignment		24.4	41	PDB header: transcription/protein binding Chain: B: PDB Molecule: 65 kda yes-associated protein; PDBTitle: crystal structure of human yap and tead complex
2	c3j20E_	 Alignment		23.4	31	PDB header: ribosome Chain: E: PDB Molecule: 30s ribosomal protein s4e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
3	d2r8oa2	 Alignment		22.1	29	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
4	d1cw0a_	 Alignment		22.0	17	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
5	c2xzmW_	 Alignment		21.5	35	PDB header: ribosome Chain: W: PDB Molecule: 40s ribosomal protein s4; 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 1
6	d1bs0a_	 Alignment		21.3	24	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
7	d1wjwa_	 Alignment		20.5	11	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
8	c5xyiE_	 Alignment		20.3	46	PDB header: ribosome Chain: E: PDB Molecule: 40s ribosomal protein s4; PDBTitle: small subunit of trichomonas vaginalis ribosome
9	d1xbta2	 Alignment		17.5	29	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
10	c3u5cE_	 Alignment		17.4	31	PDB header: ribosome Chain: E: PDB Molecule: 40s ribosomal protein s4-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
11	c5xxuE_	 Alignment		16.8	38	PDB header: ribosome Chain: E: PDB Molecule: ribosomal protein es4; PDBTitle: small subunit of toxoplasma gondii ribosome

12	c3ahhA	Alignment		16.7	15	PDB header: lyase Chain: A: PDB Molecule: xylulose 5-phosphate/fructose 6-phosphate phosphoketolase; PDBTitle: h142a mutant of phosphoketolase from bifidobacterium breve complexed2 with acetyl thiamine diphosphate
13	d1gpua1	Alignment		15.7	27	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
14	d1oi1a1	Alignment		15.6	20	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
15	c3r3pB	Alignment		15.2	8	PDB header: hydrolase Chain: B: PDB Molecule: mobile intron protein; PDBTitle: homing endonuclease i-bth0305i catalytic domain
16	d1yf2a2	Alignment		14.0	33	Fold: DNA methylase specificity domain Superfamily: DNA methylase specificity domain Family: Type I restriction modification DNA specificity domain
17	d2b8ta2	Alignment		14.0	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
18	c2kywA	Alignment		13.8	45	PDB header: cell adhesion Chain: A: PDB Molecule: adhesion exoprotein; PDBTitle: solution nmr structure of a domain of adhesion exoprotein from2 pediococcus pentosaceus, northeast structural genomics consortium3 target ptr41o
19	c3hr1A	Alignment		12.5	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: endonuclease-like protein; PDBTitle: crystal structure of a putative endonuclease-like protein (ngo0050)2 from neisseria gonorrhoeae
20	c4o3vA	Alignment		12.2	18	PDB header: protein transport Chain: A: PDB Molecule: virb8-like protein of type iv secretion system; PDBTitle: crystal structure of a virb8-like protein of type iv secretion system2 from rickettsia typhi
21	c5abvF	Alignment	not modelled	11.3	56	PDB header: translation Chain: F: PDB Molecule: gh11071p; PDBTitle: complex of d. melanogaster eif4e with the 4e-binding2 protein mextli
22	c1xx6B	Alignment	not modelled	11.1	18	PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: x-ray structure of clostridium acetobutylicum thymidine kinase with2 adp. northeast structural genomics target car26.
23	c2n5dA	Alignment	not modelled	10.9	44	PDB header: protein binding Chain: A: PDB Molecule: fusion protein of two pks domains; PDBTitle: nmr structure of pks domains
24	c3nqjA	Alignment	not modelled	10.4	60	PDB header: dna binding protein Chain: A: PDB Molecule: histone h3-like centromeric protein a; PDBTitle: crystal structure of (cenp-a/h4)2 heterotetramer
25	c2hueB	Alignment	not modelled	10.2	60	PDB header: dna binding protein Chain: B: PDB Molecule: histone h3; PDBTitle: structure of the h3-h4 chaperone asf1 bound to histones h3 and h4
26	d1id3a	Alignment	not modelled	10.2	45	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
27	c3nquA	Alignment	not modelled	9.9	55	PDB header: dna binding protein Chain: A: PDB Molecule: histone h3-like centromeric protein a; PDBTitle: crystal structure of partially trypsinized (cenp-a/h4)2 heterotetramer
28	d1dw0a	Alignment	not modelled	9.8	36	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
29	d1e8ga1	Alignment	not modelled	9.4	33	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like

30	c2xcmE	Alignment	not modelled	9.2	26	PDB header: chaperone/protein binding Chain: E: PDB Molecule: rar1; PDBTitle: complex of hsp90 n-terminal, sgt1 cs and rar1 chord2 domain
31	d1pvma3	Alignment	not modelled	9.1	57	Fold: Rubredoxin-like Superfamily: Hypothetical protein Ta0289 C-terminal domain Family: Hypothetical protein Ta0289 C-terminal domain
32	c2yfwC	Alignment	not modelled	9.1	60	PDB header: cell cycle Chain: C: PDB Molecule: histone h3-like centromeric protein cse4; PDBTitle: heterotetramer structure of kluyveromyces lactis cse4,h4
33	c6hrhA	Alignment	not modelled	8.9	28	PDB header: oxidoreductase Chain: A: PDB Molecule: 5-aminolevulinate synthase, erythroid-specific, PDBTitle: structure of human erythroid-specific 5'-aminolevulinate synthase,2 alas2
34	d1p3ie	Alignment	not modelled	8.7	60	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
35	d1yf2a1	Alignment	not modelled	8.6	40	Fold: DNA methylase specificity domain Superfamily: DNA methylase specificity domain Family: Type I restriction modification DNA specificity domain
36	c6e0cA	Alignment	not modelled	8.5	55	PDB header: nuclear protein Chain: A: PDB Molecule: histone h3-like centromeric protein a; PDBTitle: cryo-em structure of the cenp-a nucleosome (w601) in complex with a2 single chain antibody fragment
37	d1w8oa1	Alignment	not modelled	8.4	22	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
38	c2hwkA	Alignment	not modelled	8.2	29	PDB header: hydrolase Chain: A: PDB Molecule: helicase nsp2; PDBTitle: crystal structure of venezuelan equine encephalitis alphavirus nsp22 protease domain
39	d1eqzq	Alignment	not modelled	8.1	60	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
40	d1r9ja2	Alignment	not modelled	8.0	21	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
41	d2f21a1	Alignment	not modelled	7.9	45	Fold: WW domain-like Superfamily: WW domain Family: WW domain
42	c3trkA	Alignment	not modelled	7.9	36	PDB header: hydrolase Chain: A: PDB Molecule: nonstructural polyprotein; PDBTitle: structure of the chikungunya virus nsp2 protease
43	c3okgB	Alignment	not modelled	7.9	56	PDB header: dna binding protein Chain: B: PDB Molecule: restriction endonuclease s subunits; PDBTitle: crystal structure of hdsd subunit from thermoanaerobacter2 tengcongensis
44	c2l5aA	Alignment	not modelled	7.9	60	PDB header: nuclear protein Chain: A: PDB Molecule: histone h3-like centromeric protein cse4, protein scm3, PDBTitle: structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3
45	d1bhia	Alignment	not modelled	7.8	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
46	c6nf8n	Alignment	not modelled	7.8	57	PDB header: ribosomal protein Chain: N: PDB Molecule: 28s ribosomal protein s14, mitochondrial; PDBTitle: structure of human mitochondrial translation initiation factor 3 bound2 to the small ribosomal subunit -class i
47	d1fc4a	Alignment	not modelled	7.7	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
48	c5aj3n	Alignment	not modelled	7.6	50	PDB header: ribosome Chain: N: PDB Molecule: mitoribosomal protein us14m, mrps14; PDBTitle: structure of the small subunit of the mammalian mitoribosome
49	d1tzyc	Alignment	not modelled	7.5	55	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
50	c2lb0A	Alignment	not modelled	7.3	50	PDB header: signaling protein/transcription Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf1; PDBTitle: structure of the first ww domain of human smurf1 in complex with a di-2 phosphorylated human smad1 derived peptide
51	c2lazA	Alignment	not modelled	7.3	50	PDB header: signaling protein/transcription Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf1; PDBTitle: structure of the first ww domain of human smurf1 in complex with a2 mono-phosphorylated human smad1 derived peptide
52	c4k3vA	Alignment	not modelled	7.1	11	PDB header: transport protein Chain: A: PDB Molecule: abc superfamily atp binding cassette transporter, binding PDBTitle: structure of staphylococcus aureus mntc
53	d1kx5a	Alignment	not modelled	7.1	60	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
54	c5vrbb	Alignment	not modelled	7.1	26	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of a transketolase from neisseria gonorrhoeae
55	c4wrnB	Alignment	not modelled	6.7	26	PDB header: structural protein Chain: B: PDB Molecule: maltose-binding periplasmic protein,uromodulin;

						PDBTitle: crystal structure of the polymerization region of human2 uromodulin/tamm-horsfall protein
56	c6c23Q_	Alignment	not modelled	6.6	20	PDB header: gene regulation Chain: Q: PDB Molecule: polycomb protein suz12; PDBTitle: cryo-em structure of prc2 bound to cofactors aebp2 and jarid2 in the2 compact active state
57	d2uuyb1	Alignment	not modelled	6.6	57	Fold: BPTI-like Superfamily: BPTI-like Family: Tick tryptase inhibitor-like
58	c3nctC_	Alignment	not modelled	6.6	33	PDB header: dna binding protein, chaperone Chain: C: PDB Molecule: protein psib; PDBTitle: x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
59	d1gu2a_	Alignment	not modelled	6.5	29	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
60	c6c24Q_	Alignment	not modelled	6.5	20	PDB header: gene regulation Chain: Q: PDB Molecule: polycomb protein suz12; PDBTitle: cryo-em structure of prc2 bound to cofactors aebp2 and jarid2 in the2 extended active state
61	c3n3fB_	Alignment	not modelled	6.4	21	PDB header: protein binding Chain: B: PDB Molecule: collagen alpha-1(xv) chain; PDBTitle: crystal structure of the human collagen xv trimerization domain: a2 potent trimerizing unit common to multiplexin collagens
62	c3komB_	Alignment	not modelled	6.4	35	PDB header: transferase Chain: B: PDB Molecule: transketolase; PDBTitle: crystal structure of apo transketolase from francisella tularensis
63	c2uuxA_	Alignment	not modelled	6.3	45	PDB header: inhibitor Chain: A: PDB Molecule: tryptase inhibitor; PDBTitle: structure of the tryptase inhibitor tdpi from a tick
64	d1wjsa_	Alignment	not modelled	6.3	21	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
65	c3hshA_	Alignment	not modelled	6.3	15	PDB header: protein binding Chain: A: PDB Molecule: collagen alpha-1(xviii) chain; PDBTitle: crystal structure of human collagen xviii trimerization domain2 (tetragonal crystal form)
66	d2ieaa2	Alignment	not modelled	6.1	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
67	c5v6fA_	Alignment	not modelled	6.1	23	PDB header: sugar binding protein Chain: A: PDB Molecule: hemolysin-related protein; PDBTitle: crystal structure of the second beta-prism domain of rbmc from v.2 cholerae bound to mannitriose
68	d2ozla1	Alignment	not modelled	5.9	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
69	d1oz2a1	Alignment	not modelled	5.9	13	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
70	c2orvB_	Alignment	not modelled	5.8	29	PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: human thymidine kinase 1 in complex with tp4a
71	d1oz2a2	Alignment	not modelled	5.7	21	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: MBT repeat
72	c5jayB_	Alignment	not modelled	5.7	26	PDB header: transferase Chain: B: PDB Molecule: 8-amino-7-oxonanoate synthase; PDBTitle: crystal structure of an 8-amino-7-oxonanoate synthase from2 burkholderia xenovorans
73	d1umga_	Alignment	not modelled	5.7	23	Fold: Sulfolobus fructose-1,6-bisphosphatase-like Superfamily: Sulfolobus fructose-1,6-bisphosphatase-like Family: Sulfolobus fructose-1,6-bisphosphatase-like
74	c4cgbE_	Alignment	not modelled	5.6	75	PDB header: cell cycle Chain: E: PDB Molecule: echinoderm microtubule-associated protein-like 2; PDBTitle: crystal structure of the trimerization domain of eml2
75	d1wvfa1	Alignment	not modelled	5.6	47	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
76	c5h6sB_	Alignment	not modelled	5.5	26	PDB header: hydrolase Chain: B: PDB Molecule: amidase; PDBTitle: crystal structure of hydrazidase s179a mutant complexed with a2 substrate
77	d1x64a2	Alignment	not modelled	5.5	44	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
78	c5n02B_	Alignment	not modelled	5.4	18	PDB header: lyase Chain: B: PDB Molecule: glutaconate coa-transferase family, subunit b; PDBTitle: crystal structure of the decarboxylase aiba/aibb c56s variant
79	c3hqtB_	Alignment	not modelled	5.3	9	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
80	c3t2dA_	Alignment	not modelled	5.3	29	PDB header: lyase, hydrolase Chain: A: PDB Molecule: fructose-1,6-bisphosphate aldolase/phosphatase; PDBTitle: fructose-1,6-bisphosphate aldolase/phosphatase from thermoproteus2 neutrophilus, fbp-bound form
81	d2zjrl1	Alignment	not modelled	5.3	75	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11

82	d1p5dx4	Alignment	not modelled	5.3	31	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
83	c3rimA_	Alignment	not modelled	5.2	17	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: crystal structure of mycobacterium tuberculosis transketolase2 (rv1449c)
84	c2kxqA_	Alignment	not modelled	5.2	33	PDB header: protein binding Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf2; PDBTitle: solution structure of smurf2 ww2 and ww3 bound to smad7 py motif2 containing peptide
85	c5vobE_	Alignment	not modelled	5.1	60	PDB header: viral protein/immune system Chain: E: PDB Molecule: envelope glycoprotein ul131a; PDBTitle: crystal structure of hcmv pentamer in complex with neutralizing2 antibody 8i21
86	c2o1xA_	Alignment	not modelled	5.1	17	PDB header: transferase Chain: A: PDB Molecule: 1-deoxy-d-xylulose-5-phosphate synthase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from deinococcus2 radiodurans