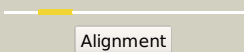
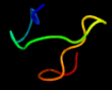
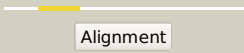
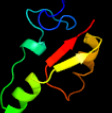


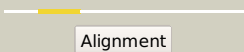

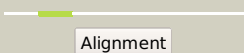

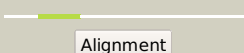



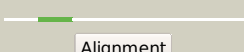

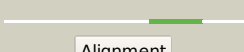

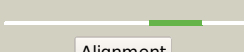

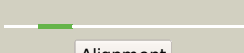



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0622_(-)_715373_716320
Date	Fri Jul 26 01:50:18 BST 2019
Unique Job ID	e43ef4750064cbfe

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cngC_	 Alignment		78.7	45	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
2	d1vdda_	 Alignment		77.2	20	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
3	d1iq8a3	 Alignment		74.4	24	Fold: PUA domain-like Superfamily: PUA domain-like Family: PUA domain
4	c1vddC_	 Alignment		71.8	20	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
5	d1pfva3	 Alignment		67.9	32	Fold: Rubredoxin-like Superfamily: Methionyl-tRNA synthetase (MetRS), Zn-domain Family: Methionyl-tRNA synthetase (MetRS), Zn-domain
6	c5zvqA_	 Alignment		65.4	25	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
7	c3zv0D_	 Alignment		64.6	20	PDB header: cell cycle Chain: D: PDB Molecule: h/aca ribonucleoprotein complex subunit 4; PDBTitle: structure of the shq1p-cbf5p complex
8	c5flml_	 Alignment		59.6	25	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: structure of transcribing mammalian rna polymerase ii
9	c1zxuA_	 Alignment		56.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: at5g01750 protein; PDBTitle: x-ray structure of protein from arabidopsis thaliana at5g01750
10	d2q4ma1	 Alignment		56.0	18	Fold: Tubby C-terminal domain-like Superfamily: Tubby C-terminal domain-like Family: At5g01750-like
11	c6cnbR_	 Alignment		53.9	33	PDB header: transcription/dna Chain: R: PDB Molecule: transcription factor iiib 70 kda subunit,tata-box-binding PDBTitle: yeast rna polymerase iii initial transcribing complex

12	c1i3ql_	Alignment		51.3	29	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii 14.2kd PDBTitle: rna polymerase ii crystal form i at 3.1 a resolution
13	c3gzkA_	Alignment		50.4	13	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: structure of a. acidocaldarius cellulase cela
14	d1r3ea1	Alignment		47.8	22	Fold: PUA domain-like Superfamily: PUA domain-like Family: PUA domain
15	c3ve5D_	Alignment		46.6	16	PDB header: recombination Chain: D: PDB Molecule: recombination protein recr; PDBTitle: structure of recombination mediator protein recr16-196 deletion mutant
16	d1k8ia2	Alignment		46.0	44	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
17	d2as0a1	Alignment		43.5	35	Fold: PUA domain-like Superfamily: PUA domain-like Family: Hypothetical RNA methyltransferase domain (HRMD)
18	c3h0gl_	Alignment		39.0	24	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
19	c2p9rA_	Alignment		38.1	21	PDB header: signaling protein Chain: A: PDB Molecule: alpha-2-macroglobulin; PDBTitle: human alpha2-macroglobulin is composed of multiple domains,2 as predicted by homology with complement component c3
20	c5z2vB_	Alignment		37.6	24	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
21	c4c2mX_	Alignment	not modelled	36.7	38	PDB header: transcription Chain: X: PDB Molecule: dna-directed rna polymerase i subunit rpa12; PDBTitle: structure of rna polymerase i at 2.8 a resolution
22	d2apoa1	Alignment	not modelled	36.6	32	Fold: PUA domain-like Superfamily: PUA domain-like Family: PUA domain
23	c2gb5B_	Alignment	not modelled	35.7	38	PDB header: hydrolase Chain: B: PDB Molecule: nadh pyrophosphatase; PDBTitle: crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
24	c3hkzP_	Alignment	not modelled	34.7	50	PDB header: transferase Chain: P: PDB Molecule: dna-directed rna polymerase subunit p; PDBTitle: the x-ray crystal structure of rna polymerase from archaea
25	c6o3pA_	Alignment	not modelled	34.0	21	PDB header: hydrolase Chain: A: PDB Molecule: peroxisomal nadh pyrophosphatase nudt12; PDBTitle: crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
26	d2fiya1	Alignment	not modelled	31.3	35	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
27	d2j0151	Alignment	not modelled	29.5	33	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
28	c3k7aM_	Alignment	not modelled	29.1	28	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of an rna polymerase ii-tfiib complex

29	c4zzkA	Alignment	not modelled	29.0	17	PDB header: motor protein Chain: A: PDB Molecule: basal-body rod modification protein flgd; PDBTitle: crystal structure of truncated flgd (monoclinic form) from the human2 pathogen helicobacter pylori
30	d2k4xa1	Alignment	not modelled	28.7	63	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein S27a
31	c1oazH	Alignment	not modelled	28.1	16	PDB header: immune system Chain: H: PDB Molecule: immunoglobulin e; PDBTitle: ige fv spe7 complexed with a recombinant thioredoxin
32	d2ey4a1	Alignment	not modelled	27.2	23	Fold: PUA domain-like Superfamily: PUA domain-like Family: PUA domain
33	d1ooya1	Alignment	not modelled	26.1	11	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like
34	d2zjrz1	Alignment	not modelled	26.0	25	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
35	c6em5l	Alignment	not modelled	25.8	17	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
36	c5fja_	Alignment	not modelled	25.8	45	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase iii subunit rpc10; PDBTitle: cryo-em structure of yeast rna polymerase iii at 4.7 a
37	c3j3v0_	Alignment	not modelled	25.4	38	PDB header: ribosome Chain: 0: PDB Molecule: 50s ribosomal protein l32; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
38	d1q7ha1	Alignment	not modelled	25.0	23	Fold: PUA domain-like Superfamily: PUA domain-like Family: PUA domain
39	c2apoA	Alignment	not modelled	24.9	26	PDB header: isomerase/rna binding protein Chain: A: PDB Molecule: probable trna pseudouridine synthase b; PDBTitle: crystal structure of the methanococcus jannaschii cbf52 nop10 complex
40	d1hdma2	Alignment	not modelled	24.1	29	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
41	c4bpo9	Alignment	not modelled	23.2	47	PDB header: ribosome Chain: 9: PDB Molecule: 40s ribosomal protein rps31e; PDBTitle: the crystal structure of the eukaryotic 40s ribosomal subunit in2 complex with eif1 and eif1a - complex 3
42	d1x63a2	Alignment	not modelled	22.7	56	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
43	c2ey4A	Alignment	not modelled	21.2	26	PDB header: isomerase/biosynthetic protein Chain: A: PDB Molecule: probable trna pseudouridine synthase b; PDBTitle: crystal structure of a cbf5-nop10-gar1 complex
44	c2wjvA	Alignment	not modelled	20.9	30	PDB header: hydrolase Chain: A: PDB Molecule: regulator of nonsense transcripts 1; PDBTitle: crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 orthorhombic form
45	c4v1oM	Alignment	not modelled	20.9	28	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: architecture of the rna polymerase ii-mediator core transcription2 initiation complex
46	c2k9yB	Alignment	not modelled	19.3	55	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
47	c2k9yA	Alignment	not modelled	19.3	55	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
48	d2cu8a1	Alignment	not modelled	19.1	24	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
49	c4iu2A	Alignment	not modelled	19.0	14	PDB header: structural protein Chain: A: PDB Molecule: cell-wall anchoring protein; PDBTitle: cohesin-dockerin -x domain complex from ruminococcus flavefacience
50	d1owqa2	Alignment	not modelled	19.0	28	Fold: FKBP-like Superfamily: Chitinase insertion domain Family: Chitinase insertion domain
51	d1zbfa1	Alignment	not modelled	18.8	29	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
52	d2pi6a2	Alignment	not modelled	17.1	31	Fold: FKBP-like Superfamily: Chitinase insertion domain Family: Chitinase insertion domain
53	c5waiF	Alignment	not modelled	17.1	25	PDB header: transcription Chain: F: PDB Molecule: polycomb protein suz12; PDBTitle: crystal structure of a suz12-rbbp4-jarid2-aebp2 heterotetrameric2 complex
54	c5fz5M	Alignment	not modelled	16.9	28	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: transcription initiation complex structures elucidate dna opening (cc)
55	c2l7xA	Alignment	not modelled	16.7	31	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein;

						PDBTitle: crimean congo hemorrhagic fever gn zinc finger
56	d1hxa2	Alignment	not modelled	16.7	34	Fold: FKBP-like Superfamily: Chitinase insertion domain Family: Chitinase insertion domain
57	c3wnwB	Alignment	not modelled	16.6	53	PDB header: metal binding protein/transferase Chain: B: PDB Molecule: orff; PDBTitle: crystal structure of lysz from thermus thermophilus complex with lysw
58	c2xz1A	Alignment	not modelled	16.6	30	PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent helicase nam7; PDBTitle: upf1-rna complex
59	c3osvC	Alignment	not modelled	16.4	16	PDB header: structural protein Chain: C: PDB Molecule: flagellar basal-body rod modification protein flgd; PDBTitle: the crytsal structure of flgd from p. aeruginosa
60	d1k78a1	Alignment	not modelled	16.4	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
61	c4pchE	Alignment	not modelled	16.0	50	PDB header: viral protein Chain: E: PDB Molecule: vp1; PDBTitle: structure of human polyomavirus 7 (hpyv7) vp1 pentamer
62	c4pcgD	Alignment	not modelled	15.9	50	PDB header: viral protein Chain: D: PDB Molecule: vp1; PDBTitle: structure of human polyomavirus 6 (hpyv6) vp1 pentamer
63	c2q07A	Alignment	not modelled	15.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein af0587; PDBTitle: crystal structure of af0587, a protein of unknown function
64	c3k1fM	Alignment	not modelled	15.5	33	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of rna polymerase ii in complex with tfiib
65	c6elhA	Alignment	not modelled	15.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide reductase; PDBTitle: low resolution structure of neisseria meningitidis qnor
66	d1dgsa1	Alignment	not modelled	15.3	26	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
67	d2qam01	Alignment	not modelled	14.9	22	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
68	d2o14a1	Alignment	not modelled	14.5	29	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: YxiM N-terminal domain-like
69	c4giwP	Alignment	not modelled	14.5	50	PDB header: transcription Chain: P: PDB Molecule: dna-directed rna polymerase subunit p; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
70	c2g9tT	Alignment	not modelled	14.3	36	PDB header: viral protein Chain: T: PDB Molecule: PDBTitle: crystal structure of the sars coronavirus nsp10 at 2.1a
71	c3bwrC	Alignment	not modelled	14.1	50	PDB header: viral protein Chain: C: PDB Molecule: capsid protein vp1; PDBTitle: sv40 vp1 pentamer in complex with gm1 oligosaccharide
72	c4u62D	Alignment	not modelled	13.8	43	PDB header: viral protein Chain: D: PDB Molecule: structural protein vp1; PDBTitle: trichodysplasia spinulosa-associated polyomavirus (tspyv) vp1 in2 complex with 3'-sialyllactose
73	d1vpsa	Alignment	not modelled	13.7	50	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group I dsDNA viruses Family: Papovaviridae-like VP
74	c2elpA	Alignment	not modelled	13.7	50	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
75	d1tfva2	Alignment	not modelled	13.6	28	Fold: FKBP-like Superfamily: Chitinase insertion domain Family: Chitinase insertion domain
76	c4fmiN	Alignment	not modelled	13.5	43	PDB header: viral protein Chain: N: PDB Molecule: vp1; PDBTitle: merkel cell polyomavirus vp1 in complex with 3'-sialyllactosamine
77	c4mbyB	Alignment	not modelled	13.5	43	PDB header: viral protein Chain: B: PDB Molecule: major capsid protein vp1; PDBTitle: structure of b-lymphotropic polyomavirus vp1 in complex with 3'-2 sialyllactose
78	c3uv1B	Alignment	not modelled	13.4	13	PDB header: allergen Chain: B: PDB Molecule: der f 7 allergen; PDBTitle: crystal structure a major allergen from dust mite
79	c2iykB	Alignment	not modelled	13.4	30	PDB header: hydrolase Chain: B: PDB Molecule: regulator of nonsense transcripts 1; PDBTitle: crystal structure of the upf2-interacting domain of2 nonsense mediated mrna decay factor upf1
80	d1y0ja1	Alignment	not modelled	13.4	48	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
81	d2gmga1	Alignment	not modelled	13.0	41	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF0610-like
82	c4u3eA	Alignment	not modelled	12.9	31	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside triphosphate reductase; PDBTitle: anaerobic ribonucleotide reductase

83	c3iysA_	Alignment	not modelled	12.8	43	PDB header: virus Chain: A: PDB Molecule: major capsid protein vp1; PDBTitle: homology model of avian polyomavirus asymmetric unit
84	c3t0yD_	Alignment	not modelled	12.7	46	PDB header: transcription regulator/protein binding Chain: D: PDB Molecule: nepr; PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
85	c3t0yB_	Alignment	not modelled	12.5	46	PDB header: transcription regulator/protein binding Chain: B: PDB Molecule: nepr; PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
86	c6egxA_	Alignment	not modelled	12.5	26	PDB header: virus Chain: A: PDB Molecule: structural protein vp1; PDBTitle: sacbrood virus of honeybee - expansion state i
87	c6flkA_	Alignment	not modelled	12.5	16	PDB header: structural protein Chain: A: PDB Molecule: cep120; PDBTitle: crystal structure of cep120 c2c domain
88	c3s7xC_	Alignment	not modelled	12.4	43	PDB header: viral protein Chain: C: PDB Molecule: major capsid protein vp1; PDBTitle: unassembled washington university polyomavirus vp1 pentamer r198k2 mutant
89	c4acqA_	Alignment	not modelled	12.3	23	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: alpha-2-macroglobulin; PDBTitle: alpha-2 macroglobulin
90	d1pfta_	Alignment	not modelled	12.2	32	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
91	d1rzsA_	Alignment	not modelled	12.1	58	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
92	c4a17Y_	Alignment	not modelled	11.8	30	PDB header: ribosome Chain: Y: PDB Molecule: rpl37a; 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 2.
93	c3c12A_	Alignment	not modelled	11.5	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: flagellar protein; PDBTitle: crystal structure of flgd from xanthomonas campestris:2 insights into the hook capping essential for flagellar3 assembly
94	d1dl6a_	Alignment	not modelled	11.5	33	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
95	c5iy9M_	Alignment	not modelled	11.5	33	PDB header: transcription, transferase/dna/rna Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: human holo-pic in the initial transcribing state (no iis)
96	c2xzn9_	Alignment	not modelled	11.4	42	PDB header: ribosome Chain: 9: PDB Molecule: rps31e; 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
97	d1sva1_	Alignment	not modelled	11.4	50	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group I dsDNA viruses Family: Papovaviridae-like VP
98	c3bd1B_	Alignment	not modelled	11.3	50	PDB header: transcription Chain: B: PDB Molecule: cro protein; PDBTitle: structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
99	c1ze2B_	Alignment	not modelled	11.3	24	PDB header: lyase/rna Chain: B: PDB Molecule: trna pseudouridine synthase b; PDBTitle: conformational change of pseudouridine 55 synthase upon its2 association with rna substrate