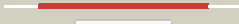



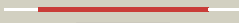

















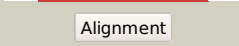
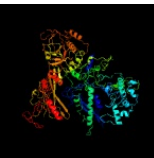

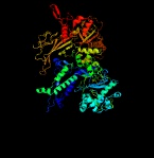


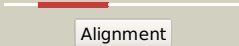


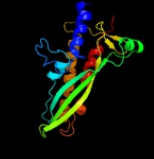



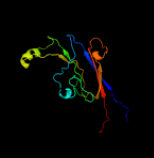
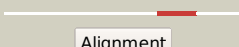

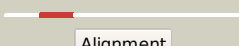

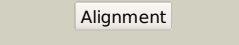



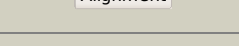
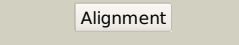
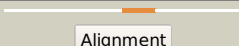
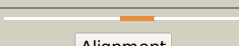


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0667_(rpoB)_759810_763328
Date	Fri Jul 26 01:50:23 BST 2019
Unique Job ID	45c45dc0742dc1a2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lu0C_	 Alignment		100.0	58	PDB header: transferase Chain: C: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: molecular model of escherichia coli core rna polymerase
2	c6j9eC_	 Alignment		100.0	56	PDB header: transcription Chain: C: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: cryo-em structure of xanthomonas oryzae transcription elongation2 complex with nusa and the bacteriophage protein p7
3	c5tw1C_	 Alignment		100.0	93	PDB header: transcription activator/transferase/dna Chain: C: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpA
4	d1smyc_	 Alignment		100.0	52	Fold: beta and beta-prime subunits of DNA dependent RNA-polymerase Superfamily: beta and beta-prime subunits of DNA dependent RNA-polymerase Family: RNA-polymerase beta
5	d1ynjc1	 Alignment		100.0	51	Fold: beta and beta-prime subunits of DNA dependent RNA-polymerase Superfamily: beta and beta-prime subunits of DNA dependent RNA-polymerase Family: RNA-polymerase beta
6	c6dcfc_	 Alignment		100.0	95	PDB header: transcription/dna/antibiotic Chain: C: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rifampicin-resistant rna polymerase and bound3 to kanglemycin a
7	c4c2mQ_	 Alignment		100.0	24	PDB header: transcription Chain: Q: PDB Molecule: dna-directed rna polymerase i subunit rpa135; PDBTitle: structure of rna polymerase i at 2.8 a resolution
8	c3iydC_	 Alignment		100.0	57	PDB header: transcription/dna Chain: C: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
9	c5flmB_	 Alignment		100.0	27	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase ii subunit rpb2; PDBTitle: structure of transcribing mammalian rna polymerase ii
10	c5fj9B_	 Alignment		100.0	27	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase iii subunit rpc2; PDBTitle: cryo-em structure of yeast apo rna polymerase iii at 4.6 a
11	c2pmzB_	 Alignment		100.0	31	PDB header: translation, transferase Chain: B: PDB Molecule: dna-directed rna polymerase subunit b; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus

12	c3h0gN_	 Alignment		100.0	27	PDB header: transcription Chain: N: PDB Molecule: dna-directed rna polymerase ii subunit rpb2; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
13	d1twfb_	 Alignment		100.0	27	Fold: beta and beta-prime subunits of DNA dependent RNA-polymerase Superfamily: beta and beta-prime subunits of DNA dependent RNA-polymerase Family: RNA-polymerase beta
14	c4qiwB_	 Alignment		100.0	31	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
15	c4kbmA_	 Alignment		100.0	99	PDB header: transferase/transcription Chain: A: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: structure of the mtb card/rnap beta subunit b1-b2 domains complex
16	c3mlqD_	 Alignment		100.0	55	PDB header: transferase/transcription Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain
17	c3mlqB_	 Alignment		100.0	44	PDB header: transferase/transcription Chain: B: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain
18	c2ly7A_	 Alignment		100.0	74	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: b-flap domain of rna polymerase (b. subtilis)
19	c3tbiB_	 Alignment		100.0	44	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of t4 gp33 bound to e. coli rnap beta-flap domain
20	c3ltiA_	 Alignment		100.0	50	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-beta4 domains
21	c3qqcA_	 Alignment	not modelled	99.4	22	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase subunit b, dna-directed rna PDBTitle: crystal structure of archaeal spt4/5 bound to the rnap clamp domain
22	c5j1lA_	 Alignment	not modelled	93.5	26	PDB header: hydrolase Chain: A: PDB Molecule: toxR-activated gene (tage); PDBTitle: crystal structure of csd1-csd2 dimer i
23	c2lmcB_	 Alignment	not modelled	92.8	27	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: structure of t7 transcription factor gp2-e. coli rnap jaw domain2 complex
24	c2gu1A_	 Alignment	not modelled	89.9	28	PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae
25	c2hsiB_	 Alignment	not modelled	89.3	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative peptidase m23; PDBTitle: crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
26	c3sluB_	 Alignment	not modelled	84.0	27	PDB header: hydrolase Chain: B: PDB Molecule: m23 peptidase domain protein; PDBTitle: crystal structure of nmb0315
27	c5j1mD_	 Alignment	not modelled	80.6	23	PDB header: hydrolase Chain: D: PDB Molecule: toxR-activated gene (tage); PDBTitle: crystal structure of csd1-csd2 dimer ii
28	d1qwya_	 Alignment	not modelled	80.4	31	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Peptidoglycan hydrolase LytM

29	c4bh5B	Alignment	not modelled	79.7	33	PDB header: cell cycle Chain: B: PDB Molecule: murein hydrolase activator envc; PDBTitle: lytm domain of envc, an activator of cell wall amidases in2 escherichia coli
30	c4rnzA	Alignment	not modelled	74.6	24	PDB header: hydrolase Chain: A: PDB Molecule: conserved hypothetical secreted protein; PDBTitle: structure of helicobacter pylori csd3 from the hexagonal crystal
31	c5gt1A	Alignment	not modelled	73.9	24	PDB header: choline-binding protein Chain: A: PDB Molecule: choline binding protein a; PDBTitle: crystal structure of cbpa from I. salivarius ren
32	c2aujD	Alignment	not modelled	73.4	25	PDB header: transferase Chain: D: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of thermus aquaticus rna polymerase beta'-subunit2 insert
33	c4lxcA	Alignment	not modelled	73.1	29	PDB header: hydrolase Chain: A: PDB Molecule: lysostaphin; PDBTitle: the antimicrobial peptidase lysostaphin from staphylococcus simulans
34	c4qpbB	Alignment	not modelled	71.5	32	PDB header: hydrolase Chain: B: PDB Molecule: lysostaphin; PDBTitle: catalytic domain of the antimicrobial peptidase lysostaphin from2 staphylococcus simulans crystallized in the absence of phosphate
35	c3tufB	Alignment	not modelled	71.3	30	PDB header: signaling protein Chain: B: PDB Molecule: stage ii sporulation protein q; PDBTitle: structure of the spoiii-spoiiiah pore forming complex.
36	c5kvpA	Alignment	not modelled	68.4	22	PDB header: hydrolase Chain: A: PDB Molecule: zoocin a endopeptidase; PDBTitle: solution structure of the catalytic domain of zoocin a
37	c2b44A	Alignment	not modelled	64.3	29	PDB header: hydrolase Chain: A: PDB Molecule: glycyl-glycine endopeptidase lytm; PDBTitle: truncated s. aureus lytm, p 32 2 1 crystal form
38	c3uz0D	Alignment	not modelled	61.5	29	PDB header: transport protein Chain: D: PDB Molecule: stage ii sporulation protein q; PDBTitle: crystal structure of spoiiih and spoiiq complex
39	c2aukA	Alignment	not modelled	56.6	24	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of e. coli rna polymerase beta' g/g' insert
40	d1r46a1	Alignment	not modelled	54.4	24	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
41	c6ekaB	Alignment	not modelled	47.1	86	PDB header: protein fibril Chain: B: PDB Molecule: podospora anserina s mat+ genomic dna chromosome 3, PDBTitle: solid-state mas nmr structure of the helix prion amyloid fibrils
42	c5kqbA	Alignment	not modelled	47.0	26	PDB header: hydrolase Chain: A: PDB Molecule: peptidase m23; PDBTitle: identification and structural characterization of lytu
43	c5b0hB	Alignment	not modelled	44.6	11	PDB header: metal binding protein Chain: B: PDB Molecule: leukocyte cell-derived chemotaxin-2; PDBTitle: crystal structure of human leukocyte cell-derived chemotaxin 2
44	c3nyyA	Alignment	not modelled	44.6	28	PDB header: hydrolase Chain: A: PDB Molecule: putative glycyl-glycine endopeptidase lytm; PDBTitle: crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution
45	c4yk3B	Alignment	not modelled	42.1	30	PDB header: protein binding Chain: B: PDB Molecule: bepe protein; PDBTitle: crystal structure of the bid domain of bepe from bartonella henselae
46	c4yk2B	Alignment	not modelled	42.1	20	PDB header: protein binding Chain: B: PDB Molecule: bartonella effector protein (bep) substrate of virb t4ss; PDBTitle: crystal structure of the bid domain of bep9 from bartonella2 clarridgeiae
47	d2gprra	Alignment	not modelled	42.1	16	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
48	d1glaf	Alignment	not modelled	40.3	20	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
49	d2f3ga	Alignment	not modelled	36.5	20	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
50	d1gprra	Alignment	not modelled	35.9	28	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
51	c2ivfC	Alignment	not modelled	35.0	16	PDB header: oxidoreductase Chain: C: PDB Molecule: ethylbenzene dehydrogenase gamma-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
52	d1uc8a1	Alignment	not modelled	32.3	18	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Lysine biosynthesis enzyme LysX, N-terminal domain
53	c2gtiA	Alignment	not modelled	32.2	16	PDB header: viral protein Chain: A: PDB Molecule: replicase polyprotein 1ab; PDBTitle: mutation of mhv coronavirus non-structural protein nsp15 (f3071) PDB header: protein binding

54	c4yk1A	Alignment	not modelled	29.7	10	Chain: A: PDB Molecule: bartonella effector protein (bep) substrate of virb t4ss; PDBTitle: crystal structure of the bid domain of bep6 from bartonella rochalimae
55	c1wcoN	Alignment	not modelled	29.1	86	PDB header: peptide/antibiotic Chain: N: PDB Molecule: nisin z; PDBTitle: the solution structure of the nisin-lipid ii complex
56	d1y4oa1	Alignment	not modelled	28.8	53	Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
57	c6h5nA	Alignment	not modelled	27.8	27	PDB header: cell invasion Chain: A: PDB Molecule: gametocyte surface protein p45/48; PDBTitle: plasmodium falciparum pfs48/45 c-terminal domain bound to monoclonal2 antibody 85rf45.1
58	d1n26a2	Alignment	not modelled	26.6	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
59	c4p6vA	Alignment	not modelled	25.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit a; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
60	d1gm5a4	Alignment	not modelled	25.6	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
61	c2db3D	Alignment	not modelled	24.8	33	PDB header: hydrolase/rna Chain: D: PDB Molecule: atp-dependent rna helicase vasa; PDBTitle: structural basis for rna unwinding by the dead-box protein2 drosophila vasa
62	c4iqzD	Alignment	not modelled	24.2	16	PDB header: unknown function Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: the crystal structure of a large insert in rna polymerase (rpoC)2 subunit from e. coli
63	d1ni7a	Alignment	not modelled	23.8	18	Fold: SufE/NifU Superfamily: SufE/NifU Family: SufE-like
64	c4nhoA	Alignment	not modelled	22.5	38	PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx23; PDBTitle: structure of the spliceosomal dead-box protein prp28
65	d1lk5a2	Alignment	not modelled	22.4	17	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
66	d2eyqa5	Alignment	not modelled	22.3	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
67	d1mzga	Alignment	not modelled	21.8	14	Fold: SufE/NifU Superfamily: SufE/NifU Family: SufE-like
68	c4meiA	Alignment	not modelled	21.2	16	PDB header: protein transport Chain: A: PDB Molecule: virb8 protein; PDBTitle: crystal structure of a virb8 type iv secretion system machinery2 soluble domain from bartonella tribocorum
69	c5m88A	Alignment	not modelled	21.0	23	PDB header: splicing Chain: A: PDB Molecule: core; PDBTitle: spliceosome component
70	c5c22A	Alignment	not modelled	21.0	53	PDB header: protein transport Chain: A: PDB Molecule: chromosomal hemolysin d; PDBTitle: crystal structure of zn-bound hlyd from e. coli
71	c4bmjC	Alignment	not modelled	20.4	50	PDB header: apoptosis Chain: C: PDB Molecule: tax1-binding protein 1; PDBTitle: structure of the ubz1and2 tandem of the ubiquitin-binding adaptor2 protein tax1bp1
72	c4l0zA	Alignment	not modelled	20.4	21	PDB header: transcription/dna Chain: A: PDB Molecule: runt-related transcription factor 1; PDBTitle: crystal structure of runx1 and ets1 bound to tcr alpha promoter2 (crystal form 2)
73	c1rb8J	Alignment	not modelled	20.2	55	PDB header: virus/dna Chain: J: PDB Molecule: small core protein; PDBTitle: the phix174 dna binding protein j in two different capsid2 environments.
74	c3mjhD	Alignment	not modelled	19.9	50	PDB header: protein transport Chain: D: PDB Molecule: early endosome antigen 1; PDBTitle: crystal structure of human rab5a in complex with the c2h2 zinc finger2 of eea1
75	c3bxzA	Alignment	not modelled	19.7	39	PDB header: transport protein Chain: A: PDB Molecule: preprotein translocase subunit seca; PDBTitle: crystal structure of the isolated dead motor domains from escherichia2 coli seca
76	c4upcA	Alignment	not modelled	19.7	20	PDB header: protein binding Chain: A: PDB Molecule: nicastrin; PDBTitle: structure of a extracellular domain
77	c5xytI	Alignment	not modelled	19.5	20	PDB header: ribosome Chain: T: PDB Molecule: ribosomal protein s19e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
78	c2vb0A	Alignment	not modelled	19.2	21	PDB header: hydrolase Chain: A: PDB Molecule: polyprotein 3bcd; PDBTitle: crystal structure of coxsackievirus b3 proteinase 3c
79	c2nu9E	Alignment	not modelled	18.3	21	PDB header: ligase Chain: E: PDB Molecule: succinyl-coa synthetase beta chain; PDBTitle: c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form Fold: FwdE/GAPDH domain-like

80	d1cf2o2	Alignment	not modelled	18.3	29	Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
81	c5xxu1	Alignment	not modelled	17.3	35	PDB header: ribosome Chain: I: PDB Molecule: ribosomal protein es8; PDBTitle: small subunit of toxoplasma gondii ribosome
82	c5gmkq	Alignment	not modelled	17.2	24	PDB header: rna binding protein/rna Chain: Q: PDB Molecule: pre-mrna-splicing factor slt11; PDBTitle: cryo-em structure of the catalytic step i spliceosome (c complex) at 2.3.4 angstrom resolution
83	c3it5B	Alignment	not modelled	17.0	22	PDB header: hydrolase Chain: B: PDB Molecule: protease lasa; PDBTitle: crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
84	c3cwiA	Alignment	not modelled	16.8	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: thiamine-biosynthesis protein this; PDBTitle: crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
85	d1tf5a4	Alignment	not modelled	15.8	39	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
86	d1d02a	Alignment	not modelled	15.5	17	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease MunI
87	d1px5a1	Alignment	not modelled	15.3	28	Fold: PAP/OAS1 substrate-binding domain Superfamily: PAP/OAS1 substrate-binding domain Family: 2'-5'-oligoadenylate synthetase 1, OAS1, second domain
88	c6em5b	Alignment	not modelled	15.3	25	PDB header: ribosome Chain: B: PDB Molecule: 60s ribosomal protein l3; PDBTitle: state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
89	c6g2iy	Alignment	not modelled	15.2	38	PDB header: oxidoreductase Chain: Y: PDB Molecule: mcg5603; PDBTitle: mouse mitochondrial complex i in the active state
90	c4nhf	Alignment	not modelled	15.2	17	PDB header: protein transport Chain: F: PDB Molecule: trwg protein; PDBTitle: crystal structure of the soluble domain of trwg type iv secretion2 machinery from bartonella grahamii
91	c3izbX	Alignment	not modelled	15.2	42	PDB header: ribosome Chain: X: PDB Molecule: 40s ribosomal protein rps27 (s27e); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
92	c3j20W	Alignment	not modelled	15.1	33	PDB header: ribosome Chain: W: PDB Molecule: 30s ribosomal protein s27e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
93	c1gjjA	Alignment	not modelled	15.0	35	PDB header: membrane protein Chain: A: PDB Molecule: lap2; PDBTitle: n-terminal constant region of the nuclear envelope protein2 lap2
94	c2qhoB	Alignment	not modelled	14.9	52	PDB header: protein binding/ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase edd1; PDBTitle: crystal structure of the uba domain from edd ubiquitin2 ligase in complex with ubiquitin
95	c1m1jA	Alignment	not modelled	14.9	50	PDB header: blood clotting Chain: A: PDB Molecule: fibrinogen alpha subunit; PDBTitle: crystal structure of native chicken fibrinogen with two different2 bound ligands
96	c2f1mA	Alignment	not modelled	14.8	20	PDB header: transport protein Chain: A: PDB Molecule: acriflavine resistance protein a; PDBTitle: conformational flexibility in the multidrug efflux system protein acra
97	c3wfoB	Alignment	not modelled	14.8	34	PDB header: transferase Chain: B: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme (apo form 1)
98	c1bplA	Alignment	not modelled	14.6	26	PDB header: glycosyltransferase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: glycosyltransferase
99	c2bhmE	Alignment	not modelled	14.6	8	PDB header: bacterial protein Chain: E: PDB Molecule: type iv secretion system protein virb8; PDBTitle: crystal structure of virb8 from brucella suis