











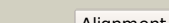

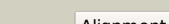











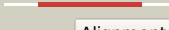












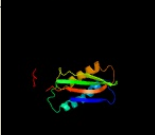

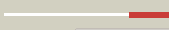

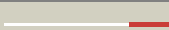
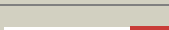




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1537_(dinX)_1739862_1741253
Date	Fri Aug 2 13:30:12 BST 2019
Unique Job ID	7efcc37a6faea0df

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gqcB_	 Alignment		100.0	31	PDB header: transferase/dna Chain: B: PDB Molecule: dna repair protein rev1; PDBTitle: structure of human rev1-dna-dntp ternary complex
2	c2oh2B_	 Alignment		100.0	29	PDB header: transferase/dna Chain: B: PDB Molecule: dna polymerase kappa; PDBTitle: ternary complex of human dna polymerase
3	c4ir1A_	 Alignment		100.0	30	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase iv; PDBTitle: polymerase-dna complex
4	c2aq4A_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: dna repair protein rev1; PDBTitle: ternary complex of the catalytic core of rev1 with dna and dctp.
5	c1jihA_	 Alignment		100.0	25	PDB header: translation Chain: A: PDB Molecule: dna polymerase eta; PDBTitle: yeast dna polymerase eta
6	c1s97D_	 Alignment		100.0	28	PDB header: transferase/dna Chain: D: PDB Molecule: dna polymerase iv; PDBTitle: dpo4 with gt mismatch
7	c2r8kB_	 Alignment		100.0	25	PDB header: replication, transferase/dna Chain: B: PDB Molecule: dna polymerase eta; PDBTitle: structure of the eukaryotic dna polymerase eta in complex with 1,2-d(gpp)-cisplatin containing dna
8	c3mr2A_	 Alignment		100.0	29	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase eta; PDBTitle: human dna polymerase eta in complex with normal dna and incoming2 nucleotide (nrm)
9	c1t94B_	 Alignment		100.0	28	PDB header: replication Chain: B: PDB Molecule: polymerase (dna directed) kappa; PDBTitle: crystal structure of the catalytic core of human dna polymerase kappa
10	c1t3nB_	 Alignment		100.0	24	PDB header: replication/dna Chain: B: PDB Molecule: polymerase (dna directed) iota; PDBTitle: structure of the catalytic core of dna polymerase iota in complex with2 dna and dttp
11	c2filA_	 Alignment		100.0	25	PDB header: replication/dna Chain: A: PDB Molecule: dna polymerase iota; PDBTitle: ternary complex of human dna polymerase iota with dna and dttp

12	c1k1qA	 Alignment		100.0	24	PDB header: transcription Chain: A: PDB Molecule: dbh protein; PDBTitle: crystal structure of a dinb family error prone dna2 polymerase from sulfolobus solfataricus
13	d1t94a2	 Alignment		100.0	30	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
14	d1jx4a2	 Alignment		100.0	30	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
15	d1jha2	 Alignment		100.0	30	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
16	d1k1sa2	 Alignment		100.0	29	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
17	d1lzeta2	 Alignment		100.0	29	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
18	c4dezA	 Alignment		100.0	41	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iv 1; PDBTitle: structure of msdpo4
19	d1im4a	 Alignment		100.0	30	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
20	d1unnc	 Alignment		99.7	23	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
21	d1t94a1	 Alignment	not modelled	99.5	29	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
22	d1lzeta1	 Alignment	not modelled	99.4	18	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
23	d1jha1	 Alignment	not modelled	98.7	14	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
24	d1jx4a1	 Alignment	not modelled	98.1	21	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
25	d1k1sa1	 Alignment	not modelled	97.9	15	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
26	d1szpa1	 Alignment	not modelled	97.1	23	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
27	d1pzna1	 Alignment	not modelled	97.0	27	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain

28	d2i1qa1	Alignment	not modelled	96.7	25	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
29	d1b22a_	Alignment	not modelled	96.1	26	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
30	c1b22A	Alignment	not modelled	96.1	26	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
31	c2zj8A_	Alignment	not modelled	95.8	20	PDB header: hydrolase Chain: A: PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 2
32	d2aq0a1	Alignment	not modelled	95.7	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
33	d1lb2b_	Alignment	not modelled	95.6	20	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
34	d1doqa_	Alignment	not modelled	95.3	27	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
35	d2p6ra2	Alignment	not modelled	95.2	24	Fold: Sec63 N-terminal domain-like Superfamily: Sec63 N-terminal domain-like Family: Achaeal helicase C-terminal domain
36	d1gm5a2	Alignment	not modelled	95.2	39	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RecG "wedge" domain
37	d2a1ja1	Alignment	not modelled	95.2	28	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
38	c1kdhA_	Alignment	not modelled	95.1	16	PDB header: transferase/dna Chain: A: PDB Molecule: terminal deoxynucleotidyltransferase short PDBTitle: binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
39	d1cooa_	Alignment	not modelled	95.1	23	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
40	d1z3eb1	Alignment	not modelled	95.1	18	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
41	c3bqsB_	Alignment	not modelled	94.9	32	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from2 listeria monocytogenes, trigonal form
42	c1kftA_	Alignment	not modelled	94.9	16	PDB header: dna binding protein Chain: A: PDB Molecule: excinuclease abc subunit c; PDBTitle: solution structure of the c-terminal domain of uvrc from e-2 coli
43	d1kfta_	Alignment	not modelled	94.9	16	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
44	c2lyhA_	Alignment	not modelled	94.7	24	PDB header: dna binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215
45	c2va8A_	Alignment	not modelled	94.4	24	PDB header: hydrolase Chain: A: PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
46	c1t4gA_	Alignment	not modelled	93.5	31	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: atpase in complex with amp-pnp
47	c8icza_	Alignment	not modelled	93.4	16	PDB header: transferase/dna Chain: A: PDB Molecule: protein (dna polymerase beta (e.c.2.7.7.7)); PDBTitle: dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with2 seven base pairs of dna; soaked in the presence of of datp3 (1 millimolar), mncl2 (5 millimolar), and lithium sulfate4 (75 millimolar)
48	c2ihmA_	Alignment	not modelled	93.4	15	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase mu; PDBTitle: polymerase mu in ternary complex with gapped 11mer dna duplex and2 bound incoming nucleotide
49	c1nomA_	Alignment	not modelled	93.4	18	PDB header: nucleotidyltransferase Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: dna polymerase beta (pol b) (e.c.2.7.7.7), 31-kd domain; soaked in the2 presence of mncl2 (5 millimolar)
50	c2bcuA_	Alignment	not modelled	93.3	12	PDB header: transferase, lyase/dna Chain: A: PDB Molecule: dna polymerase lambda; PDBTitle: dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a tt mismatch
51	d2q0zx1	Alignment	not modelled	93.1	13	Fold: Sec63 N-terminal domain-like Superfamily: Sec63 N-terminal domain-like Family: Sec63 N-terminal domain
52	d1jmsa3	Alignment	not modelled	92.9	25	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
53	c5agaA_	Alignment	not modelled	92.9	22	PDB header: transferase Chain: A: PDB Molecule: dna polymerase theta; PDBTitle: crystal structure of the helicase domain of human dna2 polymerase theta in complex with amppnp
						Fold: SAM domain-like

54	d2bcqa2	Alignment	not modelled	92.7	16	Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
55	d2vana1	Alignment	not modelled	92.7	43	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
56	c2maxA	Alignment	not modelled	92.6	16	PDB header: transferase Chain: A; PDB Molecule: dna-directed rna polymerase subunit alpha; PDBTitle: nmr structure of the rna polymerase alpha subunit c-terminal domain2 from helicobacter pylori
57	d2fmpa2	Alignment	not modelled	92.5	39	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
58	d1szpb1	Alignment	not modelled	92.5	26	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
59	c1pznA	Alignment	not modelled	92.3	33	PDB header: recombination Chain: A; PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada)
60	c4bxoB	Alignment	not modelled	92.2	24	PDB header: hydrolase/dna Chain: B; PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex
61	c1gm5A	Alignment	not modelled	92.0	41	PDB header: helicase Chain: A; PDB Molecule: recg; PDBTitle: structure of recg bound to three-way dna junction
62	c2p6uA	Alignment	not modelled	91.9	24	PDB header: dna binding protein Chain: A; PDB Molecule: afuhel308 helicase; PDBTitle: apo structure of the hel308 superfamily 2 helicase
63	d1x2ia1	Alignment	not modelled	91.6	18	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
64	d2bgwa1	Alignment	not modelled	91.4	16	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
65	c5tw1T	Alignment	not modelled	90.9	20	PDB header: transcription activator/transferase/dna Chain: T; PDB Molecule: dna-directed rna polymerase subunit alpha; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpA
66	c3im2A	Alignment	not modelled	90.9	23	PDB header: hydrolase Chain: A; PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: structure of the c-terminal sec63 unit of yeast brr2, p41212 form
67	c2kz3A	Alignment	not modelled	90.7	23	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein rad51l3; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83
68	c2w9mB	Alignment	not modelled	90.6	25	PDB header: dna replication Chain: B; PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
69	c4p4oA	Alignment	not modelled	90.6	36	PDB header: transferase/dna Chain: A; PDB Molecule: dna polymerase beta; PDBTitle: crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
70	c4bgdA	Alignment	not modelled	90.5	24	PDB header: transcription Chain: A; PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: crystal structure of brr2 in complex with the jab1/mpn domain of prp8
71	c5m52B	Alignment	not modelled	90.1	23	PDB header: hydrolase Chain: B; PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: crystal structure of yeast brr2 full-length in complex with prp8 jab12 domain
72	c5dcaA	Alignment	not modelled	90.1	25	PDB header: hydrolase Chain: A; PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: crystal structure of yeast full length brr2 in complex with prp8 jab12 domain
73	c4bxoA	Alignment	not modelled	90.0	10	PDB header: hydrolase/dna Chain: A; PDB Molecule: fanconi anemia group m protein; PDBTitle: architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex
74	c5lqwC	Alignment	not modelled	89.6	22	PDB header: splicing Chain: C; PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: yeast activated spliceosome
75	d2a1jb1	Alignment	not modelled	89.3	18	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
76	c2nrzB	Alignment	not modelled	88.9	22	PDB header: hydrolase Chain: B; PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal half of uvrC bound to its2 catalytic divalent cation
77	c3auoB	Alignment	not modelled	88.5	36	PDB header: transferase/dna Chain: B; PDB Molecule: dna polymerase beta family (x family); PDBTitle: dna polymerase x from thermus thermophilus hb8 ternary complex with 1-2 nt gapped dna and dddgtp
78	c2dfIA	Alignment	not modelled	88.2	26	PDB header: recombination Chain: A; PDB Molecule: dna repair and recombination protein rada; PDBTitle: crystal structure of left-handed rada filament
79	c5i2dA	Alignment	not modelled	88.1	26	PDB header: transcription/dna/rna Chain: A; PDB Molecule: dna-directed rna polymerase subunit alpha; PDBTitle: crystal structure of t. thermophilus tthb099 class ii

					transcription2 activation complex: tap-rpo PDB header: hydrolase Chain: A: PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region
80	c2mutA_	Alignment	not modelled	86.7	18
81	c4f92B_	Alignment	not modelled	86.6	13
82	d1qw2a_	Alignment	not modelled	85.9	24
83	c5jzcG_	Alignment	not modelled	85.5	32
84	d1dgsa1	Alignment	not modelled	83.1	22
85	c2q0zX_	Alignment	not modelled	81.9	13
86	c3ezuA_	Alignment	not modelled	81.6	25
87	c6flqF_	Alignment	not modelled	81.3	23
88	d1ci4a_	Alignment	not modelled	81.1	28
89	c3i5aA_	Alignment	not modelled	81.1	19
90	c3iydA_	Alignment	not modelled	79.7	20
91	c4glxA_	Alignment	not modelled	79.6	15
92	c2owoA_	Alignment	not modelled	79.1	15
93	c3ldaA_	Alignment	not modelled	78.6	27
94	c1szpC_	Alignment	not modelled	73.1	26
95	c1dgsB_	Alignment	not modelled	71.2	22
96	c6ah0D_	Alignment	not modelled	70.6	13
97	c1wcnA_	Alignment	not modelled	68.6	31
98	c2bhnD_	Alignment	not modelled	63.9	16
99	c3breA_	Alignment	not modelled	63.4	23
100	c4mntA_	Alignment	not modelled	62.0	20
101	c1w25B_	Alignment	not modelled	58.5	18
102	c1v9pB_	Alignment	not modelled	55.5	22
103	c3jcrC_	Alignment	not modelled	55.3	13
104	d2phna1	Alignment	not modelled	54.3	22
					PDB header: hydrolase

105	c1ixrA_	Alignment	not modelled	52.6	14	Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
106	d1bvsa2	Alignment	not modelled	52.3	29	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
107	c5lm7A_	Alignment	not modelled	50.2	24	PDB header: transcription Chain: A: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: crystal structure of the lambda n-nus factor complex
108	c1vddC_	Alignment	not modelled	49.6	44	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
109	c2csdB_	Alignment	not modelled	48.2	36	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
110	c4dmzB_	Alignment	not modelled	48.1	20	PDB header: nucleotide-binding protein Chain: B: PDB Molecule: putative uncharacterized protein peld; PDBTitle: peld 156-455 from pseudomonas aeruginosa pa14, apo form
111	d1ykgA1	Alignment	not modelled	47.8	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
112	c4itqA_	Alignment	not modelled	47.6	28	PDB header: gene regulation, structural protein/dna Chain: A: PDB Molecule: putative uncharacterized protein sco1480; PDBTitle: crystal structure of hypothetical protein sco1480 bound to dna
113	d2axtu1	Alignment	not modelled	47.3	10	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: PsbU-like
114	c1s5lu_	Alignment	not modelled	47.2	10	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
115	c5m59C_	Alignment	not modelled	47.1	17	PDB header: splicing Chain: C: PDB Molecule: pre-mrna splicing helicase-like protein; PDBTitle: crystal structure of chaetomium thermophilum brr2 helicase core in2 complex with prp8 jab1 domain
116	c5z2vB_	Alignment	not modelled	46.3	25	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
117	c2vp8A_	Alignment	not modelled	46.2	21	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase 2; PDBTitle: structure of mycobacterium tuberculosis rv1207
118	d1vdda_	Alignment	not modelled	45.9	44	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
119	c5zvqA_	Alignment	not modelled	45.6	44	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
120	c1wwuA_	Alignment	not modelled	39.5	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein flj21935; PDBTitle: solution structure of the sam_pnt domain of human protein2 flj21935