Phyre2

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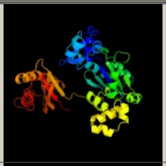
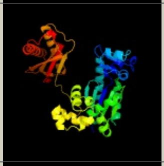
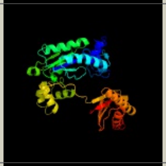
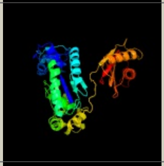
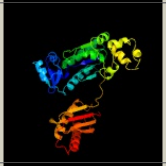
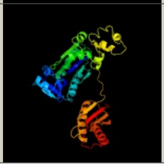
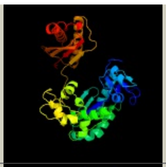
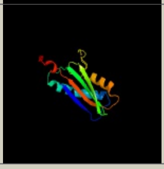
Description	RVBD3394c_(-)_3809622_3811205
Date	Fri Aug 9 18:20:06 BST 2019
Unique Job ID	16d840166d4c7004

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ir1A_	Alignment		100.0	18	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase iv; **PDBTitle:** polymerase-dna complex
2	c1s97D_	Alignment		100.0	14	**PDB header:**transferase/dna **Chain:** D: **PDB Molecule:**dna polymerase iv; **PDBTitle:** dpo4 with gt mismatch
3	c1t94B_	Alignment		100.0	15	**PDB header:**replication **Chain:** B: **PDB Molecule:**polymerase (dna directed) kappa; **PDBTitle:** crystal structure of the catalytic core of human dna polymerase kappa
4	c3gqcB_	Alignment		100.0	16	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** structure of human rev1-dna-dntp ternary complex
5	c2oh2B_	Alignment		100.0	15	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase kappa; **PDBTitle:** ternary complex of human dna polymerase
6	c2fllA_	Alignment		100.0	18	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** ternary complex of human dna polymerase iota with dna and dttp
7	c1t3nB_	Alignment		100.0	16	**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
8	c3mr2A_	Alignment		100.0	19	**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	c1k1qA_	Alignment		100.0	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dbh protein; **PDBTitle:** crystal structure of a dinb family error prone dna2 polymerase from sulfolobus solfataricus
10	c1jihA_	Alignment		100.0	16	**PDB header:**translation **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** yeast dna polymerase eta
11	c2r8kB_	Alignment		100.0	16	**PDB header:**replication, transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase eta; **PDBTitle:** structure of the eukaryotic dna polymerase eta in complex with 1,2-2 d(gpg)-cisplatin containing dna

12	c2aq4A_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** ternary complex of the catalytic core of rev1 with dna and dctp.
13	d1jx4a2	Alignment		100.0	16	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
14	d1zeta2	Alignment		100.0	17	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
15	d1k1sa2	Alignment		100.0	14	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
16	c4dezA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iv 1; **PDBTitle:** structure of msdpo4
17	d1t94a2	Alignment		100.0	17	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
18	d1jiha2	Alignment		100.0	23	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
19	d1im4a_	Alignment		100.0	16	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
20	d1unnc_	Alignment		99.2	17	**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	98.6	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
22	d1zeta1	Alignment	not modelled	98.1	13	**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	d1jiha1	Alignment	not modelled	97.1	11	**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	d1lb2b_	Alignment	not modelled	94.4	12	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
25	d1z3eb1	Alignment	not modelled	93.5	19	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
26	d1doqa_	Alignment	not modelled	93.0	20	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
27	d1cooa_	Alignment	not modelled	92.1	15	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
28	d1qw2a_	Alignment	not modelled	90.0	24	**Fold:**Hypothetical protein Ta1206 **Superfamily:**Hypothetical protein Ta1206

						Family: Hypothetical protein Ta1206
29	c2maxA_	Alignment	not modelled	89.8	17	**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
30	d1szpa1	Alignment	not modelled	89.5	22	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
31	c5tw1T_	Alignment	not modelled	88.6	21	**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
32	c2kz3A_	Alignment	not modelled	87.1	20	**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
33	d1pzna1	Alignment	not modelled	86.8	17	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
34	d1gm5a2	Alignment	not modelled	83.3	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RecG "wedge" domain
35	d1szpb1	Alignment	not modelled	81.5	21	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
36	d2i1qa1	Alignment	not modelled	80.6	13	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
37	d1jx4a1	Alignment	not modelled	79.1	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
38	c5i2dA_	Alignment	not modelled	76.2	20	**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
39	d1b22a_	Alignment	not modelled	74.3	15	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
40	c1b22A_	Alignment	not modelled	74.3	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** rad51 (n-terminal domain)
41	c1t4gA_	Alignment	not modelled	72.0	11	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rada; **PDBTitle:** atpase in complex with amp-pnp
42	c3bqsB_	Alignment	not modelled	68.6	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 listeria monocytogenes, trigonal form
43	c1nomA_	Alignment	not modelled	67.0	7	**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)
44	c8iczA_	Alignment	not modelled	62.7	8	**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)
45	c1gm5A_	Alignment	not modelled	62.5	18	**PDB header:**helicase **Chain:** A: **PDB Molecule:**recg; **PDBTitle:** structure of recg bound to three-way dna junction
46	c2bcuA_	Alignment	not modelled	62.3	8	**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 t:t mismatch
47	c1pznA_	Alignment	not modelled	62.1	16	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rad51; **PDBTitle:** rad51 (rada)
48	c3iydA_	Alignment	not modelled	60.7	15	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit alpha; **PDBTitle:** three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
49	d1jmsa3	Alignment	not modelled	60.0	19	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
50	d2bcqa2	Alignment	not modelled	58.1	8	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
51	c1szpC_	Alignment	not modelled	57.9	21	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** a crystal structure of the rad51 filament
52	d2vana1	Alignment	not modelled	57.4	15	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
53	d2fmpa2	Alignment	not modelled	56.5	12	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like

						Family:DNA polymerase beta-like, second domain
54	c1wcnA_	Alignment	not modelled	56.0	26	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** nmr structure of the carboxyterminal domains of escherichia2 coli nusa
55	c1kdhA_	Alignment	not modelled	55.1	12	**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
56	c2ihmA_	Alignment	not modelled	49.2	12	**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
57	d1k1sa1	Alignment	not modelled	45.1	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
58	c1wwuA_	Alignment	not modelled	42.5	19	**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
59	d2p6ra2	Alignment	not modelled	42.0	21	**Fold:**Sec63 N-terminal domain-like **Superfamily:**Sec63 N-terminal domain-like **Family:**Achaeal helicase C-terminal domain
60	c5jzcG_	Alignment	not modelled	41.7	13	**PDB header:**dna binding protein **Chain:** G: **PDB Molecule:**dna repair protein rad51 homolog 1; **PDBTitle:** helical filament
61	c2dflA_	Alignment	not modelled	41.6	16	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rada; **PDBTitle:** crystal structure of left-handed rada filament
62	c2iruA_	Alignment	not modelled	38.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative dna ligase-like protein rv0938/mt0965; **PDBTitle:** crystal structure of the polymerase domain from mycobacterium2 tuberculosis ligase d
63	c2zj8A_	Alignment	not modelled	37.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ski2-type helicase; **PDBTitle:** archaeal dna helicase hjm apo state in form 2
64	c4p4oA_	Alignment	not modelled	37.1	19	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase beta; **PDBTitle:** crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
65	c5dmuA_	Alignment	not modelled	36.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nhej polymerase; **PDBTitle:** structure of the nhej polymerase from methanocella paludicola
66	c2w9mB_	Alignment	not modelled	35.6	15	**PDB header:**dna replication **Chain:** B: **PDB Molecule:**polymerase x; **PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
67	d2a1ja1	Alignment	not modelled	31.0	22	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
68	d2q0zx1	Alignment	not modelled	29.6	3	**Fold:**Sec63 N-terminal domain-like **Superfamily:**Sec63 N-terminal domain-like **Family:**Sec63 N-terminal domain
69	c5ezbB_	Alignment	not modelled	26.0	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**chicken prestin stas domain,chicken prestin stas domain; **PDBTitle:** chicken prestin stas domain
70	c2faoB_	Alignment	not modelled	22.3	16	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**probable atp-dependent dna ligase; **PDBTitle:** crystal structure of pseudomonas aeruginosa ligd polymerase2 domain
71	c3auoB_	Alignment	not modelled	20.3	19	**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 ddgtp
72	c3ldaA_	Alignment	not modelled	19.5	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** yeast rad51 h352y filament interface mutant
73	c5agaA_	Alignment	not modelled	18.1	13	**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
74	c3idwA_	Alignment	not modelled	17.4	23	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**actin cytoskeleton-regulatory complex protein sla1; **PDBTitle:** crystal structure of sla1 homology domain 2
75	c1hl8B_	Alignment	not modelled	17.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of thermotoga maritima alpha-fucosidase
76	c2e8mA_	Alignment	not modelled	15.7	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**epidermal growth factor receptor kinase **PDBTitle:** solution structure of the c-terminal sam-domain of2 epidermal growth receptor pathway substrate 8
77	c2l05A_	Alignment	not modelled	14.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase b-raf; **PDBTitle:** solution nmr structure of the ras-binding domain of serine/threonine-2 protein kinase b-raf from homo sapiens, northeast structural genomics3 consortium target hr4694f
78	c3im2A_	Alignment	not modelled	14.5	9	**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
79	d1dgsa1	Alignment	not modelled	14.0	19	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
80	c6ogdD_	Alignment	not modelled	13.9	20	**PDB header:**toxin **Chain:** D: **PDB Molecule:**toxin subunit yena1; **PDBTitle:** cryo-em structure of yentca in its prepore state
81	d2fomb1	Alignment	not modelled	13.0	18	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
82	c1rrbA_	Alignment	not modelled	12.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**raf proto-oncogene serine/threonine-protein **PDBTitle:** the ras-binding domain of raf-1 from rat, nmr, 1 structure
83	d1c1yb_	Alignment	not modelled	12.8	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
84	c4h2dB_	Alignment	not modelled	12.8	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-dependent diflavin oxidoreductase 1; **PDBTitle:** crystal structure of ndor1
85	c4wwrE_	Alignment	not modelled	12.5	54	**PDB header:**transport protein **Chain:** E: **PDB Molecule:**large proline-rich protein bag6; **PDBTitle:** crystal structure of bag6-ubl4a dimerization domain
86	c5yxiA_	Alignment	not modelled	12.4	43	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**drafx6; **PDBTitle:** designed protein drafx6
87	d2fp7b1	Alignment	not modelled	12.3	17	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
88	d1befa_	Alignment	not modelled	10.7	18	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
89	c1loiA_	Alignment	not modelled	10.5	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyclic 3',5'-amp specific phosphodiesterase rd1; **PDBTitle:** n-terminal splice region of rat c-amp phosphodiesterase,2 nmr, 7 structures
90	c4jmrA_	Alignment	not modelled	9.6	25	**PDB header:**viral protein/peptide **Chain:** A: **PDB Molecule:**gag protein; **PDBTitle:** a unique spumavirus gag n-terminal domain with functional properties2 of orthoretroviral matrix and capsid
91	d1ttea1	Alignment	not modelled	9.5	24	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
92	d1u9la_	Alignment	not modelled	9.5	16	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**NusA extra C-terminal domains
93	c2va8A_	Alignment	not modelled	9.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ski2-type helicase; **PDBTitle:** dna repair helicase hel308
94	c1dgsB_	Alignment	not modelled	9.1	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
95	d1kfta_	Alignment	not modelled	8.9	9	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
96	c1kftA_	Alignment	not modelled	8.9	9	**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
97	c4m9mA_	Alignment	not modelled	8.9	18	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**ns2b-ns3 protease; **PDBTitle:** ns2b-ns3 protease from dengue virus at ph 8.5
98	c2owoA_	Alignment	not modelled	8.7	18	**PDB header:**ligase/dna **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
99	d2ijob1	Alignment	not modelled	8.6	18	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases