












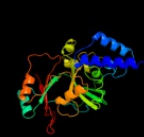










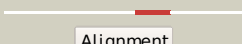
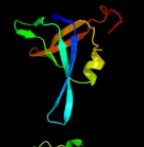
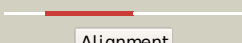

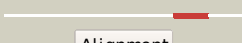







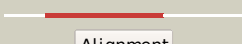

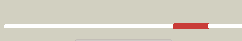


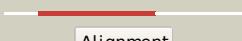

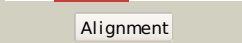



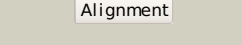
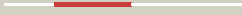


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2owoA	 Alignment		100.0	23	PDB header: ligase/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
2	c1v9pB	 Alignment		100.0	23	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
3	c1dgsB	 Alignment		100.0	22	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
4	c3pn1A	 Alignment		100.0	25	PDB header: ligase/ligase inhibitor Chain: A: PDB Molecule: dna ligase; PDBTitle: novel bacterial nad+-dependent dna ligase inhibitors with broad2 spectrum potency and antibacterial efficacy in vivo
5	d1b04a	 Alignment		100.0	25	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
6	d1ta8a	 Alignment		100.0	24	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
7	c3jslA	 Alignment		100.0	26	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: crystal structure of the adenylation domain of nad+-2 dependent dna ligase from staphylococcus aureus
8	d1v9pa3	 Alignment		100.0	25	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
9	c1zauA	 Alignment		100.0	23	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: adenylation domain of nad+ dependent dna ligase from2 m.tuberculosis
10	d1dgsa3	 Alignment		100.0	24	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
11	c3bacA	 Alignment		100.0	24	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: structural basis for the inhibition of bacterial nad+2 dependent dna ligase

12	d1dgsa1	 <div>Alignment</div>		100.0	15	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
13	d1dgsa2	 <div>Alignment</div>		100.0	28	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA ligase/mRNA capping enzyme postcatalytic domain
14	d1x9na3	 <div>Alignment</div>		99.6	15	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: ATP-dependent DNA ligase catalytic domain
15	d2a1jb1	 <div>Alignment</div>		99.0	14	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
16	c2hivA_	 <div>Alignment</div>		98.9	18	PDB header: ligase Chain: A: PDB Molecule: thermostable dna ligase; PDBTitle: atp-dependent dna ligase from s. solfataricus
17	c3gdeA_	 <div>Alignment</div>		98.9	20	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: the closed conformation of atp-dependent dna ligase from2 archaeoglobus fulgidus
18	c2vugB_	 <div>Alignment</div>		98.8	23	PDB header: ligase Chain: B: PDB Molecule: pab1020; PDBTitle: the structure of an archaeal homodimeric rna ligase
19	c3l2pA_	 <div>Alignment</div>		98.8	13	PDB header: ligase/dna Chain: A: PDB Molecule: dna ligase 3; PDBTitle: human dna ligase iii recognizes dna ends by dynamic switching between2 two dna bound states
20	d1x2ia1	 <div>Alignment</div>		98.7	14	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
21	c2cfmA_	 <div>Alignment</div>	not modelled	98.6	14	PDB header: ligase Chain: A: PDB Molecule: thermostable dna ligase; PDBTitle: atp-dependent dna ligase from pyrococcus furiosus
22	c1x9nA_	 <div>Alignment</div>	not modelled	98.6	16	PDB header: ligase/dna Chain: A: PDB Molecule: dna ligase i; PDBTitle: crystal structure of human dna ligase i bound to 5'-adenylated, nicked2 dna
23	d2bgwa1	 <div>Alignment</div>	not modelled	98.6	16	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
24	c3qwUa_	 <div>Alignment</div>	not modelled	98.3	13	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: putative atp-dependent dna ligase from aquifex aeolicus.
25	c1p8lA_	 <div>Alignment</div>	not modelled	98.3	15	PDB header: ligase Chain: A: PDB Molecule: pbcv-1 dna ligase; PDBTitle: new crystal structure of chlorella virus dna ligase-adenylate
26	c1a0iA_	 <div>Alignment</div>	not modelled	98.1	16	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: atp-dependent dna ligase from bacteriophage t7 complex with2 atp
27	d1kfta_	 <div>Alignment</div>	not modelled	98.1	15	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
28	c1kftA_	 <div>Alignment</div>	not modelled	98.1	15	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
		 <div></div>				Fold: ATP-grasp

29	d1fvia2	Alignment	not modelled	98.0	14	Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: ATP-dependent DNA ligase catalytic domain
30	c1vs0A	Alignment	not modelled	97.8	22	PDB header: ligase Chain: A: PDB Molecule: putative dna ligase-like protein rv0938/mt0965; PDBTitle: crystal structure of the ligase domain from m. tuberculosis ligd at2 2.4a
31	c2nrzB	Alignment	not modelled	97.7	16	PDB header: hydrolase Chain: B: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal half of uvrC bound to2 its catalytic divalent cation
32	c3c1zA	Alignment	not modelled	97.7	15	PDB header: dna binding protein Chain: A: PDB Molecule: dna integrity scanning protein disa; PDBTitle: structure of the ligand-free form of a bacterial dna damage2 sensor protein
33	d2i1qa1	Alignment	not modelled	97.6	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
34	d1szpa1	Alignment	not modelled	97.6	19	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
35	c2bhnD	Alignment	not modelled	97.6	18	PDB header: hydrolase Chain: D: PDB Molecule: xpf endonuclease; PDBTitle: xpf from aeropyrum pernix
36	d1a0ia2	Alignment	not modelled	97.6	14	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: ATP-dependent DNA ligase catalytic domain
37	d1pzna1	Alignment	not modelled	97.5	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
38	c1b22A	Alignment	not modelled	97.5	20	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
39	d1b22a	Alignment	not modelled	97.5	20	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
40	d1ckma2	Alignment	not modelled	97.3	14	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: mRNA capping enzyme
41	d2aq0a1	Alignment	not modelled	97.3	10	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
42	c3kyhC	Alignment	not modelled	97.1	19	PDB header: protein binding Chain: C: PDB Molecule: mrna-capping enzyme subunit alpha; PDBTitle: saccharomyces cerevisiae cet1-ceg1 capping apparatus
43	c1p16A	Alignment	not modelled	96.9	17	PDB header: transferase Chain: A: PDB Molecule: mrna capping enzyme alpha subunit; PDBTitle: structure of an mrna capping enzyme bound to the2 phosphorylated carboxyl-terminal domain of rna polymerase3 ii
44	c1cknA	Alignment	not modelled	96.9	16	PDB header: capping enzyme Chain: A: PDB Molecule: mrna capping enzyme; PDBTitle: structure of guanylylated mrna capping enzyme complexed2 with gtp
45	d1szpb1	Alignment	not modelled	96.8	19	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
46	c3s24F	Alignment	not modelled	96.5	16	PDB header: hydrolase, transferase Chain: F: PDB Molecule: mrna-capping enzyme; PDBTitle: crystal structure of human mrna guanylyltransferase
47	d1p16a2	Alignment	not modelled	96.5	18	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: mRNA capping enzyme
48	c2w9mB	Alignment	not modelled	96.5	16	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
49	c2csdB	Alignment	not modelled	96.1	16	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
50	d1pu6a	Alignment	not modelled	96.0	18	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)
51	d1doqa	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
52	d1lb2b	Alignment	not modelled	95.6	14	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
53	d1z3eb1	Alignment	not modelled	95.3	6	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
54	d1coa	Alignment	not modelled	95.2	14	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
55	d2p6ra2	Alignment	not modelled	94.8	10	Fold: Sec63 N-terminal domain-like Superfamily: Sec63 N-terminal domain-like Family: Achaeal helicase C-terminal domain
56	c2f10A	Alignment	not modelled	94.8	14	PDB header: hydrolase, lyase Chain: A: PDB Molecule: 8-oxoguanine-dna-glycosylase;

56	c31vA	Alignment	not modelled	94.8	14	PDBTitle: crystal structure of clostridium acetobutylicum 8-2 oxoguanine dna glycosylase in complex with 8-oxoguanosine PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
57	c2h5xA	Alignment	not modelled	94.8	13	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
58	d1cuka2	Alignment	not modelled	94.4	15	PDB header: ligase/dna/rna Chain: A: PDB Molecule: t4 rna ligase 2; PDBTitle: structure of t4 rna ligase 2 with nicked 5'-adenylated2 nucleic acid duplex containing a 2'-deoxyribonucleotide at3 the nick
59	c2hvsA	Alignment	not modelled	94.3	15	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
60	clixrA	Alignment	not modelled	94.2	13	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
61	c1s5lu	Alignment	not modelled	93.4	11	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
62	d1lixrA1	Alignment	not modelled	93.3	13	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HhH-containing domain-like
63	d3bzka1	Alignment	not modelled	93.2	12	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: RNA ligase
64	d1s68a	Alignment	not modelled	93.0	15	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
65	d1keaa	Alignment	not modelled	92.9	14	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
66	c1rrqA	Alignment	not modelled	92.6	13	PDB header: gene regulation Chain: A: PDB Molecule: protein (holliday junction dna helicase ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region2 lacking domain iii
67	c1d81A	Alignment	not modelled	92.5	17	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
68	d2abka	Alignment	not modelled	92.4	14	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: PsbU-like
69	d2axtu1	Alignment	not modelled	92.2	11	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase mu; PDBTitle: polymerase mu in ternary complex with gapped 11mer dna2 duplex and bound incoming nucleotide
70	c2ihmA	Alignment	not modelled	92.2	11	PDB header: hydrolase Chain: A: PDB Molecule: 8-oxoguanine dna glycosylase; PDBTitle: native structure of the human 8-oxoguanine dna glycosylase2 hogg1
71	c1ko9A	Alignment	not modelled	91.6	15	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
72	d2noha1	Alignment	not modelled	91.4	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
73	d2edua1	Alignment	not modelled	91.1	17	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
74	c1kdhA	Alignment	not modelled	90.5	9	PDB header: dna binding protein Chain: A: PDB Molecule: afuhel308 helicase; PDBTitle: apo structure of the hel308 superfamily 2 helicase
75	c2p6uA	Alignment	not modelled	90.2	11	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
76	c1hjpA	Alignment	not modelled	90.2	17	PDB header: hydrolase Chain: B: PDB Molecule: dna-3-methyladenine glycosidase ii, putative; PDBTitle: structure of an unusual 3-methyladenine dna glycosylase ii (2 alka) from deinococcus radiodurans
77	c2yg8B	Alignment	not modelled	90.2	22	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 mnc12 (5 millimolar)
78	c1nomA	Alignment	not modelled	90.1	13	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
79	d1rrqa1	Alignment	not modelled	89.8	13	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
80	d1kg2a	Alignment	not modelled	89.7	14	PDB header: hydrolase/dna Chain: A: PDB Molecule: dna-3-methyladenine glycosylase 1; PDBTitle: schizosaccaromyces pombe 3-methyladenine dna glycosylase (mag1) in2 complex with abasic-dna.
81	c3s6iA	Alignment	not modelled	89.6	13	PDB header: rna-binding protein

82	c1wcna_	Alignment	not modelled	89.2	16	Chain: A: PDB Molecule: transcription elongation protein nusa; PDBTitle: nmr structure of the carboxyterminal domains of escherichia2 coli nusa
83	c8iczA_	Alignment	not modelled	89.1	7	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), mnc12 (5 millimolar), and lithium sulfate4 (75 millimolar)
84	d1bvsa2	Alignment	not modelled	89.0	13	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
85	d2q0zx1	Alignment	not modelled	88.5	12	Fold: Sec63 N-terminal domain-like Superfamily: Sec63 N-terminal domain-like Family: Sec63 N-terminal domain
86	d1u9la_	Alignment	not modelled	88.4	10	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: NusA extra C-terminal domains
87	d2duya1	Alignment	not modelled	88.2	30	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
88	c2va8A_	Alignment	not modelled	87.9	13	PDB header: hydrolase Chain: A: PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
89	d1orna_	Alignment	not modelled	87.5	14	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
90	d1ngna_	Alignment	not modelled	86.3	13	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
91	c2bcuA_	Alignment	not modelled	85.9	11	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
92	d2a1ja1	Alignment	not modelled	85.3	11	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
93	c3n5nX_	Alignment	not modelled	85.0	21	PDB header: hydrolase Chain: X: PDB Molecule: a/g-specific adenine dna glycosylase; PDBTitle: crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue
94	c1yqmA_	Alignment	not modelled	84.9	19	PDB header: hydrolase/dna Chain: A: PDB Molecule: n-glycosylase/dna lyase; PDBTitle: catalytically inactive human 8-oxoguanine glycosylase2 crosslinked to 7-deazaguanine containing dna
95	c3gqcB_	Alignment	not modelled	84.5	17	PDB header: transferase/dna Chain: B: PDB Molecule: dna repair protein rev1; PDBTitle: structure of human rev1-dna-dntp ternary complex
96	d1mpga1	Alignment	not modelled	84.4	22	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
97	c1t3nB_	Alignment	not modelled	83.8	15	PDB header: replication/dna Chain: B: PDB Molecule: polymerase (dna directed) iota; PDBTitle: structure of the catalytic core of dna polymerase iota in2 complex with dna and dttp
98	d1jx4a2	Alignment	not modelled	83.3	20	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
99	c2ziuA_	Alignment	not modelled	81.9	15	PDB header: hydrolase Chain: A: PDB Molecule: mus81 protein; PDBTitle: crystal structure of the mus81-eme1 complex
100	c3n0uB_	Alignment	not modelled	81.4	11	PDB header: hydrolase, lyase Chain: B: PDB Molecule: probable n-glycosylase/dna lyase; PDBTitle: crystal structure of tm1821, the 8-oxoguanine dna glycosylase of2 thermotoga maritima
101	c1t4gA_	Alignment	not modelled	80.8	17	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: atpase in complex with amp-pnp
102	d2bcqa1	Alignment	not modelled	80.8	31	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
103	d1k1sa2	Alignment	not modelled	80.4	22	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
104	c1k1qA_	Alignment	not modelled	80.4	22	PDB header: transcription Chain: A: PDB Molecule: dbh protein; PDBTitle: crystal structure of a dinb family error prone dna2 polymerase from sulfolobus solfataricus
105	d2fmpa1	Alignment	not modelled	80.2	25	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
106	c3senD_	Alignment	not modelled	79.7	12	PDB header: signaling protein Chain: D: PDB Molecule: caskin-1; PDBTitle: structure of caskin1 tandem sams
107	d1nzpa_	Alignment	not modelled	79.1	31	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
108	c2c5uA_	Alignment	not modelled	79.1	18	PDB header: ligase Chain: A: PDB Molecule: rna ligase;

					PDBTitle: t4 rna ligase (rnl1) crystal structure
109	d1t94a2	Alignment	not modelled	78.8	13 Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
110	d1coka_	Alignment	not modelled	78.1	15 Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
111	c2fliA_	Alignment	not modelled	77.7	15 PDB header: replication/dna Chain: A: PDB Molecule: dna polymerase iota; PDBTitle: ternary complex of human dna polymerase iota with dna and dttp
112	c1szpC_	Alignment	not modelled	75.4	18 PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein rad51; PDBTitle: a crystal structure of the rad51 filament
113	c1mpgB_	Alignment	not modelled	75.2	20 PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna glycosylase ii; PDBTitle: 3-methyladenine dna glycosylase ii from escherichia coli
114	d2bcqa2	Alignment	not modelled	74.9	17 Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain
115	d1dk2a_	Alignment	not modelled	74.5	23 Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
116	d2fmpa2	Alignment	not modelled	74.4	15 Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain
117	d1jmsa1	Alignment	not modelled	74.0	9 Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
118	c2kp7A_	Alignment	not modelled	73.9	16 PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endonuclease mus81; PDBTitle: solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
119	c1s97D_	Alignment	not modelled	73.5	19 PDB header: transferase/dna Chain: D: PDB Molecule: dna polymerase iv; PDBTitle: dpo4 with gt mismatch
120	c1vddC_	Alignment	not modelled	73.4	19 PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr