











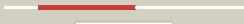



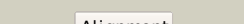

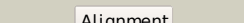
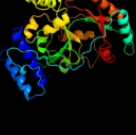
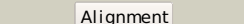










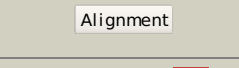
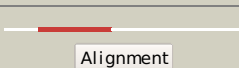
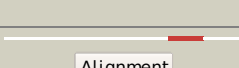
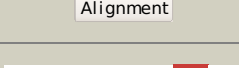
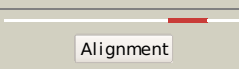
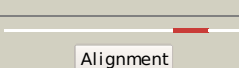
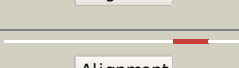
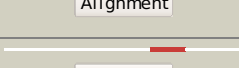
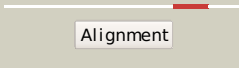
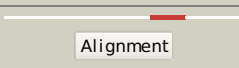
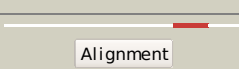
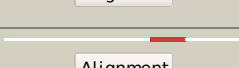


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2owoA	 Alignment		100.0	100	PDB header: ligase/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
2	c1v9pB	 Alignment		100.0	46	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
3	c1dgsB	 Alignment		100.0	45	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	62	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	d1ta8a	 Alignment		100.0	47	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
6	c3jslA	 Alignment		100.0	45	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
7	d1b04a	 Alignment		100.0	50	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
8	d1v9pa3	 Alignment		100.0	48	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
9	c1zauA	 Alignment		100.0	45	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	46	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
11	c3bacA	 Alignment		100.0	62	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: structural basis for the inhibition of bacterial nad+2 dependent dna ligase

12	d1dgsa1	Alignment		100.0	40	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
13	d1dgsa2	Alignment		100.0	50	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA ligase/mRNA capping enzyme postcatalytic domain
14	d1x9na3	Alignment		99.7	18	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: ATP-dependent DNA ligase catalytic domain
15	c2ebuA_	Alignment		99.7	38	PDB header: replication Chain: A: PDB Molecule: replication factor c subunit 1; PDBTitle: solution structure of the brct domain from human2 replication factor c large subunit 1
16	d1l7ba_	Alignment		99.6	48	Fold: BRCT domain Superfamily: BRCT domain Family: DNA ligase
17	c2cokA_	Alignment		99.3	24	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase-1; PDBTitle: solution structure of brct domain of poly(adp-ribose)2 polymerase-1
18	d2a1jb1	Alignment		99.2	30	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
19	c3gdeA_	Alignment		99.2	23	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: the closed conformation of atp-dependent dna ligase from2 archaeoglobus fulgidus
20	c2hivA_	Alignment		99.2	19	PDB header: ligase Chain: A: PDB Molecule: thermostable dna ligase; PDBTitle: atp-dependent dna ligase from s. solfataricus
21	c3l2pA_	Alignment	not modelled	99.0	17	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
22	d1x2ia1	Alignment	not modelled	99.0	27	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
23	d2bgwa1	Alignment	not modelled	98.9	29	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
24	c2cfmA_	Alignment	not modelled	98.9	20	PDB header: ligase Chain: A: PDB Molecule: thermostable dna ligase; PDBTitle: atp-dependent dna ligase from pyrococcus furiosus
25	c2vugB_	Alignment	not modelled	98.9	19	PDB header: ligase Chain: B: PDB Molecule: pab1020; PDBTitle: the structure of an archaeal homodimeric rna ligase
26	c1x9nA_	Alignment	not modelled	98.8	19	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
27	c2d8mA_	Alignment	not modelled	98.7	24	PDB header: dna binding protein Chain: A: PDB Molecule: dna-repair protein xrcc1; PDBTitle: solution structure of the first brct domain of dna-repair2 protein xrcc1
28	c1kftA_	Alignment	not modelled	98.6	32	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
						Fold: SAM domain-like

29	d1kfta_	Alignment	not modelled	98.6	32	Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
30	c3ef0A_	Alignment	not modelled	98.6	21	PDB header: hydrolase Chain: A: PDB Molecule: rna polymerase ii subunit a c-terminal domain PDBTitle: the structure of fcp1, an essential rna polymerase ii ctd2 phosphatase
31	c3qwuA_	Alignment	not modelled	98.5	18	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: putative atp-dependent dna ligase from aquifex aeolicus.
32	c3l3eA_	Alignment	not modelled	98.5	19	PDB header: cell cycle Chain: A: PDB Molecule: dna topoisomerase 2-binding protein 1; PDBTitle: crystal structure of the sixth brct domain of human topbp1
33	c2xnkA_	Alignment	not modelled	98.5	17	PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase 2-binding protein 1; PDBTitle: structure and function of the rad9-binding region of the dna damage2 checkpoint adaptor topbp1
34	d1fvia2	Alignment	not modelled	98.4	16	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: ATP-dependent DNA ligase catalytic domain
35	c1p8lA_	Alignment	not modelled	98.4	15	PDB header: ligase Chain: A: PDB Molecule: pbcv-1 dna ligase; PDBTitle: new crystal structure of chlorella virus dna ligase-adenylate
36	c2couA_	Alignment	not modelled	98.4	11	PDB header: cell cycle Chain: A: PDB Molecule: ect2 protein; PDBTitle: solution structure of the second brct domain of epithelial2 cell transforming 2
37	c2nrzB_	Alignment	not modelled	98.4	27	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
38	c3ef1A_	Alignment	not modelled	98.3	23	PDB header: hydrolase Chain: A: PDB Molecule: rna polymerase ii subunit a c-terminal domain PDBTitle: the structure of fcp1, an essential rna polymerase ii ctd2 phosphatase
39	c3c1zA_	Alignment	not modelled	98.3	25	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
40	d1cdza_	Alignment	not modelled	98.3	14	Fold: BRCT domain Superfamily: BRCT domain Family: DNA-repair protein XRCC1
41	c2e2wA_	Alignment	not modelled	98.3	17	PDB header: ligase Chain: A: PDB Molecule: dna ligase 4; PDBTitle: solution structure of the first brct domain of human dna2 ligase iv
42	d1wf6a_	Alignment	not modelled	98.2	14	Fold: BRCT domain Superfamily: BRCT domain Family: DNA topoisomerase II binding protein 1, TopBP1
43	c3ktfB_	Alignment	not modelled	98.2	19	PDB header: cell cycle Chain: B: PDB Molecule: microcephalin; PDBTitle: structure of the n-terminal brct domain of human2 microcephalin (mcph1).
44	c2bhnD_	Alignment	not modelled	98.2	26	PDB header: hydrolase Chain: D: PDB Molecule: xpf endonuclease; PDBTitle: xpf from aeropyrum pernix
45	c3ii6Y_	Alignment	not modelled	98.1	19	PDB header: ligase/dna binding protein Chain: Y: PDB Molecule: dna ligase 4; PDBTitle: structure of human xrcc4 in complex with the tandem brct2 domains of dna ligaseiv.
46	d1kzyc1	Alignment	not modelled	98.1	14	Fold: BRCT domain Superfamily: BRCT domain Family: 53BP1
47	d2ilqa1	Alignment	not modelled	98.1	18	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
48	d2aq0a1	Alignment	not modelled	98.1	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
49	d1t15a2	Alignment	not modelled	98.0	21	Fold: BRCT domain Superfamily: BRCT domain Family: BRCT domain
50	c1a0iA_	Alignment	not modelled	98.0	16	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: atp-dependent dna ligase from bacteriophage t7 complex with2 atp
51	d1a0ia2	Alignment	not modelled	98.0	16	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: ATP-dependent DNA ligase catalytic domain
52	c1vs0A_	Alignment	not modelled	98.0	18	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
53	c1kzyD_	Alignment	not modelled	97.9	14	PDB header: dna binding protein, protein binding Chain: D: PDB Molecule: tumor suppressor p53-binding protein 1; PDBTitle: crystal structure of the 53bp1 brct region complexed to2 tumor suppressor p53
54	c2ebwA_	Alignment	not modelled	97.9	19	PDB header: transferase Chain: A: PDB Molecule: dna repair protein rev1; PDBTitle: solution structure of the brct domain from human dna repair2 protein rev1

55	d1pzna1	Alignment	not modelled	97.9	32	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
56	c2vxca	Alignment	not modelled	97.8	15	PDB header: cell cycle Chain: A: PDB Molecule: dna repair protein rhp9; PDBTitle: structure of the crb2-brct2 domain complex with2 phosphopeptide.
57	d1l0ba1	Alignment	not modelled	97.8	13	Fold: BRCT domain Superfamily: BRCT domain Family: BRCT domain
58	c3l40A	Alignment	not modelled	97.7	19	PDB header: cell cycle Chain: A: PDB Molecule: brct-containing protein 1; PDBTitle: crystal structure of s. pombe brct1 brct5-brct6 domains
59	d1szpa1	Alignment	not modelled	97.7	21	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
60	c2r1zB	Alignment	not modelled	97.6	19	PDB header: antitumor protein Chain: B: PDB Molecule: brca1-associated ring domain protein 1; PDBTitle: crystal structure of the bard1 brct repeat
61	c3al3A	Alignment	not modelled	97.6	18	PDB header: dna binding protein/protein binding Chain: A: PDB Molecule: dna topoisomerase 2-binding protein 1; PDBTitle: crystal structure of topbp1 brct7/8-bach1 peptide complex
62	c1b22A	Alignment	not modelled	97.5	15	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
63	d1b22a	Alignment	not modelled	97.5	15	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
64	c1y98A	Alignment	not modelled	97.5	12	PDB header: antitumor protein Chain: A: PDB Molecule: breast cancer type 1 susceptibility protein; PDBTitle: structure of the brct repeats of brca1 bound to a ctip2 phosphopeptide.
65	c1l0ba	Alignment	not modelled	97.4	13	PDB header: unknown function Chain: A: PDB Molecule: brca1; PDBTitle: crystal structure of rat brca1 tandem-brct region
66	c2azmB	Alignment	not modelled	97.4	11	PDB header: cell cycle Chain: B: PDB Molecule: mediator of dna damage checkpoint protein 1; PDBTitle: crystal structure of the mdc1 brct repeat in complex with2 the histone tail of gamma-h2ax
67	d1t15a1	Alignment	not modelled	97.4	12	Fold: BRCT domain Superfamily: BRCT domain Family: BRCT domain
68	c1ixrA	Alignment	not modelled	97.3	16	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
69	c2coeA	Alignment	not modelled	97.2	16	PDB header: transferase Chain: A: PDB Molecule: deoxynucleotidyltransferase, terminal variant; PDBTitle: solution structure of brct domain of terminal2 deoxynucleotidyltransferase
70	c1z56C	Alignment	not modelled	97.2	16	PDB header: ligase Chain: C: PDB Molecule: dna ligase iv; PDBTitle: co-crystal structure of lif1p-lig4p
71	c2w9mB	Alignment	not modelled	97.1	24	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
72	c1hjpA	Alignment	not modelled	97.1	21	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
73	c3kyhC	Alignment	not modelled	97.1	16	PDB header: protein binding Chain: C: PDB Molecule: mrna-capping enzyme subunit alpha; PDBTitle: saccharomyces cerevisiae cet1-ceg1 capping apparatus
74	c3s24F	Alignment	not modelled	97.0	16	PDB header: hydrolase, transferase Chain: F: PDB Molecule: mrna-capping enzyme; PDBTitle: crystal structure of human mrna guanylyltransferase
75	d1ckma2	Alignment	not modelled	97.0	16	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: mRNA capping enzyme
76	c2ihmA	Alignment	not modelled	97.0	22	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
77	c2jw5A	Alignment	not modelled	97.0	13	PDB header: protein binding Chain: A: PDB Molecule: dna polymerase lambda; PDBTitle: polymerase lambda brct domain
78	d1szpb1	Alignment	not modelled	96.9	16	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
79	c3t1nA	Alignment	not modelled	96.9	19	PDB header: cell cycle/peptide Chain: A: PDB Molecule: microcephalin; PDBTitle: structure of human microcephalin (mcph1) tandem brct domains in2 complex with a cdc27 phosphopeptide
80	c2h5xA	Alignment	not modelled	96.9	18	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
						PDB header: capping enzyme

81	c1cknA		Alignment	not modelled	96.9	16	Chain: A: PDB Molecule: mrna capping enzyme; PDBTitle: structure of guanylylated mrna capping enzyme complexed2 with gtp
82	d1ixra1		Alignment	not modelled	96.8	21	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
83	d1p16a2		Alignment	not modelled	96.7	20	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: mRNA capping enzyme
84	c2hvsA		Alignment	not modelled	96.7	17	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
85	d1cuka2		Alignment	not modelled	96.6	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
86	c1p16A		Alignment	not modelled	96.4	19	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
87	c1d8lA		Alignment	not modelled	96.1	20	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
88	d1pu6a		Alignment	not modelled	95.9	17	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)
89	d1bvsa2		Alignment	not modelled	95.8	26	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
90	c1kdhA		Alignment	not modelled	95.7	15	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
91	c2csdB		Alignment	not modelled	95.6	25	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
92	c2ep8A		Alignment	not modelled	95.6	12	PDB header: cell cycle Chain: A: PDB Molecule: pescadillo homolog 1; PDBTitle: solution structure of the brct domain from human pescadillo2 homolog 1
93	c2dunA		Alignment	not modelled	95.4	15	PDB header: transferase Chain: A: PDB Molecule: dna polymerase mu; PDBTitle: solution structure of brct domain of dna polymerase mu
94	d1lb2b		Alignment	not modelled	95.3	22	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
95	d1doqa		Alignment	not modelled	95.2	24	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
96	c8icZA		Alignment	not modelled	95.2	22	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)
97	c2bcuA		Alignment	not modelled	95.2	16	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
98	d1z3eb1		Alignment	not modelled	95.0	19	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
99	c2ziuA		Alignment	not modelled	94.9	14	PDB header: hydrolase Chain: A: PDB Molecule: mus81 protein; PDBTitle: crystal structure of the mus81-eme1 complex
100	d2p6ra2		Alignment	not modelled	94.7	20	Fold: Sec63 N-terminal domain-like Superfamily: Sec63 N-terminal domain-like Family: Achaeal helicase C-terminal domain
101	d1cooa		Alignment	not modelled	94.6	21	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
102	d1kzyc2		Alignment	not modelled	94.5	24	Fold: BRCT domain Superfamily: BRCT domain Family: 53BP1
103	d1l0ba2		Alignment	not modelled	94.5	21	Fold: BRCT domain Superfamily: BRCT domain Family: BRCT domain
104	d2a1ja1		Alignment	not modelled	94.3	22	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
105	c3f10A		Alignment	not modelled	94.2	30	PDB header: hydrolase, lyase Chain: A: PDB Molecule: 8-oxoguanine-dna-glycosylase; PDBTitle: crystal structure of clostridium acetobutylicum 8-2 oxoguanine dna glycosylase in complex with 8-oxoguanosine
106	d1s68a		Alignment	not modelled	93.9	20	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: RNA ligase

107	c1s5lu_	Alignment	not modelled	93.6	10	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
108	c2va8A_	Alignment	not modelled	93.2	18	PDB header: hydrolase Chain: A: PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
109	d2axtu1	Alignment	not modelled	92.8	10	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: PsbU-like
110	c2p6uA_	Alignment	not modelled	92.7	15	PDB header: dna binding protein Chain: A: PDB Molecule: afuhel308 helicase; PDBTitle: apo structure of the hel308 superfamily 2 helicase
111	d2noha1	Alignment	not modelled	92.3	29	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
112	d1keaa_	Alignment	not modelled	92.3	21	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
113	d1kg2a_	Alignment	not modelled	92.1	31	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
114	dlin1a_	Alignment	not modelled	91.7	11	Fold: BRCT domain Superfamily: BRCT domain Family: DNA ligase
115	c1ut8B_	Alignment	not modelled	91.5	15	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
116	d1xo1a1	Alignment	not modelled	91.3	15	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
117	c3n5nX_	Alignment	not modelled	91.0	40	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
118	d1ul1x1	Alignment	not modelled	91.0	23	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
119	d1rrqa1	Alignment	not modelled	90.9	33	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
120	d2abka_	Alignment	not modelled	90.9	24	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III