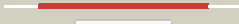



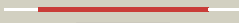








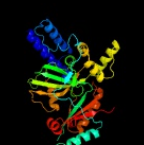



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3014c_ligA_3372555_3374630
Date	Thu Aug 8 16:20:18 BST 2019
Unique Job ID	08239361d6def205

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2owoA_	 Alignment		100.0	43	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	c1dgsB_	 Alignment		100.0	44	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
3	c1v9pB_	 Alignment		100.0	45	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
4	c4glxA_	 Alignment		100.0	44	PDB header: ligase/ligase inhibitor/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
5	c3sgIA_	 Alignment		100.0	100	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: crystal structure of dna ligase a brct domain deleted mutant of2 mycobacterium tuberculosis
6	c1zauA_	 Alignment		100.0	100	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: adenylation domain of nad+ dependent dna ligase from m.tuberculosis
7	c3pn1A_	 Alignment		100.0	43	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
8	d1ta8a_	 Alignment		100.0	41	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
9	c3jsIA_	 Alignment		100.0	40	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
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	d1b04a_	 Alignment		100.0	44	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase

12	d1v9pa3	Alignment		100.0	47	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD ⁺ -dependent DNA ligase
13	c4glwA	Alignment		100.0	39	PDB header: ligase/ligase inhibitor Chain: A: PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
14	c3bacA	Alignment		100.0	44	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: structural basis for the inhibition of bacterial nad ⁺ 2 dependent dna ligase
15	d1dgsa1	Alignment		100.0	37	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD ⁺ -dependent DNA ligase, domain 3
16	d1dgsa2	Alignment		100.0	50	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA ligase/mRNA capping enzyme postcatalytic domain
17	c6flqF	Alignment		99.8	21	PDB header: transcription Chain: F: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: cryoem structure of e.coli rna polymerase paused elongation complex2 bound to nusa
18	d1x9na3	Alignment		99.7	19	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: ATP-dependent DNA ligase catalytic domain
19	c2ebuA	Alignment		99.7	48	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
20	d1l7ba	Alignment		99.6	43	Fold: BRCT domain Superfamily: BRCT domain Family: DNA ligase
21	c2mutA	Alignment	not modelled	99.2	30	PDB header: hydrolase Chain: A: PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region
22	c2cokA	Alignment	not modelled	99.2	23	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
23	d2a1jb1	Alignment	not modelled	99.2	31	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
24	c3gdeA	Alignment	not modelled	99.1	20	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: the closed conformation of atp-dependent dna ligase from archaeoglobus2 fulgidus
25	c2hivA	Alignment	not modelled	99.0	18	PDB header: ligase Chain: A: PDB Molecule: thermostable dna ligase; PDBTitle: atp-dependent dna ligase from s. solfataricus
26	c3l2pA	Alignment	not modelled	99.0	16	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
27	c2vugB	Alignment	not modelled	99.0	20	PDB header: ligase Chain: B: PDB Molecule: pab1020; PDBTitle: the structure of an archaeal homodimeric rna ligase
28	d1x2ia1	Alignment	not modelled	99.0	32	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
						PDB header: ligase

29	c2cfmA	Alignment	not modelled	98.9	19	Chain: A: PDB Molecule: thermostable dna ligase; PDBTitle: atp-dependent dna ligase from pyrococcus furiosus
30	d2bgwa1	Alignment	not modelled	98.9	27	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
31	c4d05A	Alignment	not modelled	98.8	18	PDB header: ligase Chain: A: PDB Molecule: atp-dependent dna ligase; PDBTitle: structure and activity of a minimal-type atp-dependent dna ligase from2 a psychrotolerant bacterium
32	c3w1bA	Alignment	not modelled	98.8	16	PDB header: ligase Chain: A: PDB Molecule: dna ligase 4; PDBTitle: crystal structure of human dna ligase iv-artemis complex (mercury2 derivative)
33	c6dt1E	Alignment	not modelled	98.8	14	PDB header: ligase/dna Chain: E: PDB Molecule: dna ligase; PDBTitle: crystal structure of the ligase from bacteriophage t4 complexed with2 dna intermediate
34	c1x9nA	Alignment	not modelled	98.7	20	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
35	c6gdrA	Alignment	not modelled	98.7	19	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: dna binding with a minimal scaffold: structure-function analysis of2 lig e dna ligases
36	c2d8mA	Alignment	not modelled	98.7	16	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
37	c4bmcA	Alignment	not modelled	98.5	17	PDB header: replication Chain: A: PDB Molecule: s-m checkpoint control protein rad4; PDBTitle: crystal structure of s.pombe rad4 brct1,2
38	c6rasI	Alignment	not modelled	98.5	20	PDB header: dna binding protein Chain: I: PDB Molecule: atp-dependent dna ligase; PDBTitle: pmar-lig_pre.
39	c3ef0A	Alignment	not modelled	98.5	16	PDB header: hydrolase Chain: A: PDB Molecule: rna polymerase ii subunit a c-terminal domain phosphatase; PDBTitle: the structure of fcp1, an essential rna polymerase ii ctd phosphatase
40	d1kfta	Alignment	not modelled	98.5	26	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
41	c1kftA	Alignment	not modelled	98.5	26	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
42	c3qwua	Alignment	not modelled	98.5	19	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: putative atp-dependent dna ligase from aquifex aeolicus.
43	c6imnB	Alignment	not modelled	98.5	13	PDB header: ligase/dna Chain: B: PDB Molecule: dna ligase; PDBTitle: the crystal structure of asfvlig:ct2 complex
44	c3l3eA	Alignment	not modelled	98.4	16	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
45	c2lyhA	Alignment	not modelled	98.4	29	PDB header: dna binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215
46	c2couA	Alignment	not modelled	98.4	7	PDB header: cell cycle Chain: A: PDB Molecule: ect2 protein; PDBTitle: solution structure of the second brct domain of epithelial2 cell transforming 2
47	c2xnkA	Alignment	not modelled	98.4	25	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
48	c4bxoA	Alignment	not modelled	98.3	17	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
49	c1p8IA	Alignment	not modelled	98.3	14	PDB header: ligase Chain: A: PDB Molecule: pbcv-1 dna ligase; PDBTitle: new crystal structure of chlorella virus dna ligase-adenylate
50	c2nrzB	Alignment	not modelled	98.3	33	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
51	d1cdza	Alignment	not modelled	98.3	13	Fold: BRCT domain Superfamily: BRCT domain Family: DNA-repair protein XRCC1
52	c3ef1A	Alignment	not modelled	98.3	18	PDB header: hydrolase Chain: A: PDB Molecule: rna polymerase ii subunit a c-terminal domain phosphatase; PDBTitle: the structure of fcp1, an essential rna polymerase ii ctd phosphatase
53	c2e2wA	Alignment	not modelled	98.2	10	PDB header: ligase Chain: A: PDB Molecule: dna ligase 4; PDBTitle: solution structure of the first brct domain of human dna2 ligase iv
54	c3ii6Y	Alignment	not modelled	98.2	10	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. PDB header: cell cycle

55	c4n40A_	Alignment	not modelled	98.2	18	Chain: A: PDB Molecule: protein ect2; PDBTitle: crystal structure of human epithelial cell-transforming sequence 22 protein
56	c3ktfB_	Alignment	not modelled	98.2	22	PDB header: cell cycle Chain: B: PDB Molecule: microcephalin; PDBTitle: structure of the n-terminal brct domain of human microcephalin2 (mcph1).
57	d1fvia2	Alignment	not modelled	98.1	17	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: ATP-dependent DNA ligase catalytic domain
58	d1kzyc1	Alignment	not modelled	98.1	12	Fold: BRCT domain Superfamily: BRCT domain Family: 53BP1
59	d1w6a_	Alignment	not modelled	98.1	15	Fold: BRCT domain Superfamily: BRCT domain Family: DNA topoisomerase II binding protein 1, TopBP1
60	c3c1zA_	Alignment	not modelled	98.1	23	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 damage sensor2 protein
61	c2bhnD_	Alignment	not modelled	98.1	26	PDB header: hydrolase Chain: D: PDB Molecule: xpf endonuclease; PDBTitle: xpf from aeropyrum pernix
62	c4bxoB_	Alignment	not modelled	98.0	29	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
63	d2i1qa1	Alignment	not modelled	98.0	26	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
64	d1t15a2	Alignment	not modelled	98.0	17	Fold: BRCT domain Superfamily: BRCT domain Family: BRCT domain
65	c4bmdA_	Alignment	not modelled	98.0	19	PDB header: replication Chain: A: PDB Molecule: s-m checkpoint control protein rad4; PDBTitle: crystal structure of s.pombe rad4 brct3,4
66	d2aq0a1	Alignment	not modelled	98.0	21	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
67	c1kzyD_	Alignment	not modelled	97.9	13	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
68	c2vxCA_	Alignment	not modelled	97.9	15	PDB header: cell cycle Chain: A: PDB Molecule: dna repair protein rhp9; PDBTitle: structure of the crb2-brct2 domain complex with phosphopeptide.
69	c2ebwA_	Alignment	not modelled	97.9	20	PDB header: transferase Chain: A: PDB Molecule: dna repair protein rev1; PDBTitle: solution structure of the brct domain from human dna repair2 protein rev1
70	c1vs0A_	Alignment	not modelled	97.9	20	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
71	c1a0ia_	Alignment	not modelled	97.9	14	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: atp-dependent dna ligase from bacteriophage t7 complex with2 atp
72	c3ueoB_	Alignment	not modelled	97.8	19	PDB header: peptide binding protein Chain: B: PDB Molecule: dna topoisomerase 2-binding protein 1; PDBTitle: crystal structure of topbp1 brct4/5 domains in complex with a phospho-2 peptide
73	d1l0ba1	Alignment	not modelled	97.8	15	Fold: BRCT domain Superfamily: BRCT domain Family: BRCT domain
74	c5d1pB_	Alignment	not modelled	97.8	22	PDB header: ligase Chain: B: PDB Molecule: atp-dependent rna ligase; PDBTitle: archaeal atp-dependent rna ligase - form 2
75	d1a0ia2	Alignment	not modelled	97.8	16	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: ATP-dependent DNA ligase catalytic domain
76	d1pzna1	Alignment	not modelled	97.8	31	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
77	c3l40A_	Alignment	not modelled	97.7	17	PDB header: cell cycle Chain: A: PDB Molecule: brct-containing protein 1; PDBTitle: crystal structure of s. pombe brct5-brct6 domains
78	c2zj8A_	Alignment	not modelled	97.7	31	PDB header: hydrolase Chain: A: PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 2
79	c2r1zB_	Alignment	not modelled	97.7	20	PDB header: antitumor protein Chain: B: PDB Molecule: brca1-associated ring domain protein 1; PDBTitle: crystal structure of the bard1 brct repeat
80	c3al3A_	Alignment	not modelled	97.7	21	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
81	c4id3B_	Alianment	not modelled	97.7	19	PDB header: protein binding Chain: B: PDB Molecule: dna repair protein rev1;

					PDBTitle: crystal structure of the brct domain of s. cerevisiae rev1
82	d1t15a1	Alignment	not modelled	97.6	16 Fold: BRCT domain Superfamily: BRCT domain Family: BRCT domain
83	c1y98A	Alignment	not modelled	97.6	13 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.
84	c5covA	Alignment	not modelled	97.5	8 PDB header: ligase Chain: A; PDB Molecule: naegleria gruberi rna ligase; PDBTitle: structure and mechanism of a eukaryal nick-sealing rna ligase k170m+mn
85	d1szpa1	Alignment	not modelled	97.5	17 Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
86	c1l0bA	Alignment	not modelled	97.5	15 PDB header: unknown function Chain: A; PDB Molecule: brca1; PDBTitle: crystal structure of rat brca1 tandem-brct region
87	c3auoB	Alignment	not modelled	97.4	23 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
88	c2azmB	Alignment	not modelled	97.3	21 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
89	d1p16a2	Alignment	not modelled	97.3	19 Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: mRNA capping enzyme
90	c3kyhC	Alignment	not modelled	97.2	15 PDB header: protein binding Chain: C; PDB Molecule: mrna-capping enzyme subunit alpha; PDBTitle: saccharomyces cerevisiae cet1-ceg1 capping apparatus
91	d1ckma2	Alignment	not modelled	97.2	16 Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: mRNA capping enzyme
92	c1z56C	Alignment	not modelled	97.2	21 PDB header: ligase Chain: C; PDB Molecule: dna ligase iv; PDBTitle: co-crystal structure of lif1p-lig4p
93	c2coeA	Alignment	not modelled	97.1	16 PDB header: transferase Chain: A; PDB Molecule: deoxynucleotidyltransferase, terminal variant; PDBTitle: solution structure of brct domain of terminal2 deoxynucleotidyltransferase
94	c3t1nA	Alignment	not modelled	97.1	18 PDB header: cell cycle/peptide Chain: A; PDB Molecule: microcephalin; PDBTitle: structure of human microcephalin (mcp1) tandem brct domains in2 complex with a cdc27 phosphopeptide
95	c1cknA	Alignment	not modelled	97.1	15 PDB header: capping enzyme Chain: A; PDB Molecule: mrna capping enzyme; PDBTitle: structure of guanylated mrna capping enzyme complexed2 with gtp
96	c1p16A	Alignment	not modelled	97.1	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
97	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
98	d1b22a	Alignment	not modelled	97.0	18 Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
99	c1b22A	Alignment	not modelled	97.0	18 PDB header: dna binding protein Chain: A; PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
100	c1ixrA	Alignment	not modelled	97.0	25 PDB header: hydrolase Chain: A; PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
101	c2jw5A	Alignment	not modelled	97.0	16 PDB header: protein binding Chain: A; PDB Molecule: dna polymerase lambda; PDBTitle: polymerase lambda brct domain
102	c3vnnA	Alignment	not modelled	96.8	15 PDB header: ligase Chain: A; PDB Molecule: dna ligase 4; PDBTitle: crystal structure of a sub-domain of the nucleotidyltransferase2 (adenylation) domain of human dna ligase iv
103	c2hvsA	Alignment	not modelled	96.7	15 PDB header: ligase/dna/rna Chain: A; PDB Molecule: t4 rna ligase 2; PDBTitle: structure of t4 rna ligase 2 with nicked 5'-adenylated nucleic acid2 duplex containing a 2'-deoxyribonucleotide at the nick
104	d1ixra1	Alignment	not modelled	96.5	25 Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
105	c1hjpA	Alignment	not modelled	96.5	22 PDB header: dna recombination Chain: A; PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
106	d1cuka2	Alignment	not modelled	96.5	20 Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
107	c2h5xA	Alignment	not modelled	96.4	25 PDB header: dna binding protein Chain: A; PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis

108	c1ixrB_	Alignment	not modelled	96.3	28	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
109	d1szpb1	Alignment	not modelled	96.3	16	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
110	c2ihmA_	Alignment	not modelled	96.2	13	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
111	c2w9mB_	Alignment	not modelled	96.2	26	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
112	c2csdB_	Alignment	not modelled	96.1	20	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
113	c2ep8A_	Alignment	not modelled	95.6	10	PDB header: cell cycle Chain: A: PDB Molecule: pescadillo homolog 1; PDBTitle: solution structure of the brct domain from human pescadillo2 homolog 1
114	c2dunA_	Alignment	not modelled	95.5	15	PDB header: transferase Chain: A: PDB Molecule: dna polymerase mu; PDBTitle: solution structure of brct domain of dna polymerase mu
115	d1bvsa2	Alignment	not modelled	95.4	29	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
116	d1l0ba2	Alignment	not modelled	95.4	17	Fold: BRCT domain Superfamily: BRCT domain Family: BRCT domain
117	d1xdna_	Alignment	not modelled	95.3	14	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: RNA ligase
118	c1d8lA_	Alignment	not modelled	95.3	20	PDB header: gene regulation Chain: A: PDB Molecule: protein (holliday junction dna helicase ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region lacking2 domain iii
119	c8iczA_	Alignment	not modelled	95.3	20	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)
120	d1s68a_	Alignment	not modelled	95.0	21	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: RNA ligase