






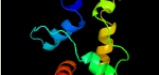















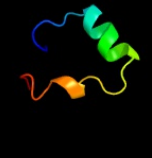

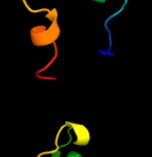
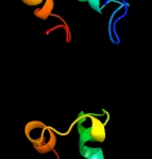
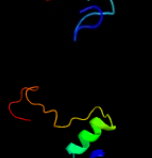
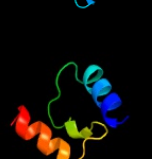

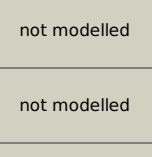


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2014 (-)_2261106_2261696
Date	Mon Aug 5 13:25:12 BST 2019
Unique Job ID	24fcf14ac768c337

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pu6a_	 Alignment		94.8	9	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)
2	c3fhgA_	 Alignment		94.8	9	PDB header: dna repair, hydrolase, lyase Chain: A: PDB Molecule: n-glycosylase/dna lyase; PDBTitle: crystal structure of sulfolobus solfataricus 8-oxoguanine dna2 glycosylase (ssogg)
3	c2h5xA_	 Alignment		94.7	19	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
4	c3n0uB_	 Alignment		94.2	13	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
5	d2bgwa1	 Alignment		94.1	20	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
6	d1cuka2	 Alignment		94.1	21	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
7	c1d8IA_	 Alignment		93.9	21	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
8	d1bvsa2	 Alignment		93.6	29	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
9	d1rrqa1	 Alignment		93.5	7	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
10	d1ixra1	 Alignment		93.5	29	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
11	c1ixrA_	 Alignment		93.4	19	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex

12	d2aq0a1	Alignment		93.4	12	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
13	d1mc8a1	Alignment		93.3	17	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
14	c4itqA_	Alignment		93.2	25	PDB header: gene regulation, structural protein/dna Chain: A: PDB Molecule: putative uncharacterized protein sco1480; PDBTitle: crystal structure of hypothetical protein sco1480 bound to dna
15	d1b43a1	Alignment		93.2	19	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
16	c1kftA_	Alignment		93.1	21	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
17	d1kfta_	Alignment		93.1	21	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
18	c4b24A_	Alignment		93.0	6	PDB header: hydrolase/dna Chain: A: PDB Molecule: probable dna-3-methyladenine glycosylase 2; PDBTitle: unprecedented sculpting of dna at abasic sites by dna glycosylase2 homolog mag2
19	c1rrqA_	Alignment		93.0	12	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
20	c3kntC_	Alignment		92.6	11	PDB header: hydrolase, lyase/dna Chain: C: PDB Molecule: n-glycosylase/dna lyase; PDBTitle: crystal structure of methanocaldococcus jannaschii 8-oxoguanine2 glycosylase/lyase in complex with 15mer dna containing 8-oxoguanine
21	d2abka_	Alignment	not modelled	92.5	17	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
22	d2a1jb1	Alignment	not modelled	92.3	20	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
23	d1orna_	Alignment	not modelled	92.2	15	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
24	d1x2ia1	Alignment	not modelled	92.1	24	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
25	d1keaa_	Alignment	not modelled	92.1	16	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
26	d1ul1x1	Alignment	not modelled	92.1	19	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
27	c1ixrB_	Alignment	not modelled	91.9	23	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
28	c2nrzB_	Alignment	not modelled	91.9	17	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
29	d3bzka1	Alignment	not modelled	91.8	14	Fold: SAM domain-like Superfamily: RuvA domain 2-like

						Family: Tex HhH-containing domain-like
30	c2mutA	Alignment	not modelled	91.7	17	PDB header: hydrolase Chain: A; PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region
31	dlrxwa1	Alignment	not modelled	91.3	20	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
32	d1a77a1	Alignment	not modelled	91.3	20	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
33	c4unfA	Alignment	not modelled	91.2	28	PDB header: lyase Chain: A; PDB Molecule: endonuclease iii-1; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-1
34	c1hjpA	Alignment	not modelled	91.1	13	PDB header: dna recombination Chain: A; PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
35	c2lyhA	Alignment	not modelled	90.3	20	PDB header: dna binding protein Chain: A; PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215
36	d2axtu1	Alignment	not modelled	90.3	14	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: PsbU-like
37	c4uobA	Alignment	not modelled	90.0	21	PDB header: lyase Chain: A; PDB Molecule: endonuclease iii-3; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-3
38	d1xo1a1	Alignment	not modelled	90.0	21	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
39	c3n5nX	Alignment	not modelled	89.8	16	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
40	c1b43A	Alignment	not modelled	89.0	19	PDB header: transferase Chain: A; PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
41	d1kg2a	Alignment	not modelled	88.7	16	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
42	c3s6iA	Alignment	not modelled	88.6	16	PDB header: hydrolase/dna Chain: A; PDB Molecule: dna-3-methyladenine glycosylase 1; PDBTitle: schizosaccharomyces pombe 3-methyladenine dna glycosylase (mag1) in2 complex with abasic-dna.
43	d1pzna1	Alignment	not modelled	88.4	25	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
44	d2edua1	Alignment	not modelled	88.4	23	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
45	d2i1qa1	Alignment	not modelled	87.9	24	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
46	c4bxoA	Alignment	not modelled	87.8	11	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
47	d1ngna	Alignment	not modelled	87.3	13	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
48	c6c34A	Alignment	not modelled	87.1	26	PDB header: dna binding protein Chain: A; PDB Molecule: 5'-3' exonuclease; PDBTitle: mycobacterium smegmatis dna flap endonuclease mutant d125n
49	c2oceA	Alignment	not modelled	86.4	17	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
50	c4q0rB	Alignment	not modelled	86.3	25	PDB header: hydrolase/dna Chain: B; PDB Molecule: dna repair protein rad2; PDBTitle: the catalytic core of rad2 (complex i)
51	c1s5lu	Alignment	not modelled	86.2	15	PDB header: photosynthesis Chain: U; PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
52	c1ut8B	Alignment	not modelled	85.6	16	PDB header: hydrolase Chain: B; PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
53	c2izoA	Alignment	not modelled	85.5	15	PDB header: hydrolase Chain: A; PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
54	d1dgsa1	Alignment	not modelled	85.4	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
55	c1rxvA	Alignment	not modelled	85.2	20	PDB header: hydrolase/dna Chain: A; PDB Molecule: flap structure-specific endonuclease; PDBTitle: crystal structure of a. fulgidus fen-1 bound to dna
56	c4bxoB	Alignment	not modelled	85.2	20	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
57	d1mpga1	Alignment	not modelled	85.0	13	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
58	c2ihmA	Alignment	not modelled	84.1	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
59	d2noha1	Alignment	not modelled	84.0	20	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
60	c3zddA	Alignment	not modelled	82.6	26	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein xni; PDBTitle: structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium
61	d2duya1	Alignment	not modelled	82.2	26	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
62	c2yg8B	Alignment	not modelled	81.7	19	PDB header: hydrolase Chain: B: PDB Molecule: dna-3-methyladenine glycosidase ii, putative; PDBTitle: structure of an unusual 3-methyladenine dna glycosylase ii (alka) from2 deinococcus radiodurans
63	c4ejyA	Alignment	not modelled	81.5	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: 3-methyladenine dna glycosylase; PDBTitle: structure of mbog1 in complex with high affinity dna ligand
64	c4wa8A	Alignment	not modelled	81.1	23	PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: methanopyrus kandleri fen-1 nuclease
65	c3f10A	Alignment	not modelled	80.9	13	PDB header: hydrolase, lyase Chain: A: PDB Molecule: 8-oxoguanine-dna-glycosylase; PDBTitle: crystal structure of clostridium acetobutylicum 8-oxoguanine dna2 glycosylase in complex with 8-oxoguanosine
66	c1ko9A	Alignment	not modelled	80.9	20	PDB header: hydrolase Chain: A: PDB Molecule: 8-oxoguanine dna glycosylase; PDBTitle: native structure of the human 8-oxoguanine dna glycosylase2 hogg1
67	c1yqmA	Alignment	not modelled	80.7	20	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
68	c1kdhA	Alignment	not modelled	80.6	14	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
69	c3q8IA	Alignment	not modelled	80.2	25	PDB header: hydrolase/dna Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of human flap endonuclease fen1 (wt) in complex with2 substrate 5'-flap dna, sm3+, and k+
70	c4p4oA	Alignment	not modelled	80.2	26	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
71	c1ul1Y	Alignment	not modelled	80.1	25	PDB header: hydrolase/dna binding protein Chain: Y: PDB Molecule: flap endonuclease-1; PDBTitle: crystal structure of the human fen1-pcna complex
72	d1cmwa1	Alignment	not modelled	79.9	28	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
73	c1mpgB	Alignment	not modelled	78.3	13	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna glycosylase ii; PDBTitle: 3-methyladenine dna glycosylase ii from escherichia coli
74	c5t9jB	Alignment	not modelled	77.5	20	PDB header: hydrolase Chain: B: PDB Molecule: flap endonuclease gen homolog 1; PDBTitle: crystal structure of human gen1 in complex with holliday junction dna2 in the upper interface
75	c1a77A	Alignment	not modelled	77.4	21	PDB header: 5'-3' exo/endo nuclease Chain: A: PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii
76	c1nomA	Alignment	not modelled	77.3	24	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)
77	c2jhnB	Alignment	not modelled	77.2	23	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna-glycosylase; PDBTitle: 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
78	c8icZA	Alignment	not modelled	77.2	18	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)
79	c3psfA	Alignment	not modelled	77.1	9	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(236-1259)
80	c2bcuA	Alignment	not modelled	77.0	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
81	c2bhnD	Alignment	not modelled	77.0	23	PDB header: hydrolase Chain: D: PDB Molecule: xpf endonuclease; PDBTitle: xpf from aeropyrum pernix

82	c3oryA	Alignment	not modelled	75.4	21	PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus
83	c2csdB	Alignment	not modelled	75.2	33	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
84	c3auoB	Alignment	not modelled	74.8	17	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
85	c3psiA	Alignment	not modelled	74.5	8	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451)
86	c2h56C	Alignment	not modelled	74.1	7	PDB header: hydrolase Chain: C: PDB Molecule: dna-3-methyladenine glycosidase; PDBTitle: crystal structure of dna-3-methyladenine glycosidase (10174367) from2 bacillus halodurans at 2.55 a resolution
87	c1vddC	Alignment	not modelled	73.7	27	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
88	c5zvqA	Alignment	not modelled	73.3	27	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
89	d1vdda	Alignment	not modelled	72.6	27	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
90	c4qlxA	Alignment	not modelled	71.3	15	PDB header: ligase/ligase inhibitor/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
91	c5z2vB	Alignment	not modelled	71.0	23	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
92	c6gmhM	Alignment	not modelled	70.6	13	PDB header: transcription Chain: M: PDB Molecule: transcription elongation factor spt6,transcription PDBTitle: structure of activated transcription complex pol ii-dsif-paf-spt6
93	c5o19A	Alignment	not modelled	69.8	11	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor, mitochondrial; PDBTitle: structure of human mitochondrial transcription elongation factor2 (tefm) n-terminal domain
94	d2fmpa1	Alignment	not modelled	67.6	21	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
95	c2w9mB	Alignment	not modelled	67.5	16	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
96	c2owoA	Alignment	not modelled	66.7	15	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
97	d2bcqa1	Alignment	not modelled	64.5	12	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
98	d1szpa1	Alignment	not modelled	64.5	14	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
99	c3qeaZ	Alignment	not modelled	63.3	15	PDB header: hydrolase/dna Chain: Z: PDB Molecule: exonuclease 1; PDBTitle: crystal structure of human exonuclease 1 exo1 (wt) in complex with dna2 (complex ii)
100	c6h5hA	Alignment	not modelled	62.9	17	PDB header: unknown function Chain: A: PDB Molecule: polb4; PDBTitle: a computationally designed drp lyase domain reconstructed from two2 heterologous fragments
101	c1cmwA	Alignment	not modelled	61.6	32	PDB header: transferase Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: crystal structure of taq dna-polymerase shows a new orientation for2 the structure-specific nuclease domain
102	c2ziuA	Alignment	not modelled	60.9	12	PDB header: hydrolase Chain: A: PDB Molecule: mus81 protein; PDBTitle: crystal structure of the mus81-eme1 complex
103	d2vana1	Alignment	not modelled	60.5	21	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
104	d1nzpa	Alignment	not modelled	60.1	10	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
105	d2fmpa2	Alignment	not modelled	59.8	17	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
106	c1dgsB	Alignment	not modelled	55.2	25	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
107	d1b0aa1	Alignment	not modelled	55.2	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
						PDB header: hydrolase

108	c2zj8A_	Alignment	not modelled	51.6	20	Chain: A: PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 2
109	c1b22A_	Alignment	not modelled	50.4	22	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
110	d1b22a_	Alignment	not modelled	50.4	22	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
111	d1jmsa1	Alignment	not modelled	49.9	9	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
112	d1d8ba_	Alignment	not modelled	49.4	13	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
113	d2bcqa2	Alignment	not modelled	49.0	21	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
114	c2kp7A_	Alignment	not modelled	48.7	9	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
115	d2a1ja1	Alignment	not modelled	48.2	10	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
116	d1szpb1	Alignment	not modelled	46.1	14	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
117	c5o9zH_	Alignment	not modelled	44.7	13	PDB header: splicing Chain: H: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp31; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
118	d1dk2a_	Alignment	not modelled	43.4	21	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
119	c1v9pB_	Alignment	not modelled	43.2	28	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
120	c2ihnA_	Alignment	not modelled	43.1	13	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate