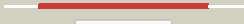



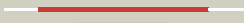

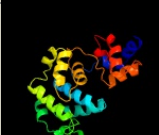
















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1870c_(-)_2120802_2121437
Date	Fri Aug 2 13:30:48 BST 2019
Unique Job ID	9c6b070ec37dd32b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1mpgB_	 Alignment		100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna glycosylase ii; PDBTitle: 3-methyladenine dna glycosylase ii from escherichia coli
2	c4b24A_	 Alignment		100.0	12	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
3	d1pu6a_	 Alignment		100.0	17	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)
4	c3s6iA_	 Alignment		100.0	20	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.
5	c2yg8B_	 Alignment		100.0	18	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
6	c2jhnB_	 Alignment		100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna-glycosylase; PDBTitle: 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
7	d1orna_	 Alignment		100.0	18	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
8	d1mpga1	 Alignment		100.0	22	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
9	c4unfA_	 Alignment		100.0	22	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-1; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-1
10	c4uobA_	 Alignment		100.0	17	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-3; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-3
11	d2abka_	 Alignment		100.0	16	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III

12	d1keaa_	Alignment		100.0	12	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
13	d1rrqa1	Alignment		100.0	18	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
14	d1kg2a_	Alignment		100.0	14	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
15	c3f10A_	Alignment		100.0	18	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
16	c3fhgA_	Alignment		100.0	23	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)
17	c3n5nX_	Alignment		100.0	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
18	c4ejyA_	Alignment		100.0	19	PDB header: hydrolase/dna Chain: A: PDB Molecule: 3-methyladenine dna glycosylase; PDBTitle: structure of mbogg1 in complex with high affinity dna ligand
19	c2h56C_	Alignment		100.0	19	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
20	c1yqmA_	Alignment		100.0	17	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
21	c3kntC_	Alignment	not modelled	100.0	16	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
22	c1rrqa_	Alignment	not modelled	100.0	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
23	c1ko9A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: 8-oxoguanine dna glycosylase; PDBTitle: native structure of the human 8-oxoguanine dna glycosylase2 hogg1
24	d2noha1	Alignment	not modelled	100.0	19	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
25	c3n0uB_	Alignment	not modelled	99.9	23	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
26	d1ngna_	Alignment	not modelled	99.9	14	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
27	d1dgsa1	Alignment	not modelled	96.8	21	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
28	c2jg6A_	Alignment	not modelled	96.6	16	PDB header: hydrolase Chain: A: PDB Molecule: dna-3-methyladenine glycosidase; PDBTitle: crystal structure of a 3-methyladenine dna glycosylase i from2 staphylococcus aureus

29	c2owoA	Alignment	not modelled	96.5	17	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
30	d1nkua	Alignment	not modelled	96.5	15	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase I (Tag)
31	c4glxA	Alignment	not modelled	96.4	17	PDB header: ligase/ligase inhibitor/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
32	c6flqF	Alignment	not modelled	96.1	22	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
33	d1szpa1	Alignment	not modelled	96.1	30	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
34	c1dgsB	Alignment	not modelled	96.0	21	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
35	c2ihmA	Alignment	not modelled	95.6	17	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
36	d2i1qa1	Alignment	not modelled	95.6	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
37	c3auoB	Alignment	not modelled	95.4	13	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
38	d1pzna1	Alignment	not modelled	95.4	20	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
39	d1szpb1	Alignment	not modelled	95.3	30	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
40	c1v9pB	Alignment	not modelled	95.2	21	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
41	c1b22A	Alignment	not modelled	95.1	24	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
42	d1b22a	Alignment	not modelled	95.1	24	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
43	c8iczA	Alignment	not modelled	95.1	32	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 datp3 (1 millimolar), mncl2 (5 millimolar), and lithium sulfate4 (75 millimolar)
44	c1ixrB	Alignment	not modelled	94.6	18	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
45	d1cuka2	Alignment	not modelled	94.5	22	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
46	c2csdB	Alignment	not modelled	94.4	19	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
47	c2h5xA	Alignment	not modelled	94.3	27	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
48	c1d8IA	Alignment	not modelled	94.3	22	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
49	c1kdhA	Alignment	not modelled	94.2	11	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
50	d2bgwa1	Alignment	not modelled	93.6	20	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
51	c2mutA	Alignment	not modelled	93.1	16	PDB header: hydrolase Chain: A: PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region
52	c2bcuA	Alignment	not modelled	93.0	20	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
53	c1vddC	Alignment	not modelled	92.9	19	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
54	c2w0mB	Alignment	not modelled	92.6	19	PDB header: dna replication Chain: B: PDB Molecule: polymerase x;

54	c2w2mb_	Alignment	not modelled	92.0	19	PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
55	d1ixra1	Alignment	not modelled	92.5	26	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
56	d1bvsa2	Alignment	not modelled	92.5	35	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
57	d1x2ia1	Alignment	not modelled	92.4	23	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
58	d1vdda_	Alignment	not modelled	92.3	19	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
59	c4p4oA_	Alignment	not modelled	92.3	16	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
60	c5zvqA_	Alignment	not modelled	92.3	23	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
61	c5z2vB_	Alignment	not modelled	91.9	13	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
62	c1kftA_	Alignment	not modelled	91.8	17	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
63	d1kfta_	Alignment	not modelled	91.8	17	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
64	c1ixrA_	Alignment	not modelled	91.7	26	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
65	c1hjpA_	Alignment	not modelled	91.4	21	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
66	c5o19A_	Alignment	not modelled	90.7	12	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor, mitochondrial; PDBTitle: structure of human mitochondrial transcription elongation factor2 (tefm) n-terminal domain
67	c1nomA_	Alignment	not modelled	89.5	29	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)
68	d2fmpa2	Alignment	not modelled	86.3	32	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
69	c5agaA_	Alignment	not modelled	85.6	18	PDB header: transferase Chain: A: PDB Molecule: dna polymerase theta; PDBTitle: crystal structure of the helicase domain of human dna2 polymerase theta in complex with amppnp
70	d2a1jb1	Alignment	not modelled	85.5	18	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
71	d2vana1	Alignment	not modelled	85.0	29	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
72	d2aq0a1	Alignment	not modelled	82.1	9	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
73	d2bcqa1	Alignment	not modelled	80.8	13	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
74	d1a77a1	Alignment	not modelled	79.4	44	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
75	d1jmsa3	Alignment	not modelled	79.3	15	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
76	c4itqA_	Alignment	not modelled	78.7	14	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
77	c4bxoB_	Alignment	not modelled	78.6	10	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
78	c3clzA_	Alignment	not modelled	77.6	26	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
79	d1mc8a1	Alignment	not modelled	77.4	44	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
80	d1jmsa1	Alignment	not modelled	76.9	11	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like

81	c2zj8A_	Alignment	not modelled	76.7	19	PDB header: hydrolase Chain: A: PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 2
82	d2bccqa2	Alignment	not modelled	76.2	12	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain
83	c2nrzB_	Alignment	not modelled	75.9	19	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
84	c1s5lu_	Alignment	not modelled	75.6	17	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
85	d1b43a1	Alignment	not modelled	75.6	44	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
86	c6h5hA_	Alignment	not modelled	75.4	25	PDB header: unknown function Chain: A: PDB Molecule: polb4; PDBTitle: a computationally designed drp lyase domain reconstructed from two2 heterologous fragments
87	d2edua1	Alignment	not modelled	74.2	18	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
88	d2axtu1	Alignment	not modelled	73.5	17	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: PsbU-like
89	d2fmpa1	Alignment	not modelled	73.4	13	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
90	d2duya1	Alignment	not modelled	73.4	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
91	c2kp7A_	Alignment	not modelled	72.6	18	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
92	d1nzpa_	Alignment	not modelled	71.7	24	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
93	d1xo1a1	Alignment	not modelled	70.5	33	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
94	d1j94m_	Alignment	not modelled	69.1	26	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
95	c3gp8A_	Alignment	not modelled	68.6	24	PDB header: hydrolase/dna Chain: A: PDB Molecule: exodeoxyribonuclease v, subunit recd, putative; PDBTitle: crystal structure of the binary complex of recd2 with dna
96	c3iz6M_	Alignment	not modelled	68.1	17	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s18 (s13p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
97	c3j20O_	Alignment	not modelled	67.6	26	PDB header: ribosome Chain: O: PDB Molecule: 30s ribosomal protein s13p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
98	d1rxwa1	Alignment	not modelled	67.1	20	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
99	c5mmjm_	Alignment	not modelled	67.0	16	PDB header: ribosome Chain: M: PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome
100	c2xznM_	Alignment	not modelled	65.9	26	PDB header: ribosome Chain: M: PDB Molecule: rps18e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
101	d3bzka1	Alignment	not modelled	65.4	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HHH-containing domain-like
102	c1ut8B_	Alignment	not modelled	63.0	33	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
103	c2zkqm_	Alignment	not modelled	62.5	22	PDB header: ribosomal protein/rna Chain: M: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
104	d2gy9m1	Alignment	not modelled	62.3	26	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
105	c2lyhA_	Alignment	not modelled	61.4	15	PDB header: dna binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215
106	c5o5jM_	Alignment	not modelled	61.1	26	PDB header: ribosome Chain: M: PDB Molecule: 30s ribosomal protein s13; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
						Fold: SAM domain-like

107	d1cmwa1	Alignment	not modelled	60.0	44	Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
108	c5lm7A	Alignment	not modelled	59.7	15	PDB header: transcription Chain: A: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: crystal structure of the lambda n-nus factor complex
109	c5xyiS	Alignment	not modelled	59.5	32	PDB header: ribosome Chain: S: PDB Molecule: ribosomal protein s13p/s18e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
110	d1ul1x1	Alignment	not modelled	59.0	27	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
111	c3ve5D	Alignment	not modelled	58.4	20	PDB header: recombination Chain: D: PDB Molecule: recombination protein recr; PDBTitle: structure of recombination mediator protein recr16-196 deletion mutant
112	d2uubm1	Alignment	not modelled	57.4	26	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
113	d1dk2a	Alignment	not modelled	56.9	13	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
114	c4bxoA	Alignment	not modelled	55.3	16	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
115	d1gm5a2	Alignment	not modelled	53.1	13	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RecG "wedge" domain
116	d1u9la	Alignment	not modelled	53.1	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: NusA extra C-terminal domains
117	d1d8ba	Alignment	not modelled	52.3	17	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
118	c3zddA	Alignment	not modelled	52.1	40	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
119	c2izoA	Alignment	not modelled	48.7	27	PDB header: hydrolase Chain: A: PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
120	c1a77A	Alignment	not modelled	47.8	44	PDB header: 5'-3' exo/endo nuclease Chain: A: PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii