

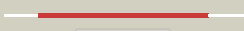





















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3674c_(nth)_4115335_4116072
Date	Fri Aug 9 18:20:36 BST 2019
Unique Job ID	48d4e24ddf4bec4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1rrqA_	 Alignment		100.0	27	PDB header: hydrolase/dna Chain: A; PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
2	d1orna_	 Alignment		100.0	41	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
3	d2abka_	 Alignment		100.0	35	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
4	c3n5nX_	 Alignment		100.0	24	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
5	d1rrqa1	 Alignment		100.0	27	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
6	d1keaa_	 Alignment		100.0	20	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
7	d1kq2a_	 Alignment		100.0	21	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
8	c4unfA_	 Alignment		100.0	23	PDB header: lyase Chain: A; PDB Molecule: endonuclease iii-1; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-1
9	c4uobA_	 Alignment		100.0	29	PDB header: lyase Chain: A; PDB Molecule: endonuclease iii-3; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-3
10	d1pu6a_	 Alignment		100.0	20	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)
11	c3f10A_	 Alignment		100.0	12	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

12	c3n0uB_	Alignment		100.0	15	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
13	c4ejyA_	Alignment		100.0	14	PDB header: hydrolase/dna Chain: A: PDB Molecule: 3-methyladenine dna glycosylase; PDBTitle: structure of mbogg1 in complex with high affinity dna ligand
14	c3kntC_	Alignment		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
15	c4b24A_	Alignment		100.0	13	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
16	c2yg8B_	Alignment		100.0	17	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
17	c3s6iA_	Alignment		100.0	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: dna-3-methyladenine glycosylase 1; PDBTitle: schizosaccaromyces pombe 3-methyladenine dna glycosylase (mag1) in2 complex with abasic-dna.
18	c1ko9A_	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: 8-oxoguanine dna glycosylase; PDBTitle: native structure of the human 8-oxoguanine dna glycosylase2 hogg1
19	c1yqmA_	Alignment		100.0	21	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
20	c3fhgA_	Alignment		100.0	17	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)
21	d1ngna_	Alignment	not modelled	100.0	18	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
22	d1mpga1	Alignment	not modelled	100.0	23	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
23	d2noha1	Alignment	not modelled	100.0	24	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
24	c2jhnB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna-glycosylase; PDBTitle: 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
25	c1mpgB_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna glycosylase ii; PDBTitle: 3-methyladenine dna glycosylase ii from escherichia coli
26	c2h56C_	Alignment	not modelled	99.9	10	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
27	c2h5xA_	Alignment	not modelled	96.9	14	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
28	c2jg6A_	Alignment	not modelled	95.6	17	PDB header: hydrolase Chain: A: PDB Molecule: dna-3-methyladenine glycosidase; PDBTitle: crystal structure of a 3-methyladenine dna glycosylase i from2 staphylococcus aureus
						Fold: DNA-glycosylase

29	d1nkua_	Alignment	not modelled	95.6	20	Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase I (Tag)
30	c1vddC	Alignment	not modelled	95.4	21	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
31	c2ihmA	Alignment	not modelled	95.3	20	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase mu; PDBTitle: polymerase mu in ternary complex with gapped 11mer dna duplex and 2 bound incoming nucleotide
32	d1vdda_	Alignment	not modelled	95.1	21	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
33	d1dgsa1	Alignment	not modelled	94.6	31	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
34	c1kdhA	Alignment	not modelled	94.4	17	PDB header: transferase/dna Chain: A: PDB Molecule: terminal deoxynucleotidyltransferase short PDBTitle: binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
35	d2fmpa1	Alignment	not modelled	94.3	20	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
36	d1cuka2	Alignment	not modelled	94.3	31	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
37	c1ixrB_	Alignment	not modelled	94.2	23	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
38	d1ixra1	Alignment	not modelled	94.2	36	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
39	c1ixrA_	Alignment	not modelled	94.1	36	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
40	c5z2vB_	Alignment	not modelled	93.9	21	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
41	c1d8IA_	Alignment	not modelled	93.9	33	PDB header: gene regulation Chain: A: PDB Molecule: protein (holliday junction dna helicase ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region lacking 2 domain iii
42	d1bvsa2	Alignment	not modelled	93.7	27	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
43	c5zvqA_	Alignment	not modelled	93.5	30	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
44	d2bccqa1	Alignment	not modelled	93.3	21	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
45	c3auoB_	Alignment	not modelled	93.3	19	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
46	c2bcuA_	Alignment	not modelled	93.0	18	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
47	c6h5hA_	Alignment	not modelled	92.9	21	PDB header: unknown function Chain: A: PDB Molecule: polb4; PDBTitle: a computationally designed drp lyase domain reconstructed from two2 heterologous fragments
48	c1hjpA_	Alignment	not modelled	92.3	14	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
49	d2bgwa1	Alignment	not modelled	92.2	24	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
50	d1nzpa_	Alignment	not modelled	92.2	21	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
51	d1jmsa1	Alignment	not modelled	92.1	14	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
52	d1dk2a_	Alignment	not modelled	91.9	20	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
53	c2w9mB_	Alignment	not modelled	91.5	24	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
54	d2i1qa1	Alignment	not modelled	91.0	28	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
55	d1szpa1	Alignment	not modelled	90.8	28	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain

56	c8iczA	Alignment	not modelled	90.2	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 with 2 seven base pairs of dna; soaked in the presence of of datp3 (1 millimolar), mnc12 (5 millimolar), and lithium sulfate4 (75 millimolar)
57	d1x2ia1	Alignment	not modelled	89.9	22	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
58	c1nomA	Alignment	not modelled	89.9	20	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 the presence of mnc12 (5 millimolar)
59	c2csdB	Alignment	not modelled	89.7	24	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
60	d2a1jb1	Alignment	not modelled	89.6	14	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
61	d1pzna1	Alignment	not modelled	88.4	23	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
62	c2owoA	Alignment	not modelled	88.3	19	PDB header: ligase/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: last stop on the road to repair: structure of e.coli dna ligase bound to nicked dna-adenylate
63	c1dgsB	Alignment	not modelled	88.0	22	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
64	d2edua1	Alignment	not modelled	86.8	32	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
65	c4glxA	Alignment	not modelled	86.6	19	PDB header: ligase/ligase inhibitor/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
66	c2kp7A	Alignment	not modelled	86.5	7	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
67	c2mutA	Alignment	not modelled	85.2	19	PDB header: hydrolase Chain: A: PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region
68	c4p4oA	Alignment	not modelled	85.0	19	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
69	c5zb8B	Alignment	not modelled	84.7	14	PDB header: dna binding protein Chain: B: PDB Molecule: pfuendoq; PDBTitle: crystal structure of the novel lesion-specific endonuclease pfuendoq2 from pyrococcus furiosus
70	c1v9pB	Alignment	not modelled	84.1	22	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
71	d2duya1	Alignment	not modelled	84.0	32	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
72	d2aq0a1	Alignment	not modelled	82.7	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
73	c3gp8A	Alignment	not modelled	82.6	25	PDB header: hydrolase/dna Chain: A: PDB Molecule: exodeoxyribonuclease v, subunit recd, putative; PDBTitle: crystal structure of the binary complex of recd2 with dna
74	d1kfta	Alignment	not modelled	82.6	12	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
75	c1kftA	Alignment	not modelled	82.6	12	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
76	c1b22A	Alignment	not modelled	81.8	24	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
77	d1b22a	Alignment	not modelled	81.8	24	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
78	d3bzka1	Alignment	not modelled	81.2	23	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HHH-containing domain-like
79	c1s5lu	Alignment	not modelled	79.7	16	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
80	c2lyhA	Alignment	not modelled	78.6	18	PDB header: dna binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215
81	d1szpb1	Alignment	not modelled	78.4	28	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
						Fold: SAM domain-like

82	d2axtu1	Alignment	not modelled	77.8	15	Superfamily: PsbU/PoIX domain-like Family: PsbU-like
83	d2vana1	Alignment	not modelled	77.6	22	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
84	d1d8ba_	Alignment	not modelled	77.4	27	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
85	c3psfA_	Alignment	not modelled	77.0	21	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)
86	d2fmpa2	Alignment	not modelled	76.5	19	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
87	d2bcqa2	Alignment	not modelled	76.4	28	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
88	c5ol9A_	Alignment	not modelled	76.0	9	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor, mitochondrial; PDBTitle: structure of human mitochondrial transcription elongation factor2 (tefm) n-terminal domain
89	d1jmsa3	Alignment	not modelled	75.8	33	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
90	d1a77a1	Alignment	not modelled	75.4	29	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
91	c2bhnD_	Alignment	not modelled	72.8	14	PDB header: hydrolase Chain: D: PDB Molecule: xpf endonuclease; PDBTitle: xpf from aeropyrum pernix
92	c3psiA_	Alignment	not modelled	72.5	24	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)
93	c3ve5D_	Alignment	not modelled	72.0	25	PDB header: recombination Chain: D: PDB Molecule: recombination protein recr; PDBTitle: structure of recombination mediator protein recr16-196 deletion mutant
94	d1xo1a1	Alignment	not modelled	71.3	29	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
95	d1rxwa1	Alignment	not modelled	71.0	33	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
96	c4itqA_	Alignment	not modelled	69.4	44	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
97	d1mc8a1	Alignment	not modelled	69.0	36	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
98	c3c1zA_	Alignment	not modelled	69.0	14	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
99	c4bxoB_	Alignment	not modelled	68.7	18	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
100	c6gmhM_	Alignment	not modelled	68.7	21	PDB header: transcription Chain: M: PDB Molecule: transcription elongation factor spt6,transcription PDBTitle: structure of activated transcription complex pol ii-dsif-paf-spt6
101	d1b43a1	Alignment	not modelled	67.0	36	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
102	d1lb2b_	Alignment	not modelled	66.2	32	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
103	d1ul1x1	Alignment	not modelled	62.6	29	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
104	c2va8A_	Alignment	not modelled	62.5	25	PDB header: hydrolase Chain: A: PDB Molecule: ski2-type helicase; PDBTitle: dna repair helicase hel308
105	c2ziuA_	Alignment	not modelled	62.1	24	PDB header: hydrolase Chain: A: PDB Molecule: mus81 protein; PDBTitle: crystal structure of the mus81-eme1 complex
106	d1z3eb1	Alignment	not modelled	61.9	21	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
107	c6flqF_	Alignment	not modelled	61.7	23	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 PDB header: hydrolase/dna

108	c4bxoA	Alignment	not modelled	60.7	11	Chain: A: PDB Molecule: fanconi anemia group m protein; PDBTitle: architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex
109	c2oceA	Alignment	not modelled	60.7	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
110	d1cooa	Alignment	not modelled	60.4	32	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
111	d1i94m	Alignment	not modelled	60.1	29	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
112	c4cdgA	Alignment	not modelled	59.9	21	PDB header: hydrolase Chain: A: PDB Molecule: bloom syndrome protein; PDBTitle: crystal structure of the bloom's syndrome helicase blm in complex with2 nanobody
113	c5agaA	Alignment	not modelled	59.6	11	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
114	d1doqa	Alignment	not modelled	59.4	26	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
115	d2i5ha1	Alignment	not modelled	59.0	33	Fold: AF1531-like Superfamily: AF1531-like Family: AF1531-like
116	c2i5hA	Alignment	not modelled	59.0	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1531; PDBTitle: crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
117	c3j20O	Alignment	not modelled	58.4	25	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)
118	c1ut8B	Alignment	not modelled	57.8	29	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
119	c2nrzB	Alignment	not modelled	56.5	12	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
120	c3iz6M	Alignment	not modelled	56.1	35	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