







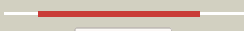















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1156_(-)_1282311_1282898
Date	Wed Jul 31 22:05:24 BST 2019
Unique Job ID	d8a1ee85cf4963f1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	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
2	c1mpgB_	 Alignment		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna glycosylase ii; PDBTitle: 3-methyladenine dna glycosylase ii from escherichia coli
3	c3s6iA_	 Alignment		100.0	15	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.
4	c4b24A_	 Alignment		100.0	10	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
5	d1mpga1	 Alignment		100.0	22	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
6	d1keaa_	 Alignment		100.0	14	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
7	c4uobA_	 Alignment		100.0	14	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-3; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-3
8	d1pu6a_	 Alignment		100.0	19	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII)
9	d1orna_	 Alignment		100.0	17	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
10	d2abka_	 Alignment		100.0	18	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
11	c4unfA_	 Alignment		100.0	20	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-1; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-1

12	c1rrqA_	Alignment		100.0	19	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
13	d2noha1	Alignment		100.0	17	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains
14	c3f10A_	Alignment		100.0	20	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
15	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
16	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
17	d1kq2a_	Alignment		100.0	14	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
18	c1ko9A_	Alignment		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
19	c3n5nX_	Alignment		100.0	18	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
20	d1ngna_	Alignment		100.0	14	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
21	c2jhnB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna-glycosylase; PDBTitle: 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
22	d1rrqa1	Alignment	not modelled	100.0	16	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
23	c3fhgA_	Alignment	not modelled	100.0	19	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)
24	c3kntC_	Alignment	not modelled	99.9	14	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
25	c3n0uB_	Alignment	not modelled	99.9	18	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	c2h56C_	Alignment	not modelled	99.9	14	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	c2jg6A_	Alignment	not modelled	97.3	19	PDB header: hydrolase Chain: A: PDB Molecule: dna-3-methyladenine glycosidase; PDBTitle: crystal structure of a 3-methyladenine dna glycosylase i from2 staphylococcus aureus
28	d1nkua_	Alignment	not modelled	97.3	17	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase I (Tag)

29	d1dgsa1	Alignment	not modelled	96.2	24	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
30	c2ihmA	Alignment	not modelled	95.9	15	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
31	c1vddC	Alignment	not modelled	95.5	36	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
32	d1vdda	Alignment	not modelled	95.5	36	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
33	c8iczA	Alignment	not modelled	95.2	21	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), mnc12 (5 millimolar), and lithium sulfate4 (75 millimolar)
34	c1kdhA	Alignment	not modelled	95.1	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
35	c5z2vB	Alignment	not modelled	95.1	29	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
36	c5zvqA	Alignment	not modelled	95.1	32	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
37	c3auoB	Alignment	not modelled	95.0	16	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	c2mutA	Alignment	not modelled	94.9	24	PDB header: hydrolase Chain: A: PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region
39	c2bcuA	Alignment	not modelled	94.0	22	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
40	c1ixrA	Alignment	not modelled	93.4	21	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
41	c1d8IA	Alignment	not modelled	93.1	24	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
42	c1kftA	Alignment	not modelled	93.0	22	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
43	d1kfta	Alignment	not modelled	93.0	22	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain
44	d2bgwa1	Alignment	not modelled	92.9	26	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
45	c2h5xA	Alignment	not modelled	92.8	25	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
46	d1cuka2	Alignment	not modelled	92.5	24	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
47	d1bvsa2	Alignment	not modelled	92.3	26	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
48	c1ixrB	Alignment	not modelled	92.1	25	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
49	c2w9mB	Alignment	not modelled	91.9	29	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
50	d1x2ia1	Alignment	not modelled	91.6	26	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
51	d1ixra1	Alignment	not modelled	91.5	25	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
52	c4p4oA	Alignment	not modelled	91.1	17	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
53	c1s5lu	Alignment	not modelled	89.7	24	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
54	d2a1jb1	Alignment	not modelled	89.4	26	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like

55	d2edua1	Alignment	not modelled	89.3	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
56	c2owoA	Alignment	not modelled	88.9	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 bound2 to nicked dna-adenylate
57	c4glxA	Alignment	not modelled	87.7	20	PDB header: ligase/ligase inhibitor/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
58	c1nomA	Alignment	not modelled	87.1	25	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 mncI2 (5 millimolar)
59	c1dgsB	Alignment	not modelled	87.0	23	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
60	c5zb8B	Alignment	not modelled	86.4	12	PDB header: dna binding protein Chain: B: PDB Molecule: pfuendoq; PDBTitle: crystal structure of the novel lesion-specific endonuclease pfuendoq2 from pyrococcus furiosus
61	d2bcqa1	Alignment	not modelled	86.4	12	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
62	c2csdB	Alignment	not modelled	86.3	16	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
63	d2axtu1	Alignment	not modelled	85.8	24	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: PsbU-like
64	c4bxoB	Alignment	not modelled	85.5	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
65	d2aq0a1	Alignment	not modelled	82.4	12	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
66	c1hjpA	Alignment	not modelled	82.4	25	PDB header: dna recombination Chain: A: PDB Molecule: ruvA; PDBTitle: holliday junction binding protein ruvA from e. coli
67	d2i1qa1	Alignment	not modelled	81.4	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
68	c2lyhA	Alignment	not modelled	81.2	45	PDB header: dna binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215
69	c6flqF	Alignment	not modelled	80.9	11	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
70	c5ol9A	Alignment	not modelled	80.9	15	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor, mitochondrial; PDBTitle: structure of human mitochondrial transcription elongation factor2 (tefm) n-terminal domain
71	d1jmsa1	Alignment	not modelled	80.8	10	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
72	c1v9pB	Alignment	not modelled	80.4	23	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad--dependent dna ligase
73	c1b22A	Alignment	not modelled	79.7	21	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain)
74	d1b22a	Alignment	not modelled	79.7	21	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
75	d1szpa1	Alignment	not modelled	77.9	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
76	d2duya1	Alignment	not modelled	77.7	38	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like
77	d2fmpa2	Alignment	not modelled	77.7	25	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
78	d1nzpa	Alignment	not modelled	77.1	12	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
79	d2vana1	Alignment	not modelled	77.0	24	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
80	d1a77a1	Alignment	not modelled	77.0	33	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
						PDB header: gene regulation, structural protein/dna

81	c4itqA_	Alignment	not modelled	76.0	33	Chain: A: PDB Molecule: putative uncharacterized protein sco1480; PDBTitle: crystal structure of hypothetical protein sco1480 bound to dna
82	d3bzka1	Alignment	not modelled	75.5	16	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HhH-containing domain-like
83	d2fmpa1	Alignment	not modelled	75.0	20	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
84	d1mc8a1	Alignment	not modelled	74.9	44	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
85	d1pzna1	Alignment	not modelled	74.3	20	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
86	c2kp7A_	Alignment	not modelled	73.6	29	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
87	d1i94m_	Alignment	not modelled	72.7	19	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
88	d1b43a1	Alignment	not modelled	72.7	44	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
89	c6h5hA_	Alignment	not modelled	71.8	24	PDB header: unknown function Chain: A: PDB Molecule: polb4; PDBTitle: a computationally designed drp lyase domain reconstructed from two2 heterologous fragments
90	c3j200_	Alignment	not modelled	71.6	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)
91	c3ve5D_	Alignment	not modelled	71.0	22	PDB header: recombination Chain: D: PDB Molecule: recombination protein recr; PDBTitle: structure of recombination mediator protein recr16-196 deletion mutant
92	c2bhnD_	Alignment	not modelled	70.8	23	PDB header: hydrolase Chain: D: PDB Molecule: xpf endonuclease; PDBTitle: xpf from aeropyrum pernix
93	d2bcqa2	Alignment	not modelled	69.5	14	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
94	c2nrzB_	Alignment	not modelled	69.3	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
95	d1jmsa3	Alignment	not modelled	68.9	10	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
96	d2gy9m1	Alignment	not modelled	68.7	25	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
97	d1rxwa1	Alignment	not modelled	68.5	44	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
98	c3iz6M_	Alignment	not modelled	68.3	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
99	c2xznM_	Alignment	not modelled	68.1	29	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
100	c5mmjm_	Alignment	not modelled	68.1	29	PDB header: ribosome Chain: M: PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome
101	c4bxoA_	Alignment	not modelled	67.0	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
102	c5o5jM_	Alignment	not modelled	66.9	25	PDB header: ribosome Chain: M: PDB Molecule: 30s ribosomal protein s13; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
103	c2zkqm_	Alignment	not modelled	66.1	17	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	d1xo1a1	Alignment	not modelled	65.3	15	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
105	d2uubm1	Alignment	not modelled	63.8	25	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
106	d1cooa_	Alignment	not modelled	63.5	18	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
						Fold: SAM domain-like

107	d1ul1x1	Alignment	not modelled	61.0	33	Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
108	d1lb2b	Alignment	not modelled	60.3	18	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
109	d1cmwa1	Alignment	not modelled	57.5	44	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
110	d1szpb1	Alignment	not modelled	56.7	17	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
111	d1dk2a	Alignment	not modelled	56.6	33	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
112	c1ut8B	Alignment	not modelled	55.7	14	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
113	c5xyiS	Alignment	not modelled	54.6	25	PDB header: ribosome Chain: S: PDB Molecule: ribosomal protein s13p/s18e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
114	d2b7ma1	Alignment	not modelled	52.4	11	Fold: alpha-alpha superhelix Superfamily: Cullin repeat-like Family: Exocyst complex component
115	d1gm5a2	Alignment	not modelled	52.2	13	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RecG "wedge" domain
116	c2ziuA	Alignment	not modelled	49.7	21	PDB header: hydrolase Chain: A: PDB Molecule: mus81 protein; PDBTitle: crystal structure of the mus81-eme1 complex
117	d1z3eb1	Alignment	not modelled	47.2	6	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
118	d1d8ba	Alignment	not modelled	47.0	17	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
119	c3gp8A	Alignment	not modelled	46.0	26	PDB header: hydrolase/dna Chain: A: PDB Molecule: exodeoxyribonuclease v, subunit recd, putative; PDBTitle: crystal structure of the binary complex of recd2 with dna
120	d1doqa	Alignment	not modelled	45.1	39	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit