Phyre^2

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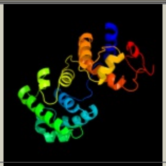
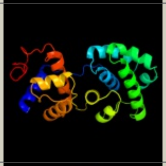
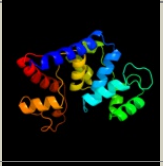
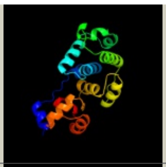
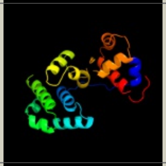
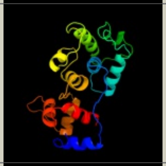
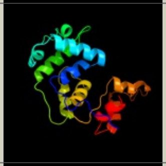
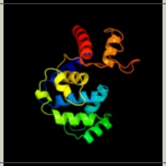
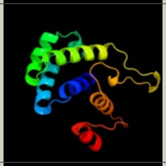
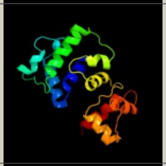
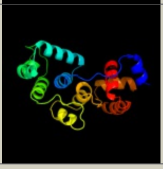
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2abka_	Alignment		100.0	100	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
2	d1orna_	Alignment		100.0	46	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
3	c1rrqA_	Alignment		100.0	22	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
4	d1keaa_	Alignment		100.0	28	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
5	d1kg2a_	Alignment		100.0	20	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
6	c3n5nX_	Alignment		100.0	21	**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
7	d1rrqa1	Alignment		100.0	22	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
8	d1pu6a_	Alignment		100.0	16	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase III (MagIII)
9	c3f10A_	Alignment		100.0	15	**PDB header:**hydrolase, lyase **Chain:** A: **PDB Molecule:**8-oxoguanine-dna-glycosylase; **PDBTitle:** crystal structure of clostridium acetobutylicum 8-2 oxoguanine dna glycosylase in complex with 8-oxoguanosine
10	c3n0uB_	Alignment		100.0	16	**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
11	c3kntC_	Alignment		100.0	18	**PDB header:**hydrolase, lyase/dna **Chain:** C: **PDB Molecule:**n-glycosylase/dna lyase; **PDBTitle:** crystal structure of methanocaldococcus jannaschii 8-2 oxoguanine glycosylase/lyase in complex with 15mer dna3 containing 8-oxoguanine

12	c3s6iA_	Alignment		100.0	17	**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.
13	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 (2 alka) from deinococcus radiodurans
14	c1ko9A_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**8-oxoguanine dna glycosylase; **PDBTitle:** native structure of the human 8-oxoguanine dna glycosylase2 hogg1
15	c1yqmA_	Alignment		100.0	19	**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	d1mpga1	Alignment		100.0	21	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
17	c3fhgA_	Alignment		100.0	20	**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)
18	d1ngna_	Alignment		100.0	18	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
19	d2noha1	Alignment		100.0	20	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
20	c2jhnB_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-methyladenine dna-glycosylase; **PDBTitle:** 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
21	c1mpgB_	Alignment	not modelled	99.9	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-methyladenine dna glycosylase ii; **PDBTitle:** 3-methyladenine dna glycosylase ii from escherichia coli
22	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
23	c2jg6A_	Alignment	not modelled	96.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna-3-methyladenine glycosidase; **PDBTitle:** crystal structure of a 3-methyladenine dna glycosylase i2 from staphylococcus aureus
24	d1nkua_	Alignment	not modelled	95.9	22	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase I (Tag)
25	c2h5xA_	Alignment	not modelled	95.9	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction atp-dependent dna helicase ruva; **PDBTitle:** ruva from mycobacterium tuberculosis
26	d1dgsa1	Alignment	not modelled	95.1	22	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
27	d2fmpa1	Alignment	not modelled	94.6	20	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
28	c2owoA_	Alignment	not modelled	93.9	23	**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
						Fold:SAM domain-like

29	d2bcqa1	Alignment	not modelled	93.7	21	**Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
30	c1vddC_	Alignment	not modelled	93.3	19	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
31	d1vdda_	Alignment	not modelled	92.8	21	**Fold:**Recombination protein RecR **Superfamily:**Recombination protein RecR **Family:**Recombination protein RecR
32	d1nzpa_	Alignment	not modelled	92.8	19	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
33	c1dgsB_	Alignment	not modelled	92.7	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
34	d1ixra1	Alignment	not modelled	92.6	27	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
35	d1cuka2	Alignment	not modelled	92.5	35	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
36	c1ixrA_	Alignment	not modelled	92.4	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruva; **PDBTitle:** ruva-ruvb complex
37	d1jmsa1	Alignment	not modelled	92.4	11	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
38	c8iczA_	Alignment	not modelled	92.3	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)
39	d1bvsa2	Alignment	not modelled	92.1	18	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
40	d1dk2a_	Alignment	not modelled	92.0	20	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
41	c2bcuA_	Alignment	not modelled	91.6	21	**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
42	c1d8lA_	Alignment	not modelled	91.4	45	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein (holliday junction dna helicase ruva); **PDBTitle:** e. coli holliday junction binding protein ruva nh2 region2 lacking domain iii
43	d2bgwa1	Alignment	not modelled	90.7	22	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
44	c1v9pB_	Alignment	not modelled	90.5	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase
45	c1kdhA_	Alignment	not modelled	90.4	22	**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
46	d2i1qa1	Alignment	not modelled	89.7	19	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
47	c2ihmA_	Alignment	not modelled	89.3	17	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase mu; **PDBTitle:** polymerase mu in ternary complex with gapped 11mer dna2 duplex and bound incoming nucleotide
48	c2csdB_	Alignment	not modelled	88.9	29	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**topoisomerase v; **PDBTitle:** crystal structure of topoisomerase v (61 kda fragment)
49	d1szpa1	Alignment	not modelled	88.6	20	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
50	c1kftA_	Alignment	not modelled	87.9	16	**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
51	d1kfta_	Alignment	not modelled	87.9	16	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
52	c1hjpA_	Alignment	not modelled	87.8	17	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**ruva; **PDBTitle:** holliday junction binding protein ruva from e. coli
53	d1x2ia1	Alignment	not modelled	87.7	18	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
54	d1pzna1	Alignment	not modelled	87.6	22	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
						PDB header:hydrolase

55	c2kp7A_	Alignment	not modelled	87.6	7	**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
56	c2w9mB_	Alignment	not modelled	87.5	22	**PDB header:**dna replication **Chain:** B: **PDB Molecule:**polymerase x; **PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
57	c1nomA_	Alignment	not modelled	86.8	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 the2 presence of mncl2 (5 millimolar)
58	d2a1jb1	Alignment	not modelled	86.8	16	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
59	d2edua1	Alignment	not modelled	84.4	23	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
60	d2duya1	Alignment	not modelled	82.5	32	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
61	d3bzka1	Alignment	not modelled	82.2	14	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Tex HhH-containing domain-like
62	c3c1zA_	Alignment	not modelled	81.6	18	**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 damage2 sensor protein
63	d1d8ba_	Alignment	not modelled	80.2	22	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
64	d2aq0a1	Alignment	not modelled	78.3	13	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
65	c1s5lu_	Alignment	not modelled	78.1	24	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**photosystem ii 12 kda extrinsic protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
66	d1b22a_	Alignment	not modelled	77.8	10	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
67	c1b22A_	Alignment	not modelled	77.8	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** rad51 (n-terminal domain)
68	d2axtu1	Alignment	not modelled	76.9	26	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**PsbU-like
69	d2vana1	Alignment	not modelled	73.9	22	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
70	d1a77a1	Alignment	not modelled	73.9	29	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
71	d2fmpa2	Alignment	not modelled	73.4	24	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
72	d1mc8a1	Alignment	not modelled	73.3	40	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
73	c3psiA_	Alignment	not modelled	72.9	16	**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)
74	d1szpb1	Alignment	not modelled	72.0	20	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
75	d1jmsa3	Alignment	not modelled	71.8	33	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
76	c3psfA_	Alignment	not modelled	71.7	18	**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)
77	d2bcqa2	Alignment	not modelled	71.5	27	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
78	d1rxwa1	Alignment	not modelled	69.7	36	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
79	d1xo1a1	Alignment	not modelled	67.2	23	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
80	d1b43a1	Alignment	not modelled	66.9	29	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
81	d1lb2b_	Alignment	not modelled	66.6	21	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
82	d2csba3	Alignment	not modelled	64.9	58	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like

						Family: Topoisomerase V repeat domain
83	d2i5ha1	Alignment	not modelled	64.1	26	**Fold:**AF1531-like **Superfamily:**AF1531-like **Family:**AF1531-like
84	c2i5hA_	Alignment	not modelled	64.1	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af1531; **PDBTitle:** crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
85	d1ul1x1	Alignment	not modelled	63.2	29	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
86	d1cooa_	Alignment	not modelled	62.7	21	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
87	d1z3eb1	Alignment	not modelled	62.6	21	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
88	d1i94m_	Alignment	not modelled	61.1	35	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
89	d1doqa_	Alignment	not modelled	60.4	21	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
90	c2nrzB_	Alignment	not modelled	58.1	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of the c-terminal half of uvrc bound to2 its catalytic divalent cation
91	c2oceA_	Alignment	not modelled	57.8	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa5201; **PDBTitle:** crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
92	c3iz6M_	Alignment	not modelled	57.7	45	**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
93	c2xznM_	Alignment	not modelled	56.4	35	**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
94	c2zkqm_	Alignment	not modelled	55.5	53	**PDB header:**ribosomal protein/rna **Chain:** M: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
95	d2gy9m1	Alignment	not modelled	55.5	35	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
96	c1ut8B_	Alignment	not modelled	55.2	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exodeoxyribonuclease; **PDBTitle:** divalent metal ions (zinc) bound to t5 5'-exonuclease
97	c2ziuA_	Alignment	not modelled	52.4	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mus81 protein; **PDBTitle:** crystal structure of the mus81-eme1 complex
98	d2uubm1	Alignment	not modelled	52.4	35	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
99	d1cmwa1	Alignment	not modelled	51.4	56	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
100	c2izoA_	Alignment	not modelled	50.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flap structure-specific endonuclease; **PDBTitle:** structure of an archaeal pcna1-pcna2-fen1 complex
101	d1wuda1	Alignment	not modelled	50.4	19	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
102	d2p6ra2	Alignment	not modelled	49.9	24	**Fold:**Sec63 N-terminal domain-like **Superfamily:**Sec63 N-terminal domain-like **Family:**Achaeal helicase C-terminal domain
103	c1a77A_	Alignment	not modelled	47.2	40	**PDB header:**5'-3' exo/endo nuclease **Chain:** A: **PDB Molecule:**flap endonuclease-1 protein; **PDBTitle:** flap endonuclease-1 from methanococcus jannaschii
104	d1gm5a2	Alignment	not modelled	46.8	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RecG "wedge" domain
105	c3q8lA_	Alignment	not modelled	45.0	29	**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+
106	c1b43A_	Alignment	not modelled	42.9	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (fen-1); **PDBTitle:** fen-1 from p. furiosus
107	c1rxvA_	Alignment	not modelled	42.1	36	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**flap structure-specific endonuclease; **PDBTitle:** crystal structure of a. fulgidus fen-1 bound to dna
108	c3mr2A_	Alignment	not modelled	40.2	8	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** human dna polymerase eta in complex with normal dna and incoming2 nucleotide (nrm)
						PDB header:helicase

109	c1gm5A_	Alignment	not modelled	39.9	14	**Chain:** A: **PDB Molecule:**recg; **PDBTitle:** structure of recg bound to three-way dna junction
110	c2bhnD_	Alignment	not modelled	39.5	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**xpf endonuclease; **PDBTitle:** xpf from aeropyrum pernix
111	c1cmwA_	Alignment	not modelled	38.5	45	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (dna polymerase i); **PDBTitle:** crystal structure of taq dna-polymerase shows a new2 orientation for the structure-specific nuclease domain
112	c3oryA_	Alignment	not modelled	37.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flap endonuclease 1; **PDBTitle:** crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus
113	c2rhfA_	Alignment	not modelled	36.9	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna helicase recq; **PDBTitle:** d. radiodurans recq hrdc domain 3
114	d1jx4a2	Alignment	not modelled	36.7	13	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
115	d1t57a_	Alignment	not modelled	36.0	23	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
116	c1ul1Y_	Alignment	not modelled	34.4	29	**PDB header:**hydrolase/dna binding protein **Chain:** Y: **PDB Molecule:**flap endonuclease-1; **PDBTitle:** crystal structure of the human fen1-pcna complex
117	c2rrdA_	Alignment	not modelled	33.6	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hrdc domain from bloom syndrome protein; **PDBTitle:** structure of hrdc domain from human bloom syndrome protein, blm
118	c3qeaZ_	Alignment	not modelled	32.2	40	**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)
119	c1k1qA_	Alignment	not modelled	31.6	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dbh protein; **PDBTitle:** crystal structure of a dinb family error prone dna2 polymerase from sulfolobus solfataricus
120	d2e1fa1	Alignment	not modelled	31.1	19	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases