Email	l.a.kelley@imperial.ac.uk
Description	P38506
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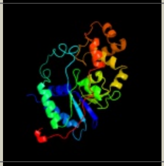
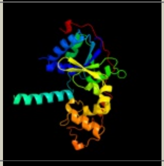
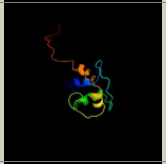
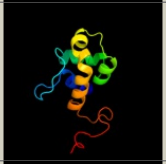
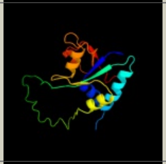
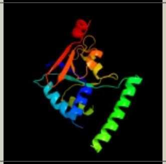
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1cmwA_	Alignment		100.0	31	**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
2	c1ut8B_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exodeoxyribonuclease; **PDBTitle:** divalent metal ions (zinc) bound to t5 5'-exonuclease
3	c2ihnA_	Alignment		100.0	16	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**ribonuclease h; **PDBTitle:** co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
4	c1rxvA_	Alignment		100.0	17	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**flap structure-specific endonuclease; **PDBTitle:** crystal structure of a. fulgidus fen-1 bound to dna
5	c3q8lA_	Alignment		100.0	21	**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+
6	c1a77A_	Alignment		100.0	16	**PDB header:**5'-3' exo/endo nuclease **Chain:** A: **PDB Molecule:**flap endonuclease-1 protein; **PDBTitle:** flap endonuclease-1 from methanococcus jannaschii
7	c1b43A_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (fen-1); **PDBTitle:** fen-1 from p. furiosus
8	c3oryA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flap endonuclease 1; **PDBTitle:** crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus
9	d1cmwa2	Alignment		100.0	27	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
10	c2izoA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flap structure-specific endonuclease; **PDBTitle:** structure of an archaeal pcna1-pcna2-fen1 complex
11	c1ul1Y_	Alignment		100.0	21	**PDB header:**hydrolase/dna binding protein **Chain:** Y: **PDB Molecule:**flap endonuclease-1; **PDBTitle:** crystal structure of the human fen1-pcna complex

12	c3qeaZ_	Alignment		100.0	16	**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)
13	d1xo1a2	Alignment		100.0	21	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
14	d1tfra2	Alignment		100.0	18	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
15	d1cmwa1	Alignment		99.9	38	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
16	d1xo1a1	Alignment		99.8	22	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
17	d1ul1x2	Alignment		99.8	17	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
18	d1b43a2	Alignment		99.8	20	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
19	d1rxwa2	Alignment		99.8	19	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
20	d1a77a2	Alignment		99.7	13	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
21	d1mc8a2	Alignment	not modelled	99.7	19	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
22	d1rxwa1	Alignment	not modelled	99.6	19	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
23	d1ul1x1	Alignment	not modelled	99.6	25	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
24	d1a77a1	Alignment	not modelled	99.6	22	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
25	d1b43a1	Alignment	not modelled	99.5	20	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
26	d1mc8a1	Alignment	not modelled	99.5	23	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
27	d1x2ia1	Alignment	not modelled	97.2	23	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
28	d2bgwa1	Alignment	not modelled	97.0	26	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
29	c2y35A_	Alignment	not modelled	96.8	18	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**ld22664p;

						PDBTitle: crystal structure of xrn1-substrate complex
30	c1kftA_	Alignment	not modelled	96.8	23	**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
31	d1kfta_	Alignment	not modelled	96.8	23	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
32	c2nrzB_	Alignment	not modelled	96.7	26	**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
33	c3fqdA_	Alignment	not modelled	96.6	18	**PDB header:**hydrolase/protein binding **Chain:** A: **PDB Molecule:**5'-3' exoribonuclease 2; **PDBTitle:** crystal structure of the s. pombe rat1-rai1 complex
34	d2a1jb1	Alignment	not modelled	96.5	19	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
35	d1dgsa1	Alignment	not modelled	96.5	20	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
36	d1cuka2	Alignment	not modelled	95.8	24	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
37	d2i1qa1	Alignment	not modelled	95.7	19	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
38	d1pzna1	Alignment	not modelled	95.6	25	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
39	d1ixra1	Alignment	not modelled	95.3	32	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
40	c3pifD_	Alignment	not modelled	94.9	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**5'->3' exoribonuclease (xrn1); **PDBTitle:** crystal structure of the 5'->3' exoribonuclease xrn1, e178q mutant in2 complex with manganese
41	c1hjpA_	Alignment	not modelled	94.9	27	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**ruva; **PDBTitle:** holliday junction binding protein ruva from e. coli
42	d2aq0a1	Alignment	not modelled	94.8	12	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
43	c1ixrA_	Alignment	not modelled	94.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruva; **PDBTitle:** ruva-ruvb complex
44	c1d8lA_	Alignment	not modelled	94.7	21	**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
45	c2owoA_	Alignment	not modelled	94.5	18	**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
46	d1bvsa2	Alignment	not modelled	94.5	16	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
47	c2h5xA_	Alignment	not modelled	94.4	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction atp-dependent dna helicase ruva; **PDBTitle:** ruva from mycobacterium tuberculosis
48	c2w9mB_	Alignment	not modelled	94.4	30	**PDB header:**dna replication **Chain:** B: **PDB Molecule:**polymerase x; **PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
49	c1dgsB_	Alignment	not modelled	94.3	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
50	c1v9pB_	Alignment	not modelled	94.2	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase
51	d2p6ra2	Alignment	not modelled	92.6	17	**Fold:**Sec63 N-terminal domain-like **Superfamily:**Sec63 N-terminal domain-like **Family:**Achaeal helicase C-terminal domain
52	c8iczA_	Alignment	not modelled	92.4	30	**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)
53	c1nomA_	Alignment	not modelled	92.2	33	**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)
54	d2vana1	Alignment	not modelled	92.0	33	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
55	d2fmpa2	Alignment	not modelled	91.7	30	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like

						Family:DNA polymerase beta-like, second domain
56	c2bhnD_	Alignment	not modelled	91.6	28	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**xpf endonuclease; **PDBTitle:** xpf from aeropyrum pernix
57	c2ihmA_	Alignment	not modelled	91.0	21	**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
58	d1szpa1	Alignment	not modelled	90.8	18	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
59	c2qipA_	Alignment	not modelled	90.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein of unknown function vpa0982; **PDBTitle:** crystal structure of a protein of unknown function vpa0982 from vibrio2 parahaemolyticus rimd 2210633
60	c2ziuA_	Alignment	not modelled	90.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mus81 protein; **PDBTitle:** crystal structure of the mus81-eme1 complex
61	c3majA_	Alignment	not modelled	89.6	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna processing chain a; **PDBTitle:** crystal structure of putative dna processing protein dpra from2 rhodopseudomonas palustris cga009
62	d2bcqa2	Alignment	not modelled	89.2	35	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
63	c1s5lu_	Alignment	not modelled	89.0	22	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**photosystem ii 12 kda extrinsic protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
64	d1jmsa3	Alignment	not modelled	88.1	19	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
65	d2axtu1	Alignment	not modelled	86.2	19	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**PsbU-like
66	c1kdhA_	Alignment	not modelled	85.7	31	**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
67	c2va8A_	Alignment	not modelled	85.5	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ski2-type helicase; **PDBTitle:** dna repair helicase hel308
68	c2bcuA_	Alignment	not modelled	85.3	35	**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
69	c3c1zA_	Alignment	not modelled	85.1	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
70	c2csdB_	Alignment	not modelled	83.7	35	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**topoisomerase v; **PDBTitle:** crystal structure of topoisomerase v (61 kda fragment)
71	d1b22a_	Alignment	not modelled	83.6	18	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
72	c1b22A_	Alignment	not modelled	83.6	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** rad51 (n-terminal domain)
73	c2p6uA_	Alignment	not modelled	83.5	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**afuhel308 helicase; **PDBTitle:** apo structure of the hel308 superfamily 2 helicase
74	d2duya1	Alignment	not modelled	81.8	18	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
75	d2i5ha1	Alignment	not modelled	81.5	19	**Fold:**AF1531-like **Superfamily:**AF1531-like **Family:**AF1531-like
76	c2i5hA_	Alignment	not modelled	81.5	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af1531; **PDBTitle:** crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
77	d2csba3	Alignment	not modelled	81.2	30	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
78	d2edua1	Alignment	not modelled	79.5	24	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
79	c3d4oA_	Alignment	not modelled	79.5	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit a; **PDBTitle:** crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
80	c3r2jC_	Alignment	not modelled	79.2	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha/beta-hydrolase-like protein; **PDBTitle:** crystal structure of pnc1 from l. infantum in complex with nicotinate
81	c1vddC_	Alignment	not modelled	77.9	32	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
						Fold: Recombination protein RecR

82	d1vdda_	Alignment	not modelled	73.7	32	**Superfamily:**Recombination protein RecR **Family:**Recombination protein RecR
83	c3fhgA_	Alignment	not modelled	72.3	28	**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)
84	c3kntC_	Alignment	not modelled	71.3	28	**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
85	c2zixA_	Alignment	not modelled	70.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**crossover junction endonuclease mus81; **PDBTitle:** crystal structure of the mus81-eme1 complex
86	c2vg2C_	Alignment	not modelled	69.2	25	**PDB header:**transferase **Chain:** C: **PDB Molecule:**undecaprenyl pyrophosphate synthetase; **PDBTitle:** rv2361 with ipp
87	c3n0uB_	Alignment	not modelled	67.7	33	**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
88	c1jp3A_	Alignment	not modelled	64.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** structure of e.coli undecaprenyl pyrophosphate synthase
89	d1pu6a_	Alignment	not modelled	63.8	43	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase III (MagIII)
90	d1ueha_	Alignment	not modelled	62.8	10	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
91	c2fq1A_	Alignment	not modelled	62.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isochorismatase; **PDBTitle:** crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
92	c1yzvA_	Alignment	not modelled	61.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** hypothetical protein from trypanosoma cruzi
93	c3s6iA_	Alignment	not modelled	60.1	36	**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.
94	c3irvA_	Alignment	not modelled	59.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cysteine hydrolase; **PDBTitle:** crystal structure of cysteine hydrolase pspph_2384 from pseudomonas2 syringae pv. phaseolicola 1448a
95	d1szpb1	Alignment	not modelled	56.9	17	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
96	d2noha1	Alignment	not modelled	56.7	21	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
97	c2d2rA_	Alignment	not modelled	56.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
98	d3bzka1	Alignment	not modelled	56.2	12	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Tex HhH-containing domain-like
99	d1jmsa1	Alignment	not modelled	55.3	17	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
100	d1keaa_	Alignment	not modelled	55.2	14	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
101	d1f75a_	Alignment	not modelled	54.8	16	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
102	d1orna_	Alignment	not modelled	54.6	18	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
103	d1nf9a_	Alignment	not modelled	53.9	17	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
104	d1yaca_	Alignment	not modelled	52.7	16	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
105	d1kg2a_	Alignment	not modelled	52.7	27	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
106	d1im5a_	Alignment	not modelled	52.6	14	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
107	c2j4dA_	Alignment	not modelled	52.6	17	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**cryptochrome dash; **PDBTitle:** cryptochrome 3 from arabidopsis thaliana
108	c3o93A_	Alignment	not modelled	52.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nicotinamidase; **PDBTitle:** high resolution crystal structures of streptococcus pneumoniae2 nicotinamidase with trapped intermediates provide

						insights into3 catalytic mechanism and inhibition by aldehydes
109	d1mpga1	Alignment	not modelled	51.8	29	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
110	c3n5nX_	Alignment	not modelled	51.8	23	**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
111	d1j2ra_	Alignment	not modelled	50.8	17	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
112	d2abka_	Alignment	not modelled	50.4	38	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
113	c3eefA_	Alignment	not modelled	50.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-carbamoylsarcosine amidase related protein; **PDBTitle:** crystal structure of n-carbamoylsarcosine amidase from thermoplasma2 acidophilum
114	c3hu5B_	Alignment	not modelled	50.2	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**isochorismatase family protein; **PDBTitle:** crystal structure of isochorismatase family protein from desulfovibrio2 vulgaris subsp. vulgaris str. hildenborough
115	c3f10A_	Alignment	not modelled	49.9	22	**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
116	c3mcwA_	Alignment	not modelled	48.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of an a putative hydrolase of the isochorismatase2 family (cv_1320) from chromobacterium violaceum atcc 12472 at 1.06 a3 resolution
117	c2jhnB_	Alignment	not modelled	48.4	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-methyladenine dna-glycosylase; **PDBTitle:** 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
118	d2a1ja1	Alignment	not modelled	48.3	16	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
119	d1rrqa1	Alignment	not modelled	48.2	29	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
120	c2yg8B_	Alignment	not modelled	47.1	38	**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