Phyre^{2}

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Description	RVBD3586_(-)_4028070_4029146
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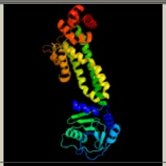
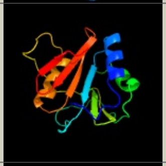
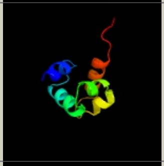
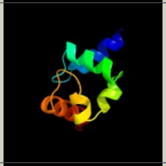
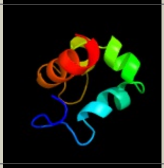
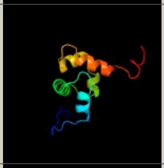
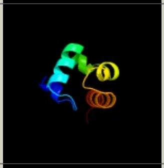
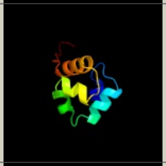
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c1zA_	Alignment		100.0	39	**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
2	d2fb5a1	Alignment		100.0	27	**Fold:**YojJ-like **Superfamily:**YojJ-like **Family:**YojJ-like
3	c4rv7C_	Alignment		100.0	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diadenylate cyclase; **PDBTitle:** characterization of an essential diadenylate cyclase
4	c6gyyB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**diadenylate cyclase; **PDBTitle:** crystal structure of daca from staphylococcus aureus, n166c/t172c2 double mutant
5	c2mutA_	Alignment		98.9	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna excision repair protein ercc-1; **PDBTitle:** solution structure of the f231l mutant ercc1-xpf dimerization region
6	d2a1jb1	Alignment		98.8	25	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
7	d1x2ia1	Alignment		98.7	28	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
8	c1dgsB_	Alignment		98.6	29	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
9	c2owoA_	Alignment		98.6	29	**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
10	d2bgwa1	Alignment		98.6	22	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
11	c1v9pB_	Alignment		98.6	29	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase

12	d1kfta_	Alignment		98.6	26	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
13	c1kftA_	Alignment		98.6	26	**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
14	d1dgsa1	Alignment		98.5	29	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
15	c4glxA_	Alignment		98.5	29	**PDB header:**ligase/ligase inhibitor/dna **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** dna ligase a in complex with inhibitor
16	d2aq0a1	Alignment		98.5	17	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
17	c2bhnD_	Alignment		98.5	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**xpf endonuclease; **PDBTitle:** xpf from aeropyrum pernix
18	c4bxoA_	Alignment		98.4	10	**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
19	c2lyhA_	Alignment		98.2	31	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**fanconi anemia-associated protein of 24 kda; **PDBTitle:** structure of faap24 residues 141-215
20	c4bxoB_	Alignment		98.2	31	**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
21	d2i1qa1	Alignment	not modelled	98.1	23	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
22	c2nrzB_	Alignment	not modelled	98.1	25	**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
23	c2zj8A_	Alignment	not modelled	97.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ski2-type helicase; **PDBTitle:** archaeal dna helicase hjm apo state in form 2
24	d1pzna1	Alignment	not modelled	97.7	28	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
25	d1szpa1	Alignment	not modelled	97.3	19	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
26	c6flqF_	Alignment	not modelled	97.2	16	**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
27	d1b22a_	Alignment	not modelled	97.0	19	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
28	c1b22A_	Alignment	not modelled	97.0	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** rad51 (n-terminal domain)
						Fold:SAM domain-like

29	d1szpb1	Alignment	not modelled	96.8	21	**Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
30	c1ixrA_	Alignment	not modelled	96.5	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruva; **PDBTitle:** ruva-ruvb complex
31	d1cuka2	Alignment	not modelled	96.4	13	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
32	d2a1ja1	Alignment	not modelled	96.3	17	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
33	d1ixra1	Alignment	not modelled	95.8	22	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
34	c1hjpA_	Alignment	not modelled	95.6	13	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**ruva; **PDBTitle:** holliday junction binding protein ruva from e. coli
35	c2va8A_	Alignment	not modelled	94.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ski2-type helicase; **PDBTitle:** dna repair helicase hel308
36	d2axtu1	Alignment	not modelled	94.5	21	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**PsbU-like
37	d1pu6a_	Alignment	not modelled	94.4	16	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase III (MagIII)
38	c2ziuA_	Alignment	not modelled	94.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mus81 protein; **PDBTitle:** crystal structure of the mus81-eme1 complex
39	c1ixrB_	Alignment	not modelled	93.9	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**holliday junction dna helicase ruva; **PDBTitle:** ruva-ruvb complex
40	c1d8lA_	Alignment	not modelled	93.8	13	**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
41	c8iczA_	Alignment	not modelled	93.6	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)
42	c2csdB_	Alignment	not modelled	93.5	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**topoisomerase v; **PDBTitle:** crystal structure of topoisomerase v (61 kda fragment)
43	c4mtnA_	Alignment	not modelled	93.4	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription termination factor nusa; **PDBTitle:** crystal structure of transcription termination factor nusa from2 planctomyces limnophilus dsm 3776
44	c2w9mB_	Alignment	not modelled	93.2	23	**PDB header:**dna replication **Chain:** B: **PDB Molecule:**polymerase x; **PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
45	d1bvsa2	Alignment	not modelled	93.2	20	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
46	c1kdhA_	Alignment	not modelled	93.1	16	**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
47	c3auoB_	Alignment	not modelled	92.9	22	**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
48	c1s5lu_	Alignment	not modelled	92.3	22	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**photosystem ii 12 kda extrinsic protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
49	c2ihmA_	Alignment	not modelled	92.1	12	**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
50	c2h5xA_	Alignment	not modelled	91.8	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction atp-dependent dna helicase ruva; **PDBTitle:** ruva from mycobacterium tuberculosis
51	c5lm7A_	Alignment	not modelled	91.5	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription termination/antitermination protein nusa; **PDBTitle:** crystal structure of the lambda n-nus factor complex
52	c2p6uA_	Alignment	not modelled	91.1	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**afuhel308 helicase; **PDBTitle:** apo structure of the hel308 superfamily 2 helicase
53	c2zixA_	Alignment	not modelled	90.5	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**crossover junction endonuclease mus81; **PDBTitle:** crystal structure of the mus81-eme1 complex
54	d1lb2b_	Alignment	not modelled	90.0	20	**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

55	d2edua1	Alignment	not modelled	89.9	36	**Superfamily:**RuvA domain 2-like **Family:**ComEA-like
56	d1kg2a_	Alignment	not modelled	89.9	14	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
57	c5ol9A_	Alignment	not modelled	89.3	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor, mitochondrial; **PDBTitle:** structure of human mitochondrial transcription elongation factor2 (tefm) n-terminal domain
58	c3f10A_	Alignment	not modelled	89.2	13	**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
59	d1cooa_	Alignment	not modelled	89.1	20	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
60	c4unfA_	Alignment	not modelled	89.1	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**endonuclease iii-1; **PDBTitle:** crystal structure of deinococcus radiodurans endonuclease iii-1
61	d2duya1	Alignment	not modelled	87.8	26	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
62	d3bzka1	Alignment	not modelled	87.8	24	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Tex HhH-containing domain-like
63	c5agaA_	Alignment	not modelled	86.9	14	**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
64	d1rrqa1	Alignment	not modelled	86.8	13	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
65	d1doqa_	Alignment	not modelled	86.1	27	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
66	c2bcuA_	Alignment	not modelled	85.5	13	**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
67	c3n5nX_	Alignment	not modelled	85.3	25	**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
68	d1z3eb1	Alignment	not modelled	85.1	24	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
69	d1mpga1	Alignment	not modelled	83.1	21	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
70	c4ejyA_	Alignment	not modelled	82.2	17	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**3-methyladenine dna glycosylase; **PDBTitle:** structure of mbogg1 in complex with high affinity dna ligand
71	c1t4gA_	Alignment	not modelled	82.0	22	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rada; **PDBTitle:** atpase in complex with amp-pnp
72	c1rrqA_	Alignment	not modelled	81.6	18	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
73	d2q0zx1	Alignment	not modelled	81.3	6	**Fold:**Sec63 N-terminal domain-like **Superfamily:**Sec63 N-terminal domain-like **Family:**Sec63 N-terminal domain
74	d1keaa_	Alignment	not modelled	80.9	10	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
75	c3zddA_	Alignment	not modelled	80.4	16	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**protein xni; **PDBTitle:** structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium
76	d1orna_	Alignment	not modelled	80.2	18	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
77	c2maxA_	Alignment	not modelled	79.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit alpha; **PDBTitle:** nmr structure of the rna polymerase alpha subunit c-terminal domain2 from helicobacter pylori
78	c4gfjA_	Alignment	not modelled	79.3	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase v; **PDBTitle:** crystal structure of topo-78, an n-terminal 78kda fragment of2 topoisomerase v
79	d2noha1	Alignment	not modelled	78.0	30	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
80	d1u9la_	Alignment	not modelled	77.1	26	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**NusA extra C-terminal domains
81	c1ut8B_	Alignment	not modelled	77.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exodeoxyribonuclease;

						PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
82	d2fmpa1	Alignment	not modelled	77.0	21	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
83	d2abka_	Alignment	not modelled	76.8	16	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
84	c5tw1T_	Alignment	not modelled	75.6	27	**PDB header:**transcription activator/transferase/dna **Chain:** T: **PDB Molecule:**dna-directed rna polymerase subunit alpha; **PDBTitle:** crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpa
85	d1xo1a1	Alignment	not modelled	75.4	11	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
86	c6ah0D_	Alignment	not modelled	74.3	4	**PDB header:**splicing **Chain:** D: **PDB Molecule:**u5 small nuclear ribonucleoprotein 200 kda helicase; **PDBTitle:** the cryo-em structure of the precusor of human pre-catalytic2 spliceosome (pre-b complex)
87	d2csba3	Alignment	not modelled	73.7	28	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
88	c3fioB_	Alignment	not modelled	73.3	18	**PDB header:**nucleotide binding protein, metal bindin **Chain:** B: **PDB Molecule:**a cystathionine beta-synthase domain protein **PDBTitle:** crystal structure of a fragment of a cystathionine beta-2 synthase domain protein fused to a zn-ribbon-like domain
89	c1pznA_	Alignment	not modelled	70.8	27	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rad51; **PDBTitle:** rad51 (rada)
90	c2jhnB_	Alignment	not modelled	69.6	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-methyladenine dna-glycosylase; **PDBTitle:** 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
91	c4uobA_	Alignment	not modelled	67.5	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**endonuclease iii-3; **PDBTitle:** crystal structure of deinococcus radiodurans endonuclease iii-3
92	d2bcqa1	Alignment	not modelled	67.4	32	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
93	c4p4oA_	Alignment	not modelled	66.5	19	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase beta; **PDBTitle:** crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
94	c4cdgA_	Alignment	not modelled	65.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bloom syndrome protein; **PDBTitle:** crystal structure of the bloom's syndrome helicase blm in complex with2 nanobody
95	c3fhgA_	Alignment	not modelled	65.2	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)
96	c2kp7A_	Alignment	not modelled	64.6	24	**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
97	d1jmsa1	Alignment	not modelled	64.6	12	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
98	c2zixB_	Alignment	not modelled	63.8	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**crossover junction endonuclease eme1; **PDBTitle:** crystal structure of the mus81-eme1 complex
99	c6c34A_	Alignment	not modelled	63.6	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**5'-3' exonuclease; **PDBTitle:** mycobacterium smegmatis dna flap endonuclease mutant d125n
100	d1nzpa_	Alignment	not modelled	62.5	32	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
101	c6h5hA_	Alignment	not modelled	61.4	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**polb4; **PDBTitle:** a computationally designed drp lyase domain reconstructed from two2 heterologous fragments
102	c1mpgB_	Alignment	not modelled	61.1	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-methyladenine dna glycosylase ii; **PDBTitle:** 3-methyladenine dna glycosylase ii from escherichia coli
103	c1ko9A_	Alignment	not modelled	60.3	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**8-oxoguanine dna glycosylase; **PDBTitle:** native structure of the human 8-oxoguanine dna glycosylase2 hogg1
104	d1ngna_	Alignment	not modelled	59.6	10	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
105	d1dk2a_	Alignment	not modelled	59.2	24	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
106	d2csba4	Alignment	not modelled	59.0	21	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
107	c1vqmA	Alignment	not modelled	58.4	29	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**n-glycosylase/dna lyase;

107	c1yqmA_	Alignment	not modelled	58.4	29	**PDBTitle:** catalytically inactive human 8-oxoguanine glycosylase2 crosslinked to 7-deazaguanine containing dna
108	d2p6ra2	Alignment	not modelled	56.6	22	**Fold:**Sec63 N-terminal domain-like **Superfamily:**Sec63 N-terminal domain-like **Family:**Achaeal helicase C-terminal domain
109	c4b24A_	Alignment	not modelled	55.5	6	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**probable dna-3-methyladenine glycosylase 2; **PDBTitle:** unprecedented sculpting of dna at abasic sites by dna glycoslase2 homolog mag2
110	d1d8ba_	Alignment	not modelled	53.6	9	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
111	c4itqA_	Alignment	not modelled	53.3	28	**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
112	c3n0uB_	Alignment	not modelled	52.7	22	**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
113	d1rxwa1	Alignment	not modelled	52.5	13	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
114	d1ul1x1	Alignment	not modelled	52.4	12	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
115	c3kntC_	Alignment	not modelled	51.5	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
116	d1a77a1	Alignment	not modelled	50.5	25	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
117	c3im2A_	Alignment	not modelled	49.4	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pre-mrna-splicing helicase brr2; **PDBTitle:** structure of the c-terminal sec63 unit of yeast brr2, p41212 form
118	d1coka_	Alignment	not modelled	49.2	19	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
119	d2e1fa1	Alignment	not modelled	48.2	11	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
120	c2dflA_	Alignment	not modelled	48.0	20	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rada; **PDBTitle:** crystal structure of left-handed rada filament