Phyre²

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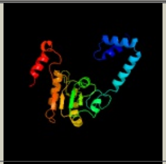
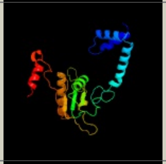
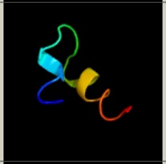
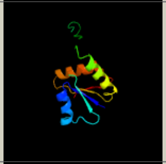
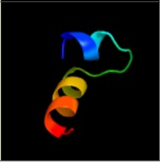
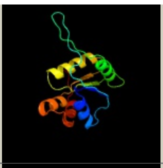
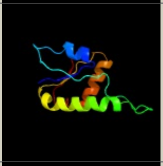
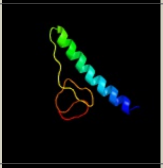
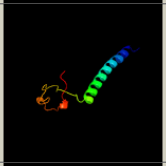
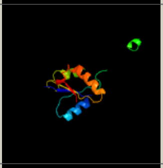
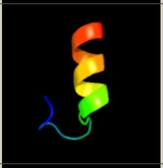
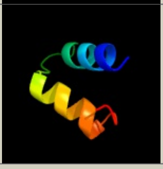
Description	RVBD3715c_(recR)_4160067_4160678
Date	Fri Aug 9 18:20:41 BST 2019
Unique Job ID	05a6f88b1d539a66

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5z2vB_	Alignment		100.0	49	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recr from pseudomonas aeruginosa pao1
2	c1vddC_	Alignment		100.0	50	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
3	d1vdda_	Alignment		100.0	50	**Fold:**Recombination protein RecR **Superfamily:**Recombination protein RecR **Family:**Recombination protein RecR
4	c5zvqA_	Alignment		100.0	51	**PDB header:**recombination **Chain:** A: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombination mediator protein recr
5	c3ve5D_	Alignment		100.0	48	**PDB header:**recombination **Chain:** D: **PDB Molecule:**recombination protein recr; **PDBTitle:** structure of recombination mediator protein recr16-196 deletion mutant
6	c2h5xA_	Alignment		96.5	36	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction atp-dependent dna helicase ruva; **PDBTitle:** ruva from mycobacterium tuberculosis
7	c1ixrB_	Alignment		96.4	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**holliday junction dna helicase ruva; **PDBTitle:** ruva-ruvb complex
8	d1bvsa2	Alignment		96.1	41	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
9	d1ixra1	Alignment		96.1	36	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
10	c4rulA_	Alignment		95.9	22	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**dna topoisomerase 1; **PDBTitle:** crystal structure of full-length e.coli topoisomerase i in complex2 with ssdna
11	d1cuka2	Alignment		95.9	45	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain

12	d1gkub3	Alignment		95.7	25	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
13	c5d5hA_	Alignment		95.5	34	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase 1; **PDBTitle:** crystal structure of mycobacterium tuberculosis topoisomerase i
14	c2hr5B_	Alignment		95.1	27	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
15	c1dvbA_	Alignment		95.0	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
16	c5gveA_	Alignment		94.9	24	**PDB header:**isomerase/protein binding **Chain:** A: **PDB Molecule:**dna topoisomerase 3-beta-1; **PDBTitle:** human top3b-tdrd3 complex
17	c1hjpA_	Alignment		94.8	53	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**ruva; **PDBTitle:** holliday junction binding protein ruva from e. coli
18	c4chtA_	Alignment		94.6	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna topoisomerase 3-alpha; **PDBTitle:** crystal structure of the human topoisomerase iii alpha-rmi1 complex2 with bound calcium ion
19	d1t6t1_	Alignment		94.5	21	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
20	c4uobA_	Alignment		94.4	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**endonuclease iii-3; **PDBTitle:** crystal structure of deinococcus radiodurans endonuclease iii-3
21	c2au3A_	Alignment	not modelled	94.2	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** crystal structure of the aquifex aeolicus primase (zinc binding and2 rna polymerase domains)
22	d2noha1	Alignment	not modelled	94.2	25	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
23	c4ddvA_	Alignment	not modelled	94.0	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**reverse gyrase; **PDBTitle:** thermotoga maritima reverse gyrase, triclinic form
24	c2o59B_	Alignment	not modelled	93.9	25	**PDB header:**isomerase/dna **Chain:** B: **PDB Molecule:**dna topoisomerase 3; **PDBTitle:** structure of e. coli topoisomerase iii in complex with an 8-base2 single stranded oligonucleotide. frozen in glycerol ph 8.0
25	c4b24A_	Alignment	not modelled	93.8	16	**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
26	c3f10A_	Alignment	not modelled	93.8	25	**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
27	c6ozwA_	Alignment	not modelled	93.8	26	**PDB header:**isomerase,dna binding protein **Chain:** A: **PDB Molecule:**dna topoisomerase 1; **PDBTitle:** crystal structure of the 65-kilodalton amino-terminal fragment of dna2 topoisomerase i from streptococcus mutans
28	c1yqmA_	Alignment	not modelled	93.7	25	**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

29	c1yuzB_	Alignment	not modelled	93.6	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
30	d1pu6a_	Alignment	not modelled	93.4	26	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase III (MagIII)
31	c1nuiA_	Alignment	not modelled	93.4	13	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna primase/helicase; **PDBTitle:** crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
32	c3s6iA_	Alignment	not modelled	93.3	22	**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.
33	c4ejyA_	Alignment	not modelled	93.2	22	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**3-methyladenine dna glycosylase; **PDBTitle:** structure of mbogg1 in complex with high affinity dna ligand
34	d1mpga1	Alignment	not modelled	93.2	25	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
35	d1nuia1	Alignment	not modelled	92.9	11	**Fold:**DNA primase core **Superfamily:**DNA primase core **Family:**Primase fragment of primase-helicase protein
36	c3fhgA_	Alignment	not modelled	92.9	21	**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)
37	d1i7da_	Alignment	not modelled	92.9	25	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
38	c1ko9A_	Alignment	not modelled	92.7	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**8-oxoguanine dna glycosylase; **PDBTitle:** native structure of the human 8-oxoguanine dna glycosylase2 hogg1
39	c4unfA_	Alignment	not modelled	92.6	32	**PDB header:**lyase **Chain:** A: **PDB Molecule:**endonuclease iii-1; **PDBTitle:** crystal structure of deinococcus radiodurans endonuclease iii-1
40	c3auoB_	Alignment	not modelled	92.6	26	**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
41	c1q57G_	Alignment	not modelled	92.5	12	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna primase/helicase; **PDBTitle:** the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
42	d2fmpa1	Alignment	not modelled	92.5	25	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
43	d2fcja1	Alignment	not modelled	92.5	23	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
44	c5gujA_	Alignment	not modelled	92.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** crystal structure of the bacillus subtilis dnag rna polymerase domain,2 natural degradation of full length dnag
45	c6o3pA_	Alignment	not modelled	92.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peroxisomal nadh pyrophosphatase nudt12; **PDBTitle:** crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
46	c2yg8B_	Alignment	not modelled	92.4	34	**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
47	c3n0uB_	Alignment	not modelled	92.3	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
48	c2jhnB_	Alignment	not modelled	92.2	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-methyladenine dna-glycosylase; **PDBTitle:** 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
49	c1mpgB_	Alignment	not modelled	92.2	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-methyladenine dna glycosylase ii; **PDBTitle:** 3-methyladenine dna glycosylase ii from escherichia coli
50	c3lpeF_	Alignment	not modelled	92.2	22	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
51	c2w9mB_	Alignment	not modelled	91.5	15	**PDB header:**dna replication **Chain:** B: **PDB Molecule:**polymerase x; **PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
52	c3n5nX_	Alignment	not modelled	91.4	26	**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
53	d2abka_	Alignment	not modelled	91.3	26	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
54	d1mw9x_	Alignment	not modelled	91.2	23	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase

55	c4edvA_	Alignment	not modelled	91.2	21	**PDB header:**transferase/transferase inhibitor **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** the structure of the s. aureus dnag rna polymerase domain bound to2 pppgpp and manganese
56	d2bcqa1	Alignment	not modelled	90.9	38	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
57	d1rrqa1	Alignment	not modelled	90.8	28	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
58	c3kntC_	Alignment	not modelled	90.6	13	**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
59	d1kg2a_	Alignment	not modelled	90.4	31	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
60	c6h5hA_	Alignment	not modelled	90.2	34	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**polb4; **PDBTitle:** a computationally designed drp lyase domain reconstructed from two2 heterologous fragments
61	d2a1jb1	Alignment	not modelled	90.1	11	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
62	d1keaa_	Alignment	not modelled	89.9	15	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
63	d1jmsa1	Alignment	not modelled	89.9	18	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
64	d1orna_	Alignment	not modelled	89.8	38	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
65	d1nzpa_	Alignment	not modelled	89.1	38	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
66	c1rrqA_	Alignment	not modelled	89.0	27	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
67	c2csdB_	Alignment	not modelled	88.8	28	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**topoisomerase v; **PDBTitle:** crystal structure of topoisomerase v (61 kda fragment)
68	c5w34A_	Alignment	not modelled	88.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** crystal structure of the rna polymerase domain (rpd) of mycobacterium2 tuberculosis primase dnag in complex with double-stranded dna3 gaccggaagtgg
69	c2gajA_	Alignment	not modelled	88.3	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
70	c8iczA_	Alignment	not modelled	88.2	24	**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)
71	c2ihmA_	Alignment	not modelled	88.2	21	**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
72	d2edua1	Alignment	not modelled	87.7	43	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
73	c1gl9B_	Alignment	not modelled	87.6	45	**PDB header:**topoisomerase **Chain:** B: **PDB Molecule:**reverse gyrase; **PDBTitle:** archaeoglobus fulgidus reverse gyrase complexed with adpnp
74	d2bgwa1	Alignment	not modelled	87.5	32	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
75	c2kp7A_	Alignment	not modelled	87.5	17	**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
76	c2mutA_	Alignment	not modelled	86.9	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna excision repair protein ercc-1; **PDBTitle:** solution structure of the f231l mutant ercc1-xpf dimerization region
77	c1ixrA_	Alignment	not modelled	86.7	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruva; **PDBTitle:** ruva-ruvb complex
78	d1dk2a_	Alignment	not modelled	86.3	34	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
79	d1kfta_	Alignment	not modelled	85.7	36	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
80	c1kftA_	Alignment	not modelled	85.7	36	**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
81	c2bcuA_	Alignment	not modelled	85.3	38	**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
82	c1kdhA_	Alignment	not modelled	85.2	17	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**terminal deoxynucleotidyltransferase short **PDBTitle:** binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
83	c2gb5B_	Alignment	not modelled	85.1	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nadh pyrophosphatase; **PDBTitle:** crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
84	d1x2ia1	Alignment	not modelled	84.9	20	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
85	c4p4oA_	Alignment	not modelled	84.4	33	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase beta; **PDBTitle:** crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
86	c2lyhA_	Alignment	not modelled	84.1	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**fanconi anemia-associated protein of 24 kda; **PDBTitle:** structure of faap24 residues 141-215
87	c1nomA_	Alignment	not modelled	84.0	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)
88	c3vrhA_	Alignment	not modelled	83.6	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph0300; **PDBTitle:** crystal structure of ph0300
89	d2duya1	Alignment	not modelled	82.8	52	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
90	d2aq0a1	Alignment	not modelled	82.7	32	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
91	c5ol9A_	Alignment	not modelled	82.2	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor, mitochondrial; **PDBTitle:** structure of human mitochondrial transcription elongation factor2 (tefm) n-terminal domain
92	c1s5lu_	Alignment	not modelled	82.2	26	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**photosystem ii 12 kda extrinsic protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
93	d1ngna_	Alignment	not modelled	81.5	16	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
94	d2axtu1	Alignment	not modelled	81.5	26	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**PsbU-like
95	d2i1qa1	Alignment	not modelled	81.4	39	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
96	d1a77a1	Alignment	not modelled	80.0	42	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
97	d2vana1	Alignment	not modelled	79.7	29	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
98	c4zbzA_	Alignment	not modelled	79.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** family 4 uracil-dna glycosylase from sulfolobus tokodaii (free form,2 x-ray wavelength=1.5418)
99	d3bzka1	Alignment	not modelled	79.5	30	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Tex HhH-containing domain-like
100	c2r8kB_	Alignment	not modelled	78.7	14	**PDB header:**replication, transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase eta; **PDBTitle:** structure of the eukaryotic dna polymerase eta in complex with 1,2-2 d(gpg)-cisplatin containing dna
101	c1b22A_	Alignment	not modelled	78.0	33	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** rad51 (n-terminal domain)
102	d1b22a_	Alignment	not modelled	78.0	33	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
103	d1jiha2	Alignment	not modelled	77.9	14	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
104	d1dgsa1	Alignment	not modelled	77.9	28	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
105	c5ghaC_	Alignment	not modelled	77.7	17	**PDB header:**transferase/transport protein **Chain:** C: **PDB Molecule:**sulfur transferase ttua; **PDBTitle:** sulfur transferase ttua in complex with sulfur carrier ttub
106	d2a1ja1	Alignment	not modelled	77.4	21	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
						PDB header:hydrolase/dna

107	c4bxoB_	Alignment	not modelled	77.2	21	**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
108	d1mc8a1	Alignment	not modelled	77.1	58	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
109	c3cngC_	Alignment	not modelled	76.9	27	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
110	c1jihA_	Alignment	not modelled	76.6	14	**PDB header:**translation **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** yeast dna polymerase eta
111	c1d8lA_	Alignment	not modelled	76.4	31	**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
112	d1rxwa1	Alignment	not modelled	76.3	33	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
113	c2h56C_	Alignment	not modelled	75.9	17	**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
114	d2fmpa2	Alignment	not modelled	74.9	39	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
115	c5vazB_	Alignment	not modelled	74.5	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna primase; **PDBTitle:** crystal structure of a dna primase domain from pseudomonas aeruginosa
116	c3qeaZ_	Alignment	not modelled	74.4	21	**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)
117	d1pzna1	Alignment	not modelled	74.3	21	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
118	d1b43a1	Alignment	not modelled	74.0	50	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
119	d2csba3	Alignment	not modelled	73.7	32	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
120	d1szpa1	Alignment	not modelled	73.6	24	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain