Phyre^{2}

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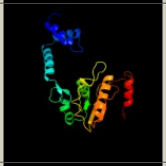
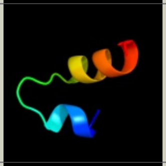
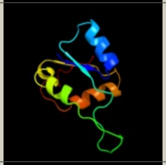
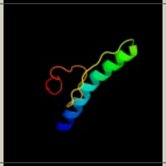
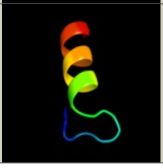
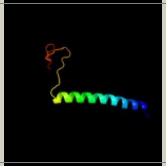
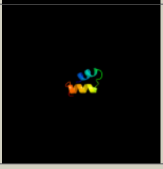
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vdda_	Alignment		100.0	46	**Fold:**Recombination protein RecR **Superfamily:**Recombination protein RecR **Family:**Recombination protein RecR
2	c1vddC_	Alignment		100.0	45	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
3	c2h5xA_	Alignment		96.3	41	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction atp-dependent dna helicase ruva; **PDBTitle:** ruva from mycobacterium tuberculosis
4	d1bvsa2	Alignment		95.9	32	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
5	d1ixra1	Alignment		95.9	36	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
6	d1cuka2	Alignment		95.7	41	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
7	d1gkub3	Alignment		95.4	23	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
8	c2o59B_	Alignment		94.9	20	**PDB header:**isomerase/dna **Chain:** B: **PDB Molecule:**dna topoisomerase 3; **PDBTitle:** structure of e. coli topoisomerase iii in complex with an 8-2 base single stranded oligonucleotide. frozen in glycerol3 ph 8.0
9	d1i7da_	Alignment		94.8	22	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
10	c2hr5B_	Alignment		94.8	27	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
11	c1hjpA_	Alignment		94.4	42	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**ruva; **PDBTitle:** holliday junction binding protein ruva from e. coli

12	c2au3A_	Alignment		94.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** crystal structure of the aquifex aeolicus primase (zinc binding and2 rna polymerase domains)
13	c1dvbA_	Alignment		94.2	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
14	d1t6t1_	Alignment		94.1	18	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
15	d2noha1	Alignment		93.8	28	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
16	c1nuiA_	Alignment		93.8	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
17	d1nuia1	Alignment		93.5	13	**Fold:**DNA primase core **Superfamily:**DNA primase core **Family:**Primase fragment of primase-helicase protein
18	c3f10A_	Alignment		93.5	26	**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
19	c1yuzB_	Alignment		93.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
20	c1yqmA_	Alignment		93.0	28	**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
21	c3n0uB_	Alignment	not modelled	93.0	21	**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
22	c3lpeF_	Alignment	not modelled	92.9	25	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
23	d1pu6a_	Alignment	not modelled	92.9	19	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase III (MagIII)
24	c3s6iA_	Alignment	not modelled	92.8	25	**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.
25	d1mw9x_	Alignment	not modelled	92.5	33	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
26	d1mpga1	Alignment	not modelled	92.5	29	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
27	c3fhgA_	Alignment	not modelled	92.4	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)
28	c1q57G_	Alignment	not modelled	92.4	11	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna primase/helicase; **PDBTitle:** the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
						PDB header:hydrolase

29	c1ko9A_	Alignment	not modelled	92.2	31	**Chain:** A: **PDB Molecule:**8-oxoguanine dna glycosylase; **PDBTitle:** native structure of the human 8-oxoguanine dna glycosylase2 hogg1
30	d2fcja1	Alignment	not modelled	92.0	21	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
31	c2yg8B_	Alignment	not modelled	91.9	25	**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
32	c1mpgB_	Alignment	not modelled	91.8	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-methyladenine dna glycosylase ii; **PDBTitle:** 3-methyladenine dna glycosylase ii from escherichia coli
33	c2jhnB_	Alignment	not modelled	91.7	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-methyladenine dna-glycosylase; **PDBTitle:** 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
34	c1gl9B_	Alignment	not modelled	91.6	25	**PDB header:**topoisomerase **Chain:** B: **PDB Molecule:**reverse gyrase; **PDBTitle:** archaeoglobus fulgidus reverse gyrase complexed with adpnp
35	d2fmpa1	Alignment	not modelled	90.9	24	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
36	d2abka_	Alignment	not modelled	90.6	38	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
37	d1rrqa1	Alignment	not modelled	90.3	20	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
38	d1kg2a_	Alignment	not modelled	90.1	31	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
39	c3kntC_	Alignment	not modelled	89.7	16	**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
40	d1orna_	Alignment	not modelled	89.6	31	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
41	c2w9mB_	Alignment	not modelled	89.5	12	**PDB header:**dna replication **Chain:** B: **PDB Molecule:**polymerase x; **PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
42	d1keaa_	Alignment	not modelled	89.4	23	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
43	c3n5nX_	Alignment	not modelled	89.3	28	**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
44	d2a1jb1	Alignment	not modelled	89.1	17	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
45	c8iczA_	Alignment	not modelled	88.9	21	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**protein (dna polymerase beta (e.c.2.7.7.7)); **PDBTitle:** dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with2 seven base pairs of dna; soaked in the presence of of datp3 (1 millimolar), mncl2 (5 millimolar), and lithium sulfate4 (75 millimolar)
46	c1rrqA_	Alignment	not modelled	88.4	19	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
47	d2bcqa1	Alignment	not modelled	88.0	23	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
48	d1jmsa1	Alignment	not modelled	87.6	15	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
49	c2csdB_	Alignment	not modelled	87.5	29	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**topoisomerase v; **PDBTitle:** crystal structure of topoisomerase v (61 kda fragment)
50	c2ihmA_	Alignment	not modelled	87.5	38	**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
51	c2gb5B_	Alignment	not modelled	87.5	18	**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
52	d2edua1	Alignment	not modelled	87.2	38	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
53	d1nzpa_	Alignment	not modelled	86.4	23	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
54	d2bgwa1	Alignment	not modelled	86.3	24	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like

55	c1ixrA_	Alignment	not modelled	85.9	43	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruva; **PDBTitle:** ruva-ruvb complex
56	d1kfta_	Alignment	not modelled	84.9	23	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
57	c1kftA_	Alignment	not modelled	84.9	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
58	c1kdhA_	Alignment	not modelled	84.2	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
59	d1x2ia1	Alignment	not modelled	83.3	20	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
60	c2gajA_	Alignment	not modelled	83.0	28	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
61	c1nomA_	Alignment	not modelled	82.9	25	**PDB header:**nucleotidyltransferase **Chain:** A: **PDB Molecule:**dna polymerase beta; **PDBTitle:** dna polymerase beta (pol b) (e.c.2.7.7.7), 31-kd domain; soaked in the2 presence of mncl2 (5 millimolar)
62	c2kp7A_	Alignment	not modelled	82.2	14	**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
63	d2duya1	Alignment	not modelled	81.8	43	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
64	d2aq0a1	Alignment	not modelled	81.6	24	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
65	c2bcuA_	Alignment	not modelled	81.6	20	**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
66	d1dk2a_	Alignment	not modelled	81.3	36	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
67	c1s5lu_	Alignment	not modelled	81.3	21	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**photosystem ii 12 kda extrinsic protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
68	d2axtu1	Alignment	not modelled	80.5	21	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**PsbU-like
69	d1ngna_	Alignment	not modelled	80.3	20	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
70	d1a77a1	Alignment	not modelled	78.5	33	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
71	d1pzna1	Alignment	not modelled	78.5	27	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
72	d3bzka1	Alignment	not modelled	78.4	19	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Tex HhH-containing domain-like
73	c1d8lA_	Alignment	not modelled	78.1	28	**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
74	d2vana1	Alignment	not modelled	77.3	21	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
75	d1dgsa1	Alignment	not modelled	77.0	36	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
76	c1b22A_	Alignment	not modelled	77.0	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** rad51 (n-terminal domain)
77	d1b22a_	Alignment	not modelled	77.0	17	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
78	d1mc8a1	Alignment	not modelled	75.6	42	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
79	c2h56C_	Alignment	not modelled	74.8	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
80	d1rxwa1	Alignment	not modelled	74.8	42	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
						Fold:2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain

81	d1o98a1	Alignment	not modelled	74.6	21	**Superfamily:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
82	d2a1ja1	Alignment	not modelled	74.5	17	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
83	d2i1qa1	Alignment	not modelled	74.5	28	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
84	c3cngC_	Alignment	not modelled	74.3	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
85	d2csba3	Alignment	not modelled	73.8	29	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
86	c3qeaZ_	Alignment	not modelled	73.6	12	**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)
87	d2fmpa2	Alignment	not modelled	73.5	28	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
88	d1b43a1	Alignment	not modelled	72.4	33	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
89	d1szpa1	Alignment	not modelled	72.3	18	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
90	d1xo1a1	Alignment	not modelled	70.6	25	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
91	c2r8kB_	Alignment	not modelled	70.2	7	**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
92	d1ul1x1	Alignment	not modelled	69.2	42	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
93	d2i5ha1	Alignment	not modelled	69.1	44	**Fold:**AF1531-like **Superfamily:**AF1531-like **Family:**AF1531-like
94	c2i5hA_	Alignment	not modelled	69.1	44	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af1531; **PDBTitle:** crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
95	c2nrzB_	Alignment	not modelled	68.5	24	**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
96	d2apob1	Alignment	not modelled	67.8	24	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
97	d1ryqa_	Alignment	not modelled	67.8	17	**Fold:**Rubredoxin-like **Superfamily:**RNA polymerase subunits **Family:**RpoE2-like
98	d2bcqa2	Alignment	not modelled	67.6	30	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
99	c1jihA_	Alignment	not modelled	67.1	7	**PDB header:**translation **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** yeast dna polymerase eta
100	d1jiha2	Alignment	not modelled	67.0	7	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
101	c1ut8B_	Alignment	not modelled	66.5	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exodeoxyribonuclease; **PDBTitle:** divalent metal ions (zinc) bound to t5 5'-exonuclease
102	d2ey4e1	Alignment	not modelled	66.2	32	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
103	d1jmsa3	Alignment	not modelled	64.6	25	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
104	d1nnqa2	Alignment	not modelled	64.5	23	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
105	c1dd9A_	Alignment	not modelled	64.2	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** structure of the dnag catalytic core
106	d1dd9a_	Alignment	not modelled	64.2	26	**Fold:**DNA primase core **Superfamily:**DNA primase core **Family:**DNA primase DnaG catalytic core
107	d2gy9m1	Alignment	not modelled	63.5	18	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
						PDB header:transferase

108	c1jr3E_	Alignment	not modelled	62.4	18	**Chain:** E: **PDB Molecule:**dna polymerase iii, delta' subunit; **PDBTitle:** crystal structure of the processivity clamp loader gamma2 complex of e. coli dna polymerase iii
109	d1vk2a_	Alignment	not modelled	61.9	10	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Mug-like
110	c2aq4A_	Alignment	not modelled	61.6	44	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** ternary complex of the catalytic core of rev1 with dna and dctp.
111	d1d8ba_	Alignment	not modelled	61.4	23	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
112	c2izoA_	Alignment	not modelled	60.3	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flap structure-specific endonuclease; **PDBTitle:** structure of an archaeal pcna1-pcna2-fen1 complex
113	c3fblA_	Alignment	not modelled	59.7	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of orf132 of the archaeal virus acidianus2 filamentous virus 1 (afv1)
114	c1o98A_	Alignment	not modelled	59.6	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
115	c2owoA_	Alignment	not modelled	57.0	33	**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
116	d1yuza2	Alignment	not modelled	57.0	27	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
117	c1a77A_	Alignment	not modelled	56.8	33	**PDB header:**5'-3' exo/endo nuclease **Chain:** A: **PDB Molecule:**flap endonuclease-1 protein; **PDBTitle:** flap endonuclease-1 from methanococcus jannaschii
118	c3q8lA_	Alignment	not modelled	55.4	42	**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+
119	d1lb2b_	Alignment	not modelled	54.8	29	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
120	d1gm5a2	Alignment	not modelled	54.3	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RecG "wedge" domain