Phyre2

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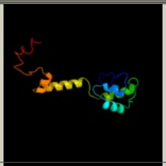
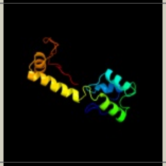
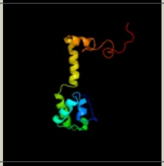
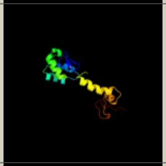
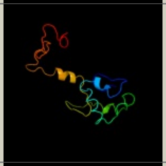
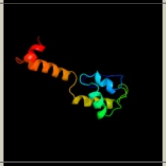
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0A7S9 |
| Date | Thu Jan 5 11:06:08 GMT 2012 |
| Unique Job ID | e55468cdaa31bbcc |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d2gy9m1 | Alignment |  | 100.0 | 100 | **Fold:**S13-like H2TH domain<br>**Superfamily:**S13-like H2TH domain<br>**Family:**Ribosomal protein S13 |
| 2 | d2uubm1 | Alignment |  | 100.0 | 57 | **Fold:**S13-like H2TH domain<br>**Superfamily:**S13-like H2TH domain<br>**Family:**Ribosomal protein S13 |
| 3 | c2xznM_ | Alignment |  | 100.0 | 33 | **PDB header:**ribosome<br>**Chain:** M: **PDB Molecule:**rps18e;<br>**PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2 |
| 4 | c3iz6M_ | Alignment |  | 100.0 | 33 | **PDB header:**ribosome<br>**Chain:** M: **PDB Molecule:**40s ribosomal protein s18 (s13p);<br>**PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 5 | c2zkqm_ | Alignment |  | 100.0 | 34 | **PDB header:**ribosomal protein/rna<br>**Chain:** M: **PDB Molecule:**<br>**PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map |
| 6 | c3bbnM_ | Alignment |  | 100.0 | 45 | **PDB header:**ribosome<br>**Chain:** M: **PDB Molecule:**ribosomal protein s13;<br>**PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome. |
| 7 | d1i94m_ | Alignment |  | 100.0 | 51 | **Fold:**S13-like H2TH domain<br>**Superfamily:**S13-like H2TH domain<br>**Family:**Ribosomal protein S13 |
| 8 | d2hkja1 | Alignment |  | 97.6 | 24 | **Fold:**S13-like H2TH domain<br>**Superfamily:**S13-like H2TH domain<br>**Family:**Topoisomerase VI-B subunit middle domain |
| 9 | c1ee8A_ | Alignment |  | 97.3 | 17 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**mutm (fpg) protein;<br>**PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8 |
| 10 | d1ee8a1 | Alignment |  | 97.2 | 17 | **Fold:**S13-like H2TH domain<br>**Superfamily:**S13-like H2TH domain<br>**Family:**Middle domain of MutM-like DNA repair proteins |
| 11 | d1tdza1 | Alignment |  | 97.1 | 24 | **Fold:**S13-like H2TH domain<br>**Superfamily:**S13-like H2TH domain<br>**Family:**Middle domain of MutM-like DNA repair proteins |

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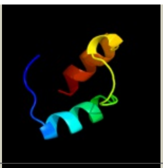
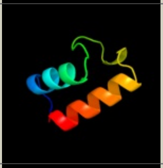
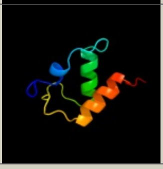
|---|---|---|---|---|---|---|
| 12 | c3a46B_ | Alignment |  | 97.0 | 28 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**formamidopyrimidine-dna glycosylase;<br>**PDBTitle:** crystal structure of mvnei1/thf complex |
| 13 | d1k82a1 | Alignment |  | 97.0 | 27 | **Fold:**S13-like H2TH domain<br>**Superfamily:**S13-like H2TH domain<br>**Family:**Middle domain of MutM-like DNA repair proteins |
| 14 | c2f5qA_ | Alignment |  | 97.0 | 24 | **PDB header:**hydrolase/dna<br>**Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase;<br>**PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2 |
| 15 | c1k82D_ | Alignment |  | 96.9 | 27 | **PDB header:**hydrolase/dna<br>**Chain:** D: **PDB Molecule:**formamidopyrimidine-dna glycosylase;<br>**PDBTitle:** crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna |
| 16 | c1nnjA_ | Alignment |  | 96.9 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosylase;<br>**PDBTitle:** crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna |
| 17 | d1r2za1 | Alignment |  | 96.9 | 26 | **Fold:**S13-like H2TH domain<br>**Superfamily:**S13-like H2TH domain<br>**Family:**Middle domain of MutM-like DNA repair proteins |
| 18 | c2opfA_ | Alignment |  | 96.7 | 22 | **PDB header:**hydrolase/dna<br>**Chain:** A: **PDB Molecule:**endonuclease viii;<br>**PDBTitle:** crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate |
| 19 | d1k3xa1 | Alignment |  | 96.7 | 24 | **Fold:**S13-like H2TH domain<br>**Superfamily:**S13-like H2TH domain<br>**Family:**Middle domain of MutM-like DNA repair proteins |
| 20 | d2i0za2 | Alignment |  | 94.7 | 20 | **Fold:**HI0933 insert domain-like<br>**Superfamily:**HI0933 insert domain-like<br>**Family:**HI0933 insert domain-like |
| 21 | d1tdha1 | Alignment | not modelled | 93.5 | 20 | **Fold:**S13-like H2TH domain<br>**Superfamily:**S13-like H2TH domain<br>**Family:**Middle domain of MutM-like DNA repair proteins |
| 22 | c1tdhA_ | Alignment | not modelled | 92.7 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**nei endonuclease viii-like 1;<br>**PDBTitle:** crystal structure of human endonuclease viii-like 1 (neil1) |
| 23 | c3fuxB_ | Alignment | not modelled | 92.2 | 29 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**dimethyladenosine transferase;<br>**PDBTitle:** t. thermophilus 16s rrna a1518 and a1519 methyltransferase (ksga) in2 complex with 5'-methylthioadenosine in space group p212121 |
| 24 | c1mx0D_ | Alignment | not modelled | 89.5 | 26 | **PDB header:**isomerase<br>**Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b;<br>**PDBTitle:** structure of topoisomerase subunit |
| 25 | d2gqfa2 | Alignment | not modelled | 88.0 | 13 | **Fold:**HI0933 insert domain-like<br>**Superfamily:**HI0933 insert domain-like<br>**Family:**HI0933 insert domain-like |
| 26 | c1s5lu_ | Alignment | not modelled | 86.3 | 26 | **PDB header:**photosynthesis<br>**Chain:** U: **PDB Molecule:**photosystem ii 12 kda extrinsic protein;<br>**PDBTitle:** architecture of the photosynthetic oxygen evolving center |
| 27 | d1qyra_ | Alignment | not modelled | 85.8 | 20 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**rRNA adenine dimethylase-like |
| 28 | d2axtu1 | Alignment | not modelled | 84.5 | 25 | **Fold:**SAM domain-like<br>**Superfamily:**PsbU/PolX domain-like<br>**Family:**PsbU-like |

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| 29 | d1pzna1 | Alignment | not modelled | 83.1 | 18 | **Fold:**SAM domain-like<br>**Superfamily:**Rad51 N-terminal domain-like<br>**Family:**DNA repair protein Rad51, N-terminal domain |
| 30 | c2zbkB_ | Alignment | not modelled | 82.5 | 22 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b;<br>**PDBTitle:** crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms |
| 31 | d2i1qa1 | Alignment | not modelled | 82.4 | 27 | **Fold:**SAM domain-like<br>**Superfamily:**Rad51 N-terminal domain-like<br>**Family:**DNA repair protein Rad51, N-terminal domain |
| 32 | d2bgwa1 | Alignment | not modelled | 82.3 | 24 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**Hef domain-like |
| 33 | c3tqsB_ | Alignment | not modelled | 80.0 | 14 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**ribosomal rna small subunit methyltransferase a;<br>**PDBTitle:** structure of the dimethyladenosine transferase (ksga) from coxiella2 burnetii |
| 34 | d2a1jb1 | Alignment | not modelled | 79.7 | 22 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**Hef domain-like |
| 35 | c1kftA_ | Alignment | not modelled | 77.6 | 27 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**excinuclease abc subunit c;<br>**PDBTitle:** solution structure of the c-terminal domain of uvrc from e-2 coli |
| 36 | d1kfta_ | Alignment | not modelled | 77.6 | 27 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**Excinuclease UvrC C-terminal domain |
| 37 | d1x2ia1 | Alignment | not modelled | 76.8 | 20 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**Hef domain-like |
| 38 | d1bvsa2 | Alignment | not modelled | 75.3 | 25 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**DNA helicase RuvA subunit, middle domain |
| 39 | c1vddC_ | Alignment | not modelled | 73.4 | 30 | **PDB header:**recombination<br>**Chain:** C: **PDB Molecule:**recombination protein recr;<br>**PDBTitle:** crystal structure of recombinational repair protein recr |
| 40 | d1ixra1 | Alignment | not modelled | 73.4 | 33 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**DNA helicase RuvA subunit, middle domain |
| 41 | d1cuka2 | Alignment | not modelled | 72.6 | 32 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**DNA helicase RuvA subunit, middle domain |
| 42 | c1d8lA_ | Alignment | not modelled | 72.3 | 25 | **PDB header:**gene regulation<br>**Chain:** A: **PDB Molecule:**protein (holliday junction dna helicase ruva);<br>**PDBTitle:** e. coli holliday junction binding protein ruva nh2 region2 lacking domain iii |
| 43 | c3fhgA_ | Alignment | not modelled | 69.5 | 26 | **PDB header:**dna repair, hydrolase, lyase<br>**Chain:** A: **PDB Molecule:**n-glycosylase/dna lyase;<br>**PDBTitle:** crystal structure of sulfolobus solfataricus 8-oxoguanine dna2 glycosylase (ssogg) |
| 44 | c2h5xA_ | Alignment | not modelled | 69.3 | 30 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**holliday junction atp-dependent dna helicase ruva;<br>**PDBTitle:** ruva from mycobacterium tuberculosis |
| 45 | c3fteA_ | Alignment | not modelled | 68.9 | 24 | **PDB header:**transferase/rna<br>**Chain:** A: **PDB Molecule:**dimethyladenosine transferase;<br>**PDBTitle:** crystal structure of a. aeolicus ksga in complex with rna |
| 46 | c1nomA_ | Alignment | not modelled | 68.0 | 23 | **PDB header:**nucleotidyltransferase<br>**Chain:** A: **PDB Molecule:**dna polymerase beta;<br>**PDBTitle:** dna polymerase beta (pol b) (e.c.2.7.7.7), 31-kd domain; soaked in the2 presence of mncl2 (5 millimolar) |
| 47 | d2fmpa2 | Alignment | not modelled | 67.8 | 30 | **Fold:**SAM domain-like<br>**Superfamily:**PsbU/PolX domain-like<br>**Family:**DNA polymerase beta-like, second domain |
| 48 | d2aq0a1 | Alignment | not modelled | 67.1 | 14 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**Hef domain-like |
| 49 | c1ixrA_ | Alignment | not modelled | 65.6 | 36 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**holliday junction dna helicase ruva;<br>**PDBTitle:** ruva-ruvb complex |
| 50 | d1jmsa3 | Alignment | not modelled | 65.0 | 30 | **Fold:**SAM domain-like<br>**Superfamily:**PsbU/PolX domain-like<br>**Family:**DNA polymerase beta-like, second domain |
| 51 | c3mr2A_ | Alignment | not modelled | 63.7 | 15 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**dna polymerase eta;<br>**PDBTitle:** human dna polymerase eta in complex with normal dna and incoming2 nucleotide (nrm) |
| 52 | d2vana1 | Alignment | not modelled | 62.9 | 30 | **Fold:**SAM domain-like<br>**Superfamily:**PsbU/PolX domain-like<br>**Family:**DNA polymerase beta-like, second domain |
| 53 | d2bcqa2 | Alignment | not modelled | 62.5 | 20 | **Fold:**SAM domain-like<br>**Superfamily:**PsbU/PolX domain-like<br>**Family:**DNA polymerase beta-like, second domain |
| 54 | d2duya1 | Alignment | not modelled | 61.4 | 19 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**ComEA-like |
| 55 | c3kntC_ | Alignment | not modelled | 60.7 | 22 | **PDB header:**hydrolase, lyase/dna<br>**Chain:** C: **PDB Molecule:**n-glycosylase/dna lyase;<br>**PDBTitle:** crystal structure of methanocaldococcus jannaschii 8-2 |

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| | | | | | | oxoguanine glycosylase/lyase in complex with 15mer dna3 containing 8-oxoguanine |
| 56 | c3uzuA_ | Alignment | not modelled | 60.4 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase a;<br>**PDBTitle:** the structure of the ribosomal rna small subunit methyltransferase a2 from burkholderia pseudomallei |
| 57 | d1dgsa1 | Alignment | not modelled | 59.3 | 18 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**NAD+-dependent DNA ligase, domain 3 |
| 58 | c1hjpA_ | Alignment | not modelled | 57.3 | 24 | **PDB header:**dna recombination<br>**Chain:** A: **PDB Molecule:**ruva;<br>**PDBTitle:** holliday junction binding protein ruva from e. coli |
| 59 | c2nrzB_ | Alignment | not modelled | 55.8 | 24 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**uvrabc system protein c;<br>**PDBTitle:** crystal structure of the c-terminal half of uvrc bound to2 its catalytic divalent cation |
| 60 | d2edua1 | Alignment | not modelled | 55.7 | 15 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**ComEA-like |
| 61 | d2noha1 | Alignment | not modelled | 52.7 | 31 | **Fold:**DNA-glycosylase<br>**Superfamily:**DNA-glycosylase<br>**Family:**DNA repair glycosylase, 2 C-terminal domains |
| 62 | d1gm5a2 | Alignment | not modelled | 51.3 | 32 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**RecG "wedge" domain |
| 63 | c1ko9A_ | Alignment | not modelled | 50.2 | 35 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**8-oxoguanine dna glycosylase;<br>**PDBTitle:** native structure of the human 8-oxoguanine dna glycosylase2 hogg1 |
| 64 | c8iczA_ | Alignment | not modelled | 50.1 | 24 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**protein (dna polymerase beta (e.c.2.7.7.7));<br>**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) |
| 65 | c3n0uB_ | Alignment | not modelled | 49.6 | 15 | **PDB header:**hydrolase, lyase<br>**Chain:** B: **PDB Molecule:**probable n-glycosylase/dna lyase;<br>**PDBTitle:** crystal structure of tm1821, the 8-oxoguanine dna glycosylase of2 thermotoga maritima |
| 66 | c2ihmA_ | Alignment | not modelled | 48.7 | 24 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**dna polymerase mu;<br>**PDBTitle:** polymerase mu in ternary complex with gapped 11mer dna2 duplex and bound incoming nucleotide |
| 67 | c3f10A_ | Alignment | not modelled | 47.5 | 29 | **PDB header:**hydrolase, lyase<br>**Chain:** A: **PDB Molecule:**8-oxoguanine-dna-glycosylase;<br>**PDBTitle:** crystal structure of clostridium acetobutylicum 8-2 oxoguanine dna glycosylase in complex with 8-oxoguanosine |
| 68 | c1yqmA_ | Alignment | not modelled | 47.5 | 35 | **PDB header:**hydrolase/dna<br>**Chain:** A: **PDB Molecule:**n-glycosylase/dna lyase;<br>**PDBTitle:** catalytically inactive human 8-oxoguanine glycosylase2 crosslinked to 7-deazaguanine containing dna |
| 69 | c2yg8B_ | Alignment | not modelled | 46.7 | 25 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**dna-3-methyladenine glycosidase ii, putative;<br>**PDBTitle:** structure of an unusual 3-methyladenine dna glycosylase ii (2 alka) from deinococcus radiodurans |
| 70 | c3s6iA_ | Alignment | not modelled | 45.7 | 35 | **PDB header:**hydrolase/dna<br>**Chain:** A: **PDB Molecule:**dna-3-methyladenine glycosylase 1;<br>**PDBTitle:** schizosaccaromyces pombe 3-methyladenine dna glycosylase (mag1) in2 complex with abasic-dna. |
| 71 | d2abka_ | Alignment | not modelled | 45.0 | 32 | **Fold:**DNA-glycosylase<br>**Superfamily:**DNA-glycosylase<br>**Family:**Endonuclease III |
| 72 | c2jhnB_ | Alignment | not modelled | 44.7 | 35 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**3-methyladenine dna-glycosylase;<br>**PDBTitle:** 3-methyladenine dna-glycosylase from archaeoglobus fulgidus |
| 73 | c2w9mB_ | Alignment | not modelled | 44.5 | 29 | **PDB header:**dna replication<br>**Chain:** B: **PDB Molecule:**polymerase x;<br>**PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans |
| 74 | c1kdhA_ | Alignment | not modelled | 44.4 | 29 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**terminal deoxynucleotidyltransferase short<br>**PDBTitle:** binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna |
| 75 | d1kg2a_ | Alignment | not modelled | 43.0 | 32 | **Fold:**DNA-glycosylase<br>**Superfamily:**DNA-glycosylase<br>**Family:**Mismatch glycosylase |
| 76 | d1szpa1 | Alignment | not modelled | 42.7 | 26 | **Fold:**SAM domain-like<br>**Superfamily:**Rad51 N-terminal domain-like<br>**Family:**DNA repair protein Rad51, N-terminal domain |
| 77 | d1mpga1 | Alignment | not modelled | 42.1 | 19 | **Fold:**DNA-glycosylase<br>**Superfamily:**DNA-glycosylase<br>**Family:**DNA repair glycosylase, 2 C-terminal domains |
| 78 | d1pu6a_ | Alignment | not modelled | 41.8 | 44 | **Fold:**DNA-glycosylase<br>**Superfamily:**DNA-glycosylase<br>**Family:**3-Methyladenine DNA glycosylase III (MagIII) |
| 79 | d1keaa_ | Alignment | not modelled | 41.5 | 35 | **Fold:**DNA-glycosylase<br>**Superfamily:**DNA-glycosylase<br>**Family:**Mismatch glycosylase |
| 80 | c2hnhA_ | Alignment | not modelled | 41.0 | 26 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dna polymerase iii alpha subunit; |

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| | | Alignment | | | | **PDBTitle:** crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii |
| 81 | c2q2eB_ | Alignment | not modelled | 40.8 | 18 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b;<br>**PDBTitle:** crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei |
| 82 | d1orna_ | Alignment | not modelled | 40.5 | 25 | **Fold:**DNA-glycosylase<br>**Superfamily:**DNA-glycosylase<br>**Family:**Endonuclease III |
| 83 | c3doaA_ | Alignment | not modelled | 38.4 | 9 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**fibrinogen binding protein;<br>**PDBTitle:** the crystal structure of the fibrinogen binding protein from2 staphylococcus aureus |
| 84 | d1a77a1 | Alignment | not modelled | 38.2 | 18 | **Fold:**SAM domain-like<br>**Superfamily:**5' to 3' exonuclease, C-terminal subdomain<br>**Family:**5' to 3' exonuclease, C-terminal subdomain |
| 85 | c2h1rA_ | Alignment | not modelled | 37.8 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dimethyladenosine transferase, putative;<br>**PDBTitle:** crystal structure of a dimethyladenosine transferase from2 plasmodium falciparum |
| 86 | c2bcuA_ | Alignment | not modelled | 37.4 | 16 | **PDB header:**transferase, lyase/dna<br>**Chain:** A: **PDB Molecule:**dna polymerase lambda;<br>**PDBTitle:** dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch |
| 87 | c1rrqA_ | Alignment | not modelled | 37.1 | 32 | **PDB header:**hydrolase/dna<br>**Chain:** A: **PDB Molecule:**muty;<br>**PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair |
| 88 | d1vdda_ | Alignment | not modelled | 35.8 | 17 | **Fold:**Recombination protein RecR<br>**Superfamily:**Recombination protein RecR<br>**Family:**Recombination protein RecR |
| 89 | d1jiha2 | Alignment | not modelled | 35.7 | 18 | **Fold:**DNA/RNA polymerases<br>**Superfamily:**DNA/RNA polymerases<br>**Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain |
| 90 | d1rrqa1 | Alignment | not modelled | 35.4 | 32 | **Fold:**DNA-glycosylase<br>**Superfamily:**DNA-glycosylase<br>**Family:**Mismatch glycosylase |
| 91 | c2h56C_ | Alignment | not modelled | 33.6 | 4 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**dna-3-methyladenine glycosidase;<br>**PDBTitle:** crystal structure of dna-3-methyladenine glycosidase (10174367) from2 bacillus halodurans at 2.55 a resolution |
| 92 | c3n5nX_ | Alignment | not modelled | 32.0 | 30 | **PDB header:**hydrolase<br>**Chain:** X: **PDB Molecule:**a/g-specific adenine dna glycosylase;<br>**PDBTitle:** crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue |
| 93 | d1zq9a1 | Alignment | not modelled | 31.7 | 11 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**rRNA adenine dimethylase-like |
| 94 | d1rxwa1 | Alignment | not modelled | 31.7 | 24 | **Fold:**SAM domain-like<br>**Superfamily:**5' to 3' exonuclease, C-terminal subdomain<br>**Family:**5' to 3' exonuclease, C-terminal subdomain |
| 95 | d1mc8a1 | Alignment | not modelled | 30.2 | 18 | **Fold:**SAM domain-like<br>**Superfamily:**5' to 3' exonuclease, C-terminal subdomain<br>**Family:**5' to 3' exonuclease, C-terminal subdomain |
| 96 | d1b43a1 | Alignment | not modelled | 29.7 | 24 | **Fold:**SAM domain-like<br>**Superfamily:**5' to 3' exonuclease, C-terminal subdomain<br>**Family:**5' to 3' exonuclease, C-terminal subdomain |
| 97 | c1mpgB_ | Alignment | not modelled | 29.2 | 19 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**3-methyladenine dna glycosylase ii;<br>**PDBTitle:** 3-methyladenine dna glycosylase ii from escherichia coli |
| 98 | d1xo1a1 | Alignment | not modelled | 28.6 | 29 | **Fold:**SAM domain-like<br>**Superfamily:**5' to 3' exonuclease, C-terminal subdomain<br>**Family:**5' to 3' exonuclease, C-terminal subdomain |
| 99 | c3grrA_ | Alignment | not modelled | 28.5 | 26 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dimethyladenosine transferase;<br>**PDBTitle:** crystal structure of the complex between s-adenosyl homocysteine and2 methanocaldococcus jannaschi dim1. |
| 100 | d3bzka1 | Alignment | not modelled | 28.2 | 31 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**Tex HhH-containing domain-like |
| 101 | c3fydA_ | Alignment | not modelled | 26.6 | 26 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**probable dimethyladenosine transferase;<br>**PDBTitle:** crystal structure of dim1 from the thermophilic archeon,2 methanocaldococcus jannaschi |
| 102 | c2zkri_ | Alignment | not modelled | 23.6 | 20 | **PDB header:**ribosomal protein/rna<br>**Chain:** I: **PDB Molecule:**rna expansion segment es15 part i;<br>**PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map |
| 103 | c2oceA_ | Alignment | not modelled | 22.6 | 25 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein pa5201;<br>**PDBTitle:** crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa |
| 104 | c2r8kB_ | Alignment | not modelled | 22.4 | 19 | **PDB header:**replication, transferase/dna<br>**Chain:** B: **PDB Molecule:**dna polymerase eta;<br>**PDBTitle:** structure of the eukaryotic dna polymerase eta in complex with 1,2-2 d(gpg)-cisplatin containing dna |
| 105 | c2kp7A_ | Alignment | not modelled | 22.2 | 5 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**crossover junction endonuclease mus81;<br>**PDBTitle:** solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a |
| 106 | d1ul1x1 | Alignment | not modelled | 22.2 | 24 | **Fold:**SAM domain-like<br>**Superfamily:**5' to 3' exonuclease, C-terminal subdomain<br>**Family:**5' to 3' exonuclease, C-terminal subdomain |

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| 107 | c1jihA_ | Alignment | not modelled | 21.6 | 19 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**dna polymerase eta;<br>**PDBTitle:** yeast dna polymerase eta |
| 108 | c2csdB_ | Alignment | not modelled | 21.5 | 38 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**topoisomerase v;<br>**PDBTitle:** crystal structure of topoisomerase v (61 kda fragment) |
| 109 | d1b22a_ | Alignment | not modelled | 21.3 | 14 | **Fold:**SAM domain-like<br>**Superfamily:**Rad51 N-terminal domain-like<br>**Family:**DNA repair protein Rad51, N-terminal domain |
| 110 | c1b22A_ | Alignment | not modelled | 21.3 | 14 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**dna repair protein rad51;<br>**PDBTitle:** rad51 (n-terminal domain) |
| 111 | c1ut8B_ | Alignment | not modelled | 20.8 | 25 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**exodeoxyribonuclease;<br>**PDBTitle:** divalent metal ions (zinc) bound to t5 5'-exonuclease |
| 112 | d2fmpa1 | Alignment | not modelled | 20.3 | 21 | **Fold:**SAM domain-like<br>**Superfamily:**DNA polymerase beta, N-terminal domain-like<br>**Family:**DNA polymerase beta, N-terminal domain-like |