





















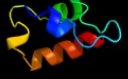










Phyre2

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|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1388_(mihF)_1563700_1564272 |
| Date | Wed Jul 31 22:05:49 BST 2019 |
| Unique Job ID | 5870fc51a757caf2 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c4itqA_ |  Alignment |  | 100.0 | 57 | 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 |
| 2 | d1i94m_ |  Alignment |  | 96.3 | 24 | Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13 |
| 3 | d2uubm1 |  Alignment |  | 96.3 | 26 | Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13 |
| 4 | c3iz6M_ |  Alignment |  | 96.2 | 16 | PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s18 (s13p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 5 | c2xznM_ |  Alignment |  | 96.2 | 20 | PDB header: ribosome Chain: M: PDB Molecule: rps18e; 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 |
| 6 | d2gy9m1 |  Alignment |  | 96.2 | 21 | Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13 |
| 7 | c5o5jM_ |  Alignment |  | 96.2 | 21 | PDB header: ribosome Chain: M: PDB Molecule: 30s ribosomal protein s13; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis |
| 8 | c2zkqm_ |  Alignment |  | 96.0 | 18 | PDB header: ribosomal protein/rna Chain: M: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map |
| 9 | c3j200_ |  Alignment |  | 96.0 | 21 | PDB header: ribosome Chain: O: PDB Molecule: 30s ribosomal protein s13p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit) |
| 10 | c5xyiS_ |  Alignment |  | 95.3 | 14 | PDB header: ribosome Chain: S: PDB Molecule: ribosomal protein s13p/s18e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome |
| 11 | c5mmjm_ |  Alignment |  | 94.5 | 15 | PDB header: ribosome Chain: M: PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome |

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|----|-------------------------|-----------|---|------|----|---|
| 12 | c3zeyM | Alignment |  | 94.5 | 18 | PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s18, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome |
| 13 | c3twkB | Alignment |  | 94.4 | 20 | PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg |
| 14 | d2hkja1 | Alignment |  | 94.2 | 21 | Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Topoisomerase VI-B subunit middle domain |
| 15 | d1r2za1 | Alignment |  | 93.8 | 19 | Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins |
| 16 | c2f5qA | Alignment |  | 93.8 | 19 | PDB header: hydrolase/dna Chain: A: PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2 |
| 17 | d1tdza1 | Alignment |  | 93.2 | 15 | Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins |
| 18 | d1ee8a1 | Alignment |  | 93.2 | 21 | Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins |
| 19 | d1k82a1 | Alignment |  | 93.1 | 23 | Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins |
| 20 | c1k82D | Alignment |  | 93.0 | 23 | PDB header: hydrolase/dna Chain: D: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna |
| 21 | c1ee8A | Alignment | not modelled | 92.9 | 21 | PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8 |
| 22 | c3fhgA | Alignment | not modelled | 92.3 | 11 | PDB header: dna repair, hydrolase, lyase Chain: A: PDB Molecule: n-glycosylase/dna lyase; PDBTitle: crystal structure of sulfobolus solfataricus 8-oxoguanine dna2 glycosylase (ssogg) |
| 23 | c3w0fA | Alignment | not modelled | 91.9 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like 3; PDBTitle: crystal structure of mouse endonuclease viii-like 3 (mnei3) |
| 24 | c1nnjA | Alignment | not modelled | 91.4 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna |
| 25 | d2aq0a1 | Alignment | not modelled | 90.5 | 17 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like |
| 26 | c1s5lu | Alignment | not modelled | 90.1 | 19 | PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center |
| 27 | c3a46B | Alignment | not modelled | 88.1 | 24 | PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of mvnei1/thf complex |
| 28 | d1x2ia1 | Alignment | not modelled | 87.9 | 20 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like |
| | | | | | | PDB header: hydrolase, lyase |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c3n0uB | Alignment | not modelled | 87.2 | 16 | Chain: B: PDB Molecule: probable n-glycosylase/dna lyase; PDBTitle: crystal structure of tm1821, the 8-oxoguanine dna glycosylase of <i>Thermotoga maritima</i> |
| 30 | d2axtu1 | Alignment | not modelled | 87.0 | 19 | Fold: SAM domain-like Superfamily: PsbU/PolX domain-like Family: PsbU-like |
| 31 | d1cuka2 | Alignment | not modelled | 86.6 | 22 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain |
| 32 | c2opfA | Alignment | not modelled | 86.0 | 22 | PDB header: hydrolase/dna Chain: A: PDB Molecule: endonuclease viii; PDBTitle: crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from <i>E. coli</i> (r252a) in complex with ap-site containing dna substrate |
| 33 | d1k3xa1 | Alignment | not modelled | 85.9 | 21 | Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins |
| 34 | c3s6iA | Alignment | not modelled | 84.1 | 9 | PDB header: hydrolase/dna Chain: A: PDB Molecule: dna-3-methyladenine glycosylase 1; PDBTitle: schizosaccharomyces pombe 3-methyladenine dna glycosylase (mag1) in2 complex with abasic-dna. |
| 35 | c1ixrA | Alignment | not modelled | 84.1 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex |
| 36 | d1kfta | Alignment | not modelled | 83.9 | 14 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Excinuclease UvrC C-terminal domain |
| 37 | c1kftA | Alignment | not modelled | 83.9 | 14 | PDB header: dna binding protein Chain: A: PDB Molecule: excinuclease abc subunit c; PDBTitle: solution structure of the c-terminal domain of uvrC from <i>E. coli</i> |
| 38 | d2bgwa1 | Alignment | not modelled | 82.5 | 20 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like |
| 39 | c4b24A | Alignment | not modelled | 81.6 | 7 | PDB header: hydrolase/dna Chain: A: PDB Molecule: probable dna-3-methyladenine glycosylase 2; PDBTitle: unprecedented sculpting of dna at abasic sites by dna glycosylase2 homolog mag2 |
| 40 | c2bhnD | Alignment | not modelled | 81.5 | 19 | PDB header: hydrolase Chain: D: PDB Molecule: xpf endonuclease; PDBTitle: xpf from <i>Aeropyrum pernix</i> |
| 41 | c4bxoA | Alignment | not modelled | 81.1 | 4 | 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 |
| 42 | c4mb7A | Alignment | not modelled | 80.4 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 8-like I720; PDBTitle: crystal structure of a viral dna glycosylase |
| 43 | d2duya1 | Alignment | not modelled | 80.1 | 24 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like |
| 44 | d1ixra1 | Alignment | not modelled | 79.6 | 24 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain |
| 45 | d2a1jb1 | Alignment | not modelled | 79.0 | 23 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like |
| 46 | d1bvsa2 | Alignment | not modelled | 78.3 | 26 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain |
| 47 | c2ihmA | Alignment | not modelled | 77.6 | 13 | 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 |
| 48 | d2edua1 | Alignment | not modelled | 77.4 | 27 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: ComEA-like |
| 49 | d1dgsa1 | Alignment | not modelled | 77.3 | 25 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3 |
| 50 | c8icza | Alignment | not modelled | 76.1 | 14 | 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 datp3 (1 millimolar), mnc12 (5 millimolar), and lithium sulfate4 (75 millimolar) |
| 51 | c2lyhA | Alignment | not modelled | 75.9 | 29 | PDB header: dna binding protein Chain: A: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215 |
| 52 | c2h5xA | Alignment | not modelled | 75.4 | 26 | PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from <i>Mycobacterium tuberculosis</i> |
| 53 | c4p4oA | Alignment | not modelled | 74.7 | 21 | PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: crystal structure of leishmania infantum polymerase beta: ternary gap2 complex |
| 54 | c3mr2A | Alignment | not modelled | 74.6 | 18 | PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase eta; PDBTitle: human dna polymerase eta in complex with normal dna and incoming2 nucleotide (nrm) |

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|----|-------------------------|-----------|--------------|------|----|--|
| 55 | c4bxoB | Alignment | not modelled | 73.6 | 29 | 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 |
| 56 | c1d8IA | Alignment | not modelled | 73.0 | 22 | 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 |
| 57 | c6erpJ | Alignment | not modelled | 72.8 | 13 | PDB header: transcription Chain: J: PDB Molecule: dimethyladenosine transferase 2, mitochondrial; PDBTitle: structure of the human mitochondrial transcription initiation complex2 at the lsp promoter |
| 58 | c2mutA | Alignment | not modelled | 72.6 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region |
| 59 | c2yg8B | Alignment | not modelled | 72.3 | 21 | 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 |
| 60 | c3f10A | Alignment | not modelled | 72.0 | 28 | 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 |
| 61 | c1hjpA | Alignment | not modelled | 70.3 | 22 | PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli |
| 62 | d1szpa1 | Alignment | not modelled | 67.3 | 20 | Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain |
| 63 | d1t94a2 | Alignment | not modelled | 66.4 | 26 | Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain |
| 64 | d2a1ja1 | Alignment | not modelled | 66.3 | 17 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like |
| 65 | c3auoB | Alignment | not modelled | 66.1 | 20 | 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 |
| 66 | c1kdhA | Alignment | not modelled | 65.1 | 14 | PDB header: transferase/dna Chain: A: PDB Molecule: terminal deoxynucleotidyltransferase short PDBTitle: binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna |
| 67 | c3epvB | Alignment | not modelled | 64.3 | 16 | PDB header: metal binding protein Chain: B: PDB Molecule: nickel and cobalt resistance protein cnrr; PDBTitle: x-ray structure of the metal-sensor cnrx in both the apo- and copper-2 bound forms |
| 68 | c1mpgB | Alignment | not modelled | 63.0 | 26 | PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna glycosylase ii; PDBTitle: 3-methyladenine dna glycosylase ii from escherichia coli |
| 69 | c2zj8A | Alignment | not modelled | 62.8 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: putative ski2-type helicase; PDBTitle: archaeal dna helicase hjm apo state in form 2 |
| 70 | d1ul1x1 | Alignment | not modelled | 62.6 | 19 | Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain |
| 71 | c3n5nX | Alignment | not modelled | 62.6 | 35 | 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 |
| 72 | d1rxwa1 | Alignment | not modelled | 62.1 | 19 | Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain |
| 73 | c1ixrB | Alignment | not modelled | 61.8 | 26 | PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex |
| 74 | d1a77a1 | Alignment | not modelled | 60.9 | 18 | Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain |
| 75 | c2nrzB | Alignment | not modelled | 59.5 | 14 | 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 |
| 76 | c2bcuA | Alignment | not modelled | 59.1 | 16 | 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 tt mismatch |
| 77 | c1mx0D | Alignment | not modelled | 58.5 | 21 | PDB header: isomerase Chain: D: PDB Molecule: type ii dna topoisomerase vi subunit b; PDBTitle: structure of topoisomerase subunit |
| 78 | c2csdB | Alignment | not modelled | 56.4 | 15 | PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment) |
| 79 | d2p6ra2 | Alignment | not modelled | 55.6 | 16 | Fold: Sec63 N-terminal domain-like Superfamily: Sec63 N-terminal domain-like Family: Achaeal helicase C-terminal domain |
| | | | | | | Fold: SAM domain-like |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 80 | d1szpb1 | Alignment | not modelled | 54.8 | 21 | Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain |
| 81 | c4l8iA | Alignment | not modelled | 54.2 | 14 | PDB header: immune system Chain: A: PDB Molecule: rsv epitope scaffold ffl_005; PDBTitle: crystal structure of rsv epitope scaffold ffl_005 |
| 82 | c3bbnM | Alignment | not modelled | 54.0 | 17 | PDB header: ribosome Chain: M: PDB Molecule: ribosomal protein s13; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome. |
| 83 | d3bzka1 | Alignment | not modelled | 53.9 | 30 | Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HhH-containing domain-like |
| 84 | c1rrqA | Alignment | not modelled | 53.9 | 16 | PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair |
| 85 | c5o19A | Alignment | not modelled | 53.9 | 9 | PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor, mitochondrial; PDBTitle: structure of human mitochondrial transcription elongation factor2 (tefm) n-terminal domain |
| 86 | c4clvB | Alignment | not modelled | 53.6 | 14 | PDB header: metal binding protein Chain: B: PDB Molecule: nickel-cobalt-cadmium resistance protein nccx; PDBTitle: crystal structure of dodecylphosphocholine-solubilized nccx2 from cupriavidus metallidurans 31a |
| 87 | c4unfA | Alignment | not modelled | 53.0 | 25 | PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-1; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-1 |
| 88 | d1mpga1 | Alignment | not modelled | 52.9 | 19 | Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: DNA repair glycosylase, 2 C-terminal domains |
| 89 | d1xo1a1 | Alignment | not modelled | 51.3 | 18 | Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain |
| 90 | c4ejyA | Alignment | not modelled | 51.2 | 21 | PDB header: hydrolase/dna Chain: A: PDB Molecule: 3-methyladenine dna glycosylase; PDBTitle: structure of mboggl1 in complex with high affinity dna ligand |
| 91 | d1b43a1 | Alignment | not modelled | 50.5 | 29 | Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain |
| 92 | c1b22A | Alignment | not modelled | 50.1 | 20 | PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: rad51 (n-terminal domain) |
| 93 | d1b22a | Alignment | not modelled | 50.1 | 20 | Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain |
| 94 | d1mc8a1 | Alignment | not modelled | 49.9 | 29 | Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain |
| 95 | d1kg2a | Alignment | not modelled | 49.9 | 39 | Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase |
| 96 | c4uobA | Alignment | not modelled | 49.3 | 30 | PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-3; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-3 |
| 97 | d1pu6a | Alignment | not modelled | 48.6 | 28 | Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase III (MagIII) |
| 98 | c2ziuA | Alignment | not modelled | 47.8 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: mus81 protein; PDBTitle: crystal structure of the mus81-eme1 complex |
| 99 | c2i5hA | Alignment | not modelled | 47.7 | 50 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1531; PDBTitle: crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655 |
| 100 | d2i5ha1 | Alignment | not modelled | 47.7 | 50 | Fold: AF1531-like Superfamily: AF1531-like Family: AF1531-like |
| 101 | d2ilqa1 | Alignment | not modelled | 47.5 | 9 | Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain |
| 102 | d1pzna1 | Alignment | not modelled | 47.5 | 14 | Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain |
| 103 | c1yqmA | Alignment | not modelled | 47.4 | 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 |
| 104 | c2jrtA | Alignment | not modelled | 47.4 | 29 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5 |
| 105 | d1keaa | Alignment | not modelled | 46.0 | 33 | Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase |
| 106 | d1rrqa1 | Alignment | not modelled | 45.9 | 17 | Fold: DNA-glycosylase Superfamily: DNA-glycosylase |

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|-----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | Family: Mismatch glycosylase |
| 107 | c3kntC_ | Alignment | not modelled | 45.9 | 17 | 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 |
| 108 | d1orna_ | Alignment | not modelled | 45.4 | 33 | Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III |
| 109 | d2abka_ | Alignment | not modelled | 45.3 | 50 | Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III |
| 110 | c2jhnB_ | Alignment | not modelled | 44.7 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: 3-methyladenine dna-glycosylase; PDBTitle: 3-methyladenine dna-glycosylase from archaeoglobus fulgidus |
| 111 | c1t3nB_ | Alignment | not modelled | 44.6 | 26 | PDB header: replication/dna Chain: B: PDB Molecule: polymerase (dna directed) iota; PDBTitle: structure of the catalytic core of dna polymerase iota in complex with2 dna and dttp |
| 112 | c2oh2B_ | Alignment | not modelled | 43.8 | 26 | PDB header: transferase/dna Chain: B: PDB Molecule: dna polymerase kappa; PDBTitle: ternary complex of human dna polymerase |
| 113 | c2owoA_ | Alignment | not modelled | 43.7 | 32 | 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 |
| 114 | d2vana1 | Alignment | not modelled | 41.8 | 18 | Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain |
| 115 | c5ituB_ | Alignment | not modelled | 41.1 | 26 | PDB header: dna binding protein/dna Chain: B: PDB Molecule: endonuclease 8-like 1; PDBTitle: crystal structure of human neil1(242k) bound to duplex dna containing2 thf |
| 116 | d1jx4a2 | Alignment | not modelled | 41.0 | 21 | Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain |
| 117 | d1tdha1 | Alignment | not modelled | 40.6 | 23 | Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins |
| 118 | d1eh1a_ | Alignment | not modelled | 38.8 | 39 | Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF |
| 119 | d2oa4a1 | Alignment | not modelled | 37.9 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: SPO1678-like |
| 120 | c1ut8B_ | Alignment | not modelled | 37.6 | 18 | PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease |