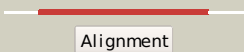

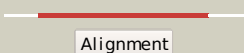

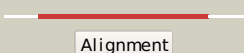

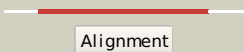

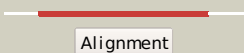

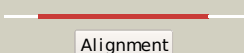

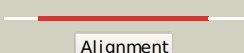

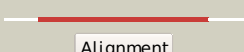

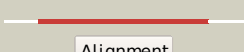

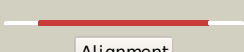

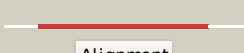
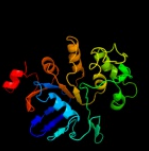











| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c2olkD_ |  Alignment |  | 100.0 | 43 | PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s |
| 2 | c2it1B_ |  Alignment |  | 100.0 | 36 | PDB header: transport protein Chain: B: PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii |
| 3 | d1g2912 |  Alignment |  | 100.0 | 31 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 4 | d1oxxk2 |  Alignment |  | 100.0 | 30 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 5 | c2yyzA_ |  Alignment |  | 100.0 | 37 | PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein |
| 6 | d1b0ua_ |  Alignment |  | 100.0 | 44 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 7 | c1oxtB_ |  Alignment |  | 100.0 | 30 | PDB header: transport protein Chain: B: PDB Molecule: abc transporter, atp binding protein; PDBTitle: crystal structure of glcv, the abc-atpase of the glucose abc2 transporter from sulfolobus solfataricus |
| 8 | c3fvqB_ |  Alignment |  | 100.0 | 32 | PDB header: hydrolase Chain: B: PDB Molecule: fe(3+) ions import atp-binding protein fbpc; PDBTitle: crystal structure of the nucleotide binding domain fbpc2 complexed with atp |
| 9 | c1z47B_ |  Alignment |  | 100.0 | 39 | PDB header: ligand binding protein Chain: B: PDB Molecule: putative abc-transporter atp-binding protein; PDBTitle: structure of the atpase subunit cysa of the putative2 sulfate atp-binding cassette (abc) transporter from3 alicyclobacillus acidocaldarius |
| 10 | d3dhwc1 |  Alignment |  | 100.0 | 38 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 11 | c1qlbD_ |  Alignment |  | 100.0 | 37 | PDB header: transport protein Chain: D: PDB Molecule: maltose/maltodextrin transport atp-binding protein malk; PDBTitle: crystal structure of e. coli malk in the nucleotide-free form |

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|----|-------------------------|-----------|---|-------|----|--|
| 12 | d1vpla_ | Alignment |  | 100.0 | 23 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 13 | c1vciA_ | Alignment |  | 100.0 | 35 | PDB header: transport protein Chain: A: PDB Molecule: sugar-binding transport atp-binding protein; PDBTitle: crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp |
| 14 | d1v43a3 | Alignment |  | 100.0 | 33 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 15 | c2d62A_ | Alignment |  | 100.0 | 31 | PDB header: sugar binding protein Chain: A: PDB Molecule: multiple sugar-binding transport atp-binding PDBTitle: crystal structure of multiple sugar binding transport atp-2 binding protein |
| 16 | c3gfoA_ | Alignment |  | 100.0 | 31 | PDB header: atp binding protein Chain: A: PDB Molecule: cobalt import atp-binding protein cbio 1; PDBTitle: structure of cbio1 from clostridium perfringens: part of2 the abc transporter complex cbionq. |
| 17 | c3dhwC_ | Alignment |  | 100.0 | 37 | PDB header: membrane protein/hydrolase Chain: C: PDB Molecule: methionine import atp-binding protein metn; PDBTitle: crystal structure of methionine importer metni |
| 18 | d1g6ha_ | Alignment |  | 100.0 | 26 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 19 | c2pcjB_ | Alignment |  | 100.0 | 37 | PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein-releasing system atp-binding protein lold; PDBTitle: crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5 |
| 20 | d3d31a2 | Alignment |  | 100.0 | 30 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 21 | d1ji0a_ | Alignment | not modelled | 100.0 | 28 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 22 | c3g5uB_ | Alignment | not modelled | 100.0 | 27 | PDB header: membrane protein Chain: B: PDB Molecule: multidrug resistance protein 1a; PDBTitle: structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding |
| 23 | c3d31B_ | Alignment | not modelled | 100.0 | 30 | PDB header: transport protein Chain: B: PDB Molecule: sulfate/molybdate abc transporter, atp-binding PDBTitle: modbc from methanosarcina acetivorans |
| 24 | c2yz2B_ | Alignment | not modelled | 100.0 | 29 | PDB header: hydrolase Chain: B: PDB Molecule: putative abc transporter atp-binding protein tm_0222; PDBTitle: crystal structure of the abc transporter in the cobalt transport2 system |
| 25 | d2pmka1 | Alignment | not modelled | 100.0 | 32 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 26 | d1mv5a_ | Alignment | not modelled | 100.0 | 25 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 27 | d3b60a1 | Alignment | not modelled | 100.0 | 29 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 28 | c2d2fA_ | Alignment | not modelled | 100.0 | 22 | PDB header: protein binding Chain: A: PDB Molecule: sufc protein; PDBTitle: crystal structure of atypical cytoplasmic abc-atpase sufc |

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|----|-------------------------|-----------|--------------|-------|----|--|
| | | | | | | from thermus2 thermophilus hb8 |
| 29 | d1jj7a_ | Alignment | not modelled | 100.0 | 27 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 30 | d1l2ta_ | Alignment | not modelled | 100.0 | 34 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 31 | c2hydB_ | Alignment | not modelled | 100.0 | 30 | PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866 |
| 32 | c2nq2C_ | Alignment | not modelled | 100.0 | 25 | PDB header: metal transport Chain: C: PDB Molecule: hypothetical abc transporter atp-binding protein PDBTitle: an inward-facing conformation of a putative metal-chelate2 type abc transporter. |
| 33 | c2yl4A_ | Alignment | not modelled | 100.0 | 30 | PDB header: membrane protein Chain: A: PDB Molecule: atp-binding cassette sub-family b member 10, PDBTitle: structure of the human mitochondrial abc transporter, abcb10 |
| 34 | c3nhaA_ | Alignment | not modelled | 100.0 | 28 | PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family b member 6, mitochondrial; PDBTitle: nucleotide binding domain of human abcb6 (adp mg bound structure) |
| 35 | d2onka1 | Alignment | not modelled | 100.0 | 32 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 36 | d2hyda1 | Alignment | not modelled | 100.0 | 31 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 37 | c3gd7C_ | Alignment | not modelled | 100.0 | 22 | PDB header: hydrolase Chain: C: PDB Molecule: fusion complex of cystic fibrosis transmembrane PDBTitle: crystal structure of human nbd2 complexed with n6-2 phenylethyl-atp (p-atp) |
| 38 | c2d3wB_ | Alignment | not modelled | 100.0 | 21 | PDB header: biosynthetic protein Chain: B: PDB Molecule: probable atp-dependent transporter sufcd; PDBTitle: crystal structure of escherichia coli sufcd, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery |
| 39 | c2ihyB_ | Alignment | not modelled | 100.0 | 29 | PDB header: hydrolase Chain: B: PDB Molecule: abc transporter, atp-binding protein; PDBTitle: structure of the staphylococcus aureus putative atpase subunit of an2 atp-binding cassette (abc) transporter |
| 40 | c2cbzA_ | Alignment | not modelled | 100.0 | 28 | PDB header: transport Chain: A: PDB Molecule: multidrug resistance-associated protein 1; PDBTitle: structure of the human multidrug resistance protein 12 nucleotide binding domain 1 |
| 41 | c3b5wE_ | Alignment | not modelled | 100.0 | 29 | PDB header: membrane protein Chain: E: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of escherichia coli msba |
| 42 | c3b5xB_ | Alignment | not modelled | 100.0 | 29 | PDB header: membrane protein Chain: B: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of msba from vibrio cholerae |
| 43 | d1pf4a1 | Alignment | not modelled | 100.0 | 30 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 44 | c2pzfB_ | Alignment | not modelled | 100.0 | 24 | PDB header: hydrolase Chain: B: PDB Molecule: cystic fibrosis transmembrane conductance regulator; PDBTitle: minimal human cftr first nucleotide binding domain as a head-to-tail2 dimer with delta f508 |
| 45 | d1xmia_ | Alignment | not modelled | 100.0 | 22 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 46 | c2ghiD_ | Alignment | not modelled | 100.0 | 25 | PDB header: transport protein Chain: D: PDB Molecule: transport protein; PDBTitle: crystal structure of plasmodium yoelii multidrug resistance2 protein 2 |
| 47 | c1yqtA_ | Alignment | not modelled | 100.0 | 29 | PDB header: hydrolase/translation Chain: A: PDB Molecule: rnase l inhibitor; PDBTitle: rnase-l inhibitor |
| 48 | d2awna2 | Alignment | not modelled | 100.0 | 38 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 49 | d1r0wa_ | Alignment | not modelled | 100.0 | 22 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 50 | c3ozxA_ | Alignment | not modelled | 100.0 | 25 | PDB header: hydrolase, translation Chain: A: PDB Molecule: rnase l inhibitor; PDBTitle: crystal structure of abce1 of sulfolobus solfataricus (-fes domain) |
| 51 | c2pjzA_ | Alignment | not modelled | 100.0 | 28 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein st1066; PDBTitle: the crystal structure of putative cobalt transport atp-2 binding protein (cbio-2), st1066 |
| 52 | d1l7vc_ | Alignment | not modelled | 100.0 | 23 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 53 | d1sgwa | Alignment | not modelled | 100.0 | 19 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 54 | c3bk7A | Alignment | not modelled | 100.0 | 28 | PDB header: hydrolase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abyssi |
| 55 | c2iw3B | Alignment | not modelled | 100.0 | 21 | PDB header: translation Chain: B: PDB Molecule: elongation factor 3a; PDBTitle: elongation factor 3 in complex with adp |
| 56 | c2r6fA | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: excinuclease abc subunit a; PDBTitle: crystal structure of bacillus stearothermophilus uvra |
| 57 | c2ygrD | Alignment | not modelled | 100.0 | 25 | PDB header: hydrolase Chain: D: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra |
| 58 | c3pihA | Alignment | not modelled | 100.0 | 24 | PDB header: hydrolase/dna Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: t. maritima uvra in complex with fluorescein-modified dna |
| 59 | c2vf7B | Alignment | not modelled | 100.0 | 22 | PDB header: dna-binding protein Chain: B: PDB Molecule: excinuclease abc, subunit a.; PDBTitle: crystal structure of uvra2 from deinococcus radiodurans |
| 60 | d1cr2a | Alignment | not modelled | 99.9 | 13 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 61 | d1w1wa | Alignment | not modelled | 99.9 | 16 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 62 | c3tauB | Alignment | not modelled | 99.9 | 18 | PDB header: transferase Chain: B: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of a putative guanylate monophosphate kinase from2 listeria monocytogenes egd-e |
| 63 | c2j41A | Alignment | not modelled | 99.9 | 17 | PDB header: transferase Chain: A: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of staphylococcus aureus guanylate2 monophosphate kinase |
| 64 | c3a4mB | Alignment | not modelled | 99.8 | 13 | PDB header: transferase Chain: B: PDB Molecule: l-seryl-trna(sec) kinase; PDBTitle: crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase |
| 65 | c1xexB | Alignment | not modelled | 99.7 | 19 | PDB header: cell cycle Chain: B: PDB Molecule: smc protein; PDBTitle: structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases. |
| 66 | d2qy9a2 | Alignment | not modelled | 99.7 | 15 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 67 | c1f2uD | Alignment | not modelled | 99.7 | 24 | PDB header: replication Chain: D: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of rad50 abc-atpase |
| 68 | c2o5vA | Alignment | not modelled | 99.7 | 26 | PDB header: replication/recombination Chain: A: PDB Molecule: dna replication and repair protein recf; PDBTitle: recombination mediator recf |
| 69 | d1lsls2 | Alignment | not modelled | 99.7 | 16 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 70 | d1vmaa2 | Alignment | not modelled | 99.6 | 13 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 71 | c1ii8B | Alignment | not modelled | 99.6 | 30 | PDB header: replication Chain: B: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of the p. furiosus rad50 atpase domain |
| 72 | c1u9iA | Alignment | not modelled | 99.6 | 15 | PDB header: circadian clock protein Chain: A: PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites |
| 73 | c3geiB | Alignment | not modelled | 99.6 | 15 | PDB header: hydrolase Chain: B: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from chlorobium tepidum in complex2 with gcp |
| 74 | d1okkd2 | Alignment | not modelled | 99.5 | 17 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 75 | c3lncB | Alignment | not modelled | 99.5 | 18 | PDB header: transferase Chain: B: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of guanylate kinase from anaplasma2 phagocytophilum |
| 76 | d1ye8a1 | Alignment | not modelled | 99.4 | 11 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 77 | d1np6a | Alignment | not modelled | 99.4 | 10 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 78 | c1q57G | Alignment | not modelled | 99.3 | 13 | PDB header: transferase Chain: G: PDB Molecule: dna primase/helicase; PDBTitle: the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7 |
| | | | | | | Fold: P-loop containing nucleoside triphosphate hydrolases |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 79 | d1e69a_ | Alignment | not modelled | 99.3 | 21 | Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 80 | c2dr3A_ | Alignment | not modelled | 99.1 | 13 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0273 protein ph0284; PDBTitle: crystal structure of reca superfamily atpase ph0284 from pyrococcus2 horikoshii ot3 |
| 81 | c3auyB_ | Alignment | not modelled | 99.1 | 27 | PDB header: recombination Chain: B: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: crystal structure of rad50 bound to adp |
| 82 | d2i3ba1 | Alignment | not modelled | 99.0 | 12 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 83 | d1qzxa3 | Alignment | not modelled | 98.9 | 15 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 84 | c2w0mA_ | Alignment | not modelled | 98.9 | 16 | PDB header: unknown function Chain: A: PDB Molecule: sso2452; PDBTitle: crystal structure of sso2452 from sulfolobus solfataricus2 p2 |
| 85 | d1ewqa2 | Alignment | not modelled | 98.8 | 22 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 86 | c2o8bA_ | Alignment | not modelled | 98.7 | 20 | PDB header: dna binding protein/dna Chain: A: PDB Molecule: dna mismatch repair protein msh2; PDBTitle: human mutsalph (msh2/msh6) bound to adp and a g t mispair |
| 87 | c3thxB_ | Alignment | not modelled | 98.7 | 17 | PDB header: dna binding protein/dna Chain: B: PDB Molecule: dna mismatch repair protein msh3; PDBTitle: human mutsbeta complexed with an idl of 3 bases (loop3) and adp |
| 88 | d1wb9a2 | Alignment | not modelled | 98.7 | 22 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 89 | c2o8dB_ | Alignment | not modelled | 98.7 | 24 | PDB header: dna binding protein/dna Chain: B: PDB Molecule: dna mismatch repair protein msh6; PDBTitle: human mutsalph (msh2/msh6) bound to adp and a g du mispair |
| 90 | d1nlfa_ | Alignment | not modelled | 98.7 | 17 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 91 | c1wxqA_ | Alignment | not modelled | 98.6 | 10 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3 |
| 92 | c1ewqA_ | Alignment | not modelled | 98.6 | 23 | PDB header: replication/dna Chain: A: PDB Molecule: dna mismatch repair protein muts; PDBTitle: crystal structure taq muts complexed with a heteroduplex2 dna at 2.2 a resolution |
| 93 | c1wbdA_ | Alignment | not modelled | 98.5 | 21 | PDB header: dna-binding Chain: A: PDB Molecule: dna mismatch repair protein muts; PDBTitle: crystal structure of e. coli dna mismatch repair enzyme2 muts, e38q mutant, in complex with a g,t mismatch |
| 94 | c3bh0A_ | Alignment | not modelled | 98.5 | 9 | PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p |
| 95 | c1ewrA_ | Alignment | not modelled | 98.5 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: dna mismatch repair protein muts; PDBTitle: crystal structure of taq muts |
| 96 | d1tf7a1 | Alignment | not modelled | 98.5 | 13 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 97 | c1pznG_ | Alignment | not modelled | 98.4 | 15 | PDB header: recombination Chain: G: PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada) |
| 98 | c2vyeA_ | Alignment | not modelled | 98.3 | 9 | PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dnac-ssdna complex |
| 99 | d1tf7a2 | Alignment | not modelled | 98.2 | 13 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 100 | c3qg5A_ | Alignment | not modelled | 98.2 | 40 | PDB header: hydrolase Chain: A: PDB Molecule: rad50; PDBTitle: the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair |
| 101 | c3bgwD_ | Alignment | not modelled | 98.2 | 9 | PDB header: replication Chain: D: PDB Molecule: dnab-like replicative helicase; PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase |
| 102 | c3qkuB_ | Alignment | not modelled | 98.2 | 32 | PDB header: replication Chain: B: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: mre11 rad50 binding domain in complex with rad50 and amp-pnp |
| 103 | d1yrba1 | Alignment | not modelled | 98.2 | 13 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 104 | d2i1qa2 | Alignment | not modelled | 98.2 | 9 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 105 | c2q6tB_ | Alignment | not modelled | 98.2 | 17 | PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer |
| 106 | d1xp8a1 | Alignment | not modelled | 98.1 | 19 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 107 | d1mo6a1 | Alignment | not modelled | 98.1 | 18 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 108 | c2recB_ | Alignment | not modelled | 98.1 | 19 | PDB header: helicase PDB COMPND: |
| 109 | c2cvhB_ | Alignment | not modelled | 98.0 | 16 | PDB header: dna binding protein Chain: B: PDB Molecule: dna repair and recombination protein radb; PDBTitle: crystal structure of the radb recombinase |
| 110 | c1szpC_ | Alignment | not modelled | 98.0 | 15 | PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein rad51; PDBTitle: a crystal structure of the rad51 filament |
| 111 | c1us8A_ | Alignment | not modelled | 98.0 | 26 | PDB header: dna repair Chain: A: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: the rad50 signature motif: essential to atp binding and2 biological function |
| 112 | d1v5wa_ | Alignment | not modelled | 98.0 | 16 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 113 | c2ztsB_ | Alignment | not modelled | 98.0 | 18 | PDB header: atp-binding protein Chain: B: PDB Molecule: putative uncharacterized protein ph0186; PDBTitle: crystal structure of kaic-like protein ph0186 from2 hyperthermophilic archaea pyrococcus horikoshii ot3 |
| 114 | d1u94a1 | Alignment | not modelled | 97.9 | 20 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 115 | d1ubea1 | Alignment | not modelled | 97.9 | 19 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 116 | c1xp8A_ | Alignment | not modelled | 97.9 | 17 | PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: "deinococcus radiodurans reca in complex with atp-gamma-s" |
| 117 | d1zp6a1 | Alignment | not modelled | 97.9 | 30 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Atu3015-like |
| 118 | c3cmvG_ | Alignment | not modelled | 97.9 | 12 | PDB header: recombination Chain: G: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-2 ssdna/dsdna structures |
| 119 | d1n0wa_ | Alignment | not modelled | 97.9 | 21 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 120 | c2zjbB_ | Alignment | not modelled | 97.9 | 15 | PDB header: recombination Chain: B: PDB Molecule: meiotic recombination protein dmc1/lim15 homolog; PDBTitle: crystal structure of the human dmc1-m200v polymorphic2 variant |