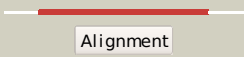

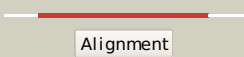
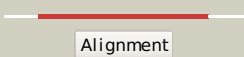

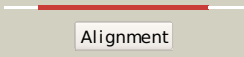

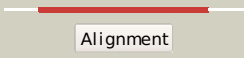


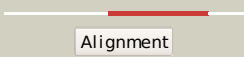

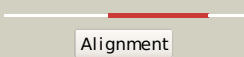
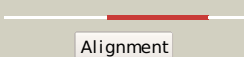

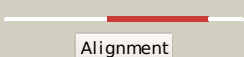



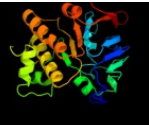










| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c2ygrD_ |  Alignment |  | 100.0 | 57 | PDB header: hydrolase Chain: D: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra |
| 2 | c3pihA_ |  Alignment |  | 100.0 | 56 | PDB header: hydrolase/dna Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: t. maritima uvra in complex with fluorescein-modified dna |
| 3 | c2vf7B_ |  Alignment |  | 100.0 | 44 | PDB header: dna-binding protein Chain: B: PDB Molecule: excinuclease abc, subunit a.; PDBTitle: crystal structure of uvra2 from deinococcus radiodurans |
| 4 | c2r6fA_ |  Alignment |  | 100.0 | 62 | PDB header: hydrolase Chain: A: PDB Molecule: excinuclease abc subunit a; PDBTitle: crystal structure of bacillus stearothermophilus uvra |
| 5 | c3g5uB_ |  Alignment |  | 100.0 | 34 | PDB header: membrane protein Chain: B: PDB Molecule: multi drug resistance protein 1a; PDBTitle: structure of p-glycoprotein reveals a molecular basis for 2 poly-specific drug binding |
| 6 | c3cmvG_ |  Alignment |  | 100.0 | 15 | PDB header: recombination Chain: G: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-2 ssdna/dsdna structures |
| 7 | c2iw3B_ |  Alignment |  | 100.0 | 16 | PDB header: translation Chain: B: PDB Molecule: elongation factor 3a; PDBTitle: elongation factor 3 in complex with adp |
| 8 | c1yqtA_ |  Alignment |  | 100.0 | 26 | PDB header: hydrolase/translation Chain: A: PDB Molecule: rnase l inhibitor; PDBTitle: rnase-l inhibitor |
| 9 | c3bk7A_ |  Alignment |  | 100.0 | 25 | 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 |
| 10 | c3ozxA_ |  Alignment |  | 100.0 | 24 | PDB header: hydrolase, translation Chain: A: PDB Molecule: rnase l inhibitor; PDBTitle: crystal structure of abce1 of sulfolobus solfataricus (-fes domain) |
| 11 | c2hydB_ |  Alignment |  | 100.0 | 24 | PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866 |

| | | | | | | |
|----|-------------------------|-----------|---|-------|----|---|
| 12 | c2yl4A_ | Alignment |  | 100.0 | 28 | 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 |
| 13 | c3b5wE_ | Alignment |  | 100.0 | 23 | PDB header: membrane protein Chain: E: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba |
| 14 | c2olkD_ | Alignment |  | 100.0 | 27 | PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s |
| 15 | c3b5xB_ | Alignment |  | 100.0 | 26 | PDB header: membrane protein Chain: B: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of msba from vibrio cholerae |
| 16 | c3nhaA_ | Alignment |  | 100.0 | 26 | 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) |
| 17 | d2pmk1 | Alignment |  | 100.0 | 25 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 18 | c2it1B_ | Alignment |  | 100.0 | 28 | PDB header: transport protein Chain: B: PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii |
| 19 | c2yyzA_ | Alignment |  | 100.0 | 27 | PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein |
| 20 | d1b0ua_ | Alignment |  | 100.0 | 29 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 21 | d1g2912 | Alignment | not modelled | 100.0 | 26 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 22 | c1oxTB_ | Alignment | not modelled | 100.0 | 26 | 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 |
| 23 | c3fvqB_ | Alignment | not modelled | 100.0 | 27 | 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 |
| 24 | c1z47B_ | Alignment | not modelled | 100.0 | 27 | 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 |
| 25 | c1vciA_ | Alignment | not modelled | 100.0 | 23 | 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 |
| 26 | c3dhwC_ | Alignment | not modelled | 100.0 | 28 | PDB header: membrane protein/hydrolase Chain: C: PDB Molecule: methionine import atp-binding protein metn; PDBTitle: crystal structure of methionine importer metni |
| 27 | d3dhwc1 | 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 Fold: P-loop containing nucleoside triphosphate hydrolases |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 28 | d1v43a3 | Alignment | not modelled | 100.0 | 24 | Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 29 | d1oxxk2 | 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 |
| 30 | d1jj7a_ | 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 |
| 31 | c3gfoA_ | Alignment | not modelled | 100.0 | 25 | 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. |
| 32 | d2hyda1 | 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 |
| 33 | d3d31a2 | 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 |
| 34 | d3b60a1 | 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 |
| 35 | c1q1bD_ | Alignment | not modelled | 100.0 | 28 | 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 |
| 36 | c2d62A_ | Alignment | not modelled | 100.0 | 27 | 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 |
| 37 | 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 |
| 38 | d1vp1a_ | Alignment | not modelled | 100.0 | 26 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 39 | d1mv5a_ | Alignment | not modelled | 100.0 | 24 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 40 | c2pcjB_ | Alignment | not modelled | 100.0 | 30 | 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 |
| 41 | d1g6ha_ | 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 |
| 42 | c2d2fA_ | Alignment | not modelled | 100.0 | 24 | PDB header: protein binding Chain: A: PDB Molecule: sufc protein; PDBTitle: crystal structure of atypical cytoplasmic abc-atpase sufc from thermus2 thermophilus hb8 |
| 43 | c3d31B_ | Alignment | not modelled | 100.0 | 25 | PDB header: transport protein Chain: B: PDB Molecule: sulfate/molybdate abc transporter, atp-binding PDBTitle: modbc from methanosarcina acetivorans |
| 44 | d1ji0a_ | Alignment | not modelled | 100.0 | 26 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 45 | d1l2ta_ | Alignment | not modelled | 100.0 | 33 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 46 | c2cbzA_ | Alignment | not modelled | 100.0 | 22 | 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 |
| 47 | c3gd7C_ | Alignment | not modelled | 100.0 | 20 | 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) |
| 48 | d1r0wa_ | Alignment | not modelled | 100.0 | 24 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 49 | d2onka1 | Alignment | not modelled | 100.0 | 24 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 50 | c2d3wB_ | Alignment | not modelled | 100.0 | 24 | PDB header: biosynthetic protein Chain: B: PDB Molecule: probable atp-dependent transporter sufc; PDBTitle: crystal structure of escherichia coli sufc, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery |
| 51 | 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 |
| | | | | | | PDB header: metal transport Chain: C: PDB Molecule: hypothetical abc transporter atp-binding |

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|----|--------------------------|-----------|--------------|-------|----|--|
| 52 | c2nq2C_ | Alignment | not modelled | 100.0 | 25 | protein PDBTitle: an inward-facing conformation of a putative metal-chelate2 type abc transporter. |
| 53 | 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 |
| 54 | c2pzfB_ | Alignment | not modelled | 100.0 | 22 | PDB header: hydrolase Chain: B: PDB Molecule: cystic fibrosis transmembrane conductance regulator; PDBTitle: minimal human cfr first nucleotide binding domain as a head-to-tail2 dimer with delta f508 |
| 55 | 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 |
| 56 | d1l7vc_ | 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 |
| 57 | c2ihyB_ | Alignment | not modelled | 100.0 | 26 | 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 |
| 58 | c2pjzA_ | Alignment | not modelled | 100.0 | 21 | 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 |
| 59 | d2awna2 | 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 |
| 60 | d1sgwa_ | Alignment | not modelled | 100.0 | 20 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 61 | d1wl1wa_ | Alignment | not modelled | 99.8 | 18 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 62 | c3fpnA_ | Alignment | not modelled | 99.7 | 47 | PDB header: dna binding protein Chain: A: PDB Molecule: geobacillus stearothermophilus uvra interaction PDBTitle: crystal structure of uvra-uvrb interaction domains |
| 63 | c1f2uD_ | Alignment | not modelled | 99.7 | 27 | PDB header: replication Chain: D: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of rad50 abc-atpase |
| 64 | c1xexB_ | Alignment | not modelled | 99.7 | 21 | PDB header: cell cycle Chain: B: PDB Molecule: smc protein; PDBTitle: structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases. |
| 65 | c1ii8B_ | Alignment | not modelled | 99.7 | 29 | PDB header: replication Chain: B: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of the p. furiosus rad50 atpase domain |
| 66 | d1cr2a_ | Alignment | not modelled | 99.6 | 16 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 67 | c1u9iA_ | Alignment | not modelled | 99.5 | 17 | PDB header: circadian clock protein Chain: A: PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites |
| 68 | c3tauB_ | Alignment | not modelled | 99.5 | 16 | PDB header: transferase Chain: B: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of a putative guanylate monophosphaste kinase from2 listeria monocytogenes egd-e |
| 69 | c2j41A_ | Alignment | not modelled | 99.4 | 18 | PDB header: transferase Chain: A: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of staphylococcus aureus guanylate2 monophosphate kinase |
| 70 | c3a4mB_ | Alignment | not modelled | 99.2 | 18 | PDB header: transferase Chain: B: PDB Molecule: l-seryl-trna(sec) kinase; PDBTitle: crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase |
| 71 | c2o5vA_ | Alignment | not modelled | 99.1 | 27 | PDB header: replication/recombination Chain: A: PDB Molecule: dna replication and repair protein recf; PDBTitle: recombination mediator recf |
| 72 | d1ls1a2 | Alignment | not modelled | 98.7 | 23 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 73 | d2qy9a2 | Alignment | not modelled | 98.7 | 13 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 74 | c3geiB_ | Alignment | not modelled | 98.7 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from chlorobium tepidum in complex2 with gcp |
| 75 | d1e69a_ | Alignment | not modelled | 98.4 | 22 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 76 | d1vmaa2 | Alignment | not modelled | 98.4 | 12 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 77 | c3lncB_ | Alignment | not modelled | 98.3 | 14 | PDB header: transferase Chain: B: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of guanylate kinase from anaplasma2 phagocytophilum |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|---|
| 78 | d1okkd2 | Alignment | not modelled | 98.2 | 17 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 79 | c1q57G_ | Alignment | not modelled | 98.1 | 16 | PDB header: transferase Chain: G: PDB Molecule: dna primase/helicase; PDBTitle: the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7 |
| 80 | c2w0mA_ | Alignment | not modelled | 97.9 | 21 | PDB header: unknown function Chain: A: PDB Molecule: ss02452; PDBTitle: crystal structure of ss02452 from sulfolobus solfataricus2 p2 |
| 81 | d1ye8a1 | Alignment | not modelled | 97.9 | 15 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 82 | c2dr3A_ | Alignment | not modelled | 97.7 | 20 | 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 |
| 83 | c3qkuB_ | Alignment | not modelled | 97.5 | 31 | 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 |
| 84 | d1znwa1 | Alignment | not modelled | 97.5 | 33 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases |
| 85 | c3qg5A_ | Alignment | not modelled | 97.5 | 33 | 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 |
| 86 | c2plrB_ | Alignment | not modelled | 97.4 | 53 | PDB header: transferase Chain: B: PDB Molecule: probable thymidylate kinase; PDBTitle: crystal structure of dtmp kinase (st1543) from sulfolobus tokodaii2 strain7 |
| 87 | d1nlfa_ | Alignment | not modelled | 97.4 | 20 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 88 | d1ak2a1 | Alignment | not modelled | 97.4 | 35 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases |
| 89 | c2yvua_ | Alignment | not modelled | 97.4 | 43 | PDB header: transferase Chain: A: PDB Molecule: probable adenyl-yl-sulfate kinase; PDBTitle: crystal structure of ape1195 |
| 90 | c1znyA_ | Alignment | not modelled | 97.4 | 33 | PDB header: transferase Chain: A: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of mycobacterium tuberculosis guanylate kinase in2 complex with gdp |
| 91 | d1ki9a_ | Alignment | not modelled | 97.4 | 42 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases |
| 92 | d1s96a_ | Alignment | not modelled | 97.4 | 47 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases |
| 93 | d1tmka_ | Alignment | not modelled | 97.4 | 42 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases |
| 94 | c2wwiC_ | Alignment | not modelled | 97.3 | 45 | PDB header: transferase Chain: C: PDB Molecule: thymidylate kinase, putative; PDBTitle: plasmodium falciparum thymidylate kinase in complex with2 aztmp and adp |
| 95 | d1np6a_ | Alignment | not modelled | 97.3 | 17 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like |
| 96 | d4tmka_ | Alignment | not modelled | 97.3 | 47 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases |
| 97 | d1nn5a_ | Alignment | not modelled | 97.3 | 26 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases |
| 98 | c3ld9D_ | Alignment | not modelled | 97.3 | 35 | PDB header: transferase Chain: D: PDB Molecule: thymidylate kinase; PDBTitle: crystal structure of thymidylate kinase from ehrlichia chaffeensis at2 2.15a resolution |
| 99 | c2w0sB_ | Alignment | not modelled | 97.3 | 47 | PDB header: transferase Chain: B: PDB Molecule: thymidylate kinase; PDBTitle: crystal structure of vaccinia virus thymidylate kinase2 bound to brivudin-5'-monophosphate |
| 100 | d1y63a_ | Alignment | not modelled | 97.3 | 45 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases |
| 101 | d1tf7a1 | Alignment | not modelled | 97.3 | 28 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 102 | d1zp6a1 | Alignment | not modelled | 97.2 | 37 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Atu3015-like |
| 103 | c1ii8A_ | Alignment | not modelled | 97.2 | 29 | PDB header: replication Chain: A: PDB Molecule: rad50 abc-atpase; |

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|-----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | PDBTitle: crystal structure of the p. furiosus rad50 atpase domain |
| 104 | d1knqa_ | Alignment | not modelled | 97.2 | 41 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Gluconate kinase |
| 105 | c3tr0A_ | Alignment | not modelled | 97.2 | 37 | PDB header: transferase Chain: A: PDB Molecule: guanylate kinase; PDBTitle: structure of guanylate kinase (gmk) from coxiella burnetii |
| 106 | d1qhxa_ | Alignment | not modelled | 97.2 | 32 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Chloramphenicol phosphotransferase |
| 107 | c2ak2A_ | Alignment | not modelled | 97.2 | 35 | PDB header: phosphotransferase Chain: A: PDB Molecule: adenylate kinase isoenzyme-2; PDBTitle: adenylate kinase isoenzyme-2 |
| 108 | d1v5wa_ | Alignment | not modelled | 97.1 | 19 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) |
| 109 | d1m8pa3 | Alignment | not modelled | 97.1 | 35 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ATP sulfurylase C-terminal domain |
| 110 | c1pznG_ | Alignment | not modelled | 97.1 | 33 | PDB header: recombination Chain: G: PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada) |
| 111 | c2bwjC_ | Alignment | not modelled | 97.1 | 33 | PDB header: transferase Chain: C: PDB Molecule: adenylate kinase 5; PDBTitle: structure of adenylate kinase 5 |
| 112 | d1khta_ | Alignment | not modelled | 97.1 | 39 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases |
| 113 | c2zjbB_ | Alignment | not modelled | 97.1 | 19 | PDB header: recombination Chain: B: PDB Molecule: meiotic recombination protein dmc1/lim15 homolog; PDBTitle: crystal structure of the human dmc1-m200v polymorphic2 variant |
| 114 | c3cm0A_ | Alignment | not modelled | 97.1 | 28 | PDB header: transferase Chain: A: PDB Molecule: adenylate kinase; PDBTitle: crystal structure of adenylate kinase from thermus2 thermophilus hb8 |
| 115 | c2vliB_ | Alignment | not modelled | 97.1 | 37 | PDB header: transferase Chain: B: PDB Molecule: antibiotic resistance protein; PDBTitle: structure of deinococcus radiodurans tunicamycin resistance2 protein |
| 116 | c3lv8A_ | Alignment | not modelled | 97.1 | 32 | PDB header: transferase Chain: A: PDB Molecule: thymidylate kinase; PDBTitle: 1.8 angstrom resolution crystal structure of a thymidylate kinase2 (tmk) from vibrio cholerae o1 biovar eltor str. n16961 in complex3 with tmp, thymidine-5'-diphosphate and adp |
| 117 | d1kgda_ | Alignment | not modelled | 97.1 | 28 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases |
| 118 | d3adka_ | Alignment | not modelled | 97.0 | 38 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases |
| 119 | c1us8A_ | Alignment | not modelled | 97.0 | 29 | 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 |
| 120 | d2bdta1 | Alignment | not modelled | 97.0 | 47 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Atu3015-like |