




















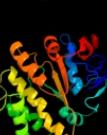


| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c2o5vA_</a> |  Alignment   |    | 100.0      | 23     | <b>PDB header:</b> replication/recombination<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna replication and repair protein recf;<br><b>PDBTitle:</b> recombination mediator recf   |
| 2  | <a href="#">c3auyB_</a> |  Alignment   |    | 100.0      | 13     | <b>PDB header:</b> recombination<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna double-strand break repair rad50 atpase;<br><b>PDBTitle:</b> crystal structure of rad50 bound to adp   |
| 3  | <a href="#">dlw1wa_</a> |  Alignment   |    | 100.0      | 17     | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like   |
| 4  | <a href="#">c3qkuB_</a> |  Alignment   |    | 99.9       | 14     | <b>PDB header:</b> replication<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna double-strand break repair rad50 atpase;<br><b>PDBTitle:</b> mre11 rad50 binding domain in complex with rad50 and amp-pnp  |
| 5  | <a href="#">dle69a_</a> |  Alignment |  | 99.9       | 16     | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like   |
| 6  | <a href="#">c3qg5A_</a> |  Alignment |  | 99.8       | 22     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> rad50;<br><b>PDBTitle:</b> the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair   |
| 7  | <a href="#">clii8A_</a> |  Alignment |  | 99.8       | 20     | <b>PDB header:</b> replication<br><b>Chain:</b> A: <b>PDB Molecule:</b> rad50 abc-atpase;<br><b>PDBTitle:</b> crystal structure of the p. furiosus rad50 atpase domain   |
| 8  | <a href="#">clvcia_</a> |  Alignment |  | 99.7       | 23     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> sugar-binding transport atp-binding protein;<br><b>PDBTitle:</b> crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp |
| 9  | <a href="#">dlv43a3</a> |  Alignment |  | 99.7       | 19     | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like   |
| 10 | <a href="#">dlg2912</a> |  Alignment |  | 99.7       | 21     | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like   |
| 11 | <a href="#">c3dhwC_</a> |  Alignment |  | 99.7       | 20     | <b>PDB header:</b> membrane protein/hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> methionine import atp-binding protein metn;<br><b>PDBTitle:</b> crystal structure of methionine importer metni  |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 12 | <a href="#">c1z47B_</a> | Alignment |              | 99.7 | 21 | <b>PDB header:</b> ligand binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative abc-transporter atp-binding protein;<br><b>PDBTitle:</b> structure of the atpase subunit cysa of the putative2 sulfate atp-binding cassette (abc) transporter from3 alicyclobacillus acidocaldarius |
| 13 | <a href="#">c1oxxB_</a> | Alignment |              | 99.7 | 21 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, atp binding protein;<br><b>PDBTitle:</b> crystal structure of glcv, the abc-atpase of the glucose abc2 transporter from sulfolobus solfataricus  |
| 14 | <a href="#">c2yz2B_</a> | Alignment |              | 99.7 | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative abc transporter atp-binding protein tm_0222;<br><b>PDBTitle:</b> crystal structure of the abc transporter in the cobalt transport2 system  |
| 15 | <a href="#">c3fvqB_</a> | Alignment |              | 99.7 | 21 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> fe(3+) ions import atp-binding protein fbpc;<br><b>PDBTitle:</b> crystal structure of the nucleotide binding domain fbpc2 complexed with atp  |
| 16 | <a href="#">c3d31B_</a> | Alignment |              | 99.7 | 21 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> sulfate/molybdate abc transporter, atp-binding<br><b>PDBTitle:</b> modbc from methanosarcina acetivorans  |
| 17 | <a href="#">d3dhwc1</a> | Alignment |              | 99.7 | 24 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like  |
| 18 | <a href="#">c3g5uB_</a> | Alignment |              | 99.7 | 21 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> multi drug resistance protein 1a;<br><b>PDBTitle:</b> structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding  |
| 19 | <a href="#">c2yl4A_</a> | Alignment |              | 99.7 | 19 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding cassette sub-family b member 10,<br><b>PDBTitle:</b> structure of the human mitochondrial abc transporter, abcb10  |
| 20 | <a href="#">c2yyzA_</a> | Alignment |              | 99.7 | 21 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter, atp-binding protein;<br><b>PDBTitle:</b> crystal structure of sugar abc transporter, atp-binding protein   |
| 21 | <a href="#">c2d2fA_</a> | Alignment | not modelled | 99.7 | 20 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> sufc protein;<br><b>PDBTitle:</b> crystal structure of atypical cytoplasmic abc-atpase sufc from thermus2 thermophilus hb8  |
| 22 | <a href="#">c2iw3B_</a> | Alignment | not modelled | 99.7 | 14 | <b>PDB header:</b> translation<br><b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor 3a;<br><b>PDBTitle:</b> elongation factor 3 in complex with adp   |
| 23 | <a href="#">d1vpla_</a> | Alignment | not modelled | 99.7 | 25 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like  |
| 24 | <a href="#">c1yqtA_</a> | Alignment | not modelled | 99.7 | 28 | <b>PDB header:</b> hydrolyase/translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> rnase i inhibitor;<br><b>PDBTitle:</b> rnase-i inhibitor   |
| 25 | <a href="#">d1ji0a_</a> | Alignment | not modelled | 99.7 | 26 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like  |
| 26 | <a href="#">d1l2ta_</a> | Alignment | not modelled | 99.7 | 20 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like  |
| 27 | <a href="#">c2olkD_</a> | Alignment | not modelled | 99.7 | 22 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> D: <b>PDB Molecule:</b> amino acid abc transporter;<br><b>PDBTitle:</b> abc protein artp in complex with adp-beta-s   |
| 28 | <a href="#">c2it1B_</a> | Alignment | not modelled | 99.7 | 24 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> 362aa long hypothetical maltose/maltodextrin<br><b>PDBTitle:</b> structure of ph0203 protein from pyrococcus horikoshii   |
|    |                         |           |              |      |    | <b>PDB header:</b> transport protein  |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | <a href="#">c2hydB</a>  | Alignment | not modelled | 99.7 | 18 | <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter homolog;<br><b>PDBTitle:</b> multidrug abc transporter sav1866   |
| 30 | <a href="#">c3gfoA</a>  | Alignment | not modelled | 99.7 | 14 | <b>PDB header:</b> atp binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cobalt import atp-binding protein cbio 1;<br><b>PDBTitle:</b> structure of cbio1 from clostridium perfringens: part of2 the abc transporter complex cbionq.                        |
| 31 | <a href="#">d1oxk2</a>  | Alignment | not modelled | 99.7 | 21 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like   |
| 32 | <a href="#">d1g6ha</a>  | Alignment | not modelled | 99.7 | 20 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like   |
| 33 | <a href="#">c1us8A</a>  | Alignment | not modelled | 99.7 | 24 | <b>PDB header:</b> dna repair<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna double-strand break repair rad50 atpase;<br><b>PDBTitle:</b> the rad50 signature motif: essential to atp binding and2 biological function   |
| 34 | <a href="#">c2pcjB</a>  | Alignment | not modelled | 99.7 | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> lipoprotein-releasing system atp-binding protein lold;<br><b>PDBTitle:</b> crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5  |
| 35 | <a href="#">d1b0ua</a>  | Alignment | not modelled | 99.7 | 20 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like   |
| 36 | <a href="#">d3b60a1</a> | Alignment | not modelled | 99.6 | 22 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like   |
| 37 | <a href="#">c2d62A</a>  | Alignment | not modelled | 99.6 | 22 | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> multiple sugar-binding transport atp-binding<br><b>PDBTitle:</b> crystal structure of multiple sugar binding transport atp-2 binding protein                                     |
| 38 | <a href="#">c2nq2C</a>  | Alignment | not modelled | 99.6 | 20 | <b>PDB header:</b> metal transport<br><b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical abc transporter atp-binding protein<br><b>PDBTitle:</b> an inward-facing conformation of a putative metal-chelate2 type abc transporter.                                  |
| 39 | <a href="#">d1mv5a</a>  | Alignment | not modelled | 99.6 | 22 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like   |
| 40 | <a href="#">d1jj7a</a>  | Alignment | not modelled | 99.6 | 22 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like   |
| 41 | <a href="#">c2pjzA</a>  | Alignment | not modelled | 99.6 | 23 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein st1066;<br><b>PDBTitle:</b> the crystal structure of putative cobalt transport atp-2 binding protein (cbio-2), st1066                       |
| 42 | <a href="#">d3d31a2</a> | Alignment | not modelled | 99.6 | 22 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like   |
| 43 | <a href="#">d2onka1</a> | Alignment | not modelled | 99.6 | 24 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like   |
| 44 | <a href="#">c3gd7C</a>  | Alignment | not modelled | 99.6 | 23 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> fusion complex of cystic fibrosis transmembrane<br><b>PDBTitle:</b> crystal structure of human nbd2 complexed with n6-2 phenylethyl-atp (p-atp)  |
| 45 | <a href="#">c1q1bD</a>  | Alignment | not modelled | 99.6 | 22 | <b>PDB header:</b> transport protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> maltose/maltodextrin transport atp-binding protein malk;<br><b>PDBTitle:</b> crystal structure of e. coli malk in the nucleotide-free form   |
| 46 | <a href="#">c2d3wB</a>  | Alignment | not modelled | 99.6 | 16 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable atp-dependent transporter sufcd;<br><b>PDBTitle:</b> crystal structure of escherichia coli sufcd, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery |
| 47 | <a href="#">d2pmka1</a> | Alignment | not modelled | 99.6 | 22 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like   |
| 48 | <a href="#">c2cbzA</a>  | Alignment | not modelled | 99.6 | 23 | <b>PDB header:</b> transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance-associated protein 1;<br><b>PDBTitle:</b> structure of the human multidrug resistance protein 12 nucleotide binding domain 1  |
| 49 | <a href="#">d1l7vc</a>  | Alignment | not modelled | 99.6 | 21 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like   |
| 50 | <a href="#">c2pzfB</a>  | Alignment | not modelled | 99.6 | 21 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cystic fibrosis transmembrane conductance regulator;<br><b>PDBTitle:</b> minimal human cfr first nucleotide binding domain as a head-to-tail2 dimer with delta f508                          |
| 51 | <a href="#">d2hyda1</a> | Alignment | not modelled | 99.6 | 21 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like   |
| 52 | <a href="#">c3nhaA</a>  | Alignment | not modelled | 99.6 | 25 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding cassette sub-family b member 6, mitochondrial;<br><b>PDBTitle:</b> nucleotide binding domain of human abcb6 (adp mg bound structure)                                     |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 53 | <a href="#">c2ihyB</a>  | Alignment | not modelled | 99.6 | 18 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, atp-binding protein;<br><b>PDBTitle:</b> structure of the staphylococcus aureus putative atpase subunit of an2 atp-binding cassette (abc) transporter  |
| 54 | <a href="#">d1r0wa</a>  | Alignment | not modelled | 99.6 | 20 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like  |
| 55 | <a href="#">c1xexA</a>  | Alignment | not modelled | 99.6 | 24 | <b>PDB header:</b> cell cycle<br><b>Chain:</b> A: <b>PDB Molecule:</b> smc protein;<br><b>PDBTitle:</b> structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.                                     |
| 56 | <a href="#">d2awna2</a> | Alignment | not modelled | 99.6 | 23 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like  |
| 57 | <a href="#">c2ygrD</a>  | Alignment | not modelled | 99.6 | 15 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> D: <b>PDB Molecule:</b> uvrabc system protein a;<br><b>PDBTitle:</b> mycobacterium tuberculosis uvra  |
| 58 | <a href="#">c3ozxA</a>  | Alignment | not modelled | 99.6 | 25 | <b>PDB header:</b> hydrolase, translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> rnase l inhibitor;<br><b>PDBTitle:</b> crystal structure of abce1 of sulfolobus solfataricus (-fes domain)   |
| 59 | <a href="#">d1xmia</a>  | Alignment | not modelled | 99.6 | 23 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like  |
| 60 | <a href="#">c3b5wE</a>  | Alignment | not modelled | 99.5 | 24 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> E: <b>PDB Molecule:</b> lipid a export atp-binding/permease protein msba;<br><b>PDBTitle:</b> crystal structure of eschericia coli msba  |
| 61 | <a href="#">c3pihA</a>  | Alignment | not modelled | 99.5 | 14 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> uvrabc system protein a;<br><b>PDBTitle:</b> t. maritima uvra in complex with fluorescein-modified dna  |
| 62 | <a href="#">d1qhla</a>  | Alignment | not modelled | 99.5 | 19 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like  |
| 63 | <a href="#">c3b5xB</a>  | Alignment | not modelled | 99.5 | 21 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> lipid a export atp-binding/permease protein msba;<br><b>PDBTitle:</b> crystal structure of msba from vibrio cholerae   |
| 64 | <a href="#">c3bk7A</a>  | Alignment | not modelled | 99.5 | 25 | <b>PDB header:</b> hydrolase/translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein;<br><b>PDBTitle:</b> structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abyssi                 |
| 65 | <a href="#">c2ghiD</a>  | Alignment | not modelled | 99.5 | 21 | <b>PDB header:</b> transport protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> transport protein;<br><b>PDBTitle:</b> crystal structure of plasmodium yoelii multidrug resistance2 protein 2   |
| 66 | <a href="#">c2vf7B</a>  | Alignment | not modelled | 99.5 | 14 | <b>PDB header:</b> dna-binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> excinuclease abc, subunit a.;<br><b>PDBTitle:</b> crystal structure of uvra2 from deinococcus radiodurans   |
| 67 | <a href="#">c1xexB</a>  | Alignment | not modelled | 99.5 | 19 | <b>PDB header:</b> cell cycle<br><b>Chain:</b> B: <b>PDB Molecule:</b> smc protein;<br><b>PDBTitle:</b> structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.                                     |
| 68 | <a href="#">d1pf4a1</a> | Alignment | not modelled | 99.4 | 21 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like  |
| 69 | <a href="#">d1sgwa</a>  | Alignment | not modelled | 99.4 | 21 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like  |
| 70 | <a href="#">c1ii8B</a>  | Alignment | not modelled | 99.3 | 25 | <b>PDB header:</b> replication<br><b>Chain:</b> B: <b>PDB Molecule:</b> rad50 abc-atpase;<br><b>PDBTitle:</b> crystal structure of the p. furiosus rad50 atpase domain  |
| 71 | <a href="#">c3eukC</a>  | Alignment | not modelled | 99.3 | 13 | <b>PDB header:</b> cell cycle<br><b>Chain:</b> C: <b>PDB Molecule:</b> chromosome partition protein mukb, linker;<br><b>PDBTitle:</b> crystal structure of muke-mukf(residues 292-443)-mukb(head2 domain)-atpgammas complex, asymmetric dimer |
| 72 | <a href="#">c1f2uD</a>  | Alignment | not modelled | 99.2 | 25 | <b>PDB header:</b> replication<br><b>Chain:</b> D: <b>PDB Molecule:</b> rad50 abc-atpase;<br><b>PDBTitle:</b> crystal structure of rad50 abc-atpase   |
| 73 | <a href="#">c2r6fA</a>  | Alignment | not modelled | 98.9 | 22 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> excinuclease abc subunit a;<br><b>PDBTitle:</b> crystal structure of bacillus stearotherophilus uvra  |
| 74 | <a href="#">d1cr2a</a>  | Alignment | not modelled | 98.5 | 16 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> RecA protein-like (ATPase-domain)   |
| 75 | <a href="#">d1wb9a2</a> | Alignment | not modelled | 98.5 | 15 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like  |
| 76 | <a href="#">d1vmaa2</a> | Alignment | not modelled | 97.8 | 24 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nitrogenase iron protein-like   |
| 77 | <a href="#">d2qy9a2</a> | Alignment | not modelled | 97.7 | 25 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nitrogenase iron protein-like   |
| 78 | <a href="#">c2j41A</a>  | Alignment | not modelled | 97.7 | 30 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> guanylate kinase;<br><b>PDBTitle:</b> crystal structure of staphylococcus aureus guanylate2   |

|     |                          |           |              |      |    |  |
|-----|--------------------------|-----------|--------------|------|----|--|
|     |                          |           |              |      |    | monophosphate kinase   |
| 79  | <a href="#">dlnp6a_</a>  | Alignment | not modelled | 97.6 | 27 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nitrogenase iron protein-like  |
| 80  | <a href="#">dlokkd2</a>  | Alignment | not modelled | 97.6 | 23 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nitrogenase iron protein-like  |
| 81  | <a href="#">d1ls1a2</a>  | Alignment | not modelled | 97.6 | 35 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nitrogenase iron protein-like  |
| 82  | <a href="#">c3tauB_</a>  | Alignment | not modelled | 97.5 | 40 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> guanylate kinase;<br><b>PDBTitle:</b> crystal structure of a putative guanylate monophosphate kinase from <i>Listeria monocytogenes</i> egd-e                    |
| 83  | <a href="#">dlqzxa3</a>  | Alignment | not modelled | 97.4 | 32 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nitrogenase iron protein-like  |
| 84  | <a href="#">c3a4mB_</a>  | Alignment | not modelled | 97.4 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> l-seryl-trna(sec) kinase;<br><b>PDBTitle:</b> crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase   |
| 85  | <a href="#">dlve8a1</a>  | Alignment | not modelled | 97.3 | 26 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> RecA protein-like (ATPase-domain)  |
| 86  | <a href="#">cllewqA_</a> | Alignment | not modelled | 97.3 | 24 | <b>PDB header:</b> replication/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein muts;<br><b>PDBTitle:</b> crystal structure taq muts complexed with a heteroduplex2 dna at 2.2 a resolution                      |
| 87  | <a href="#">d2i3ba1</a>  | Alignment | not modelled | 97.3 | 32 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> RecA protein-like (ATPase-domain)  |
| 88  | <a href="#">dllewqa2</a> | Alignment | not modelled | 97.2 | 14 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> ABC transporter ATPase domain-like                                       |
| 89  | <a href="#">clwbdA_</a>  | Alignment | not modelled | 97.1 | 16 | <b>PDB header:</b> dna-binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein muts;<br><b>PDBTitle:</b> crystal structure of e. coli dna mismatch repair enzyme2 muts, e38q mutant, in complex with a g.t mismatch |
| 90  | <a href="#">clewrA_</a>  | Alignment | not modelled | 97.1 | 18 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein muts;<br><b>PDBTitle:</b> crystal structure of taq muts  |
| 91  | <a href="#">c2o8ba_</a>  | Alignment | not modelled | 97.1 | 16 | <b>PDB header:</b> dna binding protein/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein msh2;<br><b>PDBTitle:</b> human mutsalpha (msh2/msh6) bound to adp and a g t mispair                                     |
| 92  | <a href="#">c2o8dB_</a>  | Alignment | not modelled | 97.0 | 20 | <b>PDB header:</b> dna binding protein/dna<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna mismatch repair protein msh6;<br><b>PDBTitle:</b> human mutsalpha (msh2/msh6) bound to adp and a g du mispair                                    |
| 93  | <a href="#">c3thxB_</a>  | Alignment | not modelled | 96.9 | 26 | <b>PDB header:</b> dna binding protein/dna<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna mismatch repair protein msh3;<br><b>PDBTitle:</b> human mutsbeta complexed with an idl of 3 bases (loop3) and adp                                |
| 94  | <a href="#">c3geiB_</a>  | Alignment | not modelled | 96.9 | 22 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> trna modification gtpase mnme;<br><b>PDBTitle:</b> crystal structure of mnme from chlorobium tepidum in complex2 with gcp  |
| 95  | <a href="#">dlzp6a1</a>  | Alignment | not modelled | 96.7 | 36 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Atu3015-like   |
| 96  | <a href="#">dlznwa1</a>  | Alignment | not modelled | 96.7 | 23 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases  |
| 97  | <a href="#">clwxqA_</a>  | Alignment | not modelled | 96.6 | 29 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein;<br><b>PDBTitle:</b> crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3                      |
| 98  | <a href="#">dls96a_</a>  | Alignment | not modelled | 96.5 | 24 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases  |
| 99  | <a href="#">c2flrA_</a>  | Alignment | not modelled | 96.4 | 28 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin-guanine dinucleotide biosynthesis<br><b>PDBTitle:</b> crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobbb)          |
| 100 | <a href="#">clznyA_</a>  | Alignment | not modelled | 96.4 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> guanylate kinase;<br><b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis guanylate kinase in2 complex with gdp                                      |
| 101 | <a href="#">dlyrba1</a>  | Alignment | not modelled | 96.3 | 37 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nitrogenase iron protein-like  |
| 102 | <a href="#">d1ki9a_</a>  | Alignment | not modelled | 96.3 | 18 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases  |
| 103 | <a href="#">dlgkya_</a>  | Alignment | not modelled | 96.1 | 24 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases  |
|     |                          |           |              |      |    | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases  |



|     |                         |           |              |      |    |   |
|-----|-------------------------|-----------|--------------|------|----|---|
| 104 | <a href="#">d1ly1a_</a> | Alignment | not modelled | 96.1 | 23 | <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases  |
| 105 | <a href="#">c1ly1A_</a> | Alignment | not modelled | 96.1 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> polynucleotide kinase;<br><b>PDBTitle:</b> structure and mechanism of t4 polynucleotide kinase  |
| 106 | <a href="#">c3neyC_</a> | Alignment | not modelled | 96.0 | 26 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> 55 kda erythrocyte membrane protein;<br><b>PDBTitle:</b> crystal structure of the kinase domain of mpp1/p55  |
| 107 | <a href="#">d1nija1</a> | Alignment | not modelled | 96.0 | 40 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nitrogenase iron protein-like                                     |
| 108 | <a href="#">d1sxje2</a> | Alignment | not modelled | 95.9 | 32 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Extended AAA-ATPase domain  |
| 109 | <a href="#">c2plrB_</a> | Alignment | not modelled | 95.9 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable thymidylate kinase;<br><b>PDBTitle:</b> crystal structure of dtmp kinase (st1543) from sulfolobus tokodaii2 strain7                              |
| 110 | <a href="#">c2cnwF_</a> | Alignment | not modelled | 95.9 | 28 | <b>PDB header:</b> signal recognition<br><b>Chain:</b> F: <b>PDB Molecule:</b> cell division protein ftsy;<br><b>PDBTitle:</b> gdpalf4 complex of the srp gtpases ffh and ftsy  |
| 111 | <a href="#">c1zakB_</a> | Alignment | not modelled | 95.9 | 35 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> adenylate kinase;<br><b>PDBTitle:</b> adenylate kinase from maize in complex with the inhibitor2 p1,p5-bis(adenosine-5'-)pentaphosphate (ap5a)            |
| 112 | <a href="#">c2j7pA_</a> | Alignment | not modelled | 95.9 | 35 | <b>PDB header:</b> signal recognition<br><b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein;<br><b>PDBTitle:</b> gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy                      |
| 113 | <a href="#">d1sxja2</a> | Alignment | not modelled | 95.9 | 27 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Extended AAA-ATPase domain  |
| 114 | <a href="#">c2og2A_</a> | Alignment | not modelled | 95.8 | 36 | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative signal recognition particle receptor;<br><b>PDBTitle:</b> crystal structure of chloroplast ftsy from arabidopsis2 thaliana                 |
| 115 | <a href="#">c2rhmd_</a> | Alignment | not modelled | 95.8 | 26 | <b>PDB header:</b> unknown function<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative kinase;<br><b>PDBTitle:</b> crystal structure of a putative kinase (caur_3907) from chloroflexus2 aurantiacus j-10-fl at 1.70 a resolution  |
| 116 | <a href="#">d1kgda_</a> | Alignment | not modelled | 95.8 | 24 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases                                 |
| 117 | <a href="#">c2dr3A_</a> | Alignment | not modelled | 95.7 | 23 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> upf0273 protein ph0284;<br><b>PDBTitle:</b> crystal structure of reca superfamily atpase ph0284 from pyrococcus2 horikoshii ot3 |
| 118 | <a href="#">c2wwiC_</a> | Alignment | not modelled | 95.7 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> thymidilate kinase, putative;<br><b>PDBTitle:</b> plasmodium falciparum thymidylate kinase in complex with2 aztmp and adp                                 |
| 119 | <a href="#">d3adka_</a> | Alignment | not modelled | 95.7 | 41 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nucleotide and nucleoside kinases                                 |
| 120 | <a href="#">c3lxaA_</a> | Alignment | not modelled | 95.7 | 41 | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> gtpase imap family member 1;<br><b>PDBTitle:</b> crystal structure of human gtpase imap family member 1   |