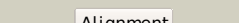
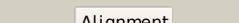
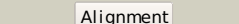


| #  | Template                | Alignment Coverage                                                                               | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                                                                                                     |
|----|-------------------------|--------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c1hqcb_</a> | <br>Alignment   |    | 100.0      | 56     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ruvb;<br><b>PDBTitle:</b> structure of ruvb from thermus thermophilus hb8                                                                                                                                                                                          |
| 2  | <a href="#">clin8A_</a> | <br>Alignment   |    | 100.0      | 54     | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction dna helicase ruvb;<br><b>PDBTitle:</b> thermotoga maritima ruvb t158v                                                                                                                                                                  |
| 3  | <a href="#">c3pfiB_</a> | <br>Alignment   |    | 100.0      | 51     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> holliday junction atp-dependent dna helicase ruvb;<br><b>PDBTitle:</b> 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate |
| 4  | <a href="#">dlixsb2</a> | <br>Alignment   |   | 100.0      | 57     | <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                                                                                                                                               |
| 5  | <a href="#">c3pvsA_</a> | <br>Alignment |  | 100.0      | 25     | <b>PDB header:</b> recombination<br><b>Chain:</b> A: <b>PDB Molecule:</b> replication-associated recombination protein a;<br><b>PDBTitle:</b> structure and biochemical activities of escherichia coli mgsa                                                                                                                              |
| 6  | <a href="#">dlin4a2</a> | <br>Alignment |  | 100.0      | 55     | <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                                                                                                                                               |
| 7  | <a href="#">clsxja_</a> | <br>Alignment |  | 100.0      | 16     | <b>PDB header:</b> replication<br><b>Chain:</b> A: <b>PDB Molecule:</b> activator 1 95 kda subunit;<br><b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)                                                         |
| 8  | <a href="#">dlsxja2</a> | <br>Alignment |  | 100.0      | 15     | <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                                                                                                                                               |
| 9  | <a href="#">dlnjfa_</a> | <br>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> Extended AAA-ATPase domain                                                                                                                                               |
| 10 | <a href="#">c1xxbB_</a> | <br>Alignment |  | 100.0      | 26     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase iii subunit gamma;<br><b>PDBTitle:</b> atpgs bound e. coli clamp loader complex                                                                                                                                                                   |
| 11 | <a href="#">dlsxjb2</a> | <br>Alignment |  | 100.0      | 24     | <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                                                                                                                                               |

|    |                         |           |                                                                                     |       |    |                                                                                                                                                                                                                                                                                  |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|-------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">c2chgB_</a> | Alignment |    | 100.0 | 23 | <b>PDB header:</b> dna-binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> replication factor c small subunit;<br><b>PDBTitle:</b> replication factor c domains 1 and 2                                                                                                     |
| 13 | <a href="#">dlsxjd2</a> | Alignment |    | 100.0 | 16 | <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                                                                                       |
| 14 | <a href="#">dlsxjc2</a> | Alignment |    | 100.0 | 18 | <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                                                                                       |
| 15 | <a href="#">dliqpa2</a> | Alignment |    | 100.0 | 20 | <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                                                                                       |
| 16 | <a href="#">clsxjC_</a> | Alignment |    | 100.0 | 20 | <b>PDB header:</b> replication<br><b>Chain:</b> C: <b>PDB Molecule:</b> activator 1 40 kda subunit;<br><b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna) |
| 17 | <a href="#">c2ce7B_</a> | Alignment |    | 100.0 | 21 | <b>PDB header:</b> cell division protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsh;<br><b>PDBTitle:</b> edta treated                                                                                                                                   |
| 18 | <a href="#">dlsxje2</a> | Alignment |  | 100.0 | 15 | <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                                                                                       |
| 19 | <a href="#">c2dhrC_</a> | Alignment |  | 99.9  | 22 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> ftsh;<br><b>PDBTitle:</b> whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)                                                                                                            |
| 20 | <a href="#">c3b9pA_</a> | Alignment |  | 99.9  | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cg5977-pa, isoform a;<br><b>PDBTitle:</b> spastin                                                                                                                                                          |
| 21 | <a href="#">cliqpF_</a> | Alignment | not modelled                                                                        | 99.9  | 24 | <b>PDB header:</b> replication<br><b>Chain:</b> F: <b>PDB Molecule:</b> rfcs;<br><b>PDBTitle:</b> crystal structure of the clamp loader small subunit from2 pyrococcus furiosus                                                                                                  |
| 22 | <a href="#">clsxjB_</a> | Alignment | not modelled                                                                        | 99.9  | 20 | <b>PDB header:</b> replication<br><b>Chain:</b> B: <b>PDB Molecule:</b> activator 1 37 kda subunit;<br><b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna) |
| 23 | <a href="#">c3h4mC_</a> | Alignment | not modelled                                                                        | 99.9  | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> proteasome-activating nucleotidase;<br><b>PDBTitle:</b> aaa atpase domain of the proteasome- activating nucleotidase                                                                                       |
| 24 | <a href="#">clsxjE_</a> | Alignment | not modelled                                                                        | 99.9  | 18 | <b>PDB header:</b> replication<br><b>Chain:</b> E: <b>PDB Molecule:</b> activator 1 40 kda subunit;<br><b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna) |
| 25 | <a href="#">clxwiA_</a> | Alignment | not modelled                                                                        | 99.9  | 20 | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> iskd1 protein;<br><b>PDBTitle:</b> crystal structure of vps4b                                                                                                                                      |
| 26 | <a href="#">d2ce7a2</a> | Alignment | not modelled                                                                        | 99.9  | 22 | <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                                                                                       |
| 27 | <a href="#">c2c9oC_</a> | Alignment | not modelled                                                                        | 99.9  | 17 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> ruvb-like 1;<br><b>PDBTitle:</b> 3d structure of the human ruvb-like helicase ruvb1                                                                                                                        |
| 28 | <a href="#">c3u5zM_</a> | Alignment | not modelled                                                                        | 99.9  | 16 | <b>PDB header:</b> dna binding protein/dna<br><b>Chain:</b> M: <b>PDB Molecule:</b> dna polymerase accessory protein 44;<br><b>PDBTitle:</b> structure of t4 bacteriophage clamp loader bound to the                                                                             |

|    |                         |           |              |      |                                                                                                                                                                                                                                                                                                 |
|----|-------------------------|-----------|--------------|------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |                         |           |              |      | t4 clamp,2 primer-template dna, and atp analog                                                                                                                                                                                                                                                  |
| 29 | <a href="#">c2chvE</a>  | Alignment | not modelled | 99.9 | 21<br><b>PDB header:</b> dna-binding protein<br><b>Chain:</b> E: <b>PDB Molecule:</b> replication factor c small subunit;<br><b>PDBTitle:</b> replication factor c adpnp complex                                                                                                                |
| 30 | <a href="#">c3d8bB</a>  | Alignment | not modelled | 99.9 | 19<br><b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> fidgetin-like protein 1;<br><b>PDBTitle:</b> crystal structure of human fidgetin-like protein 1 in complex with adp                                                                                                 |
| 31 | <a href="#">c3bosA</a>  | Alignment | not modelled | 99.9 | 13<br><b>PDB header:</b> hydrolase regulator,dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative dna replication factor;<br><b>PDBTitle:</b> crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution |
| 32 | <a href="#">c3cf1C</a>  | Alignment | not modelled | 99.9 | 17<br><b>PDB header:</b> transport protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase;<br><b>PDBTitle:</b> structure of p97/vcp in complex with adp/adp.alfx                                                                                            |
| 33 | <a href="#">c2zamA</a>  | Alignment | not modelled | 99.9 | 19<br><b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associating protein 4b;<br><b>PDBTitle:</b> crystal structure of mouse skd1/vps4b apo-form                                                                                         |
| 34 | <a href="#">c2r65A</a>  | Alignment | not modelled | 99.9 | 19<br><b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cell division protease ftsh homolog;<br><b>PDBTitle:</b> crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex                                                                         |
| 35 | <a href="#">c3eihB</a>  | Alignment | not modelled | 99.9 | 17<br><b>PDB header:</b> protein transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 4;<br><b>PDBTitle:</b> crystal structure of s.cerevisiae vps4 in the presence of atpgammas                                                                      |
| 36 | <a href="#">dlixza</a>  | Alignment | not modelled | 99.9 | 23<br><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                                                                                                |
| 37 | <a href="#">d1lv7a</a>  | Alignment | not modelled | 99.9 | 20<br><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                                                                                                |
| 38 | <a href="#">c1sxjD</a>  | Alignment | not modelled | 99.9 | 14<br><b>PDB header:</b> replication<br><b>Chain:</b> D: <b>PDB Molecule:</b> activator 1 41 kda subunit;<br><b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)          |
| 39 | <a href="#">cliy2A</a>  | Alignment | not modelled | 99.9 | 22<br><b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent metalloprotease ftsh;<br><b>PDBTitle:</b> crystal structure of the ftsh atpase domain from thermus2 thermophilus                                                                                      |
| 40 | <a href="#">c3hu2C</a>  | Alignment | not modelled | 99.9 | 22<br><b>PDB header:</b> transport protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase;<br><b>PDBTitle:</b> structure of p97 n-d1 r86a mutant in complex with atpgs                                                                                      |
| 41 | <a href="#">c2qz4A</a>  | Alignment | not modelled | 99.9 | 16<br><b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> paraplegin;<br><b>PDBTitle:</b> human paraplegin, aaa domain in complex with adp                                                                                                                                    |
| 42 | <a href="#">c1s3sA</a>  | Alignment | not modelled | 99.9 | 22<br><b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase (ter<br><b>PDBTitle:</b> crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c                                                                         |
| 43 | <a href="#">d1w5sa2</a> | Alignment | not modelled | 99.9 | 17<br><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                                                                                                |
| 44 | <a href="#">d1r6bx2</a> | Alignment | not modelled | 99.9 | 11<br><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                                                                                                |
| 45 | <a href="#">d1ofha</a>  | Alignment | not modelled | 99.9 | 20<br><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                                                                                                |
| 46 | <a href="#">d1e32a2</a> | Alignment | not modelled | 99.9 | 20<br><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                                                                                                |
| 47 | <a href="#">c2z4rB</a>  | Alignment | not modelled | 99.9 | 19<br><b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa;<br><b>PDBTitle:</b> crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa                                     |
| 48 | <a href="#">c1qvrB</a>  | Alignment | not modelled | 99.9 | 19<br><b>PDB header:</b> chaperone<br><b>Chain:</b> B: <b>PDB Molecule:</b> clpb protein;<br><b>PDBTitle:</b> crystal structure analysis of clpb                                                                                                                                                |
| 49 | <a href="#">d1g41a</a>  | Alignment | not modelled | 99.9 | 21<br><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                                                                                                |
| 50 | <a href="#">d1r6bx3</a> | Alignment | not modelled | 99.9 | 22<br><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                                                                                                |
| 51 | <a href="#">d1fnna2</a> | Alignment | not modelled | 99.9 | 21<br><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                                                                                                |
| 52 | <a href="#">d1l8qa2</a> | Alignment | not modelled | 99.9 | 20<br><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                                                                                                |
| 53 | <a href="#">d1r6bx</a>  | Alignment | not modelled | 99.9 | 22<br><b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases                                                                                                                                             |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                           |
|----|-------------------------|-----------|--------------|------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 53 | <a href="#">d1g0pa</a>  | Alignment | not modelled | 99.9 | 22 | hydrolases<br><b>Family:</b> Extended AAA-ATPase domain                                                                                                                                                                                                                   |
| 54 | <a href="#">d1um8a</a>  | Alignment | not modelled | 99.8 | 18 | hydrolases<br><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                                                                  |
| 55 | <a href="#">d1qvra3</a> | Alignment | not modelled | 99.8 | 19 | hydrolases<br><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                                                                  |
| 56 | <a href="#">d1r7ra3</a> | Alignment | not modelled | 99.8 | 19 | hydrolases<br><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                                                                  |
| 57 | <a href="#">c3pxiB</a>  | Alignment | not modelled | 99.8 | 20 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> negative regulator of genetic competence clpc/meqb;<br><b>PDBTitle:</b> structure of meca108:clpc                                                                                             |
| 58 | <a href="#">c3hteC</a>  | Alignment | not modelled | 99.8 | 20 | <b>PDB header:</b> motor protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpx;<br><b>PDBTitle:</b> crystal structure of nucleotide-free hexameric clpx                                                                    |
| 59 | <a href="#">c3kl1A</a>  | Alignment | not modelled | 99.8 | 26 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent protease lon;<br><b>PDBTitle:</b> crystal structure of lon protease from thermococcus onnurineus na1                                                                                  |
| 60 | <a href="#">c1r6bX</a>  | Alignment | not modelled | 99.8 | 22 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> X: <b>PDB Molecule:</b> clpa protein;<br><b>PDBTitle:</b> high resolution crystal structure of clpa                                                                                                                         |
| 61 | <a href="#">c2x8aA</a>  | Alignment | not modelled | 99.8 | 21 | <b>PDB header:</b> nuclear protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> nuclear valosin-containing protein-like;<br><b>PDBTitle:</b> human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain                                              |
| 62 | <a href="#">d1a5ta2</a> | Alignment | not modelled | 99.8 | 18 | hydrolases<br><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                                                                  |
| 63 | <a href="#">c2r44A</a>  | Alignment | not modelled | 99.8 | 21 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of a putative atpase (chu_0153) from cytophaga2 hutchinsonii atcc 33406 at 2.00 a resolution                                         |
| 64 | <a href="#">d1qvra2</a> | Alignment | not modelled | 99.8 | 22 | hydrolases<br><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                                                                  |
| 65 | <a href="#">c3te6A</a>  | Alignment | not modelled | 99.8 | 11 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein sir3;<br><b>PDBTitle:</b> crystal structure of the s. cerevisiae sir3 aaa+ domain                                                                                          |
| 66 | <a href="#">d1ny5a2</a> | Alignment | not modelled | 99.8 | 18 | hydrolases<br><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                                                                  |
| 67 | <a href="#">d1oz4a3</a> | Alignment | not modelled | 99.8 | 20 | hydrolases<br><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                                                                  |
| 68 | <a href="#">c2qbyA</a>  | Alignment | not modelled | 99.8 | 15 | <b>PDB header:</b> replication/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein 6 homolog 1;<br><b>PDBTitle:</b> crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)                         |
| 69 | <a href="#">c1fnbB</a>  | Alignment | not modelled | 99.8 | 21 | <b>PDB header:</b> cell cycle<br><b>Chain:</b> B: <b>PDB Molecule:</b> cell division control protein 6;<br><b>PDBTitle:</b> crystal structure of cdc6p from pyrobaculum aerophilum                                                                                        |
| 70 | <a href="#">c2hcbC</a>  | Alignment | not modelled | 99.8 | 19 | <b>PDB header:</b> replication<br><b>Chain:</b> C: <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa;<br><b>PDBTitle:</b> structure of amppcp-bound dnaa from aquifex aeolicus                                                                          |
| 71 | <a href="#">c3nbxX</a>  | Alignment | not modelled | 99.8 | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> X: <b>PDB Molecule:</b> atpase rava;<br><b>PDBTitle:</b> crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp                                                                               |
| 72 | <a href="#">c2v1uA</a>  | Alignment | not modelled | 99.7 | 19 | <b>PDB header:</b> replication<br><b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein 6 homolog;<br><b>PDBTitle:</b> structure of the aeropyrum pernix orc1 protein in complex2 with dna                                                                  |
| 73 | <a href="#">c1o1fF</a>  | Alignment | not modelled | 99.7 | 15 | <b>PDB header:</b> response regulator<br><b>Chain:</b> F: <b>PDB Molecule:</b> transcriptional regulatory protein zrar;<br><b>PDBTitle:</b> crystal structure of a sigma54-activator suggests the2 mechanism for the conformational switch necessary for3 sigma54 binding |
| 74 | <a href="#">c2c99A</a>  | Alignment | not modelled | 99.7 | 16 | <b>PDB header:</b> transcription regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> psp operon transcriptional activator;<br><b>PDBTitle:</b> structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf        |
| 75 | <a href="#">c1w5sB</a>  | Alignment | not modelled | 99.7 | 16 | <b>PDB header:</b> replication<br><b>Chain:</b> B: <b>PDB Molecule:</b> origin recognition complex subunit 2 orc2;<br><b>PDBTitle:</b> structure of the aeropyrum pernix orc2 protein (adp form)                                                                          |
| 76 | <a href="#">c3f8tA</a>  | Alignment | not modelled | 99.7 | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> predicted atpase involved in replication control;<br><b>PDBTitle:</b> crystal structure analysis of a full-length mcm homolog2 from methanopyrus kandleri                                           |
| 77 | <a href="#">d1jbka</a>  | Alignment | not modelled | 99.7 | 14 | hydrolases<br><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                                                                  |
| 78 | <a href="#">c1jr3E</a>  | Alignment | not modelled | 99.7 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> E: <b>PDB Molecule:</b> dna polymerase iii, delta' subunit;<br><b>PDBTitle:</b> crystal structure of the processivity clamp loader gamma2 complex of e. coli dna polymerase iii                                           |

|     |                         |           |              |      |    |                                                                                                                                                                                                                                                                                 |
|-----|-------------------------|-----------|--------------|------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 79  | <a href="#">dlin4a1</a> | Alignment | not modelled | 99.7 | 52 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Helicase DNA-binding domain                                                                                                                            |
| 80  | <a href="#">c1nsfA</a>  | Alignment | not modelled | 99.7 | 16 | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> n-ethylmaleimide sensitive factor;<br><b>PDBTitle:</b> d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)                                                                        |
| 81  | <a href="#">c2p65A</a>  | Alignment | not modelled | 99.7 | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pf08_0063;<br><b>PDBTitle:</b> crystal structure of the first nucleotide binding domain of 2 chaperone clpb1, putative, (pv089580) from plasmodium vivax |
| 82  | <a href="#">c2qbyB</a>  | Alignment | not modelled | 99.7 | 14 | <b>PDB header:</b> replication/dna<br><b>Chain:</b> B: <b>PDB Molecule:</b> cell division control protein 6 homolog 3;<br><b>PDBTitle:</b> crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)                               |
| 83  | <a href="#">d1d2na</a>  | Alignment | not modelled | 99.7 | 16 | <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                                                                                      |
| 84  | <a href="#">d1ixsb1</a> | Alignment | not modelled | 99.6 | 53 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Helicase DNA-binding domain                                                                                                                            |
| 85  | <a href="#">c1ny5A</a>  | Alignment | not modelled | 99.6 | 18 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family);<br><b>PDBTitle:</b> crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state                                                               |
| 86  | <a href="#">c3pxgA</a>  | Alignment | not modelled | 99.6 | 21 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> negative regulator of genetic competence clpc/mecc;<br><b>PDBTitle:</b> structure of meca121 and clpc1-485 complex                                                                                  |
| 87  | <a href="#">c3dzdA</a>  | Alignment | not modelled | 99.6 | 16 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family);<br><b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4 in the inactive2 state                                                            |
| 88  | <a href="#">c2qenA</a>  | Alignment | not modelled | 99.6 | 12 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> walker-type atpase;<br><b>PDBTitle:</b> the walker-type atpase paby2304 of pyrococcus abyssi                                                                                                       |
| 89  | <a href="#">c3m6aC</a>  | Alignment | not modelled | 99.6 | 23 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent protease la 1;<br><b>PDBTitle:</b> crystal structure of bacillus subtilis lon c-terminal domain                                                                                             |
| 90  | <a href="#">d1ixrc1</a> | Alignment | not modelled | 99.5 | 53 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Helicase DNA-binding domain                                                                                                                            |
| 91  | <a href="#">d1e94e</a>  | Alignment | not modelled | 99.5 | 22 | <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                                                                                      |
| 92  | <a href="#">c1z6tC</a>  | Alignment | not modelled | 99.5 | 15 | <b>PDB header:</b> apoptosis<br><b>Chain:</b> C: <b>PDB Molecule:</b> apoptotic protease activating factor 1;<br><b>PDBTitle:</b> structure of the apoptotic protease-activating factor 12 bound to adp                                                                         |
| 93  | <a href="#">c3f9vA</a>  | Alignment | not modelled | 99.4 | 17 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> minichromosome maintenance protein mcm;<br><b>PDBTitle:</b> crystal structure of a near full-length archaeal mcm: functional2 insights for an aaa+ hexameric helicase                                     |
| 94  | <a href="#">d2fnaa2</a> | Alignment | not modelled | 99.4 | 20 | <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                                                                                      |
| 95  | <a href="#">d2gnoa2</a> | Alignment | not modelled | 99.4 | 9  | <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                                                                                      |
| 96  | <a href="#">c2fnaA</a>  | Alignment | not modelled | 99.3 | 16 | <b>PDB header:</b> atp-binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein;<br><b>PDBTitle:</b> crystal structure of an archaeal aaa+ atpase (sso1545) from sulfolobus2 solfataricus p2 at 2.00 a resolution                                |
| 97  | <a href="#">c2p5tD</a>  | Alignment | not modelled | 99.3 | 15 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> D: <b>PDB Molecule:</b> pez2;<br><b>PDBTitle:</b> molecular and structural characterization of the pezat chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae                         |
| 98  | <a href="#">d1gvnb</a>  | Alignment | not modelled | 99.3 | 13 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Plasmid maintenance system epsilon/zeta, toxin zeta subunit                                                     |
| 99  | <a href="#">c3iytG</a>  | Alignment | not modelled | 99.3 | 15 | <b>PDB header:</b> apoptosis<br><b>Chain:</b> G: <b>PDB Molecule:</b> apoptotic protease-activating factor 1;<br><b>PDBTitle:</b> structure of an apoptosome-procaspase-9 card complex                                                                                          |
| 100 | <a href="#">c3ec2A</a>  | Alignment | not modelled | 99.3 | 21 | <b>PDB header:</b> replication<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna replication protein dnac;<br><b>PDBTitle:</b> crystal structure of the dnac helicase loader                                                                                                         |
| 101 | <a href="#">c2a5yB</a>  | Alignment | not modelled | 99.2 | 12 | <b>PDB header:</b> apoptosis<br><b>Chain:</b> B: <b>PDB Molecule:</b> ced-4;<br><b>PDBTitle:</b> structure of a ced-4/ced-9 complex                                                                                                                                             |
| 102 | <a href="#">c2kjqA</a>  | Alignment | not modelled | 99.1 | 14 | <b>PDB header:</b> replication<br><b>Chain:</b> A: <b>PDB Molecule:</b> dnaa-related protein;<br><b>PDBTitle:</b> solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.                                   |
| 103 | <a href="#">d1svma</a>  | Alignment | not modelled | 99.1 | 11 | <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                                                                                      |
|     |                         |           |              |      |    | <b>PDB header:</b> hydrolase                                                                                                                                                                                                                                                    |

|     |                         |           |              |      |    |                                                                                                                                                                                                                                                                                            |
|-----|-------------------------|-----------|--------------|------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 104 | <a href="#">c2w58B_</a> | Alignment | not modelled | 98.9 | 13 | <b>Chain:</b> B: <b>PDB Molecule:</b> primosome component (helicase loader);<br><b>PDBTitle:</b> crystal structure of the dnaI                                                                                                                                                             |
| 105 | <a href="#">c2qgzA_</a> | Alignment | not modelled | 98.9 | 21 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative primosome component;<br><b>PDBTitle:</b> crystal structure of a putative primosome component from2 streptococcus pyogenes serotype m3. northeast structural3 genomics target dr58                           |
| 106 | <a href="#">c3qmzA_</a> | Alignment | not modelled | 98.8 | 15 | <b>PDB header:</b> motor protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytoplasmic dynein heavy chain;<br><b>PDBTitle:</b> crystal structure of the cytoplasmic dynein heavy chain motor domain                                                                                         |
| 107 | <a href="#">c3co5B_</a> | Alignment | not modelled | 98.6 | 16 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative two-component system transcriptional response<br><b>PDBTitle:</b> crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae |
| 108 | <a href="#">c3tlxA_</a> | Alignment | not modelled | 98.6 | 12 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase 2;<br><b>PDBTitle:</b> crystal structure of pf10_0086, adenylate kinase from plasmodium2 falciparum                                                                                               |
| 109 | <a href="#">d1ye8a1</a> | Alignment | not modelled | 98.5 | 29 | <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)                                                                                          |
| 110 | <a href="#">c3be4A_</a> | Alignment | not modelled | 98.5 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase;<br><b>PDBTitle:</b> crystal structure of cryptosporidium parvum adenylate kinase cgd5_3360                                                                                                       |
| 111 | <a href="#">d2iyva1</a> | Alignment | not modelled | 98.5 | 33 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Shikimate kinase (AroK)                                                                                                    |
| 112 | <a href="#">d1kaga_</a> | Alignment | not modelled | 98.4 | 23 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Shikimate kinase (AroK)                                                                                                    |
| 113 | <a href="#">c3trfB_</a> | Alignment | not modelled | 98.4 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> shikimate kinase;<br><b>PDBTitle:</b> structure of a shikimate kinase (arok) from coxiella burnetii                                                                                                                |
| 114 | <a href="#">d2i3ba1</a> | Alignment | not modelled | 98.4 | 42 | <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)                                                                                          |
| 115 | <a href="#">c2gnoA_</a> | Alignment | not modelled | 98.4 | 11 | <b>PDB header:</b> replication<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii, gamma subunit-related protein;<br><b>PDBTitle:</b> crystal structure of a dna polymerase iii, gamma subunit-related2 protein (tm0771) from thermotoga maritima msb8 at 2.00 a resolution       |
| 116 | <a href="#">c1zuiA_</a> | Alignment | not modelled | 98.4 | 27 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> shikimate kinase;<br><b>PDBTitle:</b> structural basis for shikimate-binding specificity of helicobacter2 pylori shikimate kinase                                                                                  |
| 117 | <a href="#">d1lw7a2</a> | Alignment | not modelled | 98.3 | 25 | <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                                                                                          |
| 118 | <a href="#">d1rkba_</a> | Alignment | not modelled | 98.3 | 39 | <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                                                                                          |
| 119 | <a href="#">c2gxaA_</a> | Alignment | not modelled | 98.3 | 14 | <b>PDB header:</b> replication/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> replication protein e1;<br><b>PDBTitle:</b> crystal structure of papillomavirus e1 hexameric helicase2 with ssdna and mgadp                                                                                    |
| 120 | <a href="#">d1x6va3</a> | Alignment | not modelled | 98.3 | 11 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Adenosine-5'phosphosulfate kinase (APS kinase)                                                                             |