# Phyre$^2$

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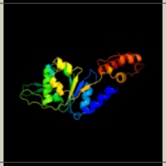
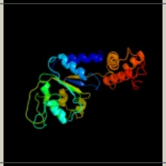
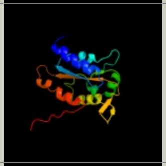
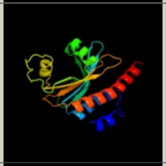
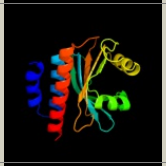
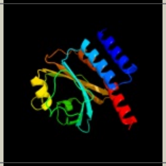
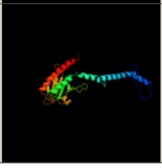
| Description | P71229 |
| Date | Thu Jan 5 12:12:26 GMT 2012 |
| Unique Job ID | ce53b58912a042eb |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1ny5A_ | Alignment |  | 100.0 | 45 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family);<br>**PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state |
| 2 | c3dzdA_ | Alignment |  | 100.0 | 47 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family);<br>**PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state |
| 3 | c2c99A_ | Alignment |  | 100.0 | 45 | **PDB header:**transcription regulation<br>**Chain:** A: **PDB Molecule:**psp operon transcriptional activator;<br>**PDBTitle:** structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf |
| 4 | d1ny5a2 | Alignment |  | 100.0 | 49 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 5 | c1ojlF_ | Alignment |  | 100.0 | 53 | **PDB header:**response regulator<br>**Chain:** F: **PDB Molecule:**transcriptional regulatory protein zrar;<br>**PDBTitle:** crystal structure of a sigma54-activator suggests the2 mechanism for the conformational switch necessary for3 sigma54 binding |
| 6 | c3co5B_ | Alignment |  | 100.0 | 26 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**putative two-component system transcriptional response<br>**PDBTitle:** crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae |
| 7 | c3p01C_ | Alignment |  | 99.9 | 15 | **PDB header:**signaling protein<br>**Chain:** C: **PDB Molecule:**two-component response regulator;<br>**PDBTitle:** crystal structure of two-component response regulator from nostoc sp.2 pcc 7120 |
| 8 | d2veaa1 | Alignment |  | 99.9 | 13 | **Fold:**Profilin-like<br>**Superfamily:**GAF domain-like<br>**Family:**GAF domain |
| 9 | d2o9ca1 | Alignment |  | 99.9 | 12 | **Fold:**Profilin-like<br>**Superfamily:**GAF domain-like<br>**Family:**GAF domain |
| 10 | c3k2nB_ | Alignment |  | 99.9 | 22 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**sigma-54-dependent transcriptional regulator;<br>**PDBTitle:** the crystal structure of sigma-54-dependent transcriptional2 regulator domain from chlorobium tepidum tls |
| 11 | c1mc0A_ | Alignment |  | 99.9 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**3',5'-cyclic nucleotide phosphodiesterase 2a;<br>**PDBTitle:** regulatory segment of mouse 3',5'-cyclic nucleotide phosphodiesterase2 2a, containing the gaf a and gaf b domains |

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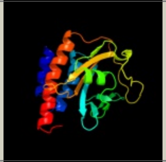
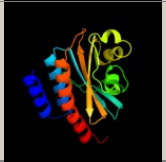
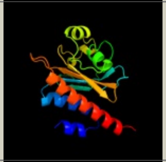
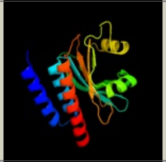
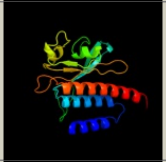
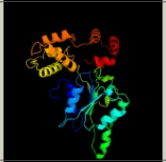
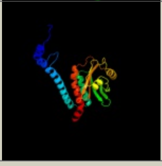
| 12 | c3p01A_ | Alignment |  | 99.9 | 15 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**two-component response regulator;<br>**PDBTitle:** crystal structure of two-component response regulator from nostoc sp.2 pcc 7120 |
| 13 | c3trcA_ | Alignment |  | 99.9 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase;<br>**PDBTitle:** structure of the gaf domain from a phosphoenolpyruvate-protein2 phosphotransferase (ptsp) from coxiella burnetii |
| 14 | c3ci6B_ | Alignment |  | 99.9 | 17 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase;<br>**PDBTitle:** crystal structure of the gaf domain from acinetobacter2 phosphoenolpyruvate-protein phosphotransferase |
| 15 | c3oovA_ | Alignment |  | 99.9 | 12 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein, putative;<br>**PDBTitle:** crystal structure of a methyl-accepting chemotaxis protein, residues2 122 to 287 |
| 16 | d2oola1 | Alignment |  | 99.9 | 11 | **Fold:**Profilin-like<br>**Superfamily:**GAF domain-like<br>**Family:**GAF domain |
| 17 | c3mmhA_ | Alignment |  | 99.9 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase;<br>**PDBTitle:** x-ray structure of free methionine-r-sulfoxide reductase from2 neisseria meningitidis in complex with its substrate |
| 18 | c2zmfA_ | Alignment |  | 99.9 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**camp and camp-inhibited cgmp 3',5'-cyclic phosphodiesterase<br>**PDBTitle:** crystal structure of the c-terminal gaf domain of human2 phosphodiesterase 10a |
| 19 | c3pfiB_ | Alignment |  | 99.9 | 16 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**holliday junction atp-dependent dna helicase ruvb;<br>**PDBTitle:** 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 |
| 20 | c1ykdB_ | Alignment |  | 99.9 | 19 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**adenylate cyclase;<br>**PDBTitle:** crystal structure of the tandem gaf domains from a cyanobacterial2 adenylyl cyclase: novel modes of ligand-binding and dimerization |
| 21 | c3mf0A_ | Alignment | not modelled | 99.9 | 12 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase;<br>**PDBTitle:** crystal structure of pde5a gaf domain (89-518) |
| 22 | c3ibjB_ | Alignment | not modelled | 99.9 | 17 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase;<br>**PDBTitle:** x-ray structure of pde2a |
| 23 | d1r6bx3 | Alignment | not modelled | 99.8 | 17 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 24 | c3eeaB_ | Alignment | not modelled | 99.8 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**gaf domain/hd domain protein;<br>**PDBTitle:** the crystal structure of the gaf domain/hd domain protein2 from geobacter sulfurreducens |
| 25 | c1vhmB_ | Alignment | not modelled | 99.8 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**protein yebr;<br>**PDBTitle:** crystal structure of an hypothetical protein |
| 26 | d1vhma_ | Alignment | not modelled | 99.8 | 12 | **Fold:**Profilin-like<br>**Superfamily:**GAF domain-like<br>**Family:**GAF domain |
| 27 | c1qvrB_ | Alignment | not modelled | 99.8 | 20 | **PDB header:**chaperone<br>**Chain:** B: **PDB Molecule:**clpb protein;<br>**PDBTitle:** crystal structure analysis of clpb |
| 28 | c2lb5A_ | Alignment | not modelled | 99.8 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sensor histidine kinase;<br>**PDBTitle:** refined structural basis for the photoconversion of a phytochrome to2 the activated far-red light-absorbing form |
| | | | | | | **PDB header:**hydrolase |

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| 29 | c2vjwA_ | Alignment | not modelled | 99.8 | 18 | **Chain:** A: **PDB Molecule:**gaf family protein;<br>**PDBTitle:** crystal structure of the second gaf domain of devs from2 mycobacterium smegmatis |
| 30 | c1in8A_ | Alignment | not modelled | 99.8 | 19 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**holliday junction dna helicase ruvb;<br>**PDBTitle:** thermotoga maritima ruvb t158v |
| 31 | c3pxiB_ | Alignment | not modelled | 99.8 | 18 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb;<br>**PDBTitle:** structure of meca108:clpc |
| 32 | c3e0yA_ | Alignment | not modelled | 99.8 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**conserved domain protein;<br>**PDBTitle:** the crystal structure of a conserved domain from a protein of2 geobacter sulfurreducens pca |
| 33 | d1mc0a1 | Alignment | not modelled | 99.8 | 15 | **Fold:**Profilin-like<br>**Superfamily:**GAF domain-like<br>**Family:**GAF domain |
| 34 | c3nbxX_ | Alignment | not modelled | 99.8 | 19 | **PDB header:**hydrolase<br>**Chain:** X: **PDB Molecule:**atpase rava;<br>**PDBTitle:** crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp |
| 35 | c3o5yA_ | Alignment | not modelled | 99.8 | 20 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**sensor protein;<br>**PDBTitle:** the crystal structure of the gaf domain of a two-component sensor2 histidine kinase from bacillus halodurans to 2.45a |
| 36 | c3dbaB_ | Alignment | not modelled | 99.8 | 10 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**cone cgmp-specific 3',5'-cyclic phosphodiesterase subunit<br>**PDBTitle:** crystal structure of the cgmp-bound gaf a domain from the2 photoreceptor phosphodiesterase 6c |
| 37 | c1r6bX_ | Alignment | not modelled | 99.8 | 20 | **PDB header:**hydrolase<br>**Chain:** X: **PDB Molecule:**clpa protein;<br>**PDBTitle:** high resolution crystal structure of clpa |
| 38 | c3ksiA_ | Alignment | not modelled | 99.8 | 10 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** structure of frmsr of staphylococcus aureus (complex with 2-propanol) |
| 39 | c2qybA_ | Alignment | not modelled | 99.8 | 18 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**membrane protein, putative;<br>**PDBTitle:** crystal structure of the gaf domain region of putative membrane2 protein from geobacter sulfurreducens pca |
| 40 | d1um8a_ | Alignment | not modelled | 99.8 | 25 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 41 | d1qvra3 | Alignment | not modelled | 99.8 | 18 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 42 | d2k2na1 | Alignment | not modelled | 99.8 | 20 | **Fold:**Profilin-like<br>**Superfamily:**GAF domain-like<br>**Family:**GAF domain |
| 43 | c2w3gA_ | Alignment | not modelled | 99.8 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**two component sensor histidine kinase devs (gaf<br>**PDBTitle:** air-oxidized structure of the first gaf domain of2 mycobacterium tuberculosis doss |
| 44 | c3hcyB_ | Alignment | not modelled | 99.8 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative two-component sensor histidine kinase protein;<br>**PDBTitle:** the crystal structure of the domain of putative two-component sensor2 histidine kinase protein from sinorhizobium meliloti 1021 |
| 45 | d3c2wa1 | Alignment | not modelled | 99.8 | 15 | **Fold:**Profilin-like<br>**Superfamily:**GAF domain-like<br>**Family:**GAF domain |
| 46 | d1l8qa2 | Alignment | not modelled | 99.7 | 18 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 47 | c3c2wB_ | Alignment | not modelled | 99.7 | 14 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**bacteriophytochrome;<br>**PDBTitle:** crystal structure of the photosensory core domain of p.2 aeruginosa bacteriophytochrome pabphp in the pfr state |
| 48 | c3pvsA_ | Alignment | not modelled | 99.7 | 19 | **PDB header:**recombination<br>**Chain:** A: **PDB Molecule:**replication-associated recombination protein a;<br>**PDBTitle:** structure and biochemical activities of escherichia coli mgsa |
| 49 | c2oolA_ | Alignment | not modelled | 99.7 | 12 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**sensor protein;<br>**PDBTitle:** crystal structure of the chromophore-binding domain of an unusual2 bacteriophytochrome rpbphp3 from r. palustris |
| 50 | c3k1jA_ | Alignment | not modelled | 99.7 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**atp-dependent protease lon;<br>**PDBTitle:** crystal structure of lon protease from thermococcus onnurineus na1 |
| 51 | c2veaA_ | Alignment | not modelled | 99.7 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phytochrome-like protein cph1;<br>**PDBTitle:** the complete sensory module of the cyanobacterial2 phytochrome cph1 in the pr-state. |
| 52 | d1mc0a2 | Alignment | not modelled | 99.7 | 14 | **Fold:**Profilin-like<br>**Superfamily:**GAF domain-like<br>**Family:**GAF domain |
| 53 | c2o9bA_ | Alignment | not modelled | 99.6 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**bacteriophytochrome;<br>**PDBTitle:** crystal structure of bacteriophytochrome chromophore binding domain |

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| 54 | c2hcbC_ | Alignment | not modelled | 99.6 | 19 | **PDB header:**replication<br>**Chain:** C: **PDB Molecule:**chromosomal replication initiator protein dnaa;<br>**PDBTitle:** structure of amppcp-bound dnaa from aquifex aeolicus |
| 55 | c2z4rB_ | Alignment | not modelled | 99.6 | 15 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**chromosomal replication initiator protein dnaa;<br>**PDBTitle:** crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa |
| 56 | c3bosA_ | Alignment | not modelled | 99.6 | 14 | **PDB header:**hydrolase regulator,dna binding protein<br>**Chain:** A: **PDB Molecule:**putative dna replication factor;<br>**PDBTitle:** crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution |
| 57 | c2k31A_ | Alignment | not modelled | 99.6 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**phosphodiesterase 5a, cgmp-specific;<br>**PDBTitle:** solution structure of cgmp-binding gaf domain of2 phosphodiesterase 5 |
| 58 | d1g8pa_ | Alignment | not modelled | 99.6 | 23 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 59 | c1nsfA_ | Alignment | not modelled | 99.6 | 19 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**n-ethylmaleimide sensitive factor;<br>**PDBTitle:** d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf) |
| 60 | c3hteC_ | Alignment | not modelled | 99.6 | 20 | **PDB header:**motor protein<br>**Chain:** C: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx;<br>**PDBTitle:** crystal structure of nucleotide-free hexameric clpx |
| 61 | c3e98B_ | Alignment | not modelled | 99.6 | 14 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**gaf domain of unknown function;<br>**PDBTitle:** crystal structure of a gaf domain containing protein that belongs to2 pfam duf484 family (pa5279) from pseudomonas aeruginosa at 2.43 a3 resolution |
| 62 | d1f5ma_ | Alignment | not modelled | 99.6 | 13 | **Fold:**Profilin-like<br>**Superfamily:**GAF domain-like<br>**Family:**GAF domain |
| 63 | c1hqcB_ | Alignment | not modelled | 99.6 | 15 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**ruvb;<br>**PDBTitle:** structure of ruvb from thermus thermophilus hb8 |
| 64 | c2xssB_ | Alignment | not modelled | 99.5 | 12 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**cgmp-specific 3', 5'-cyclic phosphodiesterase;<br>**PDBTitle:** crystal structure of gafb from the human phosphodiesterase 5 |
| 65 | c3f8tA_ | Alignment | not modelled | 99.5 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**predicted atpase involved in replication control,<br>**PDBTitle:** crystal structure analysis of a full-length mcm homolog2 from methanopyrus kandleri |
| 66 | c2r44A_ | Alignment | not modelled | 99.5 | 12 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a putative atpase (chu_0153) from cytophaga2 hutchinsonii atcc 33406 at 2.00 a resolution |
| 67 | d1ntca_ | Alignment |  | 99.5 | 26 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**FIS-like |
| 68 | d1g41a_ | Alignment | not modelled | 99.5 | 19 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 69 | d1fnna2 | Alignment | not modelled | 99.5 | 13 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 70 | d1ofha_ | Alignment | not modelled | 99.5 | 19 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 71 | d1in4a2 | Alignment | not modelled | 99.4 | 17 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 72 | d1ixsb2 | Alignment | not modelled | 99.4 | 15 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 73 | c2c9oC_ | Alignment | not modelled | 99.4 | 22 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**ruvb-like 1;<br>**PDBTitle:** 3d structure of the human ruvb-like helicase ruvbl1 |
| 74 | d1sxjd2 | Alignment | not modelled | 99.4 | 14 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 75 | d1etob_ | Alignment | not modelled | 99.4 | 20 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**FIS-like |
| 76 | d1d2na_ | Alignment | not modelled | 99.3 | 18 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 77 | d1fipa_ | Alignment | not modelled | 99.3 | 21 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**FIS-like |

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| 78 | c2dhrC_ | Alignment | not modelled | 99.3 | 22 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**ftsh;<br>**PDBTitle:** whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l) |
| 79 | c3f9vA_ | Alignment | not modelled | 99.3 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**minichromosome maintenance protein mcm;<br>**PDBTitle:** crystal structure of a near full-length archaeal mcm: functional2 insights for an aaa+ hexameric helicase |
| 80 | c3e7lD_ | Alignment | not modelled | 99.3 | 22 | **PDB header:**transcription regulator<br>**Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family);<br>**PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain |
| 81 | d1etxa_ | Alignment | not modelled | 99.3 | 23 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**FIS-like |
| 82 | c2chgB_ | Alignment | not modelled | 99.3 | 20 | **PDB header:**dna-binding protein<br>**Chain:** B: **PDB Molecule:**replication factor c small subunit;<br>**PDBTitle:** replication factor c domains 1 and 2 |
| 83 | d1njfa_ | Alignment | not modelled | 99.2 | 20 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 84 | c2ce7B_ | Alignment | not modelled | 99.2 | 21 | **PDB header:**cell division protein<br>**Chain:** B: **PDB Molecule:**cell division protein ftsh;<br>**PDBTitle:** edta treated |
| 85 | c3eihB_ | Alignment | not modelled | 99.2 | 21 | **PDB header:**protein transport<br>**Chain:** B: **PDB Molecule:**vacuolar protein sorting-associated protein 4;<br>**PDBTitle:** crystal structure of s.cerevisiae vps4 in the presence of atpgammas |
| 86 | c3b9pA_ | Alignment | not modelled | 99.2 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**cg5977-pa, isoform a;<br>**PDBTitle:** spastin |
| 87 | d1iqpa2 | Alignment | not modelled | 99.2 | 21 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 88 | c1xwiA_ | Alignment | not modelled | 99.2 | 20 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**skd1 protein;<br>**PDBTitle:** crystal structure of vps4b |
| 89 | d1umqa_ | Alignment | not modelled | 99.1 | 16 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**FIS-like |
| 90 | c1umqA_ | Alignment | not modelled | 99.1 | 16 | **PDB header:**dna-binding protein<br>**Chain:** A: **PDB Molecule:**photosynthetic apparatus regulatory protein;<br>**PDBTitle:** solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity |
| 91 | d1g2ha_ | Alignment | not modelled | 99.1 | 22 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**FIS-like |
| 92 | d1qvra2 | Alignment | not modelled | 99.1 | 17 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 93 | c2p65A_ | Alignment | not modelled | 99.1 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein pf08_0063;<br>**PDBTitle:** crystal structure of the first nucleotide binding domain of2 chaperone clpb1, putative, (pv089580) from plasmodium vivax |
| 94 | c2kjqA_ | Alignment | not modelled | 99.1 | 21 | **PDB header:**replication<br>**Chain:** A: **PDB Molecule:**dnaa-related protein;<br>**PDBTitle:** solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b. |
| 95 | d1sxjc2 | Alignment | not modelled | 99.1 | 16 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 96 | c2r65A_ | Alignment | not modelled | 99.1 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**cell division protease ftsh homolog;<br>**PDBTitle:** crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex |
| 97 | d2ce7a2 | Alignment | not modelled | 99.1 | 19 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 98 | d1sxjb2 | Alignment | not modelled | 99.1 | 14 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 99 | c1xxhB_ | Alignment | not modelled | 99.1 | 21 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**dna polymerase iii subunit gamma;<br>**PDBTitle:** atpgs bound e. coli clamp loader complex |
| 100 | c3h4mC_ | Alignment | not modelled | 99.1 | 18 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**proteasome-activating nucleotidase;<br>**PDBTitle:** aaa atpase domain of the proteasome- activating nucleotidase |
| 101 | c1sxjD_ | Alignment | not modelled | 99.0 | 14 | **PDB header:**replication<br>**Chain:** D: **PDB Molecule:**activator 1 41 kda subunit;<br>**PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna) |
| 102 | d1w5sa2 | Alignment | not modelled | 99.0 | 12 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases |

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|---|---|---|---|---|---|---|
| | | | | | | **Family:**Extended AAA-ATPase domain |
| 103 | c3u5zM_ | Alignment | not modelled | 99.0 | 18 | **PDB header:**dna binding protein/dna<br>**Chain:** M: **PDB Molecule:**dna polymerase accessory protein 44;<br>**PDBTitle:** structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog |
| 104 | c1fnnB_ | Alignment | not modelled | 99.0 | 13 | **PDB header:**cell cycle<br>**Chain:** B: **PDB Molecule:**cell division control protein 6;<br>**PDBTitle:** crystal structure of cdc6p from pyrobaculum aerophilum |
| 105 | c1sxjC_ | Alignment | not modelled | 99.0 | 17 | **PDB header:**replication<br>**Chain:** C: **PDB Molecule:**activator 1 40 kda subunit;<br>**PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna) |
| 106 | c2zamA_ | Alignment | not modelled | 99.0 | 19 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**vacuolar protein sorting-associating protein 4b;<br>**PDBTitle:** crystal structure of mouse skd1/vps4b apo-form |
| 107 | d1r6bx2 | Alignment | not modelled | 99.0 | 20 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 108 | c3d8bB_ | Alignment | not modelled | 98.9 | 21 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**fidgetin-like protein 1;<br>**PDBTitle:** crystal structure of human fidgetin-like protein 1 in complex with adp |
| 109 | c1sxjB_ | Alignment | not modelled | 98.9 | 15 | **PDB header:**replication<br>**Chain:** B: **PDB Molecule:**activator 1 37 kda subunit;<br>**PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna) |
| 110 | d1lv7a_ | Alignment | not modelled | 98.9 | 21 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 111 | c3hu2C_ | Alignment | not modelled | 98.9 | 33 | **PDB header:**transport protein<br>**Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase;<br>**PDBTitle:** structure of p97 n-d1 r86a mutant in complex with atpgs |
| 112 | c1iy2A_ | Alignment | not modelled | 98.9 | 20 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**atp-dependent metalloprotease ftsh;<br>**PDBTitle:** crystal structure of the ftsh atpase domain from thermus2 thermophilus |
| 113 | c2qbyB_ | Alignment | not modelled | 98.9 | 20 | **PDB header:**replication/dna<br>**Chain:** B: **PDB Molecule:**cell division control protein 6 homolog 3;<br>**PDBTitle:** crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus) |
| 114 | d1jbka_ | Alignment | not modelled | 98.9 | 19 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 115 | c2chvE_ | Alignment | not modelled | 98.9 | 20 | **PDB header:**dna-binding protein<br>**Chain:** E: **PDB Molecule:**replication factor c small subunit;<br>**PDBTitle:** replication factor c adpnp complex |
| 116 | c2qz4A_ | Alignment | not modelled | 98.9 | 20 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**paraplegin;<br>**PDBTitle:** human paraplegin, aaa domain in complex with adp |
| 117 | c3cf1C_ | Alignment | not modelled | 98.9 | 23 | **PDB header:**transport protein<br>**Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase;<br>**PDBTitle:** structure of p97/vcp in complex with adp/adp.alfx |
| 118 | d1e32a2 | Alignment | not modelled | 98.9 | 22 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 119 | c2v1uA_ | Alignment | not modelled | 98.8 | 17 | **PDB header:**replication<br>**Chain:** A: **PDB Molecule:**cell division control protein 6 homolog;<br>**PDBTitle:** structure of the aeropyrum pernix orc1 protein in complex2 with dna |
| 120 | c1iqpF_ | Alignment | not modelled | 98.8 | 20 | **PDB header:**replication<br>**Chain:** F: **PDB Molecule:**rfcs;<br>**PDBTitle:** crystal structure of the clamp loader small subunit from2 pyrococcus furiosus |