# Phyre$^2$

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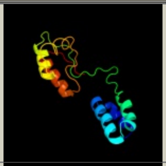
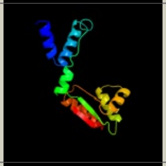
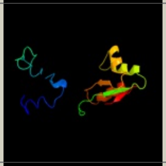
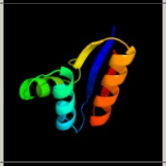
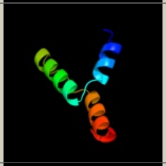
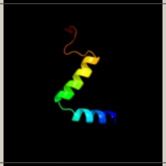
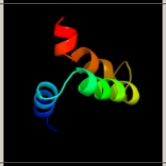
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0A7K2 |
| Date | Thu Jan 5 11:05:48 GMT 2012 |
| Unique Job ID | d023c7f9f6fa357e |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2gya3_ | Alignment |  | 100.0 | 100 | **PDB header:**ribosome<br>**Chain:** 3: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** structure of the 50s subunit of a pre-translocational e.2 coli ribosome obtained by fitting atomic models for rna and3 protein components into cryo-em map emd-1056 |
| 2 | c1giyJ_ | Alignment |  | 100.0 | 66 | **PDB header:**ribosome<br>**Chain:** J: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** crystal structure of the ribosome at 5.5 a resolution. this2 file, 1giy, contains the 50s ribosome subunit. the 30s3 ribosome subunit, three trna, and mrna molecules are in the4 file 1gix |
| 3 | c2ftcF_ | Alignment |  | 100.0 | 29 | **PDB header:**ribosome<br>**Chain:** F: **PDB Molecule:**39s ribosomal protein l12, mitochondrial;<br>**PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome |
| 4 | c2zjq5_ | Alignment |  | 99.9 | 66 | **PDB header:**ribosome<br>**Chain:** 5: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** interaction of l7 with l11 induced by microccocin binding2 to the deinococcus radiodurans 50s subunit |
| 5 | d2zjq51 | Alignment |  | 99.9 | 66 | **Fold:**ClpS-like<br>**Superfamily:**ClpS-like<br>**Family:**Ribosomal protein L7/12, C-terminal domain |
| 6 | d1ctfa_ | Alignment |  | 99.9 | 100 | **Fold:**ClpS-like<br>**Superfamily:**ClpS-like<br>**Family:**Ribosomal protein L7/12, C-terminal domain |
| 7 | d1dd3a2 | Alignment |  | 99.9 | 71 | **Fold:**ClpS-like<br>**Superfamily:**ClpS-like<br>**Family:**Ribosomal protein L7/12, C-terminal domain |
| 8 | d1dd3a1 | Alignment |  | 98.8 | 49 | **Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain |
| 9 | d1dd4d_ | Alignment |  | 98.3 | 53 | **Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain |
| 10 | d2gyc31 | Alignment |  | 97.9 | 100 | **Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain |
| 11 | d1dd4c_ | Alignment |  | 97.9 | 49 | **Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain |

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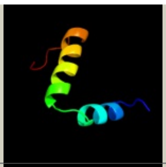
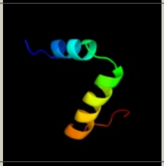
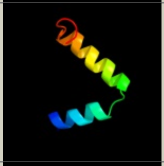
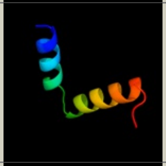
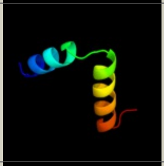
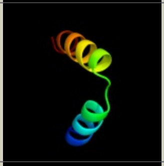
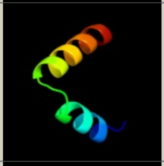
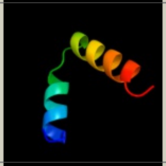
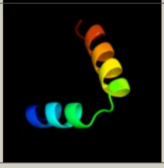
|---|---|---|---|---|---|---|
| 12 | c1rqtA_ | Alignment |  | 97.6 | 100 | **PDB header:**ribosome<br>**Chain:** A: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli |
| 13 | d1rqta_ | Alignment |  | 97.6 | 100 | **Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain |
| 14 | c1rqtB_ | Alignment |  | 97.6 | 100 | **PDB header:**ribosome<br>**Chain:** B: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli |
| 15 | c1dd3D_ | Alignment |  | 97.6 | 44 | **PDB header:**ribosome<br>**Chain:** D: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** crystal structure of ribosomal protein l12 from thermotoga maritima |
| 16 | c1dd3C_ | Alignment |  | 97.6 | 44 | **PDB header:**ribosome<br>**Chain:** C: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** crystal structure of ribosomal protein l12 from thermotoga maritima |
| 17 | c1zaxW_ | Alignment |  | 97.2 | 43 | **PDB header:**structural protein<br>**Chain:** W: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b |
| 18 | c1zavW_ | Alignment |  | 97.2 | 43 | **PDB header:**structural protein<br>**Chain:** W: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p21 |
| 19 | c1zaxV_ | Alignment |  | 97.2 | 43 | **PDB header:**structural protein<br>**Chain:** V: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b |
| 20 | c1zavU_ | Alignment |  | 97.2 | 43 | **PDB header:**structural protein<br>**Chain:** U: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p21 |
| 21 | d1zavu1 | Alignment | not modelled | 97.2 | 43 | **Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain |
| 22 | c1zaxU_ | Alignment | not modelled | 97.2 | 43 | **PDB header:**structural protein<br>**Chain:** U: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b |
| 23 | c1zavV_ | Alignment | not modelled | 97.1 | 43 | **PDB header:**structural protein<br>**Chain:** V: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p21 |
| 24 | c1zawU_ | Alignment | not modelled | 97.0 | 43 | **PDB header:**structural protein<br>**Chain:** U: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a |
| 25 | c1zawW_ | Alignment | not modelled | 97.0 | 43 | **PDB header:**structural protein<br>**Chain:** W: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a |
| 26 | c1zawV_ | Alignment | not modelled | 97.0 | 43 | **PDB header:**structural protein<br>**Chain:** V: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a |
| 27 | c1zaxZ_ | Alignment | not modelled | 96.9 | 45 | **PDB header:**structural protein<br>**Chain:** Z: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b |
| 28 | c1zavX_ | Alignment | not modelled | 96.6 | 41 | **PDB header:**structural protein<br>**Chain:** X: **PDB Molecule:**50s ribosomal protein l7/l12; |

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|---|---|---|---|---|---|---|
| | | | | | | **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p21 |
| 29 | c1zaxX_ | Alignment | not modelled | 96.6 | 41 | **PDB header:**structural protein<br>**Chain:** X: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b |
| 30 | c1zaxY_ | Alignment | not modelled | 96.6 | 41 | **PDB header:**structural protein<br>**Chain:** Y: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b |
| 31 | c1zavY_ | Alignment | not modelled | 96.6 | 41 | **PDB header:**structural protein<br>**Chain:** Y: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p21 |
| 32 | c1zawY_ | Alignment | not modelled | 96.3 | 41 | **PDB header:**structural protein<br>**Chain:** Y: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a |
| 33 | c1zawX_ | Alignment | not modelled | 96.3 | 41 | **PDB header:**structural protein<br>**Chain:** X: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a |
| 34 | c1zavZ_ | Alignment | not modelled | 94.4 | 41 | **PDB header:**structural protein<br>**Chain:** Z: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p21 |
| 35 | d1zavz1 | Alignment | not modelled | 94.4 | 41 | **Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain<br>**Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain |
| 36 | c1zawZ_ | Alignment | not modelled | 94.2 | 41 | **PDB header:**structural protein<br>**Chain:** Z: **PDB Molecule:**50s ribosomal protein l7/l12;<br>**PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a |
| 37 | d1aipc1 | Alignment | not modelled | 78.1 | 32 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**TS-N domain |
| 38 | c1aipG_ | Alignment | not modelled | 70.6 | 37 | **PDB header:**complex of two elongation factors<br>**Chain:** G: **PDB Molecule:**elongation factor ts;<br>**PDBTitle:** ef-tu ef-ts complex from thermus thermophilus |
| 39 | d1efub3 | Alignment | not modelled | 67.1 | 28 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**TS-N domain |
| 40 | d1xb2b1 | Alignment | not modelled | 61.7 | 21 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**TS-N domain |
| 41 | d2cp9a1 | Alignment | not modelled | 56.9 | 23 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**TS-N domain |
| 42 | c1xb2B_ | Alignment | not modelled | 52.3 | 21 | **PDB header:**translation<br>**Chain:** B: **PDB Molecule:**elongation factor ts, mitochondrial;<br>**PDBTitle:** crystal structure of bos taurus mitochondrial elongation2 factor tu/ts complex |
| 43 | c1efuB_ | Alignment | not modelled | 40.6 | 26 | **PDB header:**complex (two elongation factors)<br>**Chain:** B: **PDB Molecule:**elongation factor ts;<br>**PDBTitle:** elongation factor complex ef-tu/ef-ts from escherichia coli |
| 44 | c3mmpC_ | Alignment | not modelled | 29.8 | 21 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**elongation factor tu 2, elongation factor ts;<br>**PDBTitle:** structure of the qb replicase, an rna-dependent rna polymerase2 consisting of viral and host proteins |
| 45 | c2jmlA_ | Alignment | not modelled | 26.5 | 25 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**dna binding domain/transcriptional regulator;<br>**PDBTitle:** solution structure of the n-terminal domain of cara repressor |
| 46 | c2iifA_ | Alignment | not modelled | 26.1 | 21 | **PDB header:**recombination/dna<br>**Chain:** A: **PDB Molecule:**integration host factor;<br>**PDBTitle:** single chain integration host factor mutant protein (scihf2-2 k45ae) in complex with dna |
| 47 | c4a1cK_ | Alignment | not modelled | 20.8 | 6 | **PDB header:**ribosome<br>**Chain:** K: **PDB Molecule:**60s ribosomal protein l27a;<br>**PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4. |
| 48 | d1in0a2 | Alignment | not modelled | 20.5 | 24 | **Fold:**Ferredoxin-like<br>**Superfamily:**YajQ-like<br>**Family:**YajQ-like |
| 49 | d1mula_ | Alignment | not modelled | 17.4 | 33 | **Fold:**IHF-like DNA-binding proteins<br>**Superfamily:**IHF-like DNA-binding proteins<br>**Family:**Prokaryotic DNA-bending protein |
| 50 | d1vqol1 | Alignment | not modelled | 17.1 | 38 | **Fold:**Ribosomal proteins L15p and L18e<br>**Superfamily:**Ribosomal proteins L15p and L18e<br>**Family:**Ribosomal proteins L15p and L18e |
| 51 | d1p71a_ | Alignment | not modelled | 15.7 | 28 | **Fold:**IHF-like DNA-binding proteins<br>**Superfamily:**IHF-like DNA-binding proteins<br>**Family:**Prokaryotic DNA-bending protein |
| 52 | d2axtu1 | Alignment | not modelled | 14.1 | 29 | **Fold:**SAM domain-like<br>**Superfamily:**PsbU/PolX domain-like<br>**Family:**PsbU-like |
| 53 | c2zkrl_ | Alignment | not modelled | 13.1 | 6 | **PDB header:**ribosomal protein/rna<br>**Chain:** L: **PDB Molecule:**rna expansion segment es20;<br>**PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 |

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|---|---|---|---|---|---|---|
|  |  |  |  |  |  | and proteins into an 8.7 a cryo-em map |
| 54 | d1r6oc1 | Alignment | not modelled | 12.6 | 16 | **Fold:**ClpS-like<br>**Superfamily:**ClpS-like<br>**Family:**Adaptor protein ClpS (YljA) |
| 55 | d1y7ta2 | Alignment | not modelled | 12.3 | 17 | **Fold:**LDH C-terminal domain-like<br>**Superfamily:**LDH C-terminal domain-like<br>**Family:**Lactate & malate dehydrogenases, C-terminal domain |
| 56 | c1in0B_ | Alignment | not modelled | 11.8 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**yajq protein;<br>**PDBTitle:** yajq protein (hi1034) |
| 57 | d1b8za_ | Alignment | not modelled | 11.3 | 24 | **Fold:**IHF-like DNA-binding proteins<br>**Superfamily:**IHF-like DNA-binding proteins<br>**Family:**Prokaryotic DNA-bending protein |
| 58 | c3izct_ | Alignment | not modelled | 10.8 | 25 | **PDB header:**ribosome<br>**Chain:** T: **PDB Molecule:**60s ribosomal protein rpl19 (l19e);<br>**PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 59 | d1spbp_ | Alignment | not modelled | 10.4 | 27 | **Fold:**Ferredoxin-like<br>**Superfamily:**Protease propeptides/inhibitors<br>**Family:**Subtilase propeptides/inhibitors |
| 60 | d2o8ra3 | Alignment | not modelled | 10.2 | 15 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Polyphosphate kinase C-terminal domain |
| 61 | d2j01p1 | Alignment | not modelled | 9.8 | 25 | **Fold:**Ribosomal proteins L15p and L18e<br>**Superfamily:**Ribosomal proteins L15p and L18e<br>**Family:**Ribosomal proteins L15p and L18e |
| 62 | d2zjri1 | Alignment | not modelled | 9.7 | 44 | **Fold:**Ribosomal proteins L15p and L18e<br>**Superfamily:**Ribosomal proteins L15p and L18e<br>**Family:**Ribosomal proteins L15p and L18e |
| 63 | d1v5ib1 | Alignment | not modelled | 9.6 | 24 | **Fold:**Ferredoxin-like<br>**Superfamily:**Protease propeptides/inhibitors<br>**Family:**Subtilase propeptides/inhibitors |
| 64 | c2jw5A_ | Alignment | not modelled | 8.6 | 20 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**dna polymerase lambda;<br>**PDBTitle:** polymerase lambda brct domain |
| 65 | d1e0ea_ | Alignment | not modelled | 8.1 | 22 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**N-terminal Zn binding domain of HIV integrase<br>**Family:**N-terminal Zn binding domain of HIV integrase |
| 66 | c2dt5A_ | Alignment | not modelled | 8.0 | 15 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**at-rich dna-binding protein;<br>**PDBTitle:** crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8 |
| 67 | d1w5fa2 | Alignment | not modelled | 7.8 | 9 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**Tubulin C-terminal domain-like<br>**Family:**Tubulin, C-terminal domain |
| 68 | d1ofua2 | Alignment | not modelled | 7.8 | 16 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**Tubulin C-terminal domain-like<br>**Family:**Tubulin, C-terminal domain |
| 69 | d1szpa1 | Alignment | not modelled | 7.7 | 21 | **Fold:**SAM domain-like<br>**Superfamily:**Rad51 N-terminal domain-like<br>**Family:**DNA repair protein Rad51, N-terminal domain |
| 70 | d1wjfa_ | Alignment | not modelled | 7.2 | 26 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**N-terminal Zn binding domain of HIV integrase<br>**Family:**N-terminal Zn binding domain of HIV integrase |
| 71 | c3iz5t_ | Alignment | not modelled | 7.1 | 31 | **PDB header:**ribosome<br>**Chain:** T: **PDB Molecule:**60s ribosomal protein l19 (l19e);<br>**PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 72 | d1k6ya1 | Alignment | not modelled | 6.8 | 26 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**N-terminal Zn binding domain of HIV integrase<br>**Family:**N-terminal Zn binding domain of HIV integrase |
| 73 | d1kxpd3 | Alignment | not modelled | 6.7 | 20 | **Fold:**Serum albumin-like<br>**Superfamily:**Serum albumin-like<br>**Family:**Serum albumin-like |
| 74 | c3a1yF_ | Alignment | not modelled | 6.7 | 53 | **PDB header:**ribosomal protein<br>**Chain:** F: **PDB Molecule:**50s ribosomal protein p1 (l12p);<br>**PDBTitle:** the structure of protein complex |
| 75 | c3bsuF_ | Alignment | not modelled | 6.3 | 29 | **PDB header:**hydrolase/rna/dna<br>**Chain:** F: **PDB Molecule:**ribonuclease h1;<br>**PDBTitle:** hybrid-binding domain of human rnase h1 in complex with 12-2 mer rna/dna |
| 76 | c3d6zA_ | Alignment | not modelled | 6.3 | 17 | **PDB header:**transcription regulator/dna<br>**Chain:** A: **PDB Molecule:**multidrug-efflux transporter 1 regulator;<br>**PDBTitle:** crystal structure of r275e mutant of bmrr bound to dna and rhodamine |
| 77 | d1scjb_ | Alignment | not modelled | 6.0 | 23 | **Fold:**Ferredoxin-like<br>**Superfamily:**Protease propeptides/inhibitors<br>**Family:**Subtilase propeptides/inhibitors |
| 78 | c2o8rA_ | Alignment | not modelled | 6.0 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**polyphosphate kinase;<br>**PDBTitle:** crystal structure of polyphosphate kinase from2 porphyromonas gingivalis |
| 79 | d1iqoa_ | Alignment | not modelled | 5.9 | 50 | **Fold:**Hypothetical protein MTH1880<br>**Superfamily:**Hypothetical protein MTH1880<br>**Family:**Hypothetical protein MTH1880 |
| 80 | c2lbfA_ | Alignment | not modelled | 5.9 | 25 | **PDB header:**ribosomal protein<br>**Chain:** A: **PDB Molecule:**60s acidic ribosomal protein p1;<br>**PDBTitle:** solution structure of the dimerization domain of human |

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|---|---|---|---|---|---|---|
| | | | | | | ribosomal2 protein p1/p2 heterodimer |
| 81 | d1nh8a2 | Alignment | not modelled | 5.8 | 26 | **Fold:**Ferredoxin-like<br>**Superfamily:**GlnB-like<br>**Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain |
| 82 | d1lghb_ | Alignment | not modelled | 5.7 | 36 | **Fold:**Light-harvesting complex subunits<br>**Superfamily:**Light-harvesting complex subunits<br>**Family:**Light-harvesting complex subunits |
| 83 | d2o97b1 | Alignment | not modelled | 5.7 | 19 | **Fold:**IHF-like DNA-binding proteins<br>**Superfamily:**IHF-like DNA-binding proteins<br>**Family:**Prokaryotic DNA-bending protein |
| 84 | d1nxha_ | Alignment | not modelled | 5.6 | 53 | **Fold:**Hypothetical protein MTH393<br>**Superfamily:**Hypothetical protein MTH393<br>**Family:**Hypothetical protein MTH393 |
| 85 | c2l9fA_ | Alignment | not modelled | 5.5 | 29 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**cale8;<br>**PDBTitle:** nmr solution structure of meacp |
| 86 | c2fvfA_ | Alignment | not modelled | 5.3 | 33 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**acyl carrier protein;<br>**PDBTitle:** structure of 10:0-acp (protein with docked fatty acid) |
| 87 | c3nohA_ | Alignment | not modelled | 5.2 | 44 | **PDB header:**peptide binding protein<br>**Chain:** A: **PDB Molecule:**putative peptide binding protein;<br>**PDBTitle:** crystal structure of a putative peptide binding protein (rumgna_00914)2 from ruminococcus gnavus atcc 29149 at 1.60 a resolution |