# Phyre$^2$

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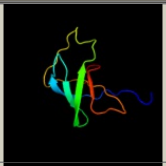
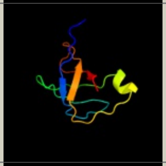
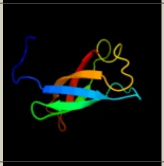
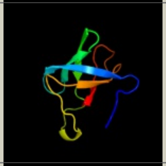
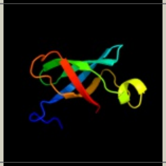
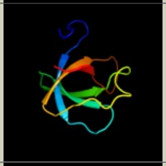
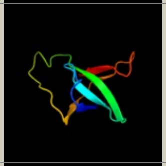
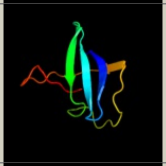
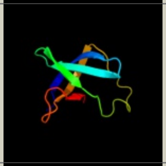
| Email | l.a.kelley@imperial.ac.uk |
| Description | P69222 |
| Date | Wed Jan 25 15:21:01 GMT 2012 |
| Unique Job ID | adb6302ace806c42 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1ah9a_ | Alignment |  | 100.0 | 100 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 2 | c3i4oA_ | Alignment |  | 100.0 | 69 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**translation initiation factor if-1;<br>**PDBTitle:** crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis |
| 3 | d1hr0w_ | Alignment |  | 99.9 | 57 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 4 | d1jt8a_ | Alignment |  | 99.9 | 24 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 5 | d1d7qa_ | Alignment |  | 99.9 | 24 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 6 | c2oqkA_ | Alignment |  | 99.9 | 31 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a;<br>**PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a |
| 7 | c2dgyA_ | Alignment |  | 99.8 | 26 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**mgc11102 protein;<br>**PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein |
| 8 | d1u0la1 | Alignment |  | 97.8 | 29 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 9 | d1t9ha1 | Alignment |  | 97.5 | 25 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 10 | c1u0lB_ | Alignment |  | 97.2 | 32 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**probable gtpase engc;<br>**PDBTitle:** crystal structure of yjeq from thermotoga maritima |
| 11 | c2yv5A_ | Alignment |  | 96.9 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**yjeq protein;<br>**PDBTitle:** crystal structure of yjeq from aquifex aeolicus |

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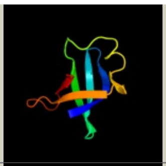
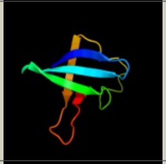
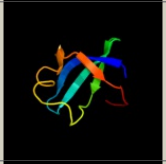
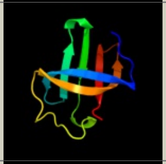
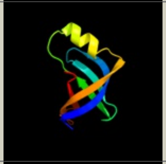
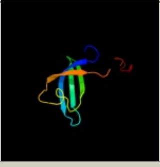
| 12 | c2rcnA_ | Alignment |  | 96.1 | 29 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**probable gtpase engc;<br>**PDBTitle:** crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium. |
| 13 | c1t9hA_ | Alignment |  | 95.5 | 27 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**probable gtpase engc;<br>**PDBTitle:** the crystal structure of yloq, a circularly permuted gtpase. |
| 14 | c4a2iV_ | Alignment |  | 94.8 | 24 | **PDB header:**ribosome/hydrolase<br>**Chain:** V: **PDB Molecule:**putative ribosome biogenesis gtpase rsga;<br>**PDBTitle:** cryo-electron microscopy structure of the 30s subunit in complex with2 the yjeq biogenesis factor |
| 15 | c3fp9E_ | Alignment |  | 93.4 | 20 | **PDB header:**hydrolase<br>**Chain:** E: **PDB Molecule:**proteasome-associated atpase;<br>**PDBTitle:** crystal structure of intern domain of proteasome-associated2 atpase, mycobacterium tuberculosis |
| 16 | c2k52A_ | Alignment |  | 91.3 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein mj1198;<br>**PDBTitle:** structure of uncharacterized protein mj1198 from2 methanocaldococcus jannaschii. northeast structural3 genomics target mjr117b |
| 17 | c1q46A_ | Alignment |  | 90.9 | 25 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**translation initiation factor 2 alpha subunit;<br>**PDBTitle:** crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia |
| 18 | c3m9bK_ | Alignment |  | 90.5 | 16 | **PDB header:**chaperone<br>**Chain:** K: **PDB Molecule:**proteasome-associated atpase;<br>**PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa |
| 19 | d1kl9a2 | Alignment |  | 89.2 | 21 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 20 | d1g2914 | Alignment |  | 89.0 | 17 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**ABC-transporter additional domain |
| 21 | c1zn1L_ | Alignment | not modelled | 87.4 | 30 | **PDB header:**biosynthetic/structural protein/rna<br>**Chain:** L: **PDB Molecule:**30s ribosomal protein s12;<br>**PDBTitle:** coordinates of rrf fitted into cryo-em map of the 70s post-2 termination complex |
| 22 | c1xniI_ | Alignment | not modelled | 85.0 | 14 | **PDB header:**cell cycle<br>**Chain:** I: **PDB Molecule:**tumor suppressor p53-binding protein 1;<br>**PDBTitle:** tandem tudor domain of 53bp1 |
| 23 | d2uubl1 | Alignment | not modelled | 84.6 | 30 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 24 | d1y14b1 | Alignment | not modelled | 83.8 | 16 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 25 | c2r7fA_ | Alignment | not modelled | 82.9 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**ribonuclease ii family protein;<br>**PDBTitle:** crystal structure of ribonuclease ii family protein from deinococcus2 radiodurans, hexagonal crystal form. northeast structural genomics3 target drr63 |
| 26 | c2oceA_ | Alignment | not modelled | 82.9 | 21 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein pa5201;<br>**PDBTitle:** crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa |
| 27 | c1yz6A_ | Alignment | not modelled | 82.1 | 27 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**probable translation initiation factor 2 alpha<br>**PDBTitle:** crystal structure of intact alpha subunit of aif2 from2 pyrococcus abyssi |
| 28 | d2qall1 | Alignment | not modelled | 78.6 | 33 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |

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| 29 | c2ix1A_ | Alignment | not modelled | 77.5 | 12 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**exoribonuclease 2;<br>**PDBTitle:** rnase ii d209n mutant |
| 30 | c2xzmL_ | Alignment | not modelled | 77.5 | 25 | **PDB header:**ribosome<br>**Chain:** L: **PDB Molecule:**40s ribosomal protein s12;<br>**PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1 |
| 31 | c1ssfA_ | Alignment | not modelled | 76.5 | 14 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**transformation related protein 53 binding<br>**PDBTitle:** solution structure of the mouse 53bp1 fragment (residues2 1463-1617) |
| 32 | d1i94l_ | Alignment | not modelled | 75.8 | 30 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 33 | c1q8kA_ | Alignment | not modelled | 75.7 | 24 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 2<br>**PDBTitle:** solution structure of alpha subunit of human eif2 |
| 34 | d1go3e1 | Alignment | not modelled | 75.3 | 26 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 35 | c2wp8J_ | Alignment | not modelled | 74.8 | 15 | **PDB header:**hydrolase<br>**Chain:** J: **PDB Molecule:**exosome complex exonuclease dis3;<br>**PDBTitle:** yeast rrp44 nuclease |
| 36 | c2khjA_ | Alignment | not modelled | 72.2 | 22 | **PDB header:**ribosomal protein<br>**Chain:** A: **PDB Molecule:**30s ribosomal protein s1;<br>**PDBTitle:** nmr structure of the domain 6 of the e. coli ribosomal2 protein s1 |
| 37 | d2ahob2 | Alignment | not modelled | 71.6 | 16 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 38 | d2g3ra1 | Alignment | not modelled | 71.5 | 14 | **Fold:**SH3-like barrel<br>**Superfamily:**Tudor/PWWP/MBT<br>**Family:**Tudor domain |
| 39 | c2k4kA_ | Alignment | not modelled | 71.3 | 27 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**general stress protein 13;<br>**PDBTitle:** solution structure of gsp13 from bacillus subtilis |
| 40 | c2khiA_ | Alignment | not modelled | 71.3 | 24 | **PDB header:**ribosomal protein<br>**Chain:** A: **PDB Molecule:**30s ribosomal protein s1;<br>**PDBTitle:** nmr structure of the domain 4 of the e. coli ribosomal2 protein s1 |
| 41 | d1smxa_ | Alignment | not modelled | 70.4 | 14 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 42 | c1kl9A_ | Alignment | not modelled | 70.2 | 19 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 2 subunit 1;<br>**PDBTitle:** crystal structure of the n-terminal segment of human eukaryotic2 initiation factor 2alpha |
| 43 | c2equA_ | Alignment | not modelled | 70.1 | 11 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**phd finger protein 20-like 1;<br>**PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1 |
| 44 | c1s1hL_ | Alignment | not modelled | 68.2 | 50 | **PDB header:**ribosome<br>**Chain:** L: **PDB Molecule:**40s ribosomal protein s23;<br>**PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i. |
| 45 | c2pmzE_ | Alignment | not modelled | 67.8 | 27 | **PDB header:**translation, transferase<br>**Chain:** E: **PDB Molecule:**dna-directed rna polymerase subunit e;<br>**PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus |
| 46 | c2c35F_ | Alignment | not modelled | 67.5 | 16 | **PDB header:**polymerase<br>**Chain:** F: **PDB Molecule:**dna-directed rna polymerase ii 19 kda<br>**PDBTitle:** subunits rpb4 and rpb7 of human rna polymerase ii |
| 47 | c1go3E_ | Alignment | not modelled | 64.7 | 25 | **PDB header:**transferase<br>**Chain:** E: **PDB Molecule:**dna-directed rna polymerase subunit e;<br>**PDBTitle:** structure of an archeal homolog of the eukaryotic rna2 polymerase ii rpb4/rpb7 complex |
| 48 | c2zkql_ | Alignment | not modelled | 63.5 | 44 | **PDB header:**ribosomal protein/rna<br>**Chain:** L: **PDB Molecule:**<br>**PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map |
| 49 | c2ahoB_ | Alignment | not modelled | 62.1 | 19 | **PDB header:**translation<br>**Chain:** B: **PDB Molecule:**translation initiation factor 2 alpha subunit;<br>**PDBTitle:** structure of the archaeal initiation factor eif2 alpha-2 gamma heterodimer from sulfolobus solfataricus complexed3 with gdpnp |
| 50 | c1h9mB_ | Alignment | not modelled | 60.7 | 13 | **PDB header:**binding protein<br>**Chain:** B: **PDB Molecule:**molybdenum-binding-protein;<br>**PDBTitle:** two crystal structures of the cytoplasmic molybdate-binding2 protein modg suggest a novel cooperative binding mechanism3 and provide insights into ligand-binding specificity.4 peg-grown form with molybdate bound |
| 51 | c2b8kG_ | Alignment | not modelled | 60.4 | 14 | **PDB header:**transferase<br>**Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kda<br>**PDBTitle:** 12-subunit rna polymerase ii |
| 52 | d1guta_ | Alignment | not modelled | 59.4 | 18 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**Molybdate/tungstate binding protein MOP |
|  |  |  |  |  |  | **PDB header:**gene regulation<br>**Chain:** A: **PDB Molecule:**multidomain protein with s1 rna-binding |

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| 53 | c3go5A_ | Alignment | not modelled | 58.8 | 12 | domains;<br>**PDBTitle:** crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution |
| 54 | c3p8dB_ | Alignment | not modelled | 56.7 | 19 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**medulloblastoma antigen mu-mb-50.72;<br>**PDBTitle:** crystal structure of the second tudor domain of human phf20 (homodimer2 form) |
| 55 | d1sroa_ | Alignment | not modelled | 56.4 | 24 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 56 | d1b12a_ | Alignment | not modelled | 55.4 | 45 | **Fold:**LexA/Signal peptidase<br>**Superfamily:**LexA/Signal peptidase<br>**Family:**Type 1 signal peptidase |
| 57 | c3psiA_ | Alignment | not modelled | 54.5 | 7 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription elongation factor spt6;<br>**PDBTitle:** crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451) |
| 58 | d1q46a2 | Alignment | not modelled | 54.0 | 21 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 59 | c1nt9G_ | Alignment | not modelled | 52.9 | 14 | **PDB header:**transcription, transferase<br>**Chain:** G: **PDB Molecule:**dna-directed rna polymerase ii 19 kd polypeptide;<br>**PDBTitle:** complete 12-subunit rna polymerase ii |
| 60 | c2wg6L_ | Alignment | not modelled | 52.0 | 18 | **PDB header:**transcription,hydrolase<br>**Chain:** L: **PDB Molecule:**general control protein gcn4,<br>**PDBTitle:** proteasome-activating nucleotidase (pan) n-domain (57-134)2 from archaeoglobus fulgidus fused to gcn4, p61a mutant |
| 61 | c3qiiA_ | Alignment | not modelled | 51.0 | 19 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**phd finger protein 20;<br>**PDBTitle:** crystal structure of tudor domain 2 of human phd finger protein 20 |
| 62 | d2nn6g1 | Alignment | not modelled | 49.3 | 17 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 63 | c2qqsB_ | Alignment | not modelled | 45.5 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**jmjc domain-containing histone demethylation<br>**PDBTitle:** jmjd2a tandem tudor domains in complex with a trimethylated2 histone h4-k20 peptide |
| 64 | c2l66B_ | Alignment | not modelled | 45.4 | 38 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family;<br>**PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea. |
| 65 | d1v43a2 | Alignment | not modelled | 44.0 | 18 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**ABC-transporter additional domain |
| 66 | c1h9sA_ | Alignment | not modelled | 43.9 | 13 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**molybdenum transport protein mode;<br>**PDBTitle:** molybdate bound complex of dimop domain of mode from e.coli |
| 67 | d2z0sa1 | Alignment | not modelled | 43.7 | 13 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 68 | c3bdlA_ | Alignment | not modelled | 42.8 | 29 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**staphylococcal nuclease domain-containing<br>**PDBTitle:** crystal structure of a truncated human tudor-sn |
| 69 | c2pqaB_ | Alignment | not modelled | 41.3 | 19 | **PDB header:**replication<br>**Chain:** B: **PDB Molecule:**replication protein a 14 kda subunit;<br>**PDBTitle:** crystal structure of full-length human rpa 14/32 heterodimer |
| 70 | d1h9ma2 | Alignment | not modelled | 40.9 | 13 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**BiMOP, duplicated molybdate-binding domain |
| 71 | d1h9ma1 | Alignment | not modelled | 40.6 | 16 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**BiMOP, duplicated molybdate-binding domain |
| 72 | c2ba0A_ | Alignment | not modelled | 38.8 | 14 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**archeal exosome rna binding protein rrp4;<br>**PDBTitle:** archaeal exosome core |
| 73 | c2bh8B_ | Alignment | not modelled | 37.6 | 18 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**1b11;<br>**PDBTitle:** combinatorial protein 1b11 |
| 74 | c2nn6G_ | Alignment | not modelled | 37.1 | 15 | **PDB header:**hydrolase/transferase<br>**Chain:** G: **PDB Molecule:**exosome complex exonuclease rrp40;<br>**PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40 |
| 75 | c2eqsA_ | Alignment | not modelled | 37.1 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**atp-dependent rna helicase dhx8;<br>**PDBTitle:** solution structure of the s1 rna binding domain of human2 atp-dependent rna helicase dhx8 |
| 76 | c2z0sA_ | Alignment | not modelled | 35.9 | 12 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**probable exosome complex rna-binding protein 1;<br>**PDBTitle:** crystal structure of putative exosome complex rna-binding2 protein |
| 77 | d2pi2e1 | Alignment | not modelled | 34.3 | 19 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Single strand DNA-binding domain, SSB |
| 78 | d2nn6i1 | Alignment | not modelled | 32.4 | 14 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |

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| 79 | d2gnra1 | Alignment | not modelled | 31.0 | 12 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**SSO2064-like |
| 80 | c2nn6I_ | Alignment | not modelled | 28.2 | 13 | **PDB header:**hydrolase/transferase<br>**Chain:** I: **PDB Molecule:**3'-5' exoribonuclease csl4 homolog;<br>**PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40 |
| 81 | c2zooA_ | Alignment | not modelled | 28.0 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**probable nitrite reductase;<br>**PDBTitle:** crystal structure of nitrite reductase from pseudoalteromonas2 haloplanktis tac125 |
| 82 | d1e32a1 | Alignment | not modelled | 27.9 | 24 | **Fold:**Double psi beta-barrel<br>**Superfamily:**ADC-like<br>**Family:**Cdc48 N-terminal domain-like |
| 83 | c3h43F_ | Alignment | not modelled | 27.7 | 18 | **PDB header:**hydrolase<br>**Chain:** F: **PDB Molecule:**proteasome-activating nucleotidase;<br>**PDBTitle:** n-terminal domain of the proteasome-activating nucleotidase2 of methanocaldococcus jannaschii |
| 84 | c2xdpA_ | Alignment | not modelled | 27.5 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**lysine-specific demethylase 4c;<br>**PDBTitle:** crystal structure of the tudor domain of human jmjd2c |
| 85 | c3h0gS_ | Alignment | not modelled | 27.4 | 15 | **PDB header:**transcription<br>**Chain:** S: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb7;<br>**PDBTitle:** rna polymerase ii from schizosaccharomyces pombe |
| 86 | d2ba0a1 | Alignment | not modelled | 27.4 | 15 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 87 | d2grea1 | Alignment | not modelled | 26.8 | 24 | **Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like<br>**Superfamily:**Aminopeptidase/glucanase lid domain<br>**Family:**Aminopeptidase/glucanase lid domain |
| 88 | d3d31a1 | Alignment | not modelled | 26.4 | 17 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**ABC-transporter additional domain |
| 89 | d2ix0a2 | Alignment | not modelled | 25.6 | 13 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 90 | d1h9ra1 | Alignment | not modelled | 25.3 | 18 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**BiMOP, duplicated molybdate-binding domain |
| 91 | c1hh2P_ | Alignment | not modelled | 25.2 | 13 | **PDB header:**transcription regulation<br>**Chain:** P: **PDB Molecule:**n utilization substance protein a;<br>**PDBTitle:** crystal structure of nusa from thermotoga maritima |
| 92 | c3iz5Y_ | Alignment | not modelled | 24.8 | 27 | **PDB header:**ribosome<br>**Chain:** Y: **PDB Molecule:**60s ribosomal protein l26 (l24p);<br>**PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 93 | d2d9ra1 | Alignment | not modelled | 24.7 | 23 | **Fold:**Double-split beta-barrel<br>**Superfamily:**AF2212/PG0164-like<br>**Family:**PG0164-like |
| 94 | d1h9ra2 | Alignment | not modelled | 24.4 | 14 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**BiMOP, duplicated molybdate-binding domain |
| 95 | d2je6i1 | Alignment | not modelled | 23.2 | 19 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 96 | d2ja9a1 | Alignment | not modelled | 22.3 | 20 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 97 | d2nn6h1 | Alignment | not modelled | 21.2 | 21 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 98 | c1l2fA_ | Alignment | not modelled | 21.0 | 13 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**n utilization substance protein a;<br>**PDBTitle:** crystal structure of nusa from thermotoga maritima: a2 structure-based role of the n-terminal domain |
| 99 | d1dcza_ | Alignment | not modelled | 20.1 | 28 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Single hybrid motif<br>**Family:**Biotinyl/lipoyl-carrier proteins and domains |