Phyre2

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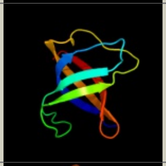
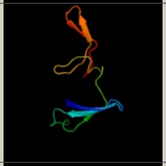
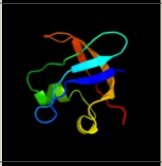
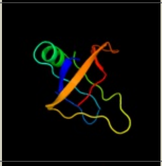
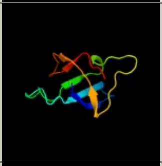
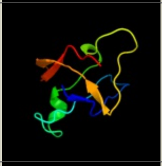
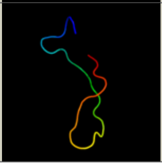
| Email | l.a.kelley@imperial.ac.uk |
| Description | P77214 |
| Date | Thu Jan 5 12:26:26 GMT 2012 |
| Unique Job ID | 4f62f0a24ea79a2f |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1zeqX_ | Alignment |  | 100.0 | 99 | **PDB header:**metal binding protein<br>**Chain:** X: **PDB Molecule:**cation efflux system protein cusf;<br>**PDBTitle:** 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli |
| 2 | c2l55A_ | Alignment |  | 99.9 | 27 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**silb,silver efflux protein, mfp component of the three<br>**PDBTitle:** solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans |
| 3 | c3camB_ | Alignment |  | 95.2 | 20 | **PDB header:**gene regulation<br>**Chain:** B: **PDB Molecule:**cold-shock domain family protein;<br>**PDBTitle:** crystal structure of the cold shock domain protein from neisseria2 meningitidis |
| 4 | c2k5nA_ | Alignment |  | 94.2 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative cold-shock protein;<br>**PDBTitle:** solution nmr structure of the n-terminal domain of protein2 eca1580 from erwinia carotovora, northeast structural3 genomics consortium target ewr156a |
| 5 | c3trzE_ | Alignment |  | 91.0 | 15 | **PDB header:**rna binding protein/rna<br>**Chain:** E: **PDB Molecule:**protein lin-28 homolog a;<br>**PDBTitle:** mouse lin28a in complex with let-7d microrna pre-element |
| 6 | d2es2a1 | Alignment |  | 90.9 | 16 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 7 | c2kcmA_ | Alignment |  | 87.9 | 18 | **PDB header:**nucleic acid binding protein<br>**Chain:** A: **PDB Molecule:**cold shock domain family protein;<br>**PDBTitle:** solution nmr structure of the n-terminal ob-domain of so_1732 from2 shewanella oneidensis. northeast structural genomics consortium3 target sor210a. |
| 8 | d1mjca_ | Alignment |  | 86.2 | 17 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 9 | d1c9oa_ | Alignment |  | 84.2 | 21 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 10 | c3aqqD_ | Alignment |  | 82.8 | 13 | **PDB header:**dna binding protein<br>**Chain:** D: **PDB Molecule:**calcium-regulated heat stable protein 1;<br>**PDBTitle:** crystal structure of human crhsp-24 |
| 11 | c2ytxA_ | Alignment |  | 81.6 | 18 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**cold shock domain-containing protein e1;<br>**PDBTitle:** solution structure of the second cold-shock domain of the human2 kiaa0885 protein (unr protein) |

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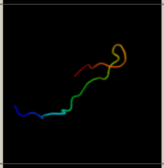
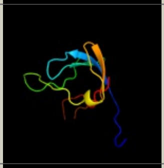
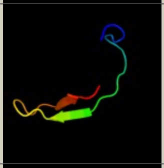
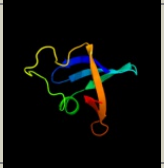
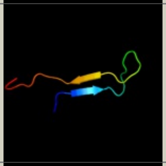
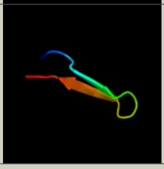
| 12 | d1g6pa_ | Alignment |  | 76.4 | 21 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 13 | d1h95a_ | Alignment |  | 76.2 | 15 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 14 | c3tdqB_ | Alignment |  | 75.0 | 21 | **PDB header:**cell adhesion<br>**Chain:** B: **PDB Molecule:**pily2 protein;<br>**PDBTitle:** crystal structure of a fimbrial biogenesis protein pily22 (pily2_pa4555) from pseudomonas aeruginosa pao1 at 2.10 a resolution |
| 15 | c2ytvA_ | Alignment |  | 72.6 | 15 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**cold shock domain-containing protein e1;<br>**PDBTitle:** solution structure of the fifth cold-shock domain of the human2 kiaa0885 protein (unr protein) |
| 16 | c1x65A_ | Alignment |  | 71.6 | 14 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**unr protein;<br>**PDBTitle:** solution structure of the third cold-shock domain of the human2 kiaa0885 protein (unr protein) |
| 17 | d1wfqa_ | Alignment |  | 68.3 | 21 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 18 | c3d0fA_ | Alignment |  | 68.1 | 8 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**penicillin-binding 1 transmembrane protein mrca;<br>**PDBTitle:** structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718 |
| 19 | d2f5va2 | Alignment |  | 62.8 | 23 | **Fold:**FAD-linked reductases, C-terminal domain<br>**Superfamily:**FAD-linked reductases, C-terminal domain<br>**Family:**GMC oxidoreductases |
| 20 | c2vc8A_ | Alignment |  | 61.9 | 28 | **PDB header:**protein-binding<br>**Chain:** A: **PDB Molecule:**enhancer of mrna-decapping protein 3;<br>**PDBTitle:** crystal structure of the lsm domain of human edc3 (enhancer2 of decapping 3) |
| 21 | c3mmlE_ | Alignment | not modelled | 60.2 | 10 | **PDB header:**hydrolase<br>**Chain:** E: **PDB Molecule:**allophanate hydrolase subunit 2;<br>**PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436 |
| 22 | c3a0jB_ | Alignment | not modelled | 57.8 | 20 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**cold shock protein;<br>**PDBTitle:** crystal structure of cold shock protein 1 from thermus2 thermophilus hb8 |
| 23 | c2khiA_ | Alignment | not modelled | 56.0 | 14 | **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 |
| 24 | d1wida_ | Alignment | not modelled | 55.2 | 21 | **Fold:**DNA-binding pseudobarrel domain<br>**Superfamily:**DNA-binding pseudobarrel domain<br>**Family:**B3 DNA binding domain |
| 25 | d1qbaa2 | Alignment | not modelled | 48.9 | 23 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**Carbohydrate-binding domain<br>**Family:**Bacterial chitobiase, n-terminal domain |
| 26 | c3kf6B_ | Alignment | not modelled | 47.6 | 29 | **PDB header:**structural protein<br>**Chain:** B: **PDB Molecule:**protein ten1;<br>**PDBTitle:** crystal structure of s. pombe stn1-ten1 complex |
| 27 | d1x9la_ | Alignment | not modelled | 43.4 | 17 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**DR1885-like metal-binding protein<br>**Family:**DR1885-like metal-binding protein |
| 28 | d2ba0a1 | Alignment | not modelled | 42.5 | 12 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| | | | | | | **Fold:**OB-fold |

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| 29 | d1hh2p1 | Alignment | not modelled | 39.8 | 23 | **Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 30 | c3u7zA_ | Alignment | not modelled | 39.4 | 14 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**putative metal binding protein rumgna_00854;<br>**PDBTitle:** crystal structure of a putative metal binding protein rumgna_008542 (zp_02040092.1) from ruminococcus gnavus atcc 29149 at 1.30 a3 resolution |
| 31 | c2vzaD_ | Alignment | not modelled | 38.9 | 31 | **PDB header:**cell adhesion<br>**Chain:** D: **PDB Molecule:**cell filamentation protein;<br>**PDBTitle:** type iv secretion system effector protein bepa |
| 32 | c2ytyA_ | Alignment | not modelled | 38.1 | 13 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**cold shock domain-containing protein e1;<br>**PDBTitle:** solution structure of the fourth cold-shock domain of the human2 kiaa0885 protein (unr protein) |
| 33 | c3m7aA_ | Alignment | not modelled | 37.7 | 22 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of saro_0823 (yp_496102.1) a protein of2 unknown function from novosphingobium aromaticivorans dsm3 12444 at 1.22 a resolution |
| 34 | c3ayhB_ | Alignment | not modelled | 36.6 | 19 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**dna-directed rna polymerase iii subunit rpc8;<br>**PDBTitle:** crystal structure of the c17/25 subcomplex from s. pombe rna2 polymerase iii |
| 35 | d1wi5a_ | Alignment | not modelled | 29.4 | 17 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 36 | d1gvha2 | Alignment | not modelled | 29.2 | 8 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Riboflavin synthase domain-like<br>**Family:**Ferredoxin reductase FAD-binding domain-like |
| 37 | d1gyca1 | Alignment | not modelled | 28.2 | 13 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Multidomain cupredoxins |
| 38 | c2k6zA_ | Alignment | not modelled | 28.1 | 21 | **PDB header:**metal transport<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha1943;<br>**PDBTitle:** solution structures of copper loaded form pcua (trans2 conformation of the peptide bond involving the nitrogen of3 p14) |
| 39 | c3i18A_ | Alignment | not modelled | 27.7 | 26 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**lmo2051 protein;<br>**PDBTitle:** crystal structure of the pdz domain of the sdrc-like protein2 (lmo2051) from listeria monocytogenes, northeast structural3 genomics consortium target lmr166b |
| 40 | d2phcb1 | Alignment | not modelled | 27.4 | 22 | **Fold:**Cyclophilin-like<br>**Superfamily:**Cyclophilin-like<br>**Family:**PH0987 C-terminal domain-like |
| 41 | c2phcB_ | Alignment | not modelled | 27.3 | 22 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein ph0987;<br>**PDBTitle:** crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii |
| 42 | d2f23a2 | Alignment | not modelled | 25.6 | 10 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**GreA transcript cleavage factor, C-terminal domain |
| 43 | c2h47C_ | Alignment | not modelled | 25.6 | 29 | **PDB header:**oxidoreductase/electron transport<br>**Chain:** C: **PDB Molecule:**azurin;<br>**PDBTitle:** crystal structure of an electron transfer complex between2 aromatic amine dephydrogenase and azurin from alcaligenes3 faecalis (form 1) |
| 44 | d1xnea_ | Alignment | not modelled | 25.5 | 24 | **Fold:**PUA domain-like<br>**Superfamily:**PUA domain-like<br>**Family:**ProFAR isomerase associated domain |
| 45 | d1qnia1 | Alignment | not modelled | 25.2 | 25 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Nitrosocyanin |
| 46 | d1u0la1 | Alignment | not modelled | 25.0 | 13 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 47 | c1t9hA_ | Alignment | not modelled | 24.1 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**probable gtpase engc;<br>**PDBTitle:** the crystal structure of yloq, a circularly permuted gtpase. |
| 48 | d2f1la1 | Alignment | not modelled | 23.9 | 35 | **Fold:**PRC-barrel domain<br>**Superfamily:**PRC-barrel domain<br>**Family:**RimM C-terminal domain-like |
| 49 | c2rf4A_ | Alignment | not modelled | 23.5 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dna-directed rna polymerase i subunit rpa4;<br>**PDBTitle:** crystal structure of the rna polymerase i subcomplex a14/43 |
| 50 | c3mmlD_ | Alignment | not modelled | 23.4 | 30 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**allophanate hydrolase subunit 1;<br>**PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436 |
| 51 | c3ie5A_ | Alignment | not modelled | 22.3 | 11 | **PDB header:**plant protein, biosynthetic protein<br>**Chain:** A: **PDB Molecule:**phenolic oxidative coupling protein hyp-1;<br>**PDBTitle:** crystal structure of hyp-1 protein from hypericum perforatum2 (st john's wort) involved in hypericin biosynthesis |
| 52 | d2cnda1 | Alignment | not modelled | 21.5 | 11 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Riboflavin synthase domain-like<br>**Family:**Ferredoxin reductase FAD-binding domain-like |
| 53 | d1v6ga2 | Alignment | not modelled | 21.4 | 42 | **Fold:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Superfamily:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Family:**LIM domain |

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| 54 | d1fwxa1 | Alignment | not modelled | 20.8 | 25 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Nitrosocyanin |
| 55 | c2aanA_ | Alignment | not modelled | 20.0 | 19 | **PDB header:**electron transport<br>**Chain:** A: **PDB Molecule:**auracyanin a;<br>**PDBTitle:** auracyanin a: a "blue" copper protein from the green thermophilic2 photosynthetic bacterium,chloroflexus aurantiacus |
| 56 | c2khjA_ | Alignment | not modelled | 19.7 | 15 | **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 |
| 57 | d1tyeb1 | Alignment | not modelled | 19.6 | 31 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Integrin domains<br>**Family:**Integrin domains |
| 58 | d1cqxa2 | Alignment | not modelled | 19.1 | 3 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Riboflavin synthase domain-like<br>**Family:**Ferredoxin reductase FAD-binding domain-like |
| 59 | c2zp2B_ | Alignment | not modelled | 19.1 | 44 | **PDB header:**transferase inhibitor<br>**Chain:** B: **PDB Molecule:**kinase a inhibitor;<br>**PDBTitle:** c-terminal domain of kipi from bacillus subtilis |
| 60 | d1joia_ | Alignment | not modelled | 18.8 | 13 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Plastocyanin/azurin-like |
| 61 | d1t9ha1 | Alignment | not modelled | 18.7 | 25 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 62 | c2p4vA_ | Alignment | not modelled | 18.3 | 13 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription elongation factor greb;<br>**PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution |
| 63 | d2ccwa1 | Alignment | not modelled | 18.2 | 13 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Plastocyanin/azurin-like |
| 64 | d2c35b1 | Alignment | not modelled | 17.8 | 17 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 65 | d1ndha1 | Alignment | not modelled | 17.4 | 18 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Riboflavin synthase domain-like<br>**Family:**Ferredoxin reductase FAD-binding domain-like |
| 66 | c3oepA_ | Alignment | not modelled | 17.2 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0988;<br>**PDBTitle:** crystal structure of ttha0988 in space group p43212 |
| 67 | d1cc3a_ | Alignment | not modelled | 17.1 | 27 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Plastocyanin/azurin-like |
| 68 | d1i94q_ | Alignment | not modelled | 16.9 | 22 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 69 | d1a5ra_ | Alignment | not modelled | 16.3 | 19 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**Ubiquitin-like<br>**Family:**Ubiquitin-related |
| 70 | d2etna2 | Alignment | not modelled | 16.1 | 10 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**GreA transcript cleavage factor, C-terminal domain |
| 71 | d2z0sa1 | Alignment | not modelled | 16.0 | 17 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 72 | d1ws8a_ | Alignment | not modelled | 15.7 | 31 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Plastocyanin/azurin-like |
| 73 | c2kjpA_ | Alignment | not modelled | 15.4 | 23 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein ylbl;<br>**PDBTitle:** solution structure of protein ylbl (bsu15050) from bacillus2 subtilis, northeast structural genomics consortium target3 sr713a |
| 74 | d1t2wa_ | Alignment | not modelled | 15.3 | 20 | **Fold:**Sortase<br>**Superfamily:**Sortase<br>**Family:**Sortase |
| 75 | c3pjyB_ | Alignment | not modelled | 15.0 | 15 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**hypothetical signal peptide protein;<br>**PDBTitle:** crystal structure of a putative transcription regulator (r01717) from2 sinorhizobium meliloti 1021 at 1.55 a resolution |
| 76 | d1k0ha_ | Alignment | not modelled | 15.0 | 6 | **Fold:**Phage tail proteins<br>**Superfamily:**Phage tail proteins<br>**Family:**gpFII-like |
| 77 | d1azca_ | Alignment | not modelled | 14.9 | 14 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Plastocyanin/azurin-like |
| 78 | d1q46a2 | Alignment | not modelled | 14.9 | 10 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 79 | d1gawa1 | Alignment | not modelled | 14.8 | 15 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Riboflavin synthase domain-like<br>**Family:**Ferredoxin reductase FAD-binding domain-like |
| 80 | c2w1kB_ | Alignment | not modelled | 14.7 | 17 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**putative sortase;<br>**PDBTitle:** crystal structure of sortase c-3 (srtc-3) from2 streptococcus pneumoniae |

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| 81 | d2z9ia1 | Alignment | not modelled | 14.5 | 16 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**HtrA-like serine proteases |
| 82 | d1jb9a1 | Alignment | not modelled | 14.5 | 28 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Riboflavin synthase domain-like<br>**Family:**Ferredoxin reductase FAD-binding domain-like |
| 83 | d1nppa2 | Alignment | not modelled | 14.1 | 35 | **Fold:**SH3-like barrel<br>**Superfamily:**Translation proteins SH3-like domain<br>**Family:**N-utilization substance G protein NusG, C-terminal domain |
| 84 | d1nz9a_ | Alignment | not modelled | 14.0 | 35 | **Fold:**SH3-like barrel<br>**Superfamily:**Translation proteins SH3-like domain<br>**Family:**N-utilization substance G protein NusG, C-terminal domain |
| 85 | c3qo6B_ | Alignment | not modelled | 13.9 | 17 | **PDB header:**photosynthesis<br>**Chain:** B: **PDB Molecule:**protease do-like 1, chloroplastic;<br>**PDBTitle:** crystal structure analysis of the plant protease deg1 |
| 86 | d1qfza1 | Alignment | not modelled | 13.6 | 19 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Riboflavin synthase domain-like<br>**Family:**Ferredoxin reductase FAD-binding domain-like |
| 87 | d2gnra1 | Alignment | not modelled | 13.3 | 10 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**SSO2064-like |
| 88 | c3mjjD_ | Alignment | not modelled | 13.3 | 20 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**predicted acetamidase/formamidase;<br>**PDBTitle:** crystal structure analysis of a recombinant predicted2 acetamidase/formamidase from the thermophile thermoanaerobacter3 tengcongensis |
| 89 | d2i6va1 | Alignment | not modelled | 13.2 | 8 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**EpsC C-terminal domain-like |
| 90 | d1n67a1 | Alignment | not modelled | 13.0 | 19 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**Bacterial adhesins<br>**Family:**Fibrinogen-binding domain |
| 91 | c2l66B_ | Alignment | not modelled | 12.9 | 32 | **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. |
| 92 | d1jzga_ | Alignment | not modelled | 12.6 | 27 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Plastocyanin/azurin-like |
| 93 | c2rcnA_ | Alignment | not modelled | 12.5 | 15 | **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. |
| 94 | d1t3qb1 | Alignment | not modelled | 12.2 | 12 | **Fold:**alpha/beta-Hammerhead<br>**Superfamily:**CO dehydrogenase molybdoprotein N-domain-like<br>**Family:**CO dehydrogenase molybdoprotein N-domain-like |
| 95 | c3ke2A_ | Alignment | not modelled | 12.2 | 31 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein yp_928783.1;<br>**PDBTitle:** crystal structure of a duf2131 family protein (sama_2911) from2 shewanella amazonensis sb2b at 2.50 a resolution |
| 96 | c3fp9E_ | Alignment | not modelled | 12.1 | 29 | **PDB header:**hydrolase<br>**Chain:** E: **PDB Molecule:**proteasome-associated atpase;<br>**PDBTitle:** crystal structure of intern domain of proteasome-associated2 atpase, mycobacterium tuberculosis |
| 97 | d1plaa_ | Alignment | not modelled | 12.1 | 27 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Plastocyanin/azurin-like |
| 98 | d1v10a2 | Alignment | not modelled | 11.8 | 14 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Multidomain cupredoxins |
| 99 | c2kw8A_ | Alignment | not modelled | 11.8 | 13 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**lpxtg-site transpeptidase family protein;<br>**PDBTitle:** solution structure of bacillus anthracis sortase a (srta)2 transpeptidase |