# Phyre2

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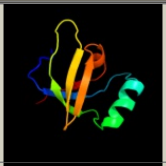
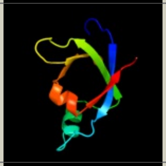
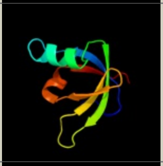
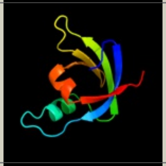
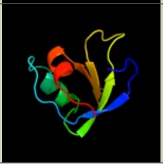
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0AEL3 |
| Date | Thu Jan 5 11:23:37 GMT 2012 |
| Unique Job ID | 4e3b14df6a10616b |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d2gcxa1 | Alignment |  | 99.9 | 89 | **Fold:**SH3-like barrel<br>**Superfamily:**C-terminal domain of transcriptional repressors<br>**Family:**FeoA-like |
| 2 | d2h3ja1 | Alignment |  | 99.9 | 53 | **Fold:**SH3-like barrel<br>**Superfamily:**C-terminal domain of transcriptional repressors<br>**Family:**FeoA-like |
| 3 | c2k5fA_ | Alignment |  | 99.8 | 28 | **PDB header:**metal transport<br>**Chain:** A: **PDB Molecule:**ferrous iron transport protein a;<br>**PDBTitle:** solution nmr structure of feoa protein from chlorobium2 tepidum. northeast structural genomics consortium target3 ctr121 |
| 4 | c2k5iA_ | Alignment |  | 99.8 | 34 | **PDB header:**metal transport<br>**Chain:** A: **PDB Molecule:**iron transport protein;<br>**PDBTitle:** solution structure of iron(ii) transport protein a from2 clostridium thermocellum , northeast structural genomics3 consortium (nesg) target vr131 |
| 5 | c2k4yA_ | Alignment |  | 99.8 | 30 | **PDB header:**metal transport<br>**Chain:** A: **PDB Molecule:**feoa-like protein;<br>**PDBTitle:** nmr structure of feoa-like protein from clostridium2 acetobutylicum: northeast structural genomics consortium3 target car178 |
| 6 | c3mhxB_ | Alignment |  | 99.7 | 21 | **PDB header:**metal transport<br>**Chain:** B: **PDB Molecule:**putative ferrous iron transport protein a;<br>**PDBTitle:** crystal structure of stenotrophomonas maltophilia feoa complexed with2 zinc: a unique procaryotic sh3 domain protein possibly acting as a3 bacterial ferrous iron transport activating factor |
| 7 | c2k5lA_ | Alignment |  | 99.7 | 30 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**feoa;<br>**PDBTitle:** solution nmr structure of protein feoa from clostridium2 thermocellum, northeast structural genomics consortium3 target cmr17 |
| 8 | c3e19D_ | Alignment |  | 99.7 | 27 | **PDB header:**transcription regulator, metal binding p<br>**Chain:** D: **PDB Molecule:**feoa;<br>**PDBTitle:** crystal structure of iron uptake regulatory protein (feoa) solved by2 sulfur sad in a monoclinic space group |
| 9 | c3hruA_ | Alignment |  | 99.5 | 10 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**metalloregulator scar;<br>**PDBTitle:** crystal structure of scar with bound zn2+ |
| 10 | c1fx7C_ | Alignment |  | 99.0 | 17 | **PDB header:**signaling protein<br>**Chain:** C: **PDB Molecule:**iron-dependent repressor ider;<br>**PDBTitle:** crystal structure of the iron-dependent regulator (ider)2 from mycobacterium tuberculosis |
| 11 | c1g3wA_ | Alignment |  | 98.4 | 17 | **PDB header:**gene regulation<br>**Chain:** A: **PDB Molecule:**diphtheria toxin repressor;<br>**PDBTitle:** cd-cys102ser dtxr |

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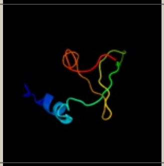
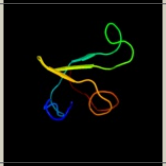
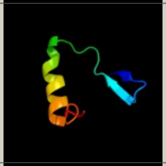
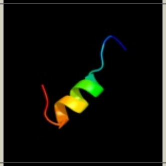
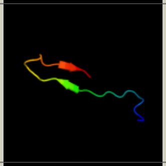
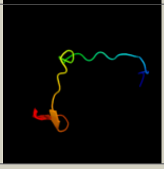
| 12 | c1qw1A_ | Alignment |  | 98.3 | 13 | **PDB header:**gene regulation<br>**Chain:** A: **PDB Molecule:**diphtheria toxin repressor;<br>**PDBTitle:** solution structure of the c-terminal domain of dtxr2 residues 110-226 |
| 13 | d1qw1a1 | Alignment |  | 91.0 | 15 | **Fold:**SH3-like barrel<br>**Superfamily:**C-terminal domain of transcriptional repressors<br>**Family:**FeoA-like |
| 14 | d1qvpa_ | Alignment |  | 79.5 | 17 | **Fold:**SH3-like barrel<br>**Superfamily:**C-terminal domain of transcriptional repressors<br>**Family:**FeoA-like |
| 15 | d1fx7a3 | Alignment |  | 74.7 | 18 | **Fold:**SH3-like barrel<br>**Superfamily:**C-terminal domain of transcriptional repressors<br>**Family:**FeoA-like |
| 16 | d1aopa2 | Alignment |  | 49.9 | 11 | **Fold:**Ferredoxin-like<br>**Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like<br>**Family:**Duplicated SiR/NiR-like domains 1 and 3 |
| 17 | c2ekkA_ | Alignment |  | 27.2 | 22 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**uba domain from e3 ubiquitin-protein ligase<br>**PDBTitle:** solution structure of ruh-074, a human uba domain |
| 18 | d1hmja_ | Alignment |  | 22.2 | 21 | **Fold:**RPB5-like RNA polymerase subunit<br>**Superfamily:**RPB5-like RNA polymerase subunit<br>**Family:**RPB5 |
| 19 | d1dzfa2 | Alignment |  | 21.7 | 20 | **Fold:**RPB5-like RNA polymerase subunit<br>**Superfamily:**RPB5-like RNA polymerase subunit<br>**Family:**RPB5 |
| 20 | d1o9ya_ | Alignment |  | 20.4 | 7 | **Fold:**Surface presentation of antigens (SPOA)<br>**Superfamily:**Surface presentation of antigens (SPOA)<br>**Family:**Surface presentation of antigens (SPOA) |
| 21 | d1eika_ | Alignment | not modelled | 19.7 | 17 | **Fold:**RPB5-like RNA polymerase subunit<br>**Superfamily:**RPB5-like RNA polymerase subunit<br>**Family:**RPB5 |
| 22 | c2pmzV_ | Alignment | not modelled | 18.4 | 17 | **PDB header:**translation, transferase<br>**Chain:** V: **PDB Molecule:**dna-directed rna polymerase subunit h;<br>**PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus |
| 23 | c1zrsB_ | Alignment | not modelled | 18.3 | 19 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** wild-type ld-carboxypeptidase |
| 24 | c2dagA_ | Alignment | not modelled | 18.0 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5;<br>**PDBTitle:** solution structure of the first uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5) |
| 25 | d1gjja2 | Alignment | not modelled | 16.5 | 18 | **Fold:**LEM/SAP HeH motif<br>**Superfamily:**LEM domain<br>**Family:**LEM domain |
| 26 | d1eeja2 | Alignment | not modelled | 15.4 | 26 | **Fold:**Cystatin-like<br>**Superfamily:**DsbC/DsbG N-terminal domain-like<br>**Family:**DsbC/DsbG N-terminal domain-like |
| 27 | c2iyjA_ | Alignment | not modelled | 14.5 | 26 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**thiol disulfide interchange protein dsbc;<br>**PDBTitle:** crystal structure of the n-terminal dimer domain of e.coli2 dsbc |
| 28 | d1zj8a1 | Alignment | not modelled | 14.0 | 18 | **Fold:**Ferredoxin-like<br>**Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like<br>**Family:**Duplicated SiR/NiR-like domains 1 and 3 |
| 29 | c1wx6A_ | Alignment | not modelled | 13.7 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**cytoplasmic protein nck2; |

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| 29 | c1wx6A_ | Alignment | not modelled | 13.7 | 15 | **PDBTitle:** solution structure of the sh3 domain of the human2 cytoplasmic protein nck2 |
| 30 | d1h9fa_ | Alignment | not modelled | 13.6 | 25 | **Fold:**LEM/SAP HeH motif<br>**Superfamily:**LEM domain<br>**Family:**LEM domain |
| 31 | c2glwA_ | Alignment | not modelled | 13.3 | 31 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**92aa long hypothetical protein;<br>**PDBTitle:** the solution structure of phs018 from pyrococcus horikoshii |
| 32 | d1y8xb1 | Alignment | not modelled | 13.2 | 21 | **Fold:**Activating enzymes of the ubiquitin-like proteins<br>**Superfamily:**Activating enzymes of the ubiquitin-like proteins<br>**Family:**Ubiquitin activating enzymes (UBA) |
| 33 | c3h0gE_ | Alignment | not modelled | 12.1 | 24 | **PDB header:**transcription<br>**Chain:** E: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii<br>**PDBTitle:** rna polymerase ii from schizosaccharomyces pombe |
| 34 | d1jeia_ | Alignment | not modelled | 12.1 | 9 | **Fold:**LEM/SAP HeH motif<br>**Superfamily:**LEM domain<br>**Family:**LEM domain |
| 35 | c2dakA_ | Alignment | not modelled | 11.9 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5;<br>**PDBTitle:** solution structure of the second uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5) |
| 36 | d1o6aa_ | Alignment | not modelled | 11.6 | 19 | **Fold:**Surface presentation of antigens (SPOA)<br>**Superfamily:**Surface presentation of antigens (SPOA)<br>**Family:**Surface presentation of antigens (SPOA) |
| 37 | c3og5A_ | Alignment | not modelled | 11.4 | 14 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**outer membrane protein assembly complex, yaet protein;<br>**PDBTitle:** crystal structure of bama potra45 tandem |
| 38 | d1t3ba2 | Alignment | not modelled | 11.3 | 25 | **Fold:**Cystatin-like<br>**Superfamily:**DsbC/DsbG N-terminal domain-like<br>**Family:**DsbC/DsbG N-terminal domain-like |
| 39 | d1guta_ | Alignment | not modelled | 11.1 | 18 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**Molybdate/tungstate binding protein MOP |
| 40 | c1y1yE_ | Alignment | not modelled | 10.4 | 20 | **PDB header:**transferase/transcription/dna-rna hybrid<br>**Chain:** E: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii 27<br>**PDBTitle:** rna polymerase ii-tfiis-dna/rna complex |
| 41 | c2crnA_ | Alignment | not modelled | 10.2 | 35 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**ubash3a protein;<br>**PDBTitle:** solution structure of the uba domain of human ubash3a2 protein |
| 42 | d2daha1 | Alignment | not modelled | 10.2 | 44 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 43 | d1oqya2 | Alignment | not modelled | 10.0 | 30 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 44 | d2auna2 | Alignment | not modelled | 9.9 | 19 | **Fold:**Flavodoxin-like<br>**Superfamily:**Class I glutamine amidotransferase-like<br>**Family:**LD-carboxypeptidase A N-terminal domain-like |
| 45 | d2crna1 | Alignment | not modelled | 9.7 | 38 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 46 | d2nzul1 | Alignment | not modelled | 9.6 | 21 | **Fold:**HPr-like<br>**Superfamily:**HPr-like<br>**Family:**HPr-like |
| 47 | d1veka_ | Alignment | not modelled | 9.4 | 23 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 48 | d3c7bb2 | Alignment | not modelled | 9.3 | 9 | **Fold:**Ferredoxin-like<br>**Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like<br>**Family:**DsrA/DsrB N-terminal-domain-like |
| 49 | d2bwba1 | Alignment | not modelled | 9.2 | 22 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 50 | d1udxa3 | Alignment | not modelled | 8.9 | 19 | **Fold:**Obg GTP-binding protein C-terminal domain<br>**Superfamily:**Obg GTP-binding protein C-terminal domain<br>**Family:**Obg GTP-binding protein C-terminal domain |
| 51 | d1ifya_ | Alignment | not modelled | 8.8 | 25 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 52 | c3bkhA_ | Alignment | not modelled | 8.7 | 12 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lytic transglycosylase;<br>**PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144 |
| 53 | d2g3qa1 | Alignment | not modelled | 8.5 | 25 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 54 | c2jy5A_ | Alignment | not modelled | 8.4 | 33 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**ubiquilin-1;<br>**PDBTitle:** nmr structure of ubiquilin 1 uba domain |
| 55 | d1wjua_ | Alignment | not modelled | 8.4 | 17 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**Ubiquitin-like<br>**Family:**Ubiquitin-related |
| 56 | c1wr1B_ | Alignment | not modelled | 8.2 | 22 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**ubiquitin-like protein dsk2; |

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| | | | | | | **PDBTitle:** the complex sturcture of dsk2p uba with ubiquitin |
| 57 | d1whca_ | Alignment | not modelled | 8.1 | 18 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 58 | c2llgA_ | Alignment | not modelled | 8.1 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** nmr structure of the protein np_814968.1 from enterococcus faecalis |
| 59 | c3le1B_ | Alignment | not modelled | 8.1 | 20 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**phosphotransferase system, hpr-related proteins;<br>**PDBTitle:** crystal structure of apohpr monomer from thermoanaerobacter2 tengcongensis |
| 60 | d2dnaa1 | Alignment | not modelled | 8.1 | 22 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 61 | d1cm3a_ | Alignment | not modelled | 8.1 | 21 | **Fold:**HPr-like<br>**Superfamily:**HPr-like<br>**Family:**HPr-like |
| 62 | d2v4jb2 | Alignment | not modelled | 8.0 | 17 | **Fold:**Ferredoxin-like<br>**Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like<br>**Family:**DsrA/DsrB N-terminal-domain-like |
| 63 | d1g3wa3 | Alignment | not modelled | 7.9 | 20 | **Fold:**SH3-like barrel<br>**Superfamily:**C-terminal domain of transcriptional repressors<br>**Family:**FeoA-like |
| 64 | d1veja1 | Alignment | not modelled | 7.9 | 33 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 65 | d2nr4a1 | Alignment | not modelled | 7.7 | 25 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**MTH863-like |
| 66 | d1fr3a_ | Alignment | not modelled | 7.5 | 18 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**Molybdate/tungstate binding protein MOP |
| 67 | c2dahA_ | Alignment | not modelled | 7.5 | 44 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**ubiquilin-3;<br>**PDBTitle:** solution structure of the c-terminal uba domain in the2 human ubiquilin 3 |
| 68 | c2daiA_ | Alignment | not modelled | 7.3 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**ubiquitin associated domain containing 1;<br>**PDBTitle:** solution structure of the first uba domain in the human2 ubiquitin associated domain containing 1 (ubadc1) |
| 69 | c2cwbA_ | Alignment | not modelled | 7.1 | 33 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**chimera of immunoglobulin g binding protein g<br>**PDBTitle:** solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin |
| 70 | d2cp8a1 | Alignment | not modelled | 7.1 | 23 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 71 | c2dnaA_ | Alignment | not modelled | 6.9 | 22 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**unnamed protein product;<br>**PDBTitle:** solution structure of rsgi ruh-056, a uba domain from mouse2 cdna |
| 72 | d1ka5a_ | Alignment | not modelled | 6.9 | 16 | **Fold:**HPr-like<br>**Superfamily:**HPr-like<br>**Family:**HPr-like |
| 73 | c3ihsB_ | Alignment | not modelled | 6.9 | 21 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**phosphocarrier protein hpr;<br>**PDBTitle:** crystal structure of a phosphocarrier protein hpr from2 bacillus anthracis str. ames |
| 74 | d2hpra_ | Alignment | not modelled | 6.7 | 21 | **Fold:**HPr-like<br>**Superfamily:**HPr-like<br>**Family:**HPr-like |
| 75 | d1mo1a_ | Alignment | not modelled | 6.7 | 21 | **Fold:**HPr-like<br>**Superfamily:**HPr-like<br>**Family:**HPr-like |
| 76 | c2kj6A_ | Alignment | not modelled | 6.6 | 16 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**tubulin folding cofactor b;<br>**PDBTitle:** nmr solution structure of a tubulin folding cofactor b2 obtained from arabidopsis thaliana: northeast structural3 genomics consortium target ar3436a |
| 77 | d1cz5a1 | Alignment | not modelled | 6.5 | 12 | **Fold:**Double psi beta-barrel<br>**Superfamily:**ADC-like<br>**Family:**Cdc48 N-terminal domain-like |
| 78 | c2ebpA_ | Alignment | not modelled | 6.5 | 9 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**sam and sh3 domain-containing protein 1;<br>**PDBTitle:** solution structure of the sh3 domain from human sam and sh32 domain containing protein 1 |
| 79 | d1oqya1 | Alignment | not modelled | 6.5 | 20 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 80 | d1udla_ | Alignment | not modelled | 6.4 | 5 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 81 | d1wiva_ | Alignment | not modelled | 6.4 | 31 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| | | | | | | **PDB header:**signaling protein |

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| 82 | c1x69A_ | Alignment | not modelled | 6.4 | 11 | **Chain:** A: **PDB Molecule:**cortactin isoform a;<br>**PDBTitle:** solution structures of the sh3 domain of human src2 substrate cortactin |
| 83 | d1wx8a1 | Alignment | not modelled | 6.4 | 39 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**Ubiquitin-like<br>**Family:**Ubiquitin-related |
| 84 | d1ja1a1 | Alignment | not modelled | 6.4 | 14 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Riboflavin synthase domain-like<br>**Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like |
| 85 | d1qmga2 | Alignment | not modelled | 6.2 | 31 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 86 | c3e4fB_ | Alignment | not modelled | 6.2 | 25 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**aminoglycoside n3-acetyltransferase;<br>**PDBTitle:** crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis |
| 87 | d1zvvj1 | Alignment | not modelled | 6.2 | 21 | **Fold:**HPr-like<br>**Superfamily:**HPr-like<br>**Family:**HPr-like |
| 88 | d1h9ra1 | Alignment | not modelled | 6.2 | 27 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**BiMOP, duplicated molybdate-binding domain |
| 89 | d1qr5a_ | Alignment | not modelled | 6.1 | 16 | **Fold:**HPr-like<br>**Superfamily:**HPr-like<br>**Family:**HPr-like |
| 90 | d2cpwa1 | Alignment | not modelled | 6.1 | 50 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 91 | d1h9ra2 | Alignment | not modelled | 5.9 | 12 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**BiMOP, duplicated molybdate-binding domain |
| 92 | d1ptfa_ | Alignment | not modelled | 5.8 | 25 | **Fold:**HPr-like<br>**Superfamily:**HPr-like<br>**Family:**HPr-like |
| 93 | c2cp8A_ | Alignment | not modelled | 5.8 | 23 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**next to brca1 gene 1 protein;<br>**PDBTitle:** solution structure of the rsgi ruh-046, a uba domain from2 human next to brca1 gene 1 protein (kiaa0049 protein)3 r923h variant |
| 94 | c2kdiA_ | Alignment | not modelled | 5.7 | 17 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**ubiquitin, vacuolar protein sorting-associated<br>**PDBTitle:** solution structure of a ubiquitin/uim fusion protein |
| 95 | c2kzrA_ | Alignment | not modelled | 5.7 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**ubiquitin thioesterase otu1;<br>**PDBTitle:** solution nmr structure of ubiquitin thioesterase otu1 (ec 3.1.2.-)2 from mus musculus, northeast structural genomics consortium target3 mmt2a |
| 96 | d1pcha_ | Alignment | not modelled | 5.6 | 5 | **Fold:**HPr-like<br>**Superfamily:**HPr-like<br>**Family:**HPr-like |
| 97 | c2lf6A_ | Alignment | not modelled | 5.6 | 33 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**effector protein hopab1;<br>**PDBTitle:** solution nmr structure of hopabpph1448_220_320 from pseudomonas2 syringae pv. phaseolicola str. 1448a, midwest center for structural3 genomics target apc40132.4 and northeast structural genomics4 consortium target pst3a |
| 98 | c1t0yA_ | Alignment | not modelled | 5.5 | 29 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**tubulin folding cofactor b;<br>**PDBTitle:** solution structure of a ubiquitin-like domain from tubulin-2 binding cofactor b |
| 99 | d1t0ya_ | Alignment | not modelled | 5.5 | 29 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**Ubiquitin-like<br>**Family:**Ubiquitin-related |