Phyre2

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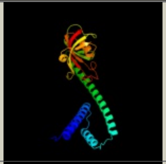
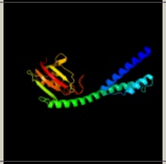
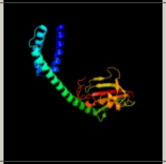
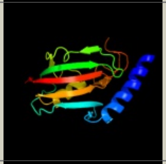
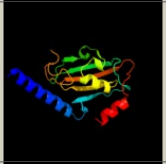
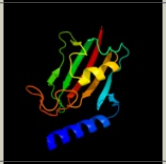
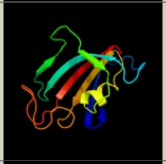
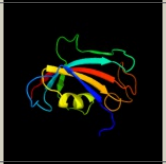
| Email | l.a.kelley@imperial.ac.uk |
| Description | P45523 |
| Date | Thu Jan 5 12:02:53 GMT 2012 |
| Unique Job ID | 9cb94ba84603fa5b |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1q6ha_ | Alignment |  | 100.0 | 99 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 2 | c1q6uA_ | Alignment |  | 100.0 | 100 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase fkpa;<br>**PDBTitle:** crystal structure of fkpa from escherichia coli |
| 3 | d1fd9a_ | Alignment |  | 100.0 | 37 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 4 | c2vcdA_ | Alignment |  | 100.0 | 41 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**outer membrane protein mip;<br>**PDBTitle:** solution structure of the fkbp-domain of legionella2 pneumophila mip in complex with rapamycin |
| 5 | d1jvwa_ | Alignment |  | 100.0 | 38 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 6 | c3oe2A_ | Alignment |  | 100.0 | 38 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase;<br>**PDBTitle:** 1.6 a crystal structure of peptidyl-prolyl cis-trans isomerase ppiase2 from pseudomonas syringae pv. tomato str. dc3000 (pspto dc3000) |
| 7 | c2lgoA_ | Alignment |  | 100.0 | 45 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**fkbp;<br>**PDBTitle:** solution nmr structure of a fkbp-type peptidyl-prolyl cis-trans2 isomerase from giardia lamblia, seattle structural genomics center3 for infectious disease target gilaa.00840.a |
| 8 | d1yata_ | Alignment |  | 100.0 | 46 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 9 | c2ke0A_ | Alignment |  | 100.0 | 50 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase;<br>**PDBTitle:** solution structure of peptidyl-prolyl cis-trans isomerase from2 burkholderia pseudomallei |
| 10 | d1q1ca1 | Alignment |  | 100.0 | 42 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 11 | c2jwxA_ | Alignment |  | 100.0 | 20 | **PDB header:**apoptosis, isomerase<br>**Chain:** A: **PDB Molecule:**fk506-binding protein 8 variant;<br>**PDBTitle:** solution structure of the n-terminal domain of human fkbp382 (fkbp38ntd) |

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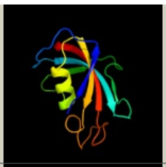
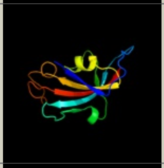
| 12 | d1c9ha_ | Alignment |  | 100.0 | 46 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 13 | d1r9ha_ | Alignment |  | 100.0 | 39 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 14 | c2f4eB_ | Alignment |  | 100.0 | 23 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**atfkbp42;<br>**PDBTitle:** n-terminal domain of fkbp42 from arabidopsis thaliana |
| 15 | c3o5fA_ | Alignment |  | 100.0 | 47 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase fkbp5;<br>**PDBTitle:** fk1 domain of fkbp51, crystal form vii |
| 16 | c2vn1A_ | Alignment |  | 100.0 | 35 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**70 kda peptidylprolyl isomerase;<br>**PDBTitle:** crystal structure of the fk506-binding domain of plasmodium2 falciparum fkbp35 in complex with fk506 |
| 17 | c1rouA_ | Alignment |  | 100.0 | 43 | **PDB header:**rotamase (isomerase)<br>**Chain:** A: **PDB Molecule:**fkbp59-i;<br>**PDBTitle:** structure of fkbp59-i, the n-terminal domain of a 59 kda2 fk506-binding protein, nmr, 22 structures |
| 18 | d2ppna1 | Alignment |  | 100.0 | 49 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 19 | d1u79a_ | Alignment |  | 100.0 | 45 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 20 | d1kt0a3 | Alignment |  | 100.0 | 24 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 21 | d1kt1a3 | Alignment | not modelled | 100.0 | 23 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 22 | c3b7xA_ | Alignment | not modelled | 100.0 | 29 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**fk506-binding protein 6;<br>**PDBTitle:** crystal structure of human fk506-binding protein 6 |
| 23 | c3o5dB_ | Alignment | not modelled | 100.0 | 46 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase fkbp5;<br>**PDBTitle:** crystal structure of a fragment of fkbp51 comprising the fk1 and fk22 domains |
| 24 | c1q1cA_ | Alignment | not modelled | 99.9 | 38 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**fk506-binding protein 4;<br>**PDBTitle:** crystal structure of n(1-260) of human fkbp52 |
| 25 | c2d9fA_ | Alignment | not modelled | 99.9 | 21 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**fk506-binding protein 8 variant;<br>**PDBTitle:** solution structure of ruh-047, an fkbp domain from human2 cdna |
| 26 | d1pbka_ | Alignment | not modelled | 99.9 | 47 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 27 | c2pbcD_ | Alignment | not modelled | 99.9 | 46 | **PDB header:**isomerase<br>**Chain:** D: **PDB Molecule:**fk506-binding protein 2;<br>**PDBTitle:** fk506-binding protein 2 |
| 28 | d1q1ca2 | Alignment | not modelled | 99.9 | 24 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| | | | | | | **PDB header:**isomerase |

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| 29 | c3jxvA_ | Alignment | not modelled | 99.9 | 31 | **Chain:** A: **PDB Molecule:**70 kda peptidyl-prolyl isomerase;<br>**PDBTitle:** crystal structure of the 3 fkbp domains of wheat fkbp73 |
| 30 | c2if4A_ | Alignment | not modelled | 99.9 | 20 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**atfkbp42;<br>**PDBTitle:** crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana |
| 31 | d1kt0a2 | Alignment | not modelled | 99.9 | 44 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 32 | d1kt1a2 | Alignment | not modelled | 99.9 | 41 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 33 | c1qz2B_ | Alignment | not modelled | 99.9 | 24 | **PDB header:**isomerase/chaperone<br>**Chain:** B: **PDB Molecule:**fk506-binding protein 4;<br>**PDBTitle:** crystal structure of fkbp52 c-terminal domain complex with2 the c-terminal peptide meevd of hsp90 |
| 34 | c1kt0A_ | Alignment | not modelled | 99.9 | 24 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**51 kda fk506-binding protein;<br>**PDBTitle:** structure of the large fkbp-like protein, fkbp51, involved in steroid2 receptor complexes |
| 35 | c2kr7A_ | Alignment | not modelled | 99.8 | 23 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase slyd;<br>**PDBTitle:** solution structure of helicobacter pylori slyd |
| 36 | c2k8iA_ | Alignment | not modelled | 99.7 | 26 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase;<br>**PDBTitle:** solution structure of e.coli slyd |
| 37 | c2kfwA_ | Alignment | not modelled | 99.7 | 27 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase<br>**PDBTitle:** solution structure of full-length slyd from e.coli |
| 38 | c3pr9A_ | Alignment | not modelled | 99.7 | 31 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase;<br>**PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26 |
| 39 | d1ix5a_ | Alignment | not modelled | 99.7 | 36 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 40 | c3prdA_ | Alignment | not modelled | 99.7 | 36 | **PDB header:**chaperone, isomerase<br>**Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase;<br>**PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26 |
| 41 | c3cgnA_ | Alignment | not modelled | 99.6 | 35 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase;<br>**PDBTitle:** crystal structure of thermophilic slyd |
| 42 | c1hxvA_ | Alignment | not modelled | 99.5 | 20 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**trigger factor;<br>**PDBTitle:** ppiase domain of the mycoplasma genitalium trigger factor |
| 43 | d1hxva_ | Alignment | not modelled | 99.5 | 20 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 44 | d1l1pa_ | Alignment | not modelled | 99.4 | 23 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 45 | d1w26a3 | Alignment | not modelled | 99.3 | 22 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 46 | d1t11a3 | Alignment | not modelled | 99.3 | 21 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 47 | c1w26B_ | Alignment | not modelled | 98.6 | 20 | **PDB header:**chaperone<br>**Chain:** B: **PDB Molecule:**trigger factor;<br>**PDBTitle:** trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins |
| 48 | c1t11A_ | Alignment | not modelled | 98.4 | 20 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**trigger factor;<br>**PDBTitle:** trigger factor |
| 49 | c3gtyX_ | Alignment | not modelled | 97.6 | 19 | **PDB header:**chaperone/ribosomal protein<br>**Chain:** X: **PDB Molecule:**trigger factor;<br>**PDBTitle:** promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone |
| 50 | c3htxA_ | Alignment | not modelled | 96.4 | 13 | **PDB header:**transferase/rna<br>**Chain:** A: **PDB Molecule:**hen1;<br>**PDBTitle:** crystal structure of small rna methyltransferase hen1 |
| 51 | d1jnsa_ | Alignment | not modelled | 46.7 | 12 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 52 | c2a2bA_ | Alignment | not modelled | 41.4 | 40 | **PDB header:**antibiotic<br>**Chain:** A: **PDB Molecule:**bacteriocin curvacin a;<br>**PDBTitle:** curvacin a |
| 53 | d2diga1 | Alignment | not modelled | 29.8 | 43 | **Fold:**SH3-like barrel<br>**Superfamily:**Tudor/PWWP/MBT<br>**Family:**Tudor domain |
| 54 | d1pina2 | Alignment | not modelled | 29.2 | 10 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 55 | d2pv2a1 | Alignment | not modelled | 28.8 | 17 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |

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| 56 | c2rqsA_ | Alignment | not modelled | 28.8 | 12 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**parvulin-like peptidyl-prolyl isomerase;<br>**PDBTitle:** 3d structure of pin from the psychrophilic archeon cenarcheaum2 symbiosum (cspin) |
| 57 | d1j6ya_ | Alignment | not modelled | 26.9 | 14 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 58 | d1ueba1 | Alignment | not modelled | 26.8 | 23 | **Fold:**SH3-like barrel<br>**Superfamily:**Translation proteins SH3-like domain<br>**Family:**eIF5a N-terminal domain-like |
| 59 | c3gpkA_ | Alignment | not modelled | 23.3 | 14 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**ppic-type peptidyl-prolyl cis-trans isomerase;<br>**PDBTitle:** crystal structure of ppic-type peptidyl-prolyl cis-trans isomerase2 domain at 1.55a resolution. |
| 60 | c3a5zF_ | Alignment | not modelled | 21.8 | 17 | **PDB header:**ligase<br>**Chain:** F: **PDB Molecule:**elongation factor p;<br>**PDBTitle:** crystal structure of escherichia coli genx in complex with elongation2 factor p |
| 61 | d1o65a_ | Alignment | not modelled | 20.3 | 23 | **Fold:**PK beta-barrel domain-like<br>**Superfamily:**PK beta-barrel domain-like<br>**Family:**MOSC (MOCO sulphurase C-terminal) domain |
| 62 | c2eqmA_ | Alignment | not modelled | 20.1 | 9 | **PDB header:**transcription<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 [homo sapiens] |
| 63 | c1yw5A_ | Alignment | not modelled | 18.0 | 17 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**peptidyl prolyl cis/trans isomerase;<br>**PDBTitle:** peptidyl-prolyl isomerase ess1 from candida albicans |
| 64 | d1m5ya3 | Alignment | not modelled | 17.8 | 14 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 65 | d1gpla1 | Alignment | not modelled | 16.6 | 14 | **Fold:**Lipase/lipooxygenase domain (PLAT/LH2 domain)<br>**Superfamily:**Lipase/lipooxygenase domain (PLAT/LH2 domain)<br>**Family:**Colipase-binding domain |
| 66 | d1orua_ | Alignment | not modelled | 16.0 | 36 | **Fold:**PK beta-barrel domain-like<br>**Superfamily:**PK beta-barrel domain-like<br>**Family:**MOSC (MOCO sulphurase C-terminal) domain |
| 67 | d1fcda2 | Alignment | not modelled | 15.1 | 20 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD/NAD-linked reductases, N-terminal and central domains |
| 68 | c3qgaD_ | Alignment | not modelled | 14.8 | 22 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**fusion of urease beta and gamma subunits;<br>**PDBTitle:** 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae |
| 69 | d2hd9a1 | Alignment | not modelled | 14.7 | 22 | **Fold:**PUA domain-like<br>**Superfamily:**PUA domain-like<br>**Family:**Atu2648/PH1033-like |
| 70 | c1zk6A_ | Alignment | not modelled | 12.6 | 9 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**foldase protein prsa;<br>**PDBTitle:** nmr solution structure of b. subtilis prsa ppiase |
| 71 | d1ejxb_ | Alignment | not modelled | 11.1 | 32 | **Fold:**beta-clip<br>**Superfamily:**Urease, beta-subunit<br>**Family:**Urease, beta-subunit |
| 72 | c3rfwA_ | Alignment | not modelled | 11.0 | 16 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**cell-binding factor 2;<br>**PDBTitle:** the virulence factor peb4 and the periplasmic protein cj1289 are two2 structurally-related sura-like chaperones in the human pathogen3 campylobacter jejuni |
| 73 | d2f8la1 | Alignment | not modelled | 10.6 | 18 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**N-6 DNA Methylase-like |
| 74 | d2vj0a1 | Alignment | not modelled | 10.6 | 17 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Clathrin adaptor appendage domain<br>**Family:**Alpha-adaptin ear subdomain-like |
| 75 | d2ih2a1 | Alignment | not modelled | 9.8 | 18 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**DNA methylase TaqI, N-terminal domain |
| 76 | d4ubpb_ | Alignment | not modelled | 9.8 | 28 | **Fold:**beta-clip<br>**Superfamily:**Urease, beta-subunit<br>**Family:**Urease, beta-subunit |
| 77 | d1e9ya1 | Alignment | not modelled | 9.3 | 36 | **Fold:**beta-clip<br>**Superfamily:**Urease, beta-subunit<br>**Family:**Urease, beta-subunit |
| 78 | c3q1jA_ | Alignment | not modelled | 8.6 | 15 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**phd finger protein 20;<br>**PDBTitle:** crystal structure of tudor domain 1 of human phd finger protein 20 |
| 79 | c2jzvA_ | Alignment | not modelled | 7.5 | 17 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**foldase protein prsa;<br>**PDBTitle:** solution structure of s. aureus prsa-ppiase |
| 80 | d1etha1 | Alignment | not modelled | 7.3 | 14 | **Fold:**Lipase/lipooxygenase domain (PLAT/LH2 domain)<br>**Superfamily:**Lipase/lipooxygenase domain (PLAT/LH2 domain)<br>**Family:**Colipase-binding domain |
| 81 | c1f8aB_ | Alignment | not modelled | 7.2 | 14 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase nima-<br>**PDBTitle:** structural basis for the phosphoserine-proline recognition2 by group iv ww domains |

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| 82 | d1qfja1 | Alignment | not modelled | 7.1 | 10 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Riboflavin synthase domain-like<br>**Family:**Ferredoxin reductase FAD-binding domain-like |
| 83 | c3on1A_ | Alignment | not modelled | 6.9 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**bh2414 protein;<br>**PDBTitle:** the structure of a protein with unknown function from bacillus2 halodurans c |
| 84 | d1eq3a_ | Alignment | not modelled | 6.9 | 13 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 85 | c1mv3A_ | Alignment | not modelled | 6.6 | 28 | **PDB header:**endocytosis/exocytosis<br>**Chain:** A: **PDB Molecule:**myc box dependent interacting protein 1;<br>**PDBTitle:** nmr structure of the tumor suppressor bin1: alternative2 splicing in melanoma and interaction with c-myc |
| 86 | c3ikmD_ | Alignment | not modelled | 6.6 | 50 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**dna polymerase subunit gamma-1;<br>**PDBTitle:** crystal structure of human mitochondrial dna polymerase2 holoenzyme |
| 87 | d2j44a1 | Alignment | not modelled | 6.6 | 50 | **Fold:**Prealbumin-like<br>**Superfamily:**Starch-binding domain-like<br>**Family:**PUD-like |
| 88 | c3oyyA_ | Alignment | not modelled | 6.4 | 14 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**elongation factor p;<br>**PDBTitle:** structure of pseudomonas aeruginosa elongation factor p |
| 89 | c2p5dA_ | Alignment | not modelled | 6.3 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**upf0310 protein mjecl36;<br>**PDBTitle:** crystal structure of mjecl36 from methanocaldococcus2 jannaschii dsm 2661 |
| 90 | c2wdtA_ | Alignment | not modelled | 6.2 | 20 | **PDB header:**hydrolase/protein binding<br>**Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase l3;<br>**PDBTitle:** crystal structure of plasmodium falciparum uchl3 in complex2 with the suicide inhibitor ubvme |
| 91 | d1js8a2 | Alignment | not modelled | 6.2 | 27 | **Fold:**C-terminal domain of mollusc hemocyanin<br>**Superfamily:**C-terminal domain of mollusc hemocyanin<br>**Family:**C-terminal domain of mollusc hemocyanin |
| 92 | d2qqra2 | Alignment | not modelled | 6.2 | 18 | **Fold:**SH3-like barrel<br>**Superfamily:**Tudor/PWWP/MBT<br>**Family:**Tudor domain |
| 93 | d1p7ka1 | Alignment | not modelled | 6.1 | 10 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Immunoglobulin<br>**Family:**V set domains (antibody variable domain-like) |
| 94 | d1xd3a_ | Alignment | not modelled | 6.0 | 20 | **Fold:**Cysteine proteinases<br>**Superfamily:**Cysteine proteinases<br>**Family:**Ubiquitin carboxyl-terminal hydrolase UCH-L |
| 95 | d1v29a_ | Alignment | not modelled | 5.9 | 17 | **Fold:**Nitrile hydratase alpha chain<br>**Superfamily:**Nitrile hydratase alpha chain<br>**Family:**Nitrile hydratase alpha chain |
| 96 | d2qqsa2 | Alignment | not modelled | 5.8 | 18 | **Fold:**SH3-like barrel<br>**Superfamily:**Tudor/PWWP/MBT<br>**Family:**Tudor domain |
| 97 | c1e9zA_ | Alignment | not modelled | 5.8 | 36 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**urease subunit alpha;<br>**PDBTitle:** crystal structure of helicobacter pylori urease |
| 98 | c1m5yB_ | Alignment | not modelled | 5.7 | 17 | **PDB header:**isomerase, cell cycle<br>**Chain:** B: **PDB Molecule:**survival protein sura;<br>**PDBTitle:** crystallographic structure of sura, a molecular chaperone2 that facilitates outer membrane porin folding |
| 99 | c3n42F_ | Alignment | not modelled | 5.5 | 29 | **PDB header:**viral protein<br>**Chain:** F: **PDB Molecule:**e1 envelope glycoprotein;<br>**PDBTitle:** crystal structures of the mature envelope glycoprotein complex (furin2 cleavage) of chikungunya virus. |