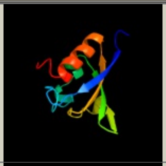
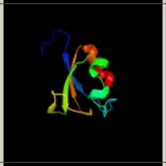
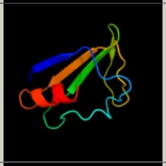
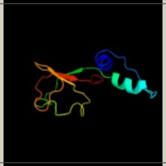
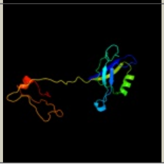
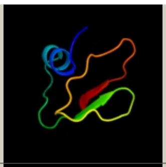
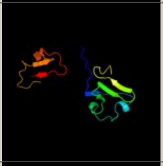
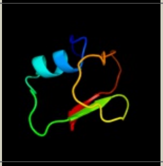
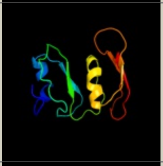
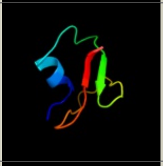
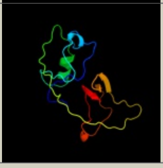
# Phyre$^2$

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P60872 |
| Date | Thu Jan 5 12:07:13 GMT 2012 |
| Unique Job ID | 5843cebe03b081a4 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1vcta2 | Alignment |  | 99.5 | 19 | **Fold:**TrkA C-terminal domain-like<br>**Superfamily:**TrkA C-terminal domain-like<br>**Family:**TrkA C-terminal domain-like |
| 2 | d2fy8a2 | Alignment |  | 99.5 | 22 | **Fold:**TrkA C-terminal domain-like<br>**Superfamily:**TrkA C-terminal domain-like<br>**Family:**TrkA C-terminal domain-like |
| 3 | c2bknA_ | Alignment |  | 99.4 | 19 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**hypothetical protein ph0236;<br>**PDBTitle:** structure analysis of unknown function protein |
| 4 | c3jxoB_ | Alignment |  | 99.1 | 26 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**trka-n domain protein;<br>**PDBTitle:** crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima |
| 5 | c2fy8A_ | Alignment |  | 99.0 | 22 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**calcium-gated potassium channel mthk;<br>**PDBTitle:** crystal structure of mthk rck domain in its ligand-free gating-ring2 form |
| 6 | c1lnqC_ | Alignment |  | 99.0 | 23 | **PDB header:**metal transport<br>**Chain:** C: **PDB Molecule:**potassium channel related protein;<br>**PDBTitle:** crystal structure of mthk at 3.3 a |
| 7 | c3l4bG_ | Alignment |  | 98.3 | 28 | **PDB header:**transport protein<br>**Chain:** G: **PDB Molecule:**trka k+ channel protien tm1088b;<br>**PDBTitle:** crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima |
| 8 | c3mt5A_ | Alignment |  | 97.5 | 11 | **PDB header:**membrane protein, transport protein<br>**Chain:** A: **PDB Molecule:**potassium large conductance calcium-activated channel,<br>**PDBTitle:** crystal structure of the human bk gating apparatus |
| 9 | c3u6nC_ | Alignment |  | 97.3 | 11 | **PDB header:**transport protein<br>**Chain:** C: **PDB Molecule:**high-conductance ca2+-activated k+ channel protein;<br>**PDBTitle:** open structure of the bk channel gating ring |
| 10 | c3nafA_ | Alignment |  | 86.1 | 17 | **PDB header:**ion transport<br>**Chain:** A: **PDB Molecule:**calcium-activated potassium channel subunit alpha-1;<br>**PDBTitle:** structure of the intracellular gating ring from the human high-2 conductance ca2+ gated k+ channel (bk channel) |
| 11 | c2ka9A_ | Alignment |  | 75.1 | 13 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**disks large homolog 4;<br>**PDBTitle:** solution structure of psd-95 pdz12 complexed with cypin2 peptide |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | d1zud21 | Alignment |  | 72.1 | 14 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**MoaD/ThiS<br>**Family:**ThiS |
| 13 | c2w8iG_ | Alignment |  | 67.3 | 20 | **PDB header:**membrane protein<br>**Chain:** G: **PDB Molecule:**putative outer membrane lipoprotein wza;<br>**PDBTitle:** crystal structure of wza24-345. |
| 14 | c2j58G_ | Alignment |  | 64.7 | 20 | **PDB header:**membrane protein<br>**Chain:** G: **PDB Molecule:**outer membrane lipoprotein wza;<br>**PDBTitle:** the structure of wza |
| 15 | d2cu3a1 | Alignment |  | 64.2 | 21 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**MoaD/ThiS<br>**Family:**ThiS |
| 16 | c2kl0A_ | Alignment |  | 63.7 | 6 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this;<br>**PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325 |
| 17 | c2zc3F_ | Alignment |  | 58.5 | 9 | **PDB header:**biosynthetic protein<br>**Chain:** F: **PDB Molecule:**penicillin-binding protein 2x;<br>**PDBTitle:** penicillin-binding protein 2x (pbp 2x) acyl-enzyme complex2 (biapenem) from streptococcus pneumoniae |
| 18 | c3cwiA_ | Alignment |  | 58.3 | 9 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**thiamine-biosynthesis protein this;<br>**PDBTitle:** crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137 |
| 19 | d1rp5a2 | Alignment |  | 57.5 | 15 | **Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain<br>**Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain<br>**Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain |
| 20 | c3r0hA_ | Alignment |  | 53.9 | 17 | **PDB header:**peptide binding protein<br>**Chain:** A: **PDB Molecule:**inactivation-no-after-potential d protein;<br>**PDBTitle:** structure of inad pdz45 in complex with ng2 peptide |
| 21 | d1tygb_ | Alignment | not modelled | 53.6 | 12 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**MoaD/ThiS<br>**Family:**ThiS |
| 22 | d1pyya2 | Alignment | not modelled | 51.4 | 13 | **Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain<br>**Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain<br>**Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain |
| 23 | c1tygG_ | Alignment | not modelled | 49.6 | 10 | **PDB header:**biosynthetic protein<br>**Chain:** G: **PDB Molecule:**yjbs;<br>**PDBTitle:** structure of the thiazole synthase/this complex |
| 24 | d1k25a2 | Alignment | not modelled | 48.8 | 13 | **Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain<br>**Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain<br>**Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain |
| 25 | d1k25a1 | Alignment | not modelled | 47.8 | 12 | **Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain<br>**Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain<br>**Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain |
| 26 | d1pyya1 | Alignment | not modelled | 45.6 | 8 | **Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain<br>**Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain<br>**Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain |
| 27 | c2anrA_ | Alignment | not modelled | 45.1 | 14 | **PDB header:**rna-binding protein/rna<br>**Chain:** A: **PDB Molecule:**neuro-oncological ventral antigen 1;<br>**PDBTitle:** crystal structure (ii) of nova-1 kh1/kh2 domain tandem with 25nt rna2 hairpin |
| 28 | d1r61a_ | Alignment | not modelled | 34.6 | 11 | **Fold:**The "swivelling" beta/beta/alpha domain<br>**Superfamily:**Putative cyclase<br>**Family:**Putative cyclase |
| | | | | | | **PDB header:**protein transport |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 29 | c1u3bA_ | Alignment | not modelled | 30.4 | 12 | **Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding,<br>**PDBTitle:** auto-inhibition mechanism of x11s/mints family scaffold2 proteins revealed by the closed conformation of the tandem3 pdz domains |
| 30 | c2dazA_ | Alignment | not modelled | 29.1 | 13 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**inad-like protein;<br>**PDBTitle:** solution structure of the 7th pdz domain of inad-like2 protein |
| 31 | c2c2xB_ | Alignment | not modelled | 27.8 | 10 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase-<br>**PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis |
| 32 | c2qndA_ | Alignment | not modelled | 27.3 | 19 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**fmr1 protein;<br>**PDBTitle:** crystal structure of the kh1-kh2 domains from human fragile x mental2 retardation protein |
| 33 | c3krmB_ | Alignment | not modelled | 25.5 | 14 | **PDB header:**rna binding protein<br>**Chain:** B: **PDB Molecule:**insulin-like growth factor 2 mrna-binding protein<br>**PDBTitle:** imp1 kh34 |
| 34 | d1v62a_ | Alignment | not modelled | 23.8 | 15 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 35 | d1wpga1 | Alignment | not modelled | 21.5 | 19 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**Calcium ATPase, transduction domain A<br>**Family:**Calcium ATPase, transduction domain A |
| 36 | c3tl6B_ | Alignment | not modelled | 21.0 | 12 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase;<br>**PDBTitle:** crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica |
| 37 | d1v6ba_ | Alignment | not modelled | 20.6 | 15 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 38 | c2eehA_ | Alignment | not modelled | 19.9 | 12 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**pdz domain-containing protein 7;<br>**PDBTitle:** solution structure of first pdz domain of pdz domain2 containing protein 7 |
| 39 | d1x6da1 | Alignment | not modelled | 19.7 | 16 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**Interleukin 16 |
| 40 | d1sdwa2 | Alignment | not modelled | 19.4 | 21 | **Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins)<br>**Superfamily:**PHM/PNGase F<br>**Family:**Peptidylglycine alpha-hydroxylating monooxygenase, PHM |
| 41 | c2hc8A_ | Alignment | not modelled | 18.5 | 21 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type;<br>**PDBTitle:** structure of the a. fulgidus copa a-domain |
| 42 | d2h1qa1 | Alignment | not modelled | 18.2 | 23 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**Dhaf3308-like<br>**Family:**Dhaf3308-like |
| 43 | d2i0ia1 | Alignment | not modelled | 17.4 | 12 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 44 | c2kegA_ | Alignment | not modelled | 17.4 | 22 | **PDB header:**antimicrobial protein<br>**Chain:** A: **PDB Molecule:**plnk;<br>**PDBTitle:** nmr structure of plantaricin k in dpc-micelles |
| 45 | c2jkdB_ | Alignment | not modelled | 16.7 | 26 | **PDB header:**gene regulation<br>**Chain:** B: **PDB Molecule:**pre-mrna leakage protein 1;<br>**PDBTitle:** structure of the yeast pml1 splicing factor and its2 integration into the res complex |
| 46 | c1yj5C_ | Alignment | not modelled | 16.2 | 38 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase fha domain;<br>**PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme |
| 47 | d1pm3a_ | Alignment | not modelled | 16.0 | 19 | **Fold:**PRC-barrel domain<br>**Superfamily:**PRC-barrel domain<br>**Family:**MTH1895 |
| 48 | d1y7ma2 | Alignment | not modelled | 15.8 | 24 | **Fold:**LysM domain<br>**Superfamily:**LysM domain<br>**Family:**LysM domain |
| 49 | c2jvzA_ | Alignment | not modelled | 15.7 | 20 | **PDB header:**splicing<br>**Chain:** A: **PDB Molecule:**far upstream element-binding protein 2;<br>**PDBTitle:** solution nmr structure of the second and third kh domains2 of ksrp |
| 50 | d1edza1 | Alignment | not modelled | 15.1 | 6 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Aminoacid dehydrogenase-like, C-terminal domain |
| 51 | c2djtA_ | Alignment | not modelled | 15.0 | 10 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**unnamed protein product;<br>**PDBTitle:** solution structures of the pdz domain of human unnamed2 protein product |
| 52 | d1ky9a1 | Alignment | not modelled | 14.9 | 15 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**HtrA-like serine proteases |
| 53 | d2ix0a3 | Alignment | not modelled | 14.8 | 18 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 54 | c2fpeB_ | Alignment | not modelled | 14.6 | 12 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**c-jun-amino-terminal kinase interacting protein |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | | | **PDBTitle:** conserved dimerization of the ib1 src-homology 3 domain |
| 55 | c3kt9A_ | Alignment | not modelled | 14.2 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**aprataxin;<br>**PDBTitle:** aprataxin fha domain |
| 56 | d2piaa1 | Alignment | not modelled | 13.9 | 15 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Riboflavin synthase domain-like<br>**Family:**Ferredoxin reductase FAD-binding domain-like |
| 57 | c2xlkB_ | Alignment | not modelled | 13.7 | 16 | **PDB header:**hydrolase/rna<br>**Chain:** B: **PDB Molecule:**csy4 endoribonuclease;<br>**PDBTitle:** crystal structure of the csy4-crrna complex, orthorhombic form |
| 58 | c2dmzA_ | Alignment | not modelled | 13.7 | 9 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**inad-like protein;<br>**PDBTitle:** solution structure of the third pdz domain of human inad-2 like protein |
| 59 | d1yjma1 | Alignment | not modelled | 13.6 | 38 | **Fold:**SMAD/FHA domain<br>**Superfamily:**SMAD/FHA domain<br>**Family:**FHA domain |
| 60 | d1ujxa_ | Alignment | not modelled | 13.5 | 41 | **Fold:**SMAD/FHA domain<br>**Superfamily:**SMAD/FHA domain<br>**Family:**FHA domain |
| 61 | d1vhwa_ | Alignment | not modelled | 13.4 | 25 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**Purine and uridine phosphorylases<br>**Family:**Purine and uridine phosphorylases |
| 62 | c2yt7A_ | Alignment | not modelled | 13.2 | 10 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding family<br>**PDBTitle:** solution structure of the pdz domain of amyloid beta a42 precursor protein-binding family a member 3 |
| 63 | c2gzvA_ | Alignment | not modelled | 13.0 | 14 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**prkca-binding protein;<br>**PDBTitle:** the cystal structure of the pdz domain of human pick1 (casp target) |
| 64 | c2d8iA_ | Alignment | not modelled | 12.9 | 15 | **PDB header:**immune system, signaling protein<br>**Chain:** A: **PDB Molecule:**t-cell lymphoma invasion and metastasis 1<br>**PDBTitle:** solution structure of the pdz domain of t-cell lymphoma2 invasion and metastasis 1 varian |
| 65 | c1zcdA_ | Alignment | not modelled | 12.9 | 20 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**na(+)/h(+) antiporter 1;<br>**PDBTitle:** crystal structure of the na+/h+ antiporter nhaa |
| 66 | d1wgka_ | Alignment | not modelled | 12.6 | 26 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**MoaD/ThiS<br>**Family:**C9orf74 homolog |
| 67 | d1efna_ | Alignment | not modelled | 12.5 | 20 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 68 | c3cqtA_ | Alignment | not modelled | 12.4 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase fyn;<br>**PDBTitle:** n53i v55l mutant of fyn sh3 domain |
| 69 | d1wi2a_ | Alignment | not modelled | 12.4 | 11 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 70 | d1shfa_ | Alignment | not modelled | 12.3 | 14 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 71 | c4a8aI_ | Alignment | not modelled | 12.2 | 18 | **PDB header:**hydrolase/hydrolase<br>**Chain:** I: **PDB Molecule:**periplasmic ph-dependent serine endoprotease degq;<br>**PDBTitle:** asymmetric cryo-em reconstruction of e. coli degq 12-mer in complex2 with lysozyme |
| 72 | c2y0oA_ | Alignment | not modelled | 12.1 | 23 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**probable d-lyxose ketol-isomerase;<br>**PDBTitle:** the structure of a d-lyxose isomerase from the sigmab2 regulon of bacillus subtilis |
| 73 | c2k9xA_ | Alignment | not modelled | 12.0 | 23 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** solution structure of urm1 from trypanosoma brucei |
| 74 | d1wi4a1 | Alignment | not modelled | 11.9 | 16 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 75 | d1k9sa_ | Alignment | not modelled | 11.8 | 23 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**Purine and uridine phosphorylases<br>**Family:**Purine and uridine phosphorylases |
| 76 | c1edzA_ | Alignment | not modelled | 11.6 | 6 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**5,10-methylenetetrahydrofolate dehydrogenase;<br>**PDBTitle:** structure of the nad-dependent 5,10-2 methylenetetrahydrofolate dehydrogenase from saccharomyces3 cerevisiae |
| 77 | c2kncA_ | Alignment | not modelled | 11.6 | 13 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**integrin alpha-iib;<br>**PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex |
| 78 | c2kfwA_ | Alignment | not modelled | 11.2 | 25 | **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 |
| 79 | c3elsA_ | Alignment | not modelled | 11.1 | 26 | **PDB header:**splicing<br>**Chain:** A: **PDB Molecule:**pre-mrna leakage protein 1;<br>**PDBTitle:** crystal structure of yeast pml1p, residues 51-204 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 80 | d1qcfa1 | Alignment | not modelled | 11.1 | 19 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 81 | d2piea1 | Alignment | not modelled | 10.9 | 20 | **Fold:**SMAD/FHA domain<br>**Superfamily:**SMAD/FHA domain<br>**Family:**FHA domain |
| 82 | d2d6fa1 | Alignment | not modelled | 10.9 | 12 | **Fold:**Sm-like fold<br>**Superfamily:**GatD N-terminal domain-like<br>**Family:**GatD N-terminal domain-like |
| 83 | c1mhsA_ | Alignment | not modelled | 10.8 | 21 | **PDB header:**membrane protein, proton transport<br>**Chain:** A: **PDB Molecule:**plasma membrane atpase;<br>**PDBTitle:** model of neurospora crassa proton atpase |
| 84 | d1lgpa_ | Alignment | not modelled | 10.7 | 29 | **Fold:**SMAD/FHA domain<br>**Superfamily:**SMAD/FHA domain<br>**Family:**FHA domain |
| 85 | d1va8a1 | Alignment | not modelled | 10.6 | 20 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 86 | c2egeA_ | Alignment | not modelled | 10.5 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein kiaa1666;<br>**PDBTitle:** solution structure of the third sh3 domain from human2 kiaa1666 protein |
| 87 | c1w9qB_ | Alignment | not modelled | 10.2 | 14 | **PDB header:**cell adhesion<br>**Chain:** B: **PDB Molecule:**syntenin 1;<br>**PDBTitle:** crystal structure of the pdz tandem of human syntenin in2 complex with tnefaf peptide |
| 88 | d1viga_ | Alignment | not modelled | 9.8 | 14 | **Fold:**Eukaryotic type KH-domain (KH-domain type I)<br>**Superfamily:**Eukaryotic type KH-domain (KH-domain type I)<br>**Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 89 | c2dgrA_ | Alignment | not modelled | 9.8 | 24 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**ring finger and kh domain-containing protein 1;<br>**PDBTitle:** solution structure of the second kh domain in ring finger2 and kh domain containing protein 1 |
| 90 | c2egaA_ | Alignment | not modelled | 9.7 | 15 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**sh3 and px domain-containing protein 2a;<br>**PDBTitle:** solution structure of the first sh3 domain from human2 kiaa0418 protein |
| 91 | d1ufxa_ | Alignment | not modelled | 9.6 | 9 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 92 | c3kw0D_ | Alignment | not modelled | 9.5 | 25 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**cysteine peptidase;<br>**PDBTitle:** crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution |
| 93 | d1g9oa_ | Alignment | not modelled | 9.5 | 14 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 94 | c2ejyA_ | Alignment | not modelled | 9.5 | 10 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**55 kda erythrocyte membrane protein;<br>**PDBTitle:** solution structure of the p55 pdz t85c domain complexed2 with the glycophorin c f127c peptide |
| 95 | d1rgwa_ | Alignment | not modelled | 9.4 | 12 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 96 | c1tuaA_ | Alignment | not modelled | 9.3 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein ape0754;<br>**PDBTitle:** 1.5 a crystal structure of a protein of unknown function2 ape0754 from aeropyrum pernix |
| 97 | c3npgD_ | Alignment | not modelled | 9.2 | 11 | **PDB header:**unknown function<br>**Chain:** D: **PDB Molecule:**uncharacterized duf364 family protein;<br>**PDBTitle:** crystal structure of a protein with unknown function from duf3642 family (ph1506) from pyrococcus horikoshii at 2.70 a resolution |
| 98 | c2dmoA_ | Alignment | not modelled | 9.2 | 12 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**neutrophil cytosol factor 2;<br>**PDBTitle:** refined solution structure of the 1st sh3 domain from human2 neutrophil cytosol factor 2 (ncf-2) |
| 99 | d1rzxa_ | Alignment | not modelled | 9.1 | 16 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |