Phyre$^2$

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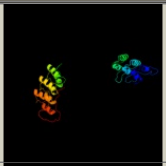
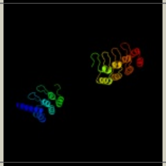
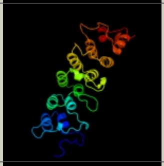
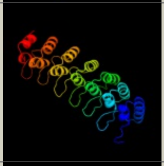
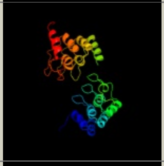
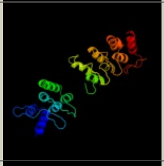
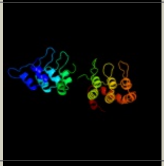
| Email | l.a.kelley@imperial.ac.uk |
| Description | P20749 |
| Date | Tue Apr 3 15:06:46 BST 2012 |
| Unique Job ID | 34106c6e40501ee3 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1n11a_ | Alignment |  | 100.0 | 36 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 2 | c1n11A_ | Alignment |  | 100.0 | 36 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**ankyrin;<br>**PDBTitle:** d34 region of human ankyrin-r and linker |
| 3 | c3utmA_ | Alignment |  | 100.0 | 31 | **PDB header:**transferase/signaling protein<br>**Chain:** A: **PDB Molecule:**tankyrase-1;<br>**PDBTitle:** crystal structure of a mouse tankyrase-axin complex |
| 4 | c3keaB_ | Alignment |  | 100.0 | 19 | **PDB header:**viral protein<br>**Chain:** B: **PDB Molecule:**k1l;<br>**PDBTitle:** structure function studies of vaccinia virus host-range protein k12 reveal a novel ankyrin repeat interaction surface for k1s function |
| 5 | d1k1aa_ | Alignment |  | 100.0 | 100 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 6 | c2fo1E_ | Alignment |  | 100.0 | 20 | **PDB header:**gene regulation/signalling protein/dna<br>**Chain:** E: **PDB Molecule:**lin-12 protein;<br>**PDBTitle:** crystal structure of the csl-notch-mastermind ternary2 complex bound to dna |
| 7 | d1s70b_ | Alignment |  | 100.0 | 24 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 8 | c3ljnA_ | Alignment |  | 100.0 | 21 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** ankyrin repeat protein from leishmania major |
| 9 | c2xaiD_ | Alignment |  | 100.0 | 20 | **PDB header:**transcription<br>**Chain:** D: **PDB Molecule:**ankyrin repeat and socs box protein 9;<br>**PDBTitle:** crystal structure of ankyrin repeat and socs box-containing2 protein 9 (asb9) in complex with elonginb and elonginc |
| 10 | d2ajaa1 | Alignment |  | 100.0 | 13 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**Pseudo ankyrin repeat-like<br>**Family:**Pseudo ankyrin repeat |
| 11 | d2fo1e1 | Alignment |  | 100.0 | 19 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |

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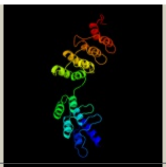
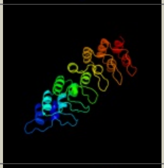
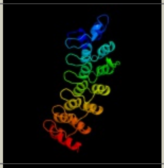
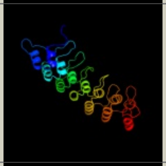
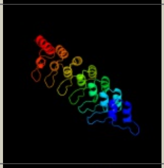
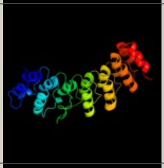
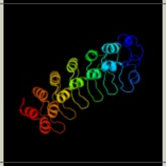
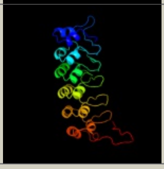
| 12 | d1wdya_ | Alignment |  | 100.0 | 24 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 13 | c3eu9B_ | Alignment |  | 100.0 | 14 | **PDB header:**protein binding, methyl-lysine-binding p<br>**Chain:** B: **PDB Molecule:**huntingtin-interacting protein 14;<br>**PDBTitle:** the ankyrin repeat domain of huntingtin interacting protein 14 |
| 14 | d1uoha_ | Alignment |  | 100.0 | 19 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 15 | c3d9hA_ | Alignment |  | 100.0 | 18 | **PDB header:**structural protein, protein binding<br>**Chain:** A: **PDB Molecule:**cdna flj77766, highly similar to homo sapiens<br>**PDBTitle:** crystal structure of the splice variant of human asb92 (hasb9-2), an ankyrin repeat protein |
| 16 | c3b7bB_ | Alignment |  | 100.0 | 22 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**euchromatic histone-lysine n-methyltransferase 1;<br>**PDBTitle:** euhmt1 (glp) ankyrin repeat domain (structure 1) |
| 17 | c2ajaA_ | Alignment |  | 100.0 | 13 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**ankyrin repeat family protein;<br>**PDBTitle:** x-ray structure of an ankyrin repeat family protein q5zsv02 from legionella pneumophila. northeast structural genomics3 consortium target lgr21. |
| 18 | d1ixva_ | Alignment |  | 100.0 | 21 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 19 | c2f8xK_ | Alignment |  | 100.0 | 21 | **PDB header:**transcription/dna<br>**Chain:** K: **PDB Molecule:**neurogenic locus notch homolog protein 1;<br>**PDBTitle:** crystal structure of activated notch, csl and maml on hes-12 promoter dna sequence |
| 20 | d1iknd_ | Alignment |  | 100.0 | 26 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 21 | c1sw6A_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**transcription regulation<br>**Chain:** A: **PDB Molecule:**regulatory protein swi6;<br>**PDBTitle:** s. cerevisiae swi6 ankyrin-repeat fragment |
| 22 | d1sw6a_ | Alignment | not modelled | 100.0 | 17 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 23 | d1ot8a_ | Alignment | not modelled | 100.0 | 23 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 24 | c3jxiA_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**vanilloid receptor-related osmotically activated channel<br>**PDBTitle:** crystal structure of the chicken trpv4 ankyrin repeat domain |
| 25 | d1oy3d_ | Alignment | not modelled | 100.0 | 30 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 26 | c1oy3D_ | Alignment | not modelled | 100.0 | 30 | **PDB header:**dna binding protein<br>**Chain:** D: **PDB Molecule:**transcription factor inhibitor i-kappa-b-beta;<br>**PDBTitle:** crystal structure of an ikbbeta/nf-kb p65 homodimer complex |
| 27 | c2vgeA_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**rela-associated inhibitor;<br>**PDBTitle:** crystal structure of the c-terminal region of human iaspp |
| 28 | c3hraA_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**ankyrin repeat family protein;<br>**PDBTitle:** crystal structure of ef0377 an ankyrin repeat protein |

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| 29 | c2f37B_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**transient receptor potential cation channel<br>**PDBTitle:** crystal structure of the ankyrin repeat domain of human2 trpv2 |
| 30 | c3t8kB_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** the crystal structure of a functionally unknown protein lebu_0176 from2 leptotrichia buccalis c-1013-b |
| 31 | c2rfaA_ | Alignment | not modelled | 100.0 | 22 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**transient receptor potential cation channel subfamily v<br>**PDBTitle:** crystal structure of the mouse trpv6 ankyrin repeat domain |
| 32 | c3ui2A_ | Alignment | not modelled | 99.9 | 31 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**signal recognition particle 43 kda protein, chloroplastic;<br>**PDBTitle:** crystal structure of the cpsrp54 tail bound to cpsrp43 |
| 33 | c2kbxA_ | Alignment | not modelled | 99.9 | 24 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**integrin-linked protein kinase;<br>**PDBTitle:** solution structure of ilk-pinch complex |
| 34 | c3ehrB_ | Alignment | not modelled | 99.9 | 21 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**osteoclast-stimulating factor 1;<br>**PDBTitle:** crystal structure of human osteoclast stimulating factor |
| 35 | c2nyjA_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**transient receptor potential cation channel<br>**PDBTitle:** crystal structure of the ankyrin repeat domain of trpv1 |
| 36 | c1ycsB_ | Alignment | not modelled | 99.9 | 19 | **PDB header:**complex (anti-oncogene/ankyrin repeats)<br>**Chain:** B: **PDB Molecule:**53bp2;<br>**PDBTitle:** p53-53bp2 complex |
| 37 | c3jueA_ | Alignment | not modelled | 99.9 | 26 | **PDB header:**protein transport/endocytosis<br>**Chain:** A: **PDB Molecule:**arfgap with coiled-coil, ank repeat and ph domain-<br>**PDBTitle:** crystal structure of arfgap and ank repeat domain of acap1 |
| 38 | c3twtD_ | Alignment | not modelled | 99.9 | 31 | **PDB header:**signaling protein/peptide<br>**Chain:** D: **PDB Molecule:**tankyrase-2;<br>**PDBTitle:** crystal structure of arc4 from human tankyrase 2 in complex with2 peptide from human mcl1 (chimeric peptide) |
| 39 | c3deoA_ | Alignment | not modelled | 99.9 | 30 | **PDB header:**protein transport, membrane protein<br>**Chain:** A: **PDB Molecule:**signal recognition particle 43 kda protein;<br>**PDBTitle:** structural basis for specific substrate recognition by the2 chloroplast signal recognition particle protein cpsrp43 |
| 40 | d1dcqa1 | Alignment | not modelled | 99.9 | 30 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 41 | c2b0oF_ | Alignment | not modelled | 99.9 | 21 | **PDB header:**metal binding protein<br>**Chain:** F: **PDB Molecule:**uplc1;<br>**PDBTitle:** crystal structure of uplc1 gap domain |
| 42 | c2rfmB_ | Alignment | not modelled | 99.9 | 26 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**putative ankyrin repeat protein tv1425;<br>**PDBTitle:** structure of a thermophilic ankyrin repeat protein |
| 43 | d2a5ea_ | Alignment | not modelled | 99.9 | 21 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 44 | c1ympB_ | Alignment | not modelled | 99.9 | 30 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**notch 1 protein;<br>**PDBTitle:** the crystal structure of a partial mouse notch-1 ankyrin2 domain: repeats 4 through 7 preserve an ankyrin fold |
| 45 | c1dcqA_ | Alignment | not modelled | 99.9 | 22 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**pyk2-associated protein beta;<br>**PDBTitle:** crystal structure of the arf-gap domain and ankyrin repeats2 of papbeta. |
| 46 | d1blxb_ | Alignment | not modelled | 99.9 | 22 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 47 | c1ympA_ | Alignment | not modelled | 99.9 | 30 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**notch 1 protein;<br>**PDBTitle:** the crystal structure of a partial mouse notch-1 ankyrin2 domain: repeats 4 through 7 preserve an ankyrin fold |
| 48 | d1ycsb1 | Alignment | not modelled | 99.9 | 27 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 49 | c3lvrE_ | Alignment | not modelled | 99.9 | 26 | **PDB header:**protein transport<br>**Chain:** E: **PDB Molecule:**arf-gap with sh3 domain, ank repeat and ph domain-<br>**PDBTitle:** the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium |
| 50 | d1awcb_ | Alignment | not modelled | 99.9 | 23 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 51 | d1myoa_ | Alignment | not modelled | 99.9 | 28 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 52 | c3c5rB_ | Alignment | not modelled | 99.9 | 35 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**brca1-associated ring domain protein 1;<br>**PDBTitle:** crystal structure of the bard1 ankyrin repeat domain and its2 functional consequences |
| 53 | d1ihba_ | Alignment | not modelled | 99.9 | 22 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| | | | | | | **PDB header:**transferase |

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| 54 | c2v5qC_ | Alignment | not modelled | 99.9 | 38 | **Chain:** C: **PDB Molecule:**design ankyrin repeat protein;<br>**PDBTitle:** crystal structure of wild-type plk-1 kinase domain in2 complex with a selective darpin |
| 55 | c3v30A_ | Alignment | not modelled | 99.9 | 24 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**dna-binding protein rfxank;<br>**PDBTitle:** crystal structure of the peptide bound complex of the ankyrin repeat2 domains of human rfxank |
| 56 | d1bd8a_ | Alignment | not modelled | 99.9 | 18 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 57 | c2zgdA_ | Alignment | not modelled | 99.8 | 26 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**3 repeat synthetic ankyrin;<br>**PDBTitle:** asn-hydroxylation stabilises the ankyrin repeat domain fold |
| 58 | c2l6bA_ | Alignment | not modelled | 99.8 | 36 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**nr1c;<br>**PDBTitle:** nrc consensus ankyrin repeat protein solution structure |
| 59 | c2jabC_ | Alignment | not modelled | 99.8 | 34 | **PDB header:**de novo protein<br>**Chain:** C: **PDB Molecule:**h10-2-g3;<br>**PDBTitle:** a designed ankyrin repeat protein evolved to picomolar2 affinity to her2 |
| 60 | d1bi7b_ | Alignment | not modelled | 99.8 | 26 | **Fold:**beta-hairpin-alpha-hairpin repeat<br>**Superfamily:**Ankyrin repeat<br>**Family:**Ankyrin repeat |
| 61 | c2xenA_ | Alignment | not modelled | 99.8 | 27 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**ni1c mut4;<br>**PDBTitle:** structural determinants for improved thermal stability of2 designed ankyrin repeat proteins with a redesigned c-3 capping module. |
| 62 | c1n0rA_ | Alignment | not modelled | 99.7 | 42 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**4 ankyrin repeats;<br>**PDBTitle:** 4ank: a designed ankyrin repeat protein with four identical2 consensus repeats |
| 63 | c1n0qB_ | Alignment | not modelled | 99.7 | 37 | **PDB header:**structural protein<br>**Chain:** B: **PDB Molecule:**3 ankyrin repeats;<br>**PDBTitle:** 3ank: a designed ankyrin repeat protein with three identical consensus2 repeats |
| 64 | c2xumS_ | Alignment | not modelled | 90.5 | 28 | **PDB header:**oxidoreductase/peptide<br>**Chain:** S: **PDB Molecule:**asp-substrate peptide 2;<br>**PDBTitle:** factor inhibiting hif (fih) q239h mutant in complex with zn(ii), nog2 and asp-substrate peptide (20-mer) |
| 65 | c2y0iS_ | Alignment | not modelled | 48.0 | 42 | **PDB header:**oxidoreductase/peptide<br>**Chain:** S: **PDB Molecule:**tankyrase-2;<br>**PDBTitle:** factor inhibiting hif-1 alpha in complex with tankyrase-2 (tnks2)2 fragment peptide (21-mer) |
| 66 | c3ix1B_ | Alignment | not modelled | 40.5 | 21 | **PDB header:**biosynthetic protein<br>**Chain:** B: **PDB Molecule:**n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding<br>**PDBTitle:** periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans |
| 67 | c3ih9A_ | Alignment | not modelled | 38.4 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**salt-tolerant glutaminase;<br>**PDBTitle:** crystal structure analysis of mglu in its tris form |
| 68 | c3ix1A_ | Alignment | not modelled | 37.0 | 21 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding<br>**PDBTitle:** periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans |
| 69 | c2x7pA_ | Alignment | not modelled | 26.6 | 16 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**possible thiamine biosynthesis enzyme;<br>**PDBTitle:** the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold |
| 70 | c3qslA_ | Alignment | not modelled | 17.5 | 30 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative exported protein;<br>**PDBTitle:** structure of cae31940 from bordetella bronchiseptica rb50 |
| 71 | c3tqwA_ | Alignment | not modelled | 16.5 | 18 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**methionine-binding protein;<br>**PDBTitle:** structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii |
| 72 | c3zrhA_ | Alignment | not modelled | 10.2 | 20 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**ubiquitin thioesterase zranb1;<br>**PDBTitle:** crystal structure of the lys29, lys33-linkage-specific trabid otu2 deubiquitinase domain reveals an ankyrin-repeat ubiquitin binding3 domain (ankubd) |
| 73 | d2cwla1 | Alignment | not modelled | 8.8 | 19 | **Fold:**Ferritin-like<br>**Superfamily:**Ferritin-like<br>**Family:**Manganese catalase (T-catalase) |
| 74 | c3e4rA_ | Alignment | not modelled | 8.3 | 16 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**nitrate transport protein;<br>**PDBTitle:** crystal structure of the alkanesulfonate binding protein2 (ssua) from the phytopathogenic bacteria xanthomonas3 axonopodis pv. citri bound to hepes |
| 75 | c2x26A_ | Alignment | not modelled | 6.4 | 9 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**periplasmic aliphatic sulphonates-binding protein;<br>**PDBTitle:** crystal structure of the periplasmic aliphatic sulphonate2 binding protein ssua from escherichia coli |
| 76 | c3sviA_ | Alignment | not modelled | 5.4 | 29 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**type iii effector hopab2;<br>**PDBTitle:** structure of the pto-binding domain of hoppmal generated by limited2 thermolysin digestion |