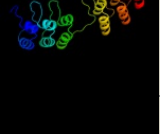
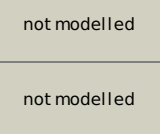


# Phyre2

|               |                             |
|---------------|-----------------------------|
| Email         | l.a.kelley@imperial.ac.uk   |
| Description   | P77736                      |
| Date          | Thu Jan 5 12:32:20 GMT 2012 |
| Unique Job ID | 11d857be92e71220            |

Detailed template information

| #  | Template                | Alignment Coverage                                                                               | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                          |
|----|-------------------------|--------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">dlwda_</a>  | <br>Alignment   |    | 100.0      | 25     | <b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                         |
| 2  | <a href="#">c3eu9B_</a> | <br>Alignment   |    | 100.0      | 15     | <b>PDB header:</b> protein binding, methyl-lysine-binding p<br><b>Chain:</b> B: <b>PDB Molecule:</b> huntingtin-interacting protein 14;<br><b>PDBTitle:</b> the ankyrin repeat domain of huntingtin interacting protein 14                                    |
| 3  | <a href="#">c3b7bB_</a> | <br>Alignment   |    | 100.0      | 15     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> euchromatic histone-lysine n-methyltransferase 1;<br><b>PDBTitle:</b> euhmt1 (glp) ankyrin repeat domain (structure 1)                                                                |
| 4  | <a href="#">dliknd_</a> | <br>Alignment   |    | 100.0      | 15     | <b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                         |
| 5  | <a href="#">dloy3d_</a> | <br>Alignment |  | 100.0      | 19     | <b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                         |
| 6  | <a href="#">cloy3D_</a> | <br>Alignment |  | 100.0      | 19     | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> transcription factor inhibitor i-kappa-b-beta;<br><b>PDBTitle:</b> crystal structure of an ikbbeta/nf-kb p65 homodimer complex                                                |
| 7  | <a href="#">c1n11A_</a> | <br>Alignment |  | 100.0      | 21     | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ankyrin;<br><b>PDBTitle:</b> d34 region of human ankyrin-r and linker                                                                                                          |
| 8  | <a href="#">dln11a_</a> | <br>Alignment |  | 100.0      | 21     | <b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                         |
| 9  | <a href="#">c3d9hA_</a> | <br>Alignment |  | 99.9       | 17     | <b>PDB header:</b> structural protein, protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> cdna flj77766, highly similar to homo sapiens<br><b>PDBTitle:</b> crystal structure of the splice variant of human asb92 (hasb9-2), an ankyrin repeat protein |
| 10 | <a href="#">c3hraA_</a> | <br>Alignment |  | 99.9       | 35     | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ankyrin repeat family protein;<br><b>PDBTitle:</b> crystal structure of ef0377 an ankyrin repeat protein                                                                       |
| 11 | <a href="#">dlixva_</a> | <br>Alignment |  | 99.9       | 12     | <b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                         |

|    |                         |           |                                                                                     |      |    |                                                                                                                                                                                                                                                          |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">c2f8xK_</a> | Alignment |     | 99.9 | 22 | <b>PDB header:</b> transcription/dna<br><b>Chain:</b> K: <b>PDB Molecule:</b> neurogenic locus notch homolog protein 1;<br><b>PDBTitle:</b> crystal structure of activated notch, csl and mam1 on hes-12 promoter dna sequence                           |
| 13 | <a href="#">c2xaiD_</a> | Alignment |    | 99.9 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> D: <b>PDB Molecule:</b> ankyrin repeat and socs box protein 9;<br><b>PDBTitle:</b> crystal structure of ankyrin repeat and socs box-containing2 protein 9 (asb9) in complex with elonginb and elonginc |
| 14 | <a href="#">d1k1aa_</a> | Alignment |    | 99.9 | 19 | <b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                    |
| 15 | <a href="#">d1uoha_</a> | Alignment |    | 99.9 | 18 | <b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                    |
| 16 | <a href="#">d1s70b_</a> | Alignment |    | 99.9 | 23 | <b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                    |
| 17 | <a href="#">c3ljnA_</a> | Alignment |   | 99.9 | 15 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein;<br><b>PDBTitle:</b> ankyrin repeat protein from leishmania major                                                                                      |
| 18 | <a href="#">c2rfaA_</a> | Alignment |  | 99.9 | 15 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily v<br><b>PDBTitle:</b> crystal structure of the mouse trpv6 ankyrin repeat domain                                      |
| 19 | <a href="#">c2fo1E_</a> | Alignment |  | 99.9 | 14 | <b>PDB header:</b> gene regulation/signalling protein/dna<br><b>Chain:</b> E: <b>PDB Molecule:</b> lin-12 protein;<br><b>PDBTitle:</b> crystal structure of the csl-notch-mastermind ternary2 complex bound to dna                                       |
| 20 | <a href="#">d2fo1e1</a> | Alignment |  | 99.9 | 14 | <b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                    |
| 21 | <a href="#">c2kbaA_</a> | Alignment | not modelled                                                                        | 99.9 | 21 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> integrin-linked protein kinase;<br><b>PDBTitle:</b> solution structure of ilk-pinch complex                                                                                    |
| 22 | <a href="#">d1blxb_</a> | Alignment | not modelled                                                                        | 99.9 | 22 | <b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                    |
| 23 | <a href="#">c3keaB_</a> | Alignment | not modelled                                                                        | 99.9 | 13 | <b>PDB header:</b> viral protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> k1l;<br><b>PDBTitle:</b> structure function studies of vaccinia virus host-range protein k12 reveal a novel ankyrin repeat interaction surface for k1s function                |
| 24 | <a href="#">d1ihba_</a> | Alignment | not modelled                                                                        | 99.9 | 19 | <b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                    |
| 25 | <a href="#">d1ot8a_</a> | Alignment | not modelled                                                                        | 99.9 | 19 | <b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                    |
| 26 | <a href="#">c1ycsB_</a> | Alignment | not modelled                                                                        | 99.9 | 35 | <b>PDB header:</b> complex (anti-oncogene/ankyrin repeats)<br><b>Chain:</b> B: <b>PDB Molecule:</b> 53bp2;<br><b>PDBTitle:</b> p53-53bp2 complex                                                                                                         |
| 27 | <a href="#">d1awcb_</a> | Alignment | not modelled                                                                        | 99.9 | 19 | <b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                    |
| 28 | <a href="#">d1bd8a_</a> | Alignment | not modelled                                                                        | 99.9 | 23 | <b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                    |
| 29 | <a href="#">c3twtd_</a> | Alignment | not modelled                                                                        | 99.9 | 27 | <b>PDB header:</b> signaling protein/peptide<br><b>Chain:</b> D: <b>PDB Molecule:</b> tankyrase-2;<br><b>PDBTitle:</b> crystal structure of arc4 from human tankyrase 2 in                                                                               |

|    |                         |           |              |      |                                                                                                                                                                                                                                                                                           |
|----|-------------------------|-----------|--------------|------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |                         |           |              |      | complex with2 peptide from human mcl1 (chimeric peptide)                                                                                                                                                                                                                                  |
| 30 | <a href="#">c2rfmB</a>  | Alignment | not modelled | 99.9 | 22<br><b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative ankyrin repeat protein tv1425;<br><b>PDBTitle:</b> structure of a thermophilic ankyrin repeat protein                                                                                          |
| 31 | <a href="#">c2jabC</a>  | Alignment | not modelled | 99.9 | 37<br><b>PDB header:</b> de novo protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> h10-2-g3;<br><b>PDBTitle:</b> a designed ankyrin repeat protein evolved to picomolar2 affinity to her2                                                                                                  |
| 32 | <a href="#">c3ui2A</a>  | Alignment | not modelled | 99.9 | 29<br><b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle 43 kda protein, chloroplastic;<br><b>PDBTitle:</b> crystal structure of the cpsrp54 tail bound to cpsrp43                                                                 |
| 33 | <a href="#">d1bi7b</a>  | Alignment | not modelled | 99.9 | 31<br><b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                                               |
| 34 | <a href="#">c2ajaA</a>  | Alignment | not modelled | 99.9 | 12<br><b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> ankyrin repeat family protein;<br><b>PDBTitle:</b> x-ray structure of an ankyrin repeat family protein q5zsv02 from legionella pneumophila. northeast structural genomics3 consortium target lgr21.     |
| 35 | <a href="#">c2v5qC</a>  | Alignment | not modelled | 99.9 | 35<br><b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> design ankyrin repeat protein;<br><b>PDBTitle:</b> crystal structure of wild-type plk-1 kinase domain in2 complex with a selective darpin                                                                   |
| 36 | <a href="#">d2a5ea</a>  | Alignment | not modelled | 99.9 | 23<br><b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                                               |
| 37 | <a href="#">c3jueA</a>  | Alignment | not modelled | 99.8 | 41<br><b>PDB header:</b> protein transport/endocytosis<br><b>Chain:</b> A: <b>PDB Molecule:</b> arfgap with coiled-coil, ank repeat and ph domain-<br><b>PDBTitle:</b> crystal structure of arfgap and ank repeat domain of acap1                                                         |
| 38 | <a href="#">d2ajaa1</a> | Alignment | not modelled | 99.8 | 15<br><b>Fold:</b> alpha-alpha superhelix<br><b>Superfamily:</b> Pseudo ankyrin repeat-like<br><b>Family:</b> Pseudo ankyrin repeat                                                                                                                                                       |
| 39 | <a href="#">c1dcqA</a>  | Alignment | not modelled | 99.8 | 30<br><b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyk2-associated protein beta;<br><b>PDBTitle:</b> crystal structure of the arf-gap domain and ankyrin repeats2 of papbeta.                                                                        |
| 40 | <a href="#">c2nyiA</a>  | Alignment | not modelled | 99.8 | 14<br><b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> transient receptor potential cation channel<br><b>PDBTitle:</b> crystal structure of the ankyrin repeat domain of trpv1                                                                               |
| 41 | <a href="#">d1myoa</a>  | Alignment | not modelled | 99.8 | 32<br><b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                                               |
| 42 | <a href="#">c3deoA</a>  | Alignment | not modelled | 99.8 | 39<br><b>PDB header:</b> protein transport, membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle 43 kda protein;<br><b>PDBTitle:</b> structural basis for specific substrate recognition by the2 chloroplast signal recognition particle protein cpsrp43 |
| 43 | <a href="#">c2xenA</a>  | Alignment | not modelled | 99.8 | 53<br><b>PDB header:</b> de novo protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ni1c mut4;<br><b>PDBTitle:</b> structural determinants for improved thermal stability of2 designed ankyrin repeat proteins with a redesigned c-3 capping module.                                        |
| 44 | <a href="#">d1sw6a</a>  | Alignment | not modelled | 99.8 | 13<br><b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                                               |
| 45 | <a href="#">c1sw6A</a>  | Alignment | not modelled | 99.8 | 13<br><b>PDB header:</b> transcription regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein swi6;<br><b>PDBTitle:</b> s. cerevisiae swi6 ankyrin-repeat fragment                                                                                                        |
| 46 | <a href="#">c1n0qB</a>  | Alignment | not modelled | 99.8 | 50<br><b>PDB header:</b> structural protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3 ankyrin repeats;<br><b>PDBTitle:</b> 3ank: a designed ankyrin repeat protein with three identical consensus2 repeats                                                                               |
| 47 | <a href="#">c2f37B</a>  | Alignment | not modelled | 99.8 | 15<br><b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> transient receptor potential cation channel<br><b>PDBTitle:</b> crystal structure of the ankyrin repeat domain of human2 trpv2                                                                         |
| 48 | <a href="#">d1dcqa1</a> | Alignment | not modelled | 99.8 | 27<br><b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                                               |
| 49 | <a href="#">c2vgeA</a>  | Alignment | not modelled | 99.8 | 17<br><b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> rela-associated inhibitor;<br><b>PDBTitle:</b> crystal structure of the c-terminal region of human iaspp                                                                                                  |
| 50 | <a href="#">c3ehrB</a>  | Alignment | not modelled | 99.8 | 27<br><b>PDB header:</b> signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> osteoclast-stimulating factor 1;<br><b>PDBTitle:</b> crystal structure of human osteoclast stimulating factor                                                                                         |
| 51 | <a href="#">d1ycsb1</a> | Alignment | not modelled | 99.8 | 24<br><b>Fold:</b> beta-hairpin-alpha-hairpin repeat<br><b>Superfamily:</b> Ankyrin repeat<br><b>Family:</b> Ankyrin repeat                                                                                                                                                               |
| 52 | <a href="#">c3c5rB</a>  | Alignment | not modelled | 99.8 | 32<br><b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> brca1-associated ring domain protein 1;<br><b>PDBTitle:</b> crystal structure of the bard1 ankyrin repeat domain and its2 functional consequences                                                       |
| 53 | <a href="#">c3t8kB</a>  | Alignment | not modelled | 99.8 | 14<br><b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> the crystal structure of a functionally unknown protein lebu_0176 from2 leptotrichia buccalis c-1013-b                               |
| 54 | <a href="#">c1ympB</a>  | Alignment | not modelled | 99.8 | 28<br><b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> notch 1 protein;<br><b>PDBTitle:</b> the crystal structure of a partial mouse notch-1 ankyrin2 domain: repeats 4 through 7 preserve an ankyrin fold                                                       |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                               |
|----|-------------------------|-----------|--------------|------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 55 | <a href="#">c1ympA_</a> | Alignment | not modelled | 99.8 | 28 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> notch 1 protein;<br><b>PDBTitle:</b> the crystal structure of a partial mouse notch-1 ankyrin2 domain: repeats 4 through 7 preserve an ankyrin fold                                                 |
| 56 | <a href="#">c2zgdA_</a> | Alignment | not modelled | 99.8 | 53 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3 repeat synthetic ankyrin;<br><b>PDBTitle:</b> asn-hydroxylation stabilises the ankyrin repeat domain fold                                                                                       |
| 57 | <a href="#">c1n0rA_</a> | Alignment | not modelled | 99.8 | 42 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> 4 ankyrin repeats;<br><b>PDBTitle:</b> 4ank: a designed ankyrin repeat protein with four identical 2 consensus repeats                                                                         |
| 58 | <a href="#">c3jxiA_</a> | Alignment | not modelled | 99.7 | 13 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> vanilloid receptor-related osmotically activated channel<br><b>PDBTitle:</b> crystal structure of the chicken trpv4 ankyrin repeat domain                                                        |
| 59 | <a href="#">c2b0oF_</a> | Alignment | not modelled | 99.7 | 21 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> uplc1;<br><b>PDBTitle:</b> crystal structure of uplc1 gap domain                                                                                                                            |
| 60 | <a href="#">c2l6bA_</a> | Alignment | not modelled | 99.7 | 44 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> nr1c;<br><b>PDBTitle:</b> nrc consensus ankyrin repeat protein solution structure                                                                                                                 |
| 61 | <a href="#">c3lvrE_</a> | Alignment | not modelled | 99.6 | 22 | <b>PDB header:</b> protein transport<br><b>Chain:</b> E: <b>PDB Molecule:</b> arf-gap with sh3 domain, ank repeat and ph domain-<br><b>PDBTitle:</b> the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium                             |
| 62 | <a href="#">c2xumS_</a> | Alignment | not modelled | 90.7 | 33 | <b>PDB header:</b> oxidoreductase/peptide<br><b>Chain:</b> S: <b>PDB Molecule:</b> asp-substrate peptide 2;<br><b>PDBTitle:</b> factor inhibiting hif (fih) q239h mutant in complex with zn(ii), nog2 and asp-substrate peptide (20-mer)                                      |
| 63 | <a href="#">c2y0iS_</a> | Alignment | not modelled | 57.1 | 31 | <b>PDB header:</b> oxidoreductase/peptide<br><b>Chain:</b> S: <b>PDB Molecule:</b> tankyrase-2;<br><b>PDBTitle:</b> factor inhibiting hif-1 alpha in complex with tankyrase-2 (tnks2)2 fragment peptide (21-mer)                                                              |
| 64 | <a href="#">c3zrhA_</a> | Alignment | not modelled | 10.7 | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin thioesterase zranb1;<br><b>PDBTitle:</b> crystal structure of the lys29, lys33-linkage-specific traid otu2 deubiquitinase domain reveals an ankyrin-repeat ubiquitin binding3 domain (ankubd) |
| 65 | <a href="#">c2do6A_</a> | Alignment | not modelled | 6.8  | 17 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase cbl-b;<br><b>PDBTitle:</b> solution structure of rsgi ruh-065, a uba domain from human2 cdna                                                                                   |
| 66 | <a href="#">d2hoea1</a> | Alignment | not modelled | 6.4  | 40 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> ROK associated domain                                                                                                                                |
| 67 | <a href="#">c2d9sA_</a> | Alignment | not modelled | 6.2  | 26 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cbl e3 ubiquitin protein ligase;<br><b>PDBTitle:</b> solution structure of rsgi ruh-049, a uba domain from mouse2 cdna                                                                                     |