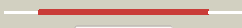














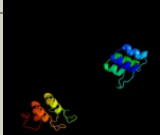

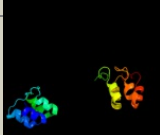






# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A0PJZ0
Date	Wed May 9 17:33:58 BST 2012
Unique Job ID	edf03199eb65a42d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3keaB_</a>	 Alignment		99.9	17	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> k11; <b>PDBTitle:</b> structure function studies of vaccinia virus host-range protein k12 reveal a novel ankyrin repeat interaction surface for k1s function
2	<a href="#">c1n11A_</a>	 Alignment		99.9	27	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> ankyrin; <b>PDBTitle:</b> d34 region of human ankyrin-r and linker
3	<a href="#">d1n11a_</a>	 Alignment		99.9	27	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
4	<a href="#">c3utmA_</a>	 Alignment		99.9	28	<b>PDB header:</b> transferase/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tankyrase-1; <b>PDBTitle:</b> crystal structure of a mouse tankyrase-axin complex
5	<a href="#">d1s70b_</a>	 Alignment		99.9	25	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
6	<a href="#">c1sw6A_</a>	 Alignment		99.9	20	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein swi6; <b>PDBTitle:</b> s. cerevisiae swi6 ankyrin-repeat fragment
7	<a href="#">d1sw6a_</a>	 Alignment		99.9	20	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
8	<a href="#">d1wdya_</a>	 Alignment		99.9	27	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
9	<a href="#">c2xaiD_</a>	 Alignment		99.8	25	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> ankyrin repeat and socs box protein 9; <b>PDBTitle:</b> crystal structure of ankyrin repeat and socs box-containing2 protein 9 (asb9) in complex with elonginb and elonginc
10	<a href="#">d1blxb_</a>	 Alignment		99.8	20	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
11	<a href="#">c2kbaA_</a>	 Alignment		99.8	24	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin-linked protein kinase; <b>PDBTitle:</b> solution structure of ilk-pinch complex

12	<a href="#">d2a5ea_</a>	Alignment		99.8	15	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
13	<a href="#">c2v5qC_</a>	Alignment		99.8	32	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> design ankyrin repeat protein; <b>PDBTitle:</b> crystal structure of wild-type plk-1 kinase domain in2 complex with a selective darpin
14	<a href="#">c1ycsB_</a>	Alignment		99.8	27	<b>PDB header:</b> complex (anti-oncogene/ankyrin repeats) <b>Chain:</b> B: <b>PDB Molecule:</b> 53bp2; <b>PDBTitle:</b> p53-53bp2 complex
15	<a href="#">c2rfaA_</a>	Alignment		99.8	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily v <b>PDBTitle:</b> crystal structure of the mouse trpv6 ankyrin repeat domain
16	<a href="#">c3hraA_</a>	Alignment		99.8	21	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> ankyrin repeat family protein; <b>PDBTitle:</b> crystal structure of ef0377 an ankyrin repeat protein
17	<a href="#">d1k1aa_</a>	Alignment		99.8	31	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
18	<a href="#">d1uoha_</a>	Alignment		99.8	29	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
19	<a href="#">d1iknd_</a>	Alignment		99.8	24	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
20	<a href="#">c3b7bB_</a>	Alignment		99.7	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> euchromatic histone-lysine n-methyltransferase 1; <b>PDBTitle:</b> euhmt1 (glp) ankyrin repeat domain (structure 1)
21	<a href="#">d1oy3d_</a>	Alignment	not modelled	99.7	30	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
22	<a href="#">c1oy3D_</a>	Alignment	not modelled	99.7	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> transcription factor inhibitor i-kappa-b-beta; <b>PDBTitle:</b> crystal structure of an ikbbeta/nf-kb p65 homodimer complex
23	<a href="#">c3eu9B_</a>	Alignment	not modelled	99.7	28	<b>PDB header:</b> protein binding, methyl-lysine-binding p <b>Chain:</b> B: <b>PDB Molecule:</b> huntingtin-interacting protein 14; <b>PDBTitle:</b> the ankyrin repeat domain of huntingtin interacting protein 14
24	<a href="#">c3ljnA_</a>	Alignment	not modelled	99.7	28	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> ankyrin repeat protein from leishmania major
25	<a href="#">d1ixva_</a>	Alignment	not modelled	99.7	25	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
26	<a href="#">c3t8kB_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of a functionally unknown protein lebu_0176 from2 leptotrichia buccalis c-1013-b
27	<a href="#">c3d9hA_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> structural protein, protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> cdna flj77766, highly similar to homo sapiens <b>PDBTitle:</b> crystal structure of the splice variant of human asb92 (hasb9-2), an ankyrin repeat protein
28	<a href="#">c2fo1E_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> gene regulation/signalling protein/dna <b>Chain:</b> E: <b>PDB Molecule:</b> lin-12 protein; <b>PDBTitle:</b> crystal structure of the csl-notch-mastermind ternary2

					complex bound to dna
29	<a href="#">d1bd8a_</a>	Alignment	not modelled	99.7	22 <b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
30	<a href="#">c2jabC_</a>	Alignment	not modelled	99.7	31 <b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> h10-2-g3; <b>PDBTitle:</b> a designed ankyrin repeat protein evolved to picomolar2 affinity to her2
31	<a href="#">c2ajaA_</a>	Alignment	not modelled	99.7	17 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ankyrin repeat family protein; <b>PDBTitle:</b> x-ray structure of an ankyrin repeat family protein q5zsv02 from legionella pneumophila. northeast structural genomics3 consortium target lgr21.
32	<a href="#">c1ympB_</a>	Alignment	not modelled	99.7	22 <b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> notch 1 protein; <b>PDBTitle:</b> the crystal structure of a partial mouse notch-1 ankyrin2 domain: repeats 4 through 7 preserve an ankyrin fold
33	<a href="#">d1ihba_</a>	Alignment	not modelled	99.7	16 <b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
34	<a href="#">c1ympA_</a>	Alignment	not modelled	99.7	22 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> notch 1 protein; <b>PDBTitle:</b> the crystal structure of a partial mouse notch-1 ankyrin2 domain: repeats 4 through 7 preserve an ankyrin fold
35	<a href="#">d2fo1e1</a>	Alignment	not modelled	99.7	18 <b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
36	<a href="#">d1bi7b_</a>	Alignment	not modelled	99.7	16 <b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
37	<a href="#">c2l6bA_</a>	Alignment	not modelled	99.7	33 <b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> nr1c; <b>PDBTitle:</b> nrc consensus ankyrin repeat protein solution structure
38	<a href="#">c2f8xK_</a>	Alignment	not modelled	99.7	21 <b>PDB header:</b> transcription/dna <b>Chain:</b> K: <b>PDB Molecule:</b> neurogenic locus notch homolog protein 1; <b>PDBTitle:</b> crystal structure of activated notch, csl and maml on hes-12 promoter dna sequence
39	<a href="#">c3v30A_</a>	Alignment	not modelled	99.6	28 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein rfxank; <b>PDBTitle:</b> crystal structure of the peptide bound complex of the ankyrin repeat2 domains of human rfxank
40	<a href="#">d2ajaa1</a>	Alignment	not modelled	99.6	13 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Pseudo ankyrin repeat-like <b>Family:</b> Pseudo ankyrin repeat
41	<a href="#">c1n0rA_</a>	Alignment	not modelled	99.6	35 <b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> 4 ankyrin repeats; <b>PDBTitle:</b> 4ank: a designed ankyrin repeat protein with four identical2 consensus repeats
42	<a href="#">c3ui2A_</a>	Alignment	not modelled	99.6	26 <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle 43 kda protein, chloroplastic; <b>PDBTitle:</b> crystal structure of the cpsrp54 tail bound to cpsrp43
43	<a href="#">c2b0oF_</a>	Alignment	not modelled	99.6	22 <b>PDB header:</b> metal binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> uplc1; <b>PDBTitle:</b> crystal structure of uplc1 gap domain
44	<a href="#">d1dcqa1</a>	Alignment	not modelled	99.6	23 <b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
45	<a href="#">c2vgeA_</a>	Alignment	not modelled	99.6	21 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rela-associated inhibitor; <b>PDBTitle:</b> crystal structure of the c-terminal region of human iasp
46	<a href="#">c3deoA_</a>	Alignment	not modelled	99.6	31 <b>PDB header:</b> protein transport, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle 43 kda protein; <b>PDBTitle:</b> structural basis for specific substrate recognition by the2 chloroplast signal recognition particle protein cpsrp43
47	<a href="#">c3ehrB_</a>	Alignment	not modelled	99.6	30 <b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> osteoclast-stimulating factor 1; <b>PDBTitle:</b> crystal structure of human osteoclast stimulating factor
48	<a href="#">c2rfmB_</a>	Alignment	not modelled	99.6	21 <b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> putative ankyrin repeat protein tv1425; <b>PDBTitle:</b> structure of a thermophilic ankyrin repeat protein
49	<a href="#">c3jueA_</a>	Alignment	not modelled	99.6	21 <b>PDB header:</b> protein transport/endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> arfgap with coiled-coil, ank repeat and ph domain- <b>PDBTitle:</b> crystal structure of arfgap and ank repeat domain of acap1
50	<a href="#">d1ot8a_</a>	Alignment	not modelled	99.5	26 <b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
51	<a href="#">c1n0qB_</a>	Alignment	not modelled	99.5	41 <b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> 3 ankyrin repeats; <b>PDBTitle:</b> 3ank: a designed ankyrin repeat protein with three identical consensus2 repeats
52	<a href="#">c3lvrE_</a>	Alignment	not modelled	99.5	23 <b>PDB header:</b> protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> arf-gap with sh3 domain, ank repeat and ph domain- <b>PDBTitle:</b> the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium
53	<a href="#">d1awcb_</a>	Alignment	not modelled	99.5	19 <b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat <b>PDB header:</b> protein binding

54	<a href="#">c3c5rB_</a>	Alignment	not modelled	99.5	30	<b>Chain:</b> B: <b>PDB Molecule:</b> brca1-associated ring domain protein 1; <b>PDBTitle:</b> crystal structure of the bard1 ankyrin repeat domain and its2 functional consequences
55	<a href="#">d1ycsb1</a>	Alignment	not modelled	99.5	23	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
56	<a href="#">c3twiD_</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> signaling protein/peptide <b>Chain:</b> D: <b>PDB Molecule:</b> tankyrase-2; <b>PDBTitle:</b> crystal structure of arc4 from human tankyrase 2 in complex with2 peptide from human mcl1 (chimeric peptide)
57	<a href="#">c1dcqA_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pyk2-associated protein beta; <b>PDBTitle:</b> crystal structure of the arf-gap domain and ankyrin repeats2 of papbeta.
58	<a href="#">d1myoa_</a>	Alignment	not modelled	99.5	26	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Ankyrin repeat <b>Family:</b> Ankyrin repeat
59	<a href="#">c2zgdA_</a>	Alignment	not modelled	99.5	34	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> 3 repeat synthetic ankyrin; <b>PDBTitle:</b> asn-hydroxylation stabilises the ankyrin repeat domain fold
60	<a href="#">c2xenA_</a>	Alignment	not modelled	99.5	37	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> ni1c mut4; <b>PDBTitle:</b> structural determinants for improved thermal stability of2 designed ankyrin repeat proteins with a redesigned c-3 capping module.
61	<a href="#">c2f37B_</a>	Alignment	not modelled	99.4	10	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> transient receptor potential cation channel <b>PDBTitle:</b> crystal structure of the ankyrin repeat domain of human2 trpv2
62	<a href="#">c3jxiA_</a>	Alignment	not modelled	99.4	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> vanilloid receptor-related osmotically activated channel <b>PDBTitle:</b> crystal structure of the chicken trpv4 ankyrin repeat domain
63	<a href="#">c2nyjA_</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> transient receptor potential cation channel <b>PDBTitle:</b> crystal structure of the ankyrin repeat domain of trpv1
64	<a href="#">c2xumS_</a>	Alignment	not modelled	95.7	39	<b>PDB header:</b> oxidoreductase/peptide <b>Chain:</b> S: <b>PDB Molecule:</b> asp-substrate peptide 2; <b>PDBTitle:</b> factor inhibiting hif (fih) q239h mutant in complex with zn(ii), nog2 and asp-substrate peptide (20-mer)
65	<a href="#">c2y0iS_</a>	Alignment	not modelled	68.1	38	<b>PDB header:</b> oxidoreductase/peptide <b>Chain:</b> S: <b>PDB Molecule:</b> tankyrase-2; <b>PDBTitle:</b> factor inhibiting hif-1 alpha in complex with tankyrase-2 (tnks2)2 fragment peptide (21-mer)
66	<a href="#">c2auaB_</a>	Alignment	not modelled	13.8	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> structure of bc2332: a protein of unknown function from bacillus2 cereus
67	<a href="#">c3zrhA_</a>	Alignment	not modelled	11.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin thioesterase zranb1; <b>PDBTitle:</b> crystal structure of the lys29, lys33-linkage-specific trabd otu2 deubiquitinase domain reveals an ankyrin-repeat ubiquitin binding3 domain (ankubd)
68	<a href="#">d2hoea1</a>	Alignment	not modelled	10.5	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
69	<a href="#">d1mv8a3</a>	Alignment	not modelled	9.6	33	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> UDP-glucose/GDP-mannose dehydrogenase C-terminal domain <b>Family:</b> UDP-glucose/GDP-mannose dehydrogenase C-terminal domain
70	<a href="#">c3sviA_</a>	Alignment	not modelled	9.4	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> type iii effector hopab2; <b>PDBTitle:</b> structure of the pto-binding domain of hoppmal generated by limited2 thermolysin digestion
71	<a href="#">c3hgkE_</a>	Alignment	not modelled	8.5	29	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> effector protein hopab2; <b>PDBTitle:</b> crystal structure of effect protein avrptob complexed with2 kinase pto
72	<a href="#">c1x3lA_</a>	Alignment	not modelled	5.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph0495; <b>PDBTitle:</b> crystal structure of the ph0495 protein from pyrococcus horikoshii2 ot3
73	<a href="#">d2b8na1</a>	Alignment	not modelled	5.4	33	<b>Fold:</b> GckA/TtuD-like <b>Superfamily:</b> GckA/TtuD-like <b>Family:</b> GckA/TtuD-like