Phyre^2

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Description	P23325
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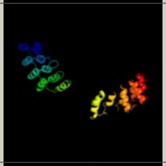
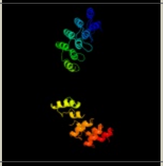
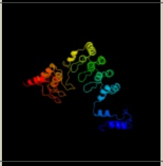
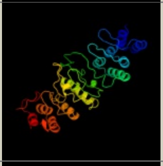
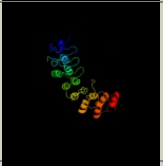
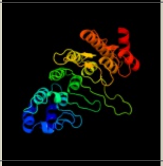
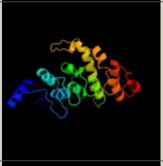
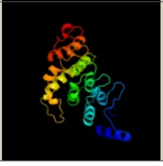
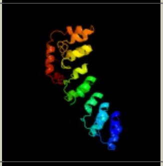
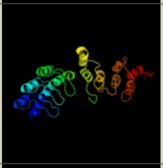
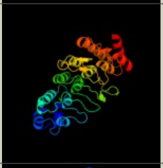
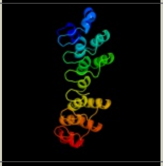
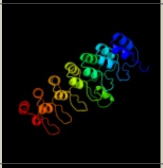
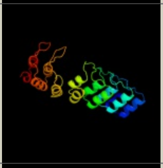
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ajaa1	Alignment		100.0	14	**Fold:**alpha-alpha superhelix **Superfamily:**Pseudo ankyrin repeat-like **Family:**Pseudo ankyrin repeat
2	c3keaB_	Alignment		100.0	20	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**k1l; **PDBTitle:** structure function studies of vaccinia virus host-range protein k12 reveal a novel ankyrin repeat interaction surface for k1s function
3	c1n11A_	Alignment		100.0	26	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ankyrin; **PDBTitle:** d34 region of human ankyrin-r and linker
4	d1n11a_	Alignment		100.0	26	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
5	c2ajaA_	Alignment		100.0	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ankyrin repeat family protein; **PDBTitle:** x-ray structure of an ankyrin repeat family protein q5zsv02 from legionella pneumophila. northeast structural genomics3 consortium target lgr21.
6	d1s70b_	Alignment		100.0	16	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
7	c3ljnA_	Alignment		100.0	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** ankyrin repeat protein from leishmania major
8	c2fo1E_	Alignment		100.0	16	**PDB header:**gene regulation/signalling protein/dna **Chain:** E: **PDB Molecule:**lin-12 protein; **PDBTitle:** crystal structure of the csl-notch-mastermind ternary2 complex bound to dna
9	c3jxiA_	Alignment		100.0	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**vanilloid receptor-related osmotically activated channel **PDBTitle:** crystal structure of the chicken trpv4 ankyrin repeat domain
10	c1sw6A_	Alignment		100.0	13	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**regulatory protein swi6; **PDBTitle:** s. cerevisiae swi6 ankyrin-repeat fragment
11	d1sw6a_	Alignment		100.0	13	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat

12	d2fo1e1	Alignment		100.0	16	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
13	c2xaiD_	Alignment		100.0	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**ankyrin repeat and socs box protein 9; **PDBTitle:** crystal structure of ankyrin repeat and socs box-containing2 protein 9 (asb9) in complex with elonginb and elonginc
14	d1wdya_	Alignment		100.0	20	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
15	c2f37B_	Alignment		100.0	17	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**transient receptor potential cation channel **PDBTitle:** crystal structure of the ankyrin repeat domain of human2 trpv2
16	d1uoha_	Alignment		99.9	19	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
17	d1k1aa_	Alignment		99.9	15	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
18	c3eu9B_	Alignment		99.9	15	**PDB header:**protein binding, methyl-lysine-binding p **Chain:** B: **PDB Molecule:**huntingtin-interacting protein 14; **PDBTitle:** the ankyrin repeat domain of huntingtin interacting protein 14
19	c3ehrB_	Alignment		99.9	14	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**osteoclast-stimulating factor 1; **PDBTitle:** crystal structure of human osteoclast stimulating factor
20	c2nyjA_	Alignment		99.9	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**transient receptor potential cation channel **PDBTitle:** crystal structure of the ankyrin repeat domain of trpv1
21	c3d9hA_	Alignment	not modelled	99.9	16	**PDB header:**structural protein, protein binding **Chain:** A: **PDB Molecule:**cdna flj77766, highly similar to homo sapiens **PDBTitle:** crystal structure of the splice variant of human asb92 (hasb9-2), an ankyrin repeat protein
22	c1ycsB_	Alignment	not modelled	99.9	15	**PDB header:**complex (anti-oncogene/ankyrin repeats) **Chain:** B: **PDB Molecule:**53bp2; **PDBTitle:** p53-53bp2 complex
23	d1ixva_	Alignment	not modelled	99.9	16	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
24	c3b7bB_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**euchromatic histone-lysine n-methyltransferase 1; **PDBTitle:** euhmt1 (glp) ankyrin repeat domain (structure 1)
25	c2f8xK_	Alignment	not modelled	99.9	18	**PDB header:**transcription/dna **Chain:** K: **PDB Molecule:**neurogenic locus notch homolog protein 1; **PDBTitle:** crystal structure of activated notch, csl and maml on hes-12 promoter dna sequence
26	c2vgeA_	Alignment	not modelled	99.9	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rela-associated inhibitor; **PDBTitle:** crystal structure of the c-terminal region of human iaspp
27	c3ui2A_	Alignment	not modelled	99.9	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**signal recognition particle 43 kda protein, chloroplastic; **PDBTitle:** crystal structure of the cpsrp54 tail bound to cpsrp43
28	c1oy3D_	Alignment	not modelled	99.9	19	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**transcription factor inhibitor i-kappa-b-beta;

						PDBTitle: crystal structure of an ikbbeta/nf-kb p65 homodimer complex
29	d1oy3d_	Alignment	not modelled	99.9	19	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
30	d1iknd_	Alignment	not modelled	99.9	21	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
31	c3t8kB_	Alignment	not modelled	99.9	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a functionally unknown protein lebu_0176 from2 leptotrichia buccalis c-1013-b
32	d1ot8a_	Alignment	not modelled	99.9	20	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
33	c2kbxA_	Alignment	not modelled	99.9	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin-linked protein kinase; **PDBTitle:** solution structure of ilk-pinch complex
34	c2rfaA_	Alignment	not modelled	99.9	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**transient receptor potential cation channel subfamily v **PDBTitle:** crystal structure of the mouse trpv6 ankyrin repeat domain
35	c3jueA_	Alignment	not modelled	99.9	14	**PDB header:**protein transport/endocytosis **Chain:** A: **PDB Molecule:**arfgap with coiled-coil, ank repeat and ph domain- **PDBTitle:** crystal structure of arfgap and ank repeat domain of acap1
36	c3deoA_	Alignment	not modelled	99.9	10	**PDB header:**protein transport, membrane protein **Chain:** A: **PDB Molecule:**signal recognition particle 43 kda protein; **PDBTitle:** structural basis for specific substrate recognition by the2 chloroplast signal recognition particle protein cpsrp43
37	c2b0oF_	Alignment	not modelled	99.9	19	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**uplc1; **PDBTitle:** crystal structure of uplc1 gap domain
38	d1dcqa1	Alignment	not modelled	99.9	16	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
39	c1dcqA_	Alignment	not modelled	99.8	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**pyk2-associated protein beta; **PDBTitle:** crystal structure of the arf-gap domain and ankyrin repeats2 of papbeta.
40	c3hraA_	Alignment	not modelled	99.8	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ankyrin repeat family protein; **PDBTitle:** crystal structure of ef0377 an ankyrin repeat protein
41	c3lvrE_	Alignment	not modelled	99.8	15	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**arf-gap with sh3 domain, ank repeat and ph domain- **PDBTitle:** the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium
42	d2a5ea_	Alignment	not modelled	99.8	16	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
43	c3twtD_	Alignment	not modelled	99.8	15	**PDB header:**signaling protein/peptide **Chain:** D: **PDB Molecule:**tankyrase-2; **PDBTitle:** crystal structure of arc4 from human tankyrase 2 in complex with2 peptide from human mcl1 (chimeric peptide)
44	c2rfmB_	Alignment	not modelled	99.8	18	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**putative ankyrin repeat protein tv1425; **PDBTitle:** structure of a thermophilic ankyrin repeat protein
45	c1ympB_	Alignment	not modelled	99.8	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**notch 1 protein; **PDBTitle:** the crystal structure of a partial mouse notch-1 ankyrin2 domain: repeats 4 through 7 preserve an ankyrin fold
46	c1ympA_	Alignment	not modelled	99.8	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**notch 1 protein; **PDBTitle:** the crystal structure of a partial mouse notch-1 ankyrin2 domain: repeats 4 through 7 preserve an ankyrin fold
47	d1blxb_	Alignment	not modelled	99.8	15	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
48	c2v5qC_	Alignment	not modelled	99.8	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**design ankyrin repeat protein; **PDBTitle:** crystal structure of wild-type plk-1 kinase domain in2 complex with a selective darpin
49	c3c5rB_	Alignment	not modelled	99.8	20	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**brca1-associated ring domain protein 1; **PDBTitle:** crystal structure of the bard1 ankyrin repeat domain and its2 functional consequences
50	d1ycsb1	Alignment	not modelled	99.8	15	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
51	c2jabC_	Alignment	not modelled	99.8	20	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**h10-2-g3; **PDBTitle:** a designed ankyrin repeat protein evolved to picomolar2 affinity to her2
52	d1myoa_	Alignment	not modelled	99.8	16	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
53	d1ihba_	Alignment	not modelled	99.8	17	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
						Fold:beta-hairpin-alpha-hairpin repeat

54	d1bi7b_	Alignment	not modelled	99.7	17	**Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
55	d1awcb_	Alignment	not modelled	99.7	22	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
56	c2l6bA_	Alignment	not modelled	99.7	18	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**nr1c; **PDBTitle:** nrc consensus ankyrin repeat protein solution structure
57	d1bd8a_	Alignment	not modelled	99.7	15	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
58	c2zgdA_	Alignment	not modelled	99.7	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**3 repeat synthetic ankyrin; **PDBTitle:** asn-hydroxylation stabilises the ankyrin repeat domain fold
59	c1n0qB_	Alignment	not modelled	99.7	26	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**3 ankyrin repeats; **PDBTitle:** 3ank: a designed ankyrin repeat protein with three identical consensus2 repeats
60	c1n0rA_	Alignment	not modelled	99.7	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**4 ankyrin repeats; **PDBTitle:** 4ank: a designed ankyrin repeat protein with four identical2 consensus repeats
61	c2xenA_	Alignment	not modelled	99.6	20	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**ni1c mut4; **PDBTitle:** structural determinants for improved thermal stability of2 designed ankyrin repeat proteins with a redesigned c-3 capping module.
62	c2xumS_	Alignment	not modelled	77.1	11	**PDB header:**oxidoreductase/peptide **Chain:** S: **PDB Molecule:**asp-substrate peptide 2; **PDBTitle:** factor inhibiting hif (fih) q239h mutant in complex with zn(ii), nog2 and asp-substrate peptide (20-mer)
63	c3zrhA_	Alignment	not modelled	60.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin thioesterase zranb1; **PDBTitle:** crystal structure of the lys29, lys33-linkage-specific trabid otu2 deubiquitinase domain reveals an ankyrin-repeat ubiquitin binding3 domain (ankubd)
64	c1iicA_	Alignment	not modelled	30.0	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**peptide n-myristoyltransferase; **PDBTitle:** crystal structure of saccharomyces cerevisiae n-myristoyltransferase2 with bound myristoylcoa
65	c2p6fA_	Alignment	not modelled	29.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycylpeptide n-tetradecanoyltransferase; **PDBTitle:** crystal structures of saccharomyces cerevisiae n-myristoyltransferase2 with bound myristoyl-coa and inhibitors
66	c2y0iS_	Alignment	not modelled	26.4	17	**PDB header:**oxidoreductase/peptide **Chain:** S: **PDB Molecule:**tankyrase-2; **PDBTitle:** factor inhibiting hif-1 alpha in complex with tankyrase-2 (tnks2)2 fragment peptide (21-mer)
67	c3i08D_	Alignment	not modelled	25.2	19	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**neurogenic locus notch homolog protein 1; **PDBTitle:** crystal structure of the s1-cleaved notch1 negative2 regulatory region (nrr)
68	c3iu2B_	Alignment	not modelled	24.5	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycylpeptide n-tetradecanoyltransferase 1; **PDBTitle:** crystal structure of human type-i n-myristoyltransferase with bound2 myristoyl-coa and inhibitor ddd90096
69	c1rxtB_	Alignment	not modelled	23.6	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycylpeptide n-tetradecanoyltransferase 1; **PDBTitle:** crystal structure of human myristoyl-coa:protein n-2 myristoyltransferase.
70	c2oo4B_	Alignment	not modelled	23.3	15	**PDB header:**cell cycle,signaling protein **Chain:** B: **PDB Molecule:**neurogenic locus notch homolog protein 2; **PDBTitle:** structure of lnr-hd (negative regulatory region) from human notch 2
71	d1iyka1	Alignment	not modelled	9.4	23	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
72	c3ix1B_	Alignment	not modelled	9.0	19	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding **PDBTitle:** periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
73	c3ix1A_	Alignment	not modelled	9.0	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding **PDBTitle:** periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
74	c3mkqB_	Alignment	not modelled	9.0	21	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** crystal structure of yeast alpha/betaprime-cop subcomplex of the copi2 vesicular coat
75	d1iica1	Alignment	not modelled	9.0	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
76	d2bosa_	Alignment	not modelled	8.7	57	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
77	c1ponB_	Alignment	not modelled	8.4	31	**PDB header:**calcium-binding protein **Chain:** B: **PDB Molecule:**troponin c; **PDBTitle:** site iii-site iv troponin c heterodimer, nmr
						PDB header:transferase **Chain:** C: **PDB Molecule:**myristoyl-coa:protein n-

78	c1iylC_	Alignment	not modelled	8.3	23	myristoyltransferase; **PDBTitle:** crystal structure of candida albicans n-myristoyltransferase with non-2 peptidic inhibitor
79	d1rxta1	Alignment	not modelled	7.7	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
80	c2be6F_	Alignment	not modelled	7.2	28	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**voltage-dependent l-type calcium channel alpha-1c subunit; **PDBTitle:** 2.0 a crystal structure of the cav1.2 iq domain-ca/cam complex
81	d2qamc2	Alignment	not modelled	7.0	50	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
82	c2jq5A_	Alignment	not modelled	6.8	38	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**sec-c motif; **PDBTitle:** solution structure of rpa3114, a sec-c motif containing2 protein from rhodopseudomonas palustris; northeast3 structural genomics consortium target rpt5 / ontario4 center for structural proteomics target rp3097
83	c2wuuA_	Alignment	not modelled	6.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-myristoyltransferase; **PDBTitle:** structure of n-myristoyltransferase from l. donovani
84	d1rl2a2	Alignment	not modelled	6.7	57	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
85	d1ukfa_	Alignment	not modelled	6.6	43	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Avirulence protein Avrpph3
86	d2i9wa1	Alignment	not modelled	6.4	38	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SEC-C associated NTF2-like domain
87	c3e4fB_	Alignment	not modelled	5.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminoglycoside n3-acetyltransferase; **PDBTitle:** crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
88	d1v47a2	Alignment	not modelled	5.5	53	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
89	c2khsB_	Alignment	not modelled	5.4	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nuclease; **PDBTitle:** solution structure of snase121:snase(111-143) complex
90	c2i9wA_	Alignment	not modelled	5.3	38	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a sec-c motif containing protein (psyc_2064) from2 psychrobacter arcticus at 1.75 a resolution