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Description	Q8CG79
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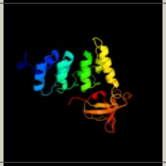
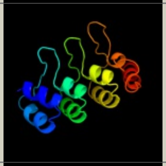
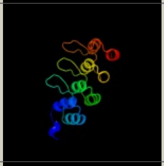
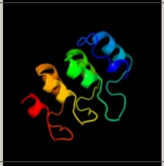
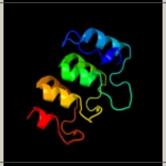
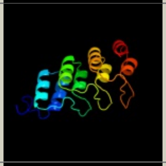
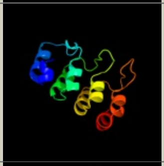
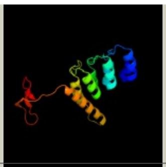
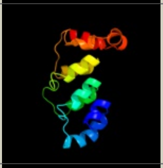
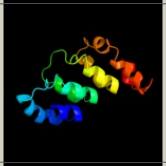
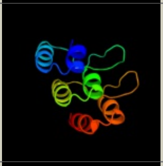
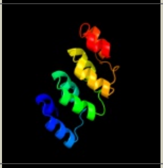
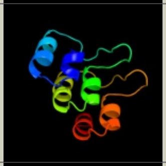
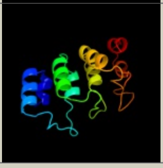
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ycsB_	Alignment		100.0	97	**PDB header:**complex (anti-oncogene/ankyrin repeats) **Chain:** B: **PDB Molecule:**53bp2; **PDBTitle:** p53-53bp2 complex
2	c2vgeA_	Alignment		100.0	54	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rela-associated inhibitor; **PDBTitle:** crystal structure of the c-terminal region of human iaspp
3	d1ycsb1	Alignment		99.9	100	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
4	c3jueA_	Alignment		99.8	25	**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
5	d1n11a_	Alignment		99.8	33	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
6	c1n11A_	Alignment		99.8	33	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ankyrin; **PDBTitle:** d34 region of human ankyrin-r and linker
7	c3t9kA_	Alignment		99.8	26	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**arf-gap with coiled-coil, ank repeat and ph domain- **PDBTitle:** crystal structure of acap1 c-portion mutant s554d fused with integrin2 beta1 peptide
8	c2b0oF_	Alignment		99.8	26	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**uplc1; **PDBTitle:** crystal structure of uplc1 gap domain
9	c3lvrE_	Alignment		99.7	26	**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
10	c1dcqA_	Alignment		99.7	25	**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.
11	c4bepB_	Alignment		99.7	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphocholine transferase ankx; **PDBTitle:** crystal structure of the legionella pneumophila fic domain-2 containing effector ankx protein (apo-form)

12	c3ui2A_	Alignment		99.7	20	**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
13	d1s70b_	Alignment		99.7	38	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
14	d2ajaa1	Alignment		99.7	16	**Fold:**alpha-alpha superhelix **Superfamily:**Pseudo ankyrin repeat-like **Family:**Pseudo ankyrin repeat
15	c2ajaA_	Alignment		99.7	15	**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.
16	c3utmA_	Alignment		99.7	24	**PDB header:**transferase/signaling protein **Chain:** A: **PDB Molecule:**tankyrase-1; **PDBTitle:** crystal structure of a mouse tankyrase-axin complex
17	d1dcqa1	Alignment		99.6	25	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
18	d1ycsb2	Alignment		99.6	92	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
19	c2fo1E_	Alignment		99.6	21	**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
20	c3keaB_	Alignment		99.6	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
21	c3ljnA_	Alignment	not modelled	99.6	31	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** ankyrin repeat protein from leishmania major
22	c4g8kA_	Alignment	not modelled	99.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**2-5a-dependent ribonuclease; **PDBTitle:** intact sensor domain of human rnase l in the inactive signaling state
23	d2fo1e1	Alignment	not modelled	99.6	21	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
24	d1sw6a_	Alignment	not modelled	99.6	19	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
25	c1sw6A_	Alignment	not modelled	99.6	19	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**regulatory protein swi6; **PDBTitle:** s. cerevisiae swi6 ankyrin-repeat fragment
26	d1wdya_	Alignment	not modelled	99.6	25	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
27	c2f8xK_	Alignment	not modelled	99.5	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
28	c4hbdA_	Alignment	not modelled	99.5	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**kn motif and ankyrin repeat domain-containing protein 2; **PDBTitle:** crystal structure of kank2 ankyrin repeats
						Fold:beta-hairpin-alpha-hairpin repeat

29	d1uoha_	Alignment	not modelled	99.5	24	**Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
30	d1iknd_	Alignment	not modelled	99.5	21	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
31	c2zgdA_	Alignment	not modelled	99.5	31	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**3 repeat synthetic ankyrin; **PDBTitle:** asn-hydroxylation stabilises the ankyrin repeat domain fold
32	c2kbxA_	Alignment	not modelled	99.5	23	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin-linked protein kinase; **PDBTitle:** solution structure of ilk-pinch complex
33	c2xaiD_	Alignment	not modelled	99.5	31	**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
34	c3eu9B_	Alignment	not modelled	99.5	25	**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
35	c3hraA_	Alignment	not modelled	99.5	25	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ankyrin repeat family protein; **PDBTitle:** crystal structure of ef0377 an ankyrin repeat protein
36	c2xenA_	Alignment	not modelled	99.5	31	**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.
37	c2uwqA_	Alignment		99.5	98	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis-stimulating of p53 protein 2; **PDBTitle:** solution structure of aspp2 n-terminus
38	d1ot8a_	Alignment	not modelled	99.5	18	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
39	c3d9hA_	Alignment	not modelled	99.5	17	**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
40	c3b7bB_	Alignment	not modelled	99.4	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**euchromatic histone-lysine n-methyltransferase 1; **PDBTitle:** euhmt1 (glp) ankyrin repeat domain (structure 1)
41	c3ehrB_	Alignment	not modelled	99.4	24	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**osteoclast-stimulating factor 1; **PDBTitle:** crystal structure of human osteoclast stimulating factor
42	c3deoA_	Alignment	not modelled	99.4	25	**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
43	d1k1aa_	Alignment	not modelled	99.4	22	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
44	d1ixva_	Alignment	not modelled	99.4	22	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
45	c1n0qB_	Alignment	not modelled	99.4	38	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**3 ankyrin repeats; **PDBTitle:** 3ank: a designed ankyrin repeat protein with three identical consensus2 repeats
46	d1oy3d_	Alignment	not modelled	99.4	24	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
47	c1oy3D_	Alignment	not modelled	99.4	24	**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
48	c2f37B_	Alignment	not modelled	99.4	18	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**transient receptor potential cation channel **PDBTitle:** crystal structure of the ankyrin repeat domain of human2 trpv2
49	c2rfaA_	Alignment	not modelled	99.4	23	**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
50	c3v31A_	Alignment	not modelled	99.4	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ankyrin repeat family a protein 2; **PDBTitle:** crystal structure of the peptide bound complex of the ankyrin repeat2 domains of human ankra2
51	d1blxb_	Alignment	not modelled	99.4	24	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
52	c3v30A_	Alignment	not modelled	99.4	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna-binding protein rfxank; **PDBTitle:** crystal structure of the peptide bound complex of the ankyrin repeat2 domains of human rfxank
53	c3jxiA_	Alignment	not modelled	99.4	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**vanilloid receptor-related osmotically activated channel

						PDBTitle: crystal structure of the chicken trpv4 ankyrin repeat domain
54	c3nmzD_	Alignment	not modelled	99.4	38	**PDB header:**cell adhesion/cell cycle **Chain:** D: **PDB Molecule:**rho guanine nucleotide exchange factor 4; **PDBTitle:** crytal structure of apc complexed with asef
55	c3t8kB_	Alignment	not modelled	99.3	12	**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
56	c1wyxA_	Alignment	not modelled	99.3	31	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**crk-associated substrate; **PDBTitle:** the crystal structure of the p130cas sh3 domain at 1.1 a2 resolution
57	c2rfmB_	Alignment	not modelled	99.3	30	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**putative ankyrin repeat protein tv1425; **PDBTitle:** structure of a thermophilic ankyrin repeat protein
58	c2kymA_	Alignment	not modelled	99.3	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**bud emergence protein 1; **PDBTitle:** solution structure of the bem1p sh3-ci domain from l.elongisporus in2 complex with ste20p peptide
59	d1ug1a_	Alignment	not modelled	99.3	20	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
60	c2nyjA_	Alignment	not modelled	99.3	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**transient receptor potential cation channel **PDBTitle:** crystal structure of the ankyrin repeat domain of trpv1
61	c4b93B_	Alignment	not modelled	99.3	26	**PDB header:**exocytosis **Chain:** B: **PDB Molecule:**ankyrin repeat domain-containing protein 27; **PDBTitle:** complex of vamp7 cytoplasmic domain with 2nd ankyrin repeat2 domain of varp
62	c1griA_	Alignment	not modelled	99.3	35	**PDB header:**signal transduction adaptor **Chain:** A: **PDB Molecule:**growth factor bound protein 2; **PDBTitle:** grb2
63	c2dnuA_	Alignment	not modelled	99.3	34	**PDB header:**structural genomics, structural protein **Chain:** A: **PDB Molecule:**sh3 multiple domains 1; **PDBTitle:** solution structure of rsgi ruh-061, a sh3 domain from human
64	c1n0rA_	Alignment	not modelled	99.3	60	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**4 ankyrin repeats; **PDBTitle:** 4ank: a designed ankyrin repeat protein with four identical2 consensus repeats
65	c2yupA_	Alignment	not modelled	99.3	24	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**vinexin; **PDBTitle:** solution structure of the second sh3 domain of human vinexin
66	c4gmrA_	Alignment	not modelled	99.3	37	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**or266 de novo protein; **PDBTitle:** crystal structure of engineered protein. northeast structural genomics2 consortium target or266.
67	c2jxbA_	Alignment	not modelled	99.3	35	**PDB header:**signaling protein complex **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd3 epsilon chain, **PDBTitle:** structure of cd3epsilon-nck2 first sh3 domain complex
68	c2egeA_	Alignment	not modelled	99.3	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein kiaa1666; **PDBTitle:** solution structure of the third sh3 domain from human2 kiaa1666 protein
69	c3jv3A_	Alignment	not modelled	99.3	31	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intersectin-1; **PDBTitle:** structure of sh3e-dh unit of murine intersectin-1l
70	d1bi7b_	Alignment	not modelled	99.3	21	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
71	c1u3oA_	Alignment	not modelled	99.3	32	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**huntingtin-associated protein-interacting **PDBTitle:** solution structure of rat kalirin n-terminal sh3 domain
72	d1ng2a2	Alignment	not modelled	99.3	31	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
73	d1i1ja_	Alignment	not modelled	99.3	22	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
74	c2i0nA_	Alignment	not modelled	99.3	30	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**class vii unconventional myosin; **PDBTitle:** structure of dictyostelium discoideum myosin vii sh3 domain2 with adjacent proline rich region
75	c2ysqA_	Alignment	not modelled	99.3	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 9; **PDBTitle:** solution structure of the sh3 domain from rho guanine2 nucleotide exchange factor 9
76	c2d8hA_	Alignment	not modelled	99.3	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**sh3yl1 protein; **PDBTitle:** solution structure of the sh3 domain of hypothetical2 protein sh3yl1
77	d1ihba_	Alignment	not modelled	99.3	26	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
78	c2k2mA_	Alignment	not modelled	99.3	31	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**eps8-like protein 1; **PDBTitle:** structural basis of pxxdy motif recognition in sh3 binding
79	c1mj0A_	Alignment	not modelled	99.3	34	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**sank e3_5 protein; **PDBTitle:** sank e3_5: an artificial ankyrin repeat protein

80	c2l6bA_	Alignment	not modelled	99.3	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**nr1c; **PDBTitle:** nrc consensus ankyrin repeat protein solution structure
81	c2yunA_	Alignment	not modelled	99.3	31	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nostrin; **PDBTitle:** solution structure of the sh3 domain of human nostrin
82	d1awcb_	Alignment	not modelled	99.2	26	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
83	d1uffa_	Alignment	not modelled	99.2	25	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
84	d1k9aa1	Alignment	not modelled	99.2	17	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
85	c1w70A_	Alignment	not modelled	99.2	21	**PDB header:**sh3 domain **Chain:** A: **PDB Molecule:**neutrophil cytosol factor 4; **PDBTitle:** sh3 domain of p40phox complexed with c-terminal polyproline2 region of p47phox
86	c2creA_	Alignment	not modelled	99.2	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hef-like protein; **PDBTitle:** solution structure of rsgi ruh-036, an sh3 domain from2 human cdna
87	c2a28D_	Alignment	not modelled	99.2	35	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**bzz1 protein; **PDBTitle:** atomic-resolution crystal structure of the second sh32 domain of yeast bzz1 determined from a pseudomerohedrally3 twinned crystal
88	c2azsA_	Alignment	not modelled	99.2	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sh2-sh3 adapter protein drk; **PDBTitle:** nmr structure of the n-terminal sh3 domain of drk2 (calculated without noe restraints)
89	c1wx6A_	Alignment	not modelled	99.2	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cytoplasmic protein nck2; **PDBTitle:** solution structure of the sh3 domain of the human2 cytoplasmic protein nck2
90	c2eywA_	Alignment	not modelled	99.2	32	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**v-crk sarcoma virus ct10 oncogene homolog **PDBTitle:** n-terminal sh3 domain of ct10-regulated kinase
91	c1x2pA_	Alignment	not modelled	99.2	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arginine n-methyltransferase 2; **PDBTitle:** solution structure of the sh3 domain of the protein2 arginine n-methyltransferase 2
92	d1bd8a_	Alignment	not modelled	99.2	26	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
93	c1x2qA_	Alignment	not modelled	99.2	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal transducing adapter molecule 2; **PDBTitle:** solution structure of the sh3 domain of the signal2 transducing adaptor molecule 2
94	c2ekhA_	Alignment	not modelled	99.2	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sh3 and px domain-containing protein 2a; **PDBTitle:** solution structures of the sh3 domain of human kiaa0418
95	d1ov3a2	Alignment	not modelled	99.2	32	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
96	c2csqA_	Alignment	not modelled	99.2	29	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**rim binding protein 2; **PDBTitle:** solution structure of the second sh3 domain of human rim-2 binding protein 2
97	c2jabC_	Alignment	not modelled	99.2	29	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**h10-2-g3; **PDBTitle:** a designed ankyrin repeat protein evolved to picomolar2 affinity to her2
98	c2xmfA_	Alignment	not modelled	99.2	32	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**myosin 1e sh3; **PDBTitle:** myosin 1e sh3
99	c2ct4A_	Alignment	not modelled	99.2	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cdc42-interacting protein 4; **PDBTitle:** solution strutcure of the sh3 domain of the cdc42-2 interacting protein 4
100	c2v5qC_	Alignment	not modelled	99.2	38	**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
101	d1gbra_	Alignment	not modelled	99.2	35	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
102	d1udla_	Alignment	not modelled	99.2	25	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
103	c2l0aA_	Alignment	not modelled	99.2	32	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal transducing adapter molecule 1; **PDBTitle:** solution nmr structure of signal transducing adapter molecule 1 stam-12 from homo sapiens, northeast structural genomics consortium target3 hr4479e
104	d2a5ea_	Alignment	not modelled	99.2	19	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
105	c1x6gA_	Alignment	not modelled	99.2	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**megakaryocyte-associated tyrosine-protein kinase; **PDBTitle:** solution structures of the sh3 domain of human2 megakaryocyte-associated tyrosine-protein kinase.

106	c1mv3A_	Alignment	not modelled	99.2	32	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**myc box dependent interacting protein 1; **PDBTitle:** nmr structure of the tumor suppressor bin1: alternative2 splicing in melanoma and interaction with c-myc
107	c2dl7A_	Alignment	not modelled	99.2	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kiaa0769 protein; **PDBTitle:** solution structure of the second sh3 domain of human2 kiaa0769 protein
108	c2dl5A_	Alignment	not modelled	99.2	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kiaa0769 protein; **PDBTitle:** solution structure of the first sh3 domain of human2 kiaa0769 protein
109	c2cudA_	Alignment	not modelled	99.2	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**src-like-adapter; **PDBTitle:** solution structure of the sh3 domain of the human src-like2 adopter protein (slap)
110	c2dl8A_	Alignment	not modelled	99.2	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**slit-robo rho gtpase-activating protein 2; **PDBTitle:** solution structure of the sh3 domain of human slit-robo rho2 gtpase-activating protein 2
111	c2yuoA_	Alignment	not modelled	99.2	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**run and tbc1 domain containing 3; **PDBTitle:** solution structure of the sh3 domain of mouse run and tbc12 domain containing 3
112	d1uuea_	Alignment	not modelled	99.2	31	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
113	d1e6ga_	Alignment	not modelled	99.2	31	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
114	c2dmoA_	Alignment	not modelled	99.2	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**neutrophil cytosol factor 2; **PDBTitle:** refined solution structure of the 1st sh3 domain from human2 neutrophil cytosol factor 2 (ncf-2)
115	d1k4us_	Alignment	not modelled	99.2	35	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
116	c2yt6A_	Alignment	not modelled	99.2	31	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**adult male urinary bladder cdna, riken full- **PDBTitle:** solution structure of the sh3_1 domain of yamaguchi sarcoma2 viral (v-yes) oncogene homolog 1
117	d1uhca_	Alignment	not modelled	99.2	25	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
118	d1uj0a_	Alignment	not modelled	99.2	34	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
119	c2cubA_	Alignment	not modelled	99.2	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cytoplasmic protein nck1; **PDBTitle:** solution structure of the sh3 domain of the human2 cytoplasmic protein nck1
120	c3nhnA_	Alignment	not modelled	99.2	44	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase hck; **PDBTitle:** crystal structure of the src-family kinase hck sh3-sh2-linker2 regulatory region