Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P46108
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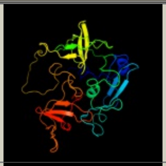
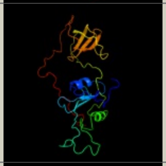
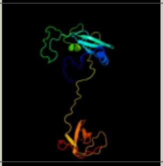
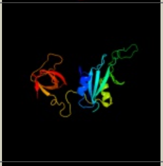
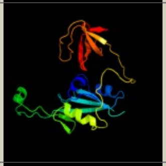
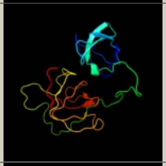
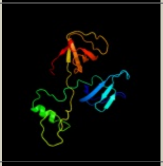
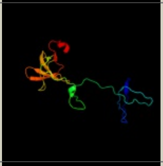
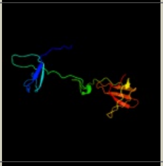
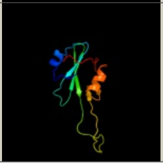
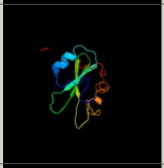
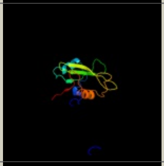
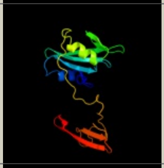
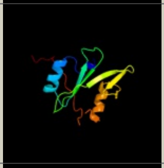
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2eyzA_	Alignment		100.0	100	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**v-crk sarcoma virus ct10 oncogene homolog **PDBTitle:** ct10-regulated kinase isoform ii
2	c2lqnA_	Alignment		100.0	61	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**crk-like protein; **PDBTitle:** solution structure of crkl
3	c2dvjA_	Alignment		100.0	97	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**v-crk sarcoma virus ct10 oncogene homolog, **PDBTitle:** phosphorylated crk-ii
4	c2eyyA_	Alignment		100.0	100	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**v-crk sarcoma virus ct10 oncogene homolog **PDBTitle:** ct10-regulated kinase isoform i
5	c3qwyA_	Alignment		100.0	38	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cell death abnormality protein 2; **PDBTitle:** ced-2
6	c3qwxX_	Alignment		100.0	38	**PDB header:**signaling protein **Chain:** X: **PDB Molecule:**cell death abnormality protein 2; **PDBTitle:** ced-2 1-174
7	c2l3sA_	Alignment		100.0	91	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**autoinhibited crk protein; **PDBTitle:** structure of the autoinhibited crk
8	c1griA_	Alignment		100.0	24	**PDB header:**signal transduction adaptor **Chain:** A: **PDB Molecule:**growth factor bound protein 2; **PDBTitle:** grb2
9	c1ng2A_	Alignment		100.0	20	**PDB header:**oxidoreductase activator **Chain:** A: **PDB Molecule:**neutrophil cytosolic factor 1; **PDBTitle:** structure of autoinhibited p47phox
10	c1ov3A_	Alignment		100.0	20	**PDB header:**oxidoreductase activator **Chain:** A: **PDB Molecule:**neutrophil cytosol factor 1; **PDBTitle:** structure of the p22phox-p47phox complex
11	d2eyva1	Alignment		99.9	100	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain

12	c2eo3A_	Alignment		99.9	78	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**crk-like protein; **PDBTitle:** solution structure of the sh2 domain from human crk-like2 protein
13	c3hizB_	Alignment		99.9	31	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit **PDBTitle:** crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha
14	d2oq1a1	Alignment		99.9	27	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
15	c2oq1A_	Alignment		99.9	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase zap-70; **PDBTitle:** tandem sh2 domains of zap-70 with 19-mer zeta1 peptide
16	c2y3aB_	Alignment		99.9	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit beta; **PDBTitle:** crystal structure of p110beta in complex with icsh2 of p85beta and2 the drug gdc-0941
17	c2shpA_	Alignment		99.9	23	**PDB header:**tyrosine phosphatase **Chain:** A: **PDB Molecule:**shp-2; **PDBTitle:** tyrosine phosphatase shp-2
18	c2gsbA_	Alignment		99.9	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ras gtpase-activating protein 1; **PDBTitle:** solution structure of the second sh2 domain of human ras2 gtpase-activating protein 1
19	c3gqiB_	Alignment		99.9	32	**PDB header:**transferase/transferase inhibitor **Chain:** B: **PDB Molecule:**phospholipase c-gamma-1; **PDBTitle:** crystal structure of activated receptor tyrosine kinase in complex2 with substrates
20	d1a81a1	Alignment		99.9	22	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
21	c2ozoA_	Alignment	not modelled	99.9	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase zap-70; **PDBTitle:** autoinhibited intact human zap-70
22	c2fo0A_	Alignment	not modelled	99.9	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase abl1 (1b isoform); **PDBTitle:** organization of the sh3-sh2 unit in active and inactive forms of the2 c-abl tyrosine kinase
23	c2dlyA_	Alignment	not modelled	99.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fyn-related kinase; **PDBTitle:** solution structure of the sh2 domain of murine fyn-related2 kinase
24	d1a81e1	Alignment	not modelled	99.8	23	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
25	c2b3oA_	Alignment	not modelled	99.8	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase, non-receptor type **PDBTitle:** crystal structure of human tyrosine phosphatase shp-1
26	d2izva2	Alignment	not modelled	99.8	26	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
27	c2eo6A_	Alignment	not modelled	99.8	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**b-cell linker protein; **PDBTitle:** solution structure of the sh2 domain from mouse b-cell2 linker protein blnk
28	c2crhA_	Alignment	not modelled	99.8	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**vav proto-oncogene; **PDBTitle:** solution structure of the sh2 domain of human proto-2 oncogene protein vav1

29	c1ka6A_	Alignment	not modelled	99.8	22	**PDB header:**immune system **Chain:** A: **PDB Molecule:**sh2 domain protein 1a; **PDBTitle:** sap/sh2d1a bound to peptide n-py
30	d1blja_	Alignment	not modelled	99.8	28	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
31	c2ysxA_	Alignment	not modelled	99.8	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signaling inositol polyphosphate phosphatase **PDBTitle:** solution structure of the human ship sh2 domain
32	d1pica_	Alignment	not modelled	99.8	33	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
33	d1csya_	Alignment	not modelled	99.8	27	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
34	c2dlzA_	Alignment	not modelled	99.8	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein vav-2; **PDBTitle:** solution structure of the sh2 domain of human protein vav-2
35	c1mv3A_	Alignment	not modelled	99.8	15	**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
36	c2ablA_	Alignment	not modelled	99.8	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**abl tyrosine kinase; **PDBTitle:** sh3-sh2 domain fragment of human bcr-abl tyrosine kinase
37	d1fhsa_	Alignment	not modelled	99.8	23	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
38	d2oq1a2	Alignment	not modelled	99.8	33	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
39	c2dbkA_	Alignment	not modelled	99.8	65	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**crk-like protein; **PDBTitle:** solution structures of the sh3 domain of human crk-like2 protein
40	d1opka2	Alignment	not modelled	99.8	35	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
41	d1rjaa_	Alignment	not modelled	99.8	34	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
42	c1oplA_	Alignment	not modelled	99.8	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase; **PDBTitle:** structural basis for the auto-inhibition of c-abl tyrosine2 kinase
43	c2vifA_	Alignment	not modelled	99.8	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**suppressor of cytokine signalling 6; **PDBTitle:** crystal structure of socs6 sh2 domain in complex with a c-kit2 phosphopeptide
44	d3c7ia1	Alignment	not modelled	99.8	28	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
45	d1a81e2	Alignment	not modelled	99.8	28	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
46	d1r1qa_	Alignment	not modelled	99.8	31	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
47	c3ps5A_	Alignment	not modelled	99.8	31	**PDB header:**hydrolase, signaling protein **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase non-receptor type 6; **PDBTitle:** crystal structure of the full-length human protein tyrosine2 phosphatase shp-1
48	c1k9aB_	Alignment	not modelled	99.8	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carboxyl-terminal src kinase; **PDBTitle:** crystal structure analysis of full-length carboxyl-terminal2 src kinase at 2.5 a resolution
49	d1k9aa2	Alignment	not modelled	99.8	33	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
50	d1nrva_	Alignment	not modelled	99.8	28	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
51	d1d4ta_	Alignment	not modelled	99.8	23	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
52	d2shpa2	Alignment	not modelled	99.8	30	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
53	d1udla_	Alignment	not modelled	99.8	25	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
54	c2c9wA_	Alignment	not modelled	99.8	25	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**suppressor of cytokine signaling 2; **PDBTitle:** crystal structure of socs-2 in complex with elongin-b and2 elongin-c at 1.9a resolution
55	d1jwoa_	Alignment	not modelled	99.8	34	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain

56	c2hmhA_	Alignment	not modelled	99.8	30	**PDB header:**cytokine regulator **Chain:** A: **PDB Molecule:**suppressor of cytokine signaling 3; **PDBTitle:** crystal structure of socs3 in complex with gp130(ptyr757)2 phosphopeptide.
57	c2ci8A_	Alignment	not modelled	99.8	33	**PDB header:**translation **Chain:** A: **PDB Molecule:**cytoplasmic protein nck1; **PDBTitle:** sh2 domain of human nck1 adaptor protein - uncomplexed
58	d1a81a2	Alignment	not modelled	99.8	28	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
59	c2lctA_	Alignment	not modelled	99.8	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** solution structure of the vav1 sh2 domain complexed with a syk-derived2 doubly phosphorylated peptide
60	d2cs0a1	Alignment	not modelled	99.8	28	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
61	d1jyra_	Alignment	not modelled	99.8	29	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
62	d1lkka_	Alignment	not modelled	99.8	32	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
63	d1rpya_	Alignment	not modelled	99.8	28	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
64	c2eobA_	Alignment	not modelled	99.8	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1-phosphatidylinositol-4,5-bisphosphate **PDBTitle:** solution structure of the second sh2 domain from rat plc2 gamma-2
65	c1y57A_	Alignment	not modelled	99.8	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase src; **PDBTitle:** structure of unphosphorylated c-src in complex with an inhibitor
66	d2c9wa2	Alignment	not modelled	99.8	25	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
67	c1x6cA_	Alignment	not modelled	99.8	37	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase, non-receptor type **PDBTitle:** solution structures of the sh2 domain of human protein-2 tyrosine phosphatase shp-1
68	c2kk6A_	Alignment	not modelled	99.8	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase fer; **PDBTitle:** solution structure of sh2 domain of proto-oncogene tyrosine-2 protein kinase fer from homo sapiens, northeast structural3 genomics consortium (nesg) target hr3461d
69	d1o48a_	Alignment	not modelled	99.8	34	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
70	c1x27F_	Alignment	not modelled	99.8	32	**PDB header:**signaling protein **Chain:** F: **PDB Molecule:**proto-oncogene tyrosine-protein kinase lck; **PDBTitle:** crystal structure of lck sh2-sh3 with sh2 binding site of2 p130cas
71	c1a81E_	Alignment	not modelled	99.8	23	**PDB header:**complex (transferase/peptide) **Chain:** E: **PDB Molecule:**syk kinase; **PDBTitle:** crystal structure of the tandem sh2 domain of the syk kinase bound to2 a dually tyrosine-phosphorylated itam
72	d1i3za_	Alignment	not modelled	99.8	31	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
73	d1ayaa_	Alignment	not modelled	99.8	33	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
74	c2izvA_	Alignment	not modelled	99.8	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**suppressor of cytokine signaling 4; **PDBTitle:** crystal structure of socs-4 in complex with elongin-b and2 elongin-c at 2.55a resolution
75	c3nhnA_	Alignment	not modelled	99.8	34	**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
76	d1qcfa2	Alignment	not modelled	99.8	33	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
77	d1luia_	Alignment	not modelled	99.8	33	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
78	c2eyxA_	Alignment	not modelled	99.8	100	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**v-crk sarcoma virus ct10 oncogene homolog **PDBTitle:** c-terminal sh3 domain of ct10-regulated kinase
79	c2ge9A_	Alignment	not modelled	99.8	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase btk; **PDBTitle:** solution structures of the sh2 domain of bruton's tyrosine2 kinase
80	d1xa6a2	Alignment	not modelled	99.8	27	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
						Fold:SH2-like

81	d1bkla_	Alignment	not modelled	99.8	34	**Superfamily:**SH2 domain **Family:**SH2 domain
82	c2dcrA_	Alignment	not modelled	99.8	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase fes/fps; **PDBTitle:** fully automated solution structure determination of the fes2 sh2 domain
83	c2el8A_	Alignment	not modelled	99.8	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal-transducing adaptor protein 2; **PDBTitle:** solution structure of the human stap2 sh2 domain
84	c2ebpA_	Alignment	not modelled	99.8	27	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**sam and sh3 domain-containing protein 1; **PDBTitle:** solution structure of the sh3 domain from human sam and sh32 domain containing protein 1
85	d1g83a2	Alignment	not modelled	99.8	31	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
86	c2knoA_	Alignment	not modelled	99.8	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tensin-like c1 domain-containing phosphatase; **PDBTitle:** nmr solution structure of sh2 domain of the human tensin like c12 domain containing phosphatase (tenc1)
87	c2h8hA_	Alignment	not modelled	99.8	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase src; **PDBTitle:** src kinase in complex with a quinazoline inhibitor
88	d1f2fa_	Alignment	not modelled	99.8	34	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
89	c1rqqC_	Alignment	not modelled	99.8	31	**PDB header:**transferase/signaling protein **Chain:** C: **PDB Molecule:**adaptor protein aps; **PDBTitle:** crystal structure of the insulin receptor kinase in complex2 with the sh2 domain of aps
90	d2qmsa1	Alignment	not modelled	99.8	32	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
91	d1mila_	Alignment	not modelled	99.8	39	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
92	c2c0iA_	Alignment	not modelled	99.8	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase hck; **PDBTitle:** src family kinase hck with bound inhibitor a-420983
93	d1fu6a_	Alignment	not modelled	99.8	32	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
94	d2fcia1	Alignment	not modelled	99.8	30	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
95	d2shpa3	Alignment	not modelled	99.8	38	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
96	d1cwea_	Alignment	not modelled	99.7	35	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
97	c2dx1A_	Alignment	not modelled	99.7	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 4; **PDBTitle:** crystal structure of rhogef protein asef
98	c2ed0A_	Alignment	not modelled	99.7	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**abl interactor 2; **PDBTitle:** solution structure of the sh3 domain of abl interactor 22 (abelson interactor 2)
99	d1qada_	Alignment	not modelled	99.7	37	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
100	c3gxxB_	Alignment	not modelled	99.7	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** structure of the sh2 domain of the candida glabrata2 transcription elongation factor spt6, crystal form b
101	d1ng2a2	Alignment	not modelled	99.7	16	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
102	c2bzxA_	Alignment	not modelled	99.7	69	**PDB header:**sh3 domain **Chain:** A: **PDB Molecule:**crk-like protein; **PDBTitle:** atomic model of crkl-sh3c monomer
103	c3nmzD_	Alignment	not modelled	99.7	17	**PDB header:**cell adhesion/cell cycle **Chain:** D: **PDB Molecule:**rho guanine nucleotide exchange factor 4; **PDBTitle:** crytal structure of apc complexed with asef
104	c2cubA_	Alignment	not modelled	99.7	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cytoplasmic protein nck1; **PDBTitle:** solution structure of the sh3 domain of the human2 cytoplasmic protein nck1
105	c1g83A_	Alignment	not modelled	99.7	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase fyn; **PDBTitle:** crystal structure of fyn sh3-sh2
106	c3mazA_	Alignment	not modelled	99.7	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal-transducing adaptor protein 1; **PDBTitle:** crystal structure of the human brdg1/stap-1 sh2 domain in complex with2 the ntal ptyr136 peptide
						PDB header:oxidoreductase

107	c2dybA_	Alignment	not modelled	99.7	20	**Chain:** A: **PDB Molecule:**neutrophil cytosol factor 4; **PDBTitle:** the crystal structure of human p40(phox)
108	c2ekxA_	Alignment	not modelled	99.7	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cytoplasmic tyrosine-protein kinase bmx; **PDBTitle:** solution structure of the human bmx sh2 domain
109	c2nwmA_	Alignment	not modelled	99.7	28	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**vinexin; **PDBTitle:** solution structure of the first sh3 domain of human vinexin2 and its interaction with the peptides from vinculin
110	c2bz8B_	Alignment	not modelled	99.7	32	**PDB header:**sh3 domain **Chain:** B: **PDB Molecule:**sh3-domain kinase binding protein 1; **PDBTitle:** n-terminal sh3 domain of cin85 bound to cbl-b peptide
111	c2kymA_	Alignment	not modelled	99.7	18	**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
112	c2ekhA_	Alignment	not modelled	99.7	16	**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
113	c2djqA_	Alignment	not modelled	99.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sh3 domain containing ring finger 2; **PDBTitle:** the solution structure of the first sh3 domain of mouse sh32 domain containing ring finger 2
114	c2yuoA_	Alignment	not modelled	99.7	23	**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
115	c2cr4A_	Alignment	not modelled	99.7	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sh3 domain-binding protein 2; **PDBTitle:** solution structure of the sh2 domain of human sh3bp2 protein
116	c1x2qA_	Alignment	not modelled	99.7	19	**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
117	c2dl8A_	Alignment	not modelled	99.7	19	**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
118	c2oi3A_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase hck; **PDBTitle:** nmr structure analysis of the hematopoetic cell kinase sh32 domain complexed with an artificial high affinity ligand3 (pd1)
119	c2ysqA_	Alignment	not modelled	99.7	20	**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
120	c2ed1A_	Alignment	not modelled	99.7	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**130 kda phosphatidylinositol 4,5-biphosphate- **PDBTitle:** solution structure of the sh3 domain of 130 kda2 phosphatidylinositol 4,5-biphosphate-dependent arf1 gtpase-3 activating protein