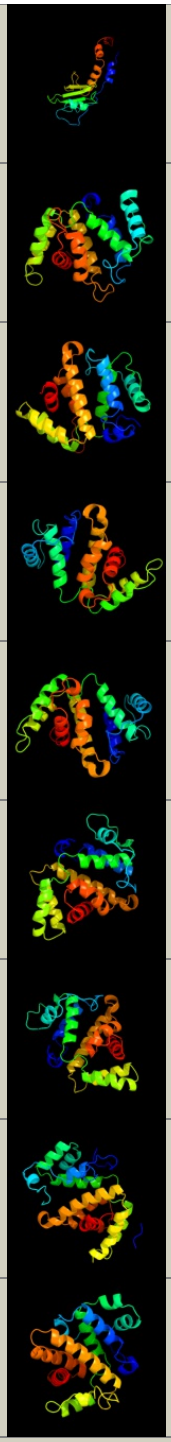
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q965N4
Date	Fri May 3 21:39:00 BST 2013
Unique Job ID	971f5ce47b1bdda5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1xa6A_	Alignment		100.0	40	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**beta2-chimaerin; **PDBTitle:** crystal structure of the human beta2-chimaerin
2	c3iugA_	Alignment		100.0	32	**PDB header:**splicing **Chain:** A: **PDB Molecule:**rho/cdc42/rac gtpase-activating protein rics; **PDBTitle:** crystal structure of the rhogap domain of rics
3	c3byiA_	Alignment		100.0	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho gtpase activating protein 15; **PDBTitle:** crystal structure of human rho gtpase activating protein 15 (arhgap15)
4	c3kuqA_	Alignment		100.0	27	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**rho gtpase-activating protein 7; **PDBTitle:** crystal structure of the dlc1 rhogap domain
5	c2ee5A_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rho gtpase activating protein 5 variant; **PDBTitle:** solution structure of the n-teruminus extended rhogap2 domain from human rho gtpase activating protein 5 variant
6	d1tx4a_	Alignment		100.0	24	**Fold:**GTPase activation domain, GAP **Superfamily:**GTPase activation domain, GAP **Family:**BCR-homology GTPase activation domain (BH-domain)
7	c2ngrB_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (gtpase activating protein (rhg)); **PDBTitle:** transition state complex for gtp hydrolysis by cdc42:2 comparisons of the high resolution structures for cdc423 bound to the active and catalytically compromised forms of4 the cdc42-gap.
8	d1xa6a1	Alignment		100.0	36	**Fold:**GTPase activation domain, GAP **Superfamily:**GTPase activation domain, GAP **Family:**BCR-homology GTPase activation domain (BH-domain)
9	c3fk2B_	Alignment		100.0	30	**PDB header:**signaling protein, hydrolase activator **Chain:** B: **PDB Molecule:**glucocorticoid receptor dna-binding factor 1; **PDBTitle:** crystal structure of the rhogap domain of human2 glucocorticoid receptor dna-binding factor 1
10	c3qisA_	Alignment		100.0	17	**PDB header:**hydrolase/protein binding **Chain:** A: **PDB Molecule:**inositol polyphosphate 5-phosphatase ocrl-1; **PDBTitle:** recognition of the f&h motif by the lowe syndrome protein ocrl
11	c3msxB_	Alignment		100.0	23	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**rho gtpase-activating protein 20; **PDBTitle:** crystal structure of rhoa.gdp.mgf3 in complex with gap domain of2 arhgap20

12	d1xa6a2	Alignment		100.0	41	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
13	c2ovjA_	Alignment		100.0	32	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rac gtpase-activating protein 1; **PDBTitle:** the crystal structure of the human rac gtpase activating protein 12 (racgap1) mgcracgap.
14	c2qv2A_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inositol polyphosphate 5-phosphatase ocrl-1; **PDBTitle:** a role of the lowe syndrome protein ocrl in early steps of2 the endocytic pathway
15	c1f7cA_	Alignment		100.0	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rhogap protein; **PDBTitle:** crystal structure of the bh domain from graf, the gtpase2 regulator associated with focal adhesion kinase
16	d1f7ca_	Alignment		100.0	30	**Fold:**GTPase activation domain, GAP **Superfamily:**GTPase activation domain, GAP **Family:**BCR-homology GTPase activation domain (BH-domain)
17	d1pbwa_	Alignment		100.0	23	**Fold:**GTPase activation domain, GAP **Superfamily:**GTPase activation domain, GAP **Family:**BCR-homology GTPase activation domain (BH-domain)
18	c1pbwB_	Alignment		100.0	22	**PDB header:**phosphotransferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase; **PDBTitle:** structure of bcr-homology (bh) domain
19	c3eapD_	Alignment		100.0	27	**PDB header:**hydrolase activator **Chain:** D: **PDB Molecule:**rho gtpase-activating protein 11a; **PDBTitle:** crystal structure of the rhogap domain of arhgap11a
20	c2xs6A_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit beta; **PDBTitle:** crystal structure of the rhogap domain of human pik3r2
21	c3ps5A_	Alignment	not modelled	99.8	27	**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
22	c2b3oA_	Alignment	not modelled	99.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase, non-receptor type **PDBTitle:** crystal structure of human tyrosine phosphatase shp-1
23	c3hizB_	Alignment	not modelled	99.7	22	**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
24	c2shpA_	Alignment	not modelled	99.7	30	**PDB header:**tyrosine phosphatase **Chain:** A: **PDB Molecule:**shp-2; **PDBTitle:** tyrosine phosphatase shp-2
25	c2fo0A_	Alignment	not modelled	99.7	36	**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
26	c1rqqC_	Alignment	not modelled	99.7	26	**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
27	c2ozoA_	Alignment	not modelled	99.7	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase zap-70; **PDBTitle:** autoinhibited intact human zap-70
						Fold:SH2-like

28	d2oq1a1	Alignment	not modelled	99.7	25	**Superfamily:**SH2 domain **Family:**SH2 domain
29	c2y3aB_	Alignment	not modelled	99.6	21	**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
30	c4fl2A_	Alignment	not modelled	99.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase syk; **PDBTitle:** structural and biophysical characterization of the syk activation2 switch
31	c2oq1A_	Alignment	not modelled	99.6	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase zap-70; **PDBTitle:** tandem sh2 domains of zap-70 with 19-mer zeta1 peptide
32	c1k9aB_	Alignment	not modelled	99.6	35	**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
33	d2izva2	Alignment	not modelled	99.6	16	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
34	c1oplA_	Alignment	not modelled	99.6	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase; **PDBTitle:** structural basis for the auto-inhibition of c-abl tyrosine2 kinase
35	c2izvA_	Alignment	not modelled	99.6	17	**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
36	d1a81a1	Alignment	not modelled	99.6	23	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
37	c2vifA_	Alignment	not modelled	99.6	24	**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
38	c2lqnA_	Alignment	not modelled	99.6	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**crk-like protein; **PDBTitle:** solution structure of crkl
39	c1x6cA_	Alignment	not modelled	99.6	29	**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
40	c2ci8A_	Alignment	not modelled	99.6	27	**PDB header:**translation **Chain:** A: **PDB Molecule:**cytoplasmic protein nck1; **PDBTitle:** sh2 domain of human nck1 adaptor protein - uncomplexed
41	d1rpya_	Alignment	not modelled	99.6	27	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
42	c2c9wA_	Alignment	not modelled	99.6	35	**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
43	c2hdxB_	Alignment	not modelled	99.6	33	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**sh2-b ph domain containing signaling mediator 1 **PDBTitle:** crystal structure of the src homology-2 domain of sh2-b in2 complex with jak2 ptyr813 phosphopeptide
44	d2shpa2	Alignment	not modelled	99.6	31	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
45	c2eo6A_	Alignment	not modelled	99.6	29	**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
46	d1nrva_	Alignment	not modelled	99.6	26	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
47	d2eyva1	Alignment	not modelled	99.6	28	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
48	d2oq1a2	Alignment	not modelled	99.6	24	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
49	d1r1qa_	Alignment	not modelled	99.6	22	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
50	d1fhsa_	Alignment	not modelled	99.6	29	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
51	c2gsbA_	Alignment	not modelled	99.6	20	**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
52	c2hmhA_	Alignment	not modelled	99.6	21	**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.
53	c2ysxA_	Alignment	not modelled	99.6	37	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signaling inositol polyphosphate phosphatase **PDBTitle:** solution structure of the human ship sh2 domain

54	c2el8A_	Alignment	not modelled	99.6	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal-transducing adaptor protein 2; **PDBTitle:** solution structure of the human stap2 sh2 domain
55	d1a81e1	Alignment	not modelled	99.6	22	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
56	c2eobA_	Alignment	not modelled	99.6	23	**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
57	c2dlzA_	Alignment	not modelled	99.6	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein vav-2; **PDBTitle:** solution structure of the sh2 domain of human protein vav-2
58	c2crhA_	Alignment	not modelled	99.6	22	**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
59	c2ablA_	Alignment	not modelled	99.6	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**abl tyrosine kinase; **PDBTitle:** sh3-sh2 domain fragment of human bcr-abl tyrosine kinase
60	c3gqiB_	Alignment	not modelled	99.6	24	**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
61	d2shpa3	Alignment	not modelled	99.6	31	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
62	d1ayaa_	Alignment	not modelled	99.6	28	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
63	c1ka6A_	Alignment	not modelled	99.6	31	**PDB header:**immune system **Chain:** A: **PDB Molecule:**sh2 domain protein 1a; **PDBTitle:** sap/sh2d1a bound to peptide n-py
64	d3c7ia1	Alignment	not modelled	99.5	27	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
65	d1rjaa_	Alignment	not modelled	99.5	26	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
66	d1jwoa_	Alignment	not modelled	99.5	33	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
67	c1y57A_	Alignment	not modelled	99.5	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase src; **PDBTitle:** structure of unphosphorylated c-src in complex with an inhibitor
68	d1jyra_	Alignment	not modelled	99.5	32	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
69	c2eo3A_	Alignment	not modelled	99.5	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**crk-like protein; **PDBTitle:** solution structure of the sh2 domain from human crk-like2 protein
70	d1k9aa2	Alignment	not modelled	99.5	35	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
71	c2dlyA_	Alignment	not modelled	99.5	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fyn-related kinase; **PDBTitle:** solution structure of the sh2 domain of murine fyn-related2 kinase
72	c1x27F_	Alignment	not modelled	99.5	22	**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
73	d1a81a2	Alignment	not modelled	99.5	31	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
74	c2kk6A_	Alignment	not modelled	99.5	26	**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
75	d1a81e2	Alignment	not modelled	99.5	27	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
76	d1d4ta_	Alignment	not modelled	99.5	28	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
77	d2c9wa2	Alignment	not modelled	99.5	33	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
78	c2lctA_	Alignment	not modelled	99.5	20	**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
79	c2c0iA_	Alignment	not modelled	99.5	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase hck; **PDBTitle:** src family kinase hck with bound inhibitor a-420983

80	c1a81E_	Alignment	not modelled	99.5	27	**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
81	c2dcrA_	Alignment	not modelled	99.5	26	**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
82	d1opka2	Alignment	not modelled	99.5	28	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
83	c2h8hA_	Alignment	not modelled	99.5	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase src; **PDBTitle:** src kinase in complex with a quinazoline inhibitor
84	c2knoA_	Alignment	not modelled	99.5	18	**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)
85	d1mila_	Alignment	not modelled	99.5	29	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
86	d1pica_	Alignment	not modelled	99.5	21	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
87	d1i3za_	Alignment	not modelled	99.5	29	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
88	d1csya_	Alignment	not modelled	99.5	32	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
89	c2eyzA_	Alignment	not modelled	99.5	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**v-crk sarcoma virus ct10 oncogene homolog **PDBTitle:** ct10-regulated kinase isoform ii
90	d1lkka_	Alignment	not modelled	99.5	29	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
91	d1blja_	Alignment	not modelled	99.5	30	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
92	c2augB_	Alignment	not modelled	99.5	28	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**growth factor receptor-bound protein 14; **PDBTitle:** crystal structure of the grb14 sh2 domain
93	d2qmsa1	Alignment	not modelled	99.5	27	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
94	d1qada_	Alignment	not modelled	99.5	22	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
95	d1cwea_	Alignment	not modelled	99.5	34	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
96	d2cs0a1	Alignment	not modelled	99.5	30	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
97	c2dvjA_	Alignment	not modelled	99.5	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**v-crk sarcoma virus ct10 oncogene homolog, **PDBTitle:** phosphorylated crk-ii
98	d1qcfa2	Alignment	not modelled	99.5	30	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
99	c3gxxB_	Alignment	not modelled	99.5	15	**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
100	d1bkla_	Alignment	not modelled	99.5	34	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
101	d1f2fa_	Alignment	not modelled	99.4	35	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
102	c2eyyA_	Alignment	not modelled	99.4	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**v-crk sarcoma virus ct10 oncogene homolog **PDBTitle:** ct10-regulated kinase isoform i
103	c3nhnA_	Alignment	not modelled	99.4	27	**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
104	d2fcia1	Alignment	not modelled	99.4	23	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
105	c3mazA_	Alignment	not modelled	99.4	17	**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
						Fold:SH2-like

106	d1fu6a_	Alignment	not modelled	99.4	22	**Superfamily:**SH2 domain **Family:**SH2 domain
107	d1o48a_	Alignment	not modelled	99.4	38	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
108	c2ge9A_	Alignment	not modelled	99.4	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase btk; **PDBTitle:** solution structures of the sh2 domain of bruton's tyrosine2 kinase
109	c3qwyA_	Alignment	not modelled	99.4	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cell death abnormality protein 2; **PDBTitle:** ced-2
110	d1g83a2	Alignment	not modelled	99.4	32	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
111	d1luia_	Alignment	not modelled	99.4	31	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
112	c3qwxX_	Alignment	not modelled	99.3	22	**PDB header:**signaling protein **Chain:** X: **PDB Molecule:**cell death abnormality protein 2; **PDBTitle:** ced-2 1-174
113	c2cr4A_	Alignment	not modelled	99.3	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sh3 domain-binding protein 2; **PDBTitle:** solution structure of the sh2 domain of human sh3bp2 protein
114	c1g83A_	Alignment	not modelled	99.3	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase fyn; **PDBTitle:** crystal structure of fyn sh3-sh2
115	c3or8A_	Alignment	not modelled	99.3	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** a tandem sh2 domain in transcription elongation factor spt6
116	c3pfqA_	Alignment	not modelled	99.3	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase c beta type; **PDBTitle:** crystal structure and allosteric activation of protein kinase c beta2 ii
117	d1xa6a3	Alignment	not modelled	99.3	52	**Fold:**Cysteine-rich domain **Superfamily:**Cysteine-rich domain **Family:**Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
118	d1uura3	Alignment	not modelled	99.3	16	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
119	c2ekxA_	Alignment	not modelled	99.3	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cytoplasmic tyrosine-protein kinase bmx; **PDBTitle:** solution structure of the human bmx sh2 domain
120	c2e73A_	Alignment	not modelled	99.3	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase c gamma type; **PDBTitle:** solution structure of the phorbol esters/diacylglycerol2 binding domain of protein kinase c gamma