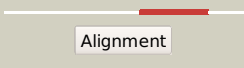

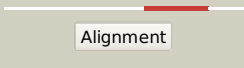

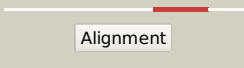

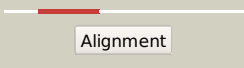

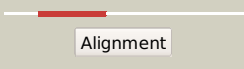

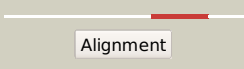

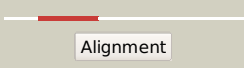

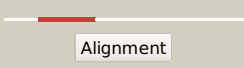

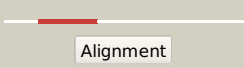

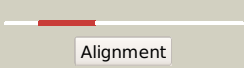

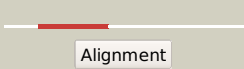

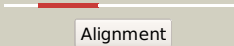

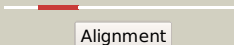

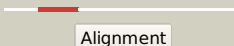

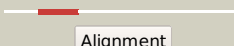

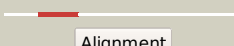

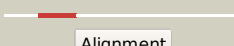

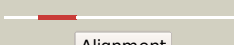
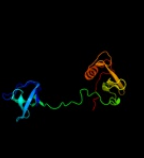




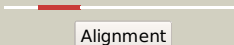
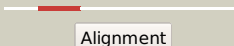
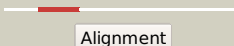


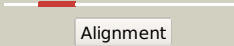
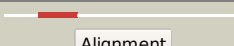
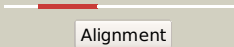


# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q95XA9
Date	Sun Jun 30 11:04:27 BST 2013
Unique Job ID	e743689df95aa392



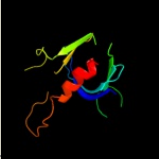
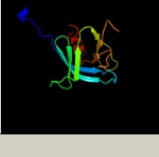
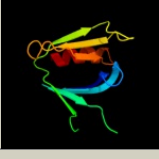
Detailed template information


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3bxjB_</a>	 Alignment		100.0	17	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ras gtpase-activating protein syngap; <b>PDBTitle:</b> crystal structure of the c2-gap fragment of syngap
2	<a href="#">d1wera_</a>	 Alignment		100.0	17	<b>Fold:</b> GTPase activation domain, GAP <b>Superfamily:</b> GTPase activation domain, GAP <b>Family:</b> p120GAP domain-like
3	<a href="#">d1nfla_</a>	 Alignment		100.0	18	<b>Fold:</b> GTPase activation domain, GAP <b>Superfamily:</b> GTPase activation domain, GAP <b>Family:</b> p120GAP domain-like
4	<a href="#">c2b3oA_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase, non-receptor type <b>PDBTitle:</b> crystal structure of human tyrosine phosphatase shp-1
5	<a href="#">c2shpA_</a>	 Alignment		100.0	21	<b>PDB header:</b> tyrosine phosphatase <b>Chain:</b> A: <b>PDB Molecule:</b> shp-2; <b>PDBTitle:</b> tyrosine phosphatase shp-2
6	<a href="#">c3fayA_</a>	 Alignment		100.0	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> ras gtpase-activating-like protein iqgap1; <b>PDBTitle:</b> crystal structure of the gap-related domain of iqgap1
7	<a href="#">c3gqiB_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> phospholipase c-gamma-1; <b>PDBTitle:</b> crystal structure of activated receptor tyrosine kinase in complex2 with substrates
8	<a href="#">c3ps5A_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase non-receptor type 6; <b>PDBTitle:</b> crystal structure of the full-length human protein tyrosine2 phosphatase shp-1
9	<a href="#">c2oq1A_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase zap-70; <b>PDBTitle:</b> tandem sh2 domains of zap-70 with 19-mer zeta1 peptide
10	<a href="#">c1a81E_</a>	 Alignment		100.0	20	<b>PDB header:</b> complex (transferase/peptide) <b>Chain:</b> E: <b>PDB Molecule:</b> syk kinase; <b>PDBTitle:</b> crystal structure of the tandem sh2 domain of the syk kinase bound to2 a dually tyrosine-phosphorylated itam
11	<a href="#">c4fi2A_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase syk; <b>PDBTitle:</b> structural and biophysical characterization of the syk activation2 switch

12	<a href="#">c2ozoA_</a>	 Alignment		99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase zap-70; <b>PDBTitle:</b> autoinhibited intact human zap-70
13	<a href="#">c2lqnA_</a>	 Alignment		99.9	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> crk-like protein; <b>PDBTitle:</b> solution structure of crkl
14	<a href="#">c2ablA_</a>	 Alignment		99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> abl tyrosine kinase; <b>PDBTitle:</b> sh3-sh2 domain fragment of human bcr-abl tyrosine kinase
15	<a href="#">c2fo0A_</a>	 Alignment		99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase abl1 (1b isoform); <b>PDBTitle:</b> organization of the sh3-sh2 unit in active and inactive forms of the2 c-abl tyrosine kinase
16	<a href="#">c2eyyA_</a>	 Alignment		99.9	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> v-crk sarcoma virus ct10 oncogene homolog <b>PDBTitle:</b> ct10-regulated kinase isoform i
17	<a href="#">c1x27F_</a>	 Alignment		99.9	21	<b>PDB header:</b> signaling protein <b>Chain:</b> F: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase lck; <b>PDBTitle:</b> crystal structure of lck sh2-sh3 with sh2 binding site of2 p130cas
18	<a href="#">c1k9aB_</a>	 Alignment		99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> carboxyl-terminal src kinase; <b>PDBTitle:</b> crystal structure analysis of full-length carboxyl-terminal2 src kinase at 2.5 a resolution
19	<a href="#">c3nhnA_</a>	 Alignment		99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase hck; <b>PDBTitle:</b> crystal structure of the src-family kinase hck sh3-sh2-linker2 regulatory region
20	<a href="#">c3qwyA_</a>	 Alignment		99.9	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cell death abnormality protein 2; <b>PDBTitle:</b> ced-2
21	<a href="#">c2h8hA_</a>	 Alignment	not modelled	99.9	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase src; <b>PDBTitle:</b> src kinase in complex with a quinazoline inhibitor
22	<a href="#">c1y57A_</a>	 Alignment	not modelled	99.9	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase src; <b>PDBTitle:</b> structure of unphosphorylated c-src in complex with an inhibitor
23	<a href="#">c1oplA_</a>	 Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase; <b>PDBTitle:</b> structural basis for the auto-inhibition of c-abl tyrosine2 kinase
24	<a href="#">c1g83A_</a>	 Alignment	not modelled	99.9	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase fyn; <b>PDBTitle:</b> crystal structure of fyn sh3-sh2
25	<a href="#">c2dviA_</a>	 Alignment	not modelled	99.9	28	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> v-crk sarcoma virus ct10 oncogene homolog, <b>PDBTitle:</b> phosphorylated crk-ii
26	<a href="#">c3qwxX_</a>	 Alignment	not modelled	99.9	16	<b>PDB header:</b> signaling protein <b>Chain:</b> X: <b>PDB Molecule:</b> cell death abnormality protein 2; <b>PDBTitle:</b> ced-2 1-174
27	<a href="#">c2eyzA_</a>	 Alignment	not modelled	99.9	30	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> v-crk sarcoma virus ct10 oncogene homolog <b>PDBTitle:</b> ct10-regulated kinase isoform ii
28	<a href="#">c2xp1A_</a>	 Alignment	not modelled	99.8	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> spt6; <b>PDBTitle:</b> structure of the tandem sh2 domains from antonospora locustae2 transcription elongation factor spt6

29	<a href="#">c2c0iA</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase hck; <b>PDBTitle:</b> src family kinase hck with bound inhibitor a-420983
30	<a href="#">c3or8A</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor spt6; <b>PDBTitle:</b> a tandem sh2 domain in transcription elongation factor spt6
31	<a href="#">c2gsbA</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ras gtpase-activating protein 1; <b>PDBTitle:</b> solution structure of the second sh2 domain of human ras2 gtpase-activating protein 1
32	<a href="#">c2eo3A</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> crk-like protein; <b>PDBTitle:</b> solution structure of the sh2 domain from human crk-like2 protein
33	<a href="#">c2hdxB</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> sh2-b ph domain containing signaling mediator 1 <b>PDBTitle:</b> crystal structure of the src homology-2 domain of sh2-b in2 complex with jak2 ptyr813 phosphopeptide
34	<a href="#">d2oq1a1</a>	Alignment	not modelled	99.5	18	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
35	<a href="#">c2crhA</a>	Alignment	not modelled	99.5	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> vav proto-oncogene; <b>PDBTitle:</b> solution structure of the sh2 domain of human proto-2 oncogene protein vav1
36	<a href="#">d1fhSA</a>	Alignment	not modelled	99.5	23	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
37	<a href="#">c2vifA</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> suppressor of cytokine signalling 6; <b>PDBTitle:</b> crystal structure of socs6 sh2 domain in complex with a c-kit2 phosphopeptide
38	<a href="#">c2dcrA</a>	Alignment	not modelled	99.5	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase fes/fps; <b>PDBTitle:</b> fully automated solution structure determination of the fes2 sh2 domain
39	<a href="#">d1i3za</a>	Alignment	not modelled	99.5	21	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
40	<a href="#">c2dlyA</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fyn-related kinase; <b>PDBTitle:</b> solution structure of the sh2 domain of murine fyn-related2 kinase
41	<a href="#">d2oq1a2</a>	Alignment	not modelled	99.5	30	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
42	<a href="#">c2ci8A</a>	Alignment	not modelled	99.5	28	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> cytoplasmic protein nck1; <b>PDBTitle:</b> sh2 domain of human nck1 adaptor protein - uncomplexed
43	<a href="#">d1a81a2</a>	Alignment	not modelled	99.5	23	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
44	<a href="#">d1xa6a2</a>	Alignment	not modelled	99.5	21	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
45	<a href="#">c2y3aB</a>	Alignment	not modelled	99.5	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit beta; <b>PDBTitle:</b> crystal structure of p110beta in complex with icsh2 of p85beta and2 the drug gdc-0941
46	<a href="#">c2kk6A</a>	Alignment	not modelled	99.5	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase fer; <b>PDBTitle:</b> solution structure of sh2 domain of proto-oncogene tyrosine-2 protein kinase fer from homo sapiens, northeast structural3 genomics consortium (nesg) target hr3461d
47	<a href="#">c3hizB</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> transferase/oncoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit <b>PDBTitle:</b> crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha
48	<a href="#">d2shpa2</a>	Alignment	not modelled	99.5	20	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
49	<a href="#">c2dlzA</a>	Alignment	not modelled	99.5	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein vav-2; <b>PDBTitle:</b> solution structure of the sh2 domain of human protein vav-2
50	<a href="#">d3c7ia1</a>	Alignment	not modelled	99.5	18	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
51	<a href="#">d1a81e2</a>	Alignment	not modelled	99.5	22	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
52	<a href="#">d1csya</a>	Alignment	not modelled	99.5	23	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
53	<a href="#">c2eobA</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-phosphatidylinositol-4,5-bisphosphate <b>PDBTitle:</b> solution structure of the second sh2 domain from rat plc2 gamma-2

54	<a href="#">d1rjaa_</a>	Alignment	not modelled	99.5	22	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
55	<a href="#">c2ysxA_</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> signaling inositol polyphosphate phosphatase <b>PDBTitle:</b> solution structure of the human ship sh2 domain
56	<a href="#">c1x6cA_</a>	Alignment	not modelled	99.4	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase, non-receptor type <b>PDBTitle:</b> solution structures of the sh2 domain of human protein-2 tyrosine phosphatase shp-1
57	<a href="#">d1jwoa_</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
58	<a href="#">c2eo6A_</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> b-cell linker protein; <b>PDBTitle:</b> solution structure of the sh2 domain from mouse b-cell2 linker protein blk
59	<a href="#">d1ayaa_</a>	Alignment	not modelled	99.4	23	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
60	<a href="#">d2shpa3</a>	Alignment	not modelled	99.4	33	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
61	<a href="#">d1k9aa2</a>	Alignment	not modelled	99.4	22	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
62	<a href="#">d1r1qa_</a>	Alignment	not modelled	99.4	30	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
63	<a href="#">c1ka6A_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> sh2 domain protein 1a; <b>PDBTitle:</b> sap/sh2d1a bound to peptide n-py
64	<a href="#">d1a81a1</a>	Alignment	not modelled	99.4	21	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
65	<a href="#">d1jyra_</a>	Alignment	not modelled	99.4	23	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
66	<a href="#">d1opka2</a>	Alignment	not modelled	99.4	15	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
67	<a href="#">d1pica_</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
68	<a href="#">d1blja_</a>	Alignment	not modelled	99.4	30	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
69	<a href="#">c2lctA_</a>	Alignment	not modelled	99.4	31	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene vav; <b>PDBTitle:</b> solution structure of the vav1 sh2 domain complexed with a syk-derived2 doubly phosphorylated peptide
70	<a href="#">d1mila_</a>	Alignment	not modelled	99.4	28	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
71	<a href="#">d2izva2</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
72	<a href="#">d2cs0a1</a>	Alignment	not modelled	99.4	27	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
73	<a href="#">d1a81e1</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
74	<a href="#">d1nrva_</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
75	<a href="#">d1qada_</a>	Alignment	not modelled	99.4	24	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
76	<a href="#">c2c9wA_</a>	Alignment	not modelled	99.4	23	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> suppressor of cytokine signaling 2; <b>PDBTitle:</b> crystal structure of socs-2 in complex with elongin-b and2 elongin-c at 1.9a resolution
77	<a href="#">c2augB_</a>	Alignment	not modelled	99.4	31	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> growth factor receptor-bound protein 14; <b>PDBTitle:</b> crystal structure of the grb14 sh2 domain
78	<a href="#">d2eyva1</a>	Alignment	not modelled	99.4	23	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
79	<a href="#">c2el8A_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal-transducing adaptor protein 2; <b>PDBTitle:</b> solution structure of the human stap2 sh2 domain
80	<a href="#">c1rqcC_</a>	Alignment	not modelled	99.4	27	<b>PDB header:</b> transferase/signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> adaptor protein aps; <b>PDBTitle:</b> crystal structure of the insulin receptor kinase in complex2 with the sh2 domain of aps

81	<a href="#">d2fcia1</a>	Alignment	not modelled	99.4	10	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
82	<a href="#">d1rpya_</a>	Alignment	not modelled	99.3	27	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
83	<a href="#">c2d9zA_</a>	Alignment		99.3	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c, nu type; <b>PDBTitle:</b> solution structure of the ph domain of protein kinase c, nu2 type from human
84	<a href="#">d1o48a_</a>	Alignment	not modelled	99.3	26	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
85	<a href="#">d1cwea_</a>	Alignment	not modelled	99.3	31	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
86	<a href="#">d1lkka_</a>	Alignment	not modelled	99.3	31	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
87	<a href="#">c1gria_</a>	Alignment	not modelled	99.3	24	<b>PDB header:</b> signal transduction adaptor <b>Chain:</b> A: <b>PDB Molecule:</b> growth factor bound protein 2; <b>PDBTitle:</b> grb2
88	<a href="#">d1qcfa2</a>	Alignment	not modelled	99.3	28	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
89	<a href="#">d1g83a2</a>	Alignment	not modelled	99.3	36	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
90	<a href="#">c3fehA_</a>	Alignment		99.3	12	<b>PDB header:</b> hydrolase activator <b>Chain:</b> A: <b>PDB Molecule:</b> centaurin-alpha-1; <b>PDBTitle:</b> crystal structure of full length centaurin alpha-1
91	<a href="#">d1bkla_</a>	Alignment	not modelled	99.3	21	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
92	<a href="#">d1d4ta_</a>	Alignment	not modelled	99.3	17	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
93	<a href="#">d2coaa1</a>	Alignment		99.3	12	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Pleckstrin-homology domain (PH domain)
94	<a href="#">c2r09A_</a>	Alignment		99.3	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytohesin-3; <b>PDBTitle:</b> crystal structure of autoinhibited form of grp1 arf gtpase exchange2 factor
95	<a href="#">c2knoA_</a>	Alignment	not modelled	99.3	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tensin-like c1 domain-containing phosphatase; <b>PDBTitle:</b> nmr solution structure of sh2 domain of the human tensin like c12 domain containing phosphatase (tenc1)
96	<a href="#">d2fjla1</a>	Alignment		99.3	16	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Pleckstrin-homology domain (PH domain)
97	<a href="#">d2c9wa2</a>	Alignment	not modelled	99.3	24	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
98	<a href="#">d1f2fa_</a>	Alignment	not modelled	99.3	27	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
99	<a href="#">c2ge9A_</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase btk; <b>PDBTitle:</b> solution structures of the sh2 domain of bruton's tyrosine2 kinase
100	<a href="#">d1luia_</a>	Alignment	not modelled	99.3	20	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
101	<a href="#">c2izvA_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> suppressor of cytokine signaling 4; <b>PDBTitle:</b> crystal structure of socs-4 in complex with elongin-b and2 elongin-c at 2.55a resolution
102	<a href="#">c3mazA_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal-transducing adaptor protein 1; <b>PDBTitle:</b> crystal structure of the human brdg1/stap-1 sh2 domain

					in complex with2 the ntal ptyr136 peptide
103	<a href="#">c2luA_</a>	Alignment		99.2	17 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase tec; <b>PDBTitle:</b> solution nmr structure of ph domain of tyrosine-protein kinase tec2 from homo sapiens, northeast structural genomics consortium (nesg)3 target hr3504c
104	<a href="#">d2dyna_</a>	Alignment	not modelled	99.2	12 <b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Pleckstrin-homology domain (PH domain)
105	<a href="#">c2dhiA_</a>	Alignment	not modelled	99.2	23 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> pleckstrin homology domain-containing family b <b>PDBTitle:</b> solution structure of the ph domain of evectin-2 from mouse
106	<a href="#">c2d9vA_</a>	Alignment	not modelled	99.2	19 <b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> pleckstrin homology domain-containing protein <b>PDBTitle:</b> solution structure of the ph domain of pleckstrin homology2 domain-containing protein family b member 1 from mouse
107	<a href="#">c3gxB_</a>	Alignment	not modelled	99.2	22 <b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription elongation factor spt6; <b>PDBTitle:</b> structure of the sh2 domain of the candida glabrata2 transcription elongation factor spt6, crystal form b
108	<a href="#">c2ekxA_</a>	Alignment	not modelled	99.2	20 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytoplasmic tyrosine-protein kinase bmx; <b>PDBTitle:</b> solution structure of the human bmx sh2 domain
109	<a href="#">d2qmsa1</a>	Alignment	not modelled	99.2	16 <b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
110	<a href="#">c2dm0A_</a>	Alignment	not modelled	99.2	23 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase txk; <b>PDBTitle:</b> solution structure of the sh2 domain of human tyrosine-2 protein kinase txk
111	<a href="#">c2hmbA_</a>	Alignment	not modelled	99.2	23 <b>PDB header:</b> cytokine regulator <b>Chain:</b> A: <b>PDB Molecule:</b> suppressor of cytokine signaling 3; <b>PDBTitle:</b> crystal structure of socs3 in complex with gp130(ptyr757)2 phosphopeptide.
112	<a href="#">d1v88a_</a>	Alignment	not modelled	99.2	22 <b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Pleckstrin-homology domain (PH domain)
113	<a href="#">d1fu6a_</a>	Alignment	not modelled	99.2	20 <b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
114	<a href="#">c3a8qB_</a>	Alignment	not modelled	99.2	19 <b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> t-lymphoma invasion and metastasis-inducing <b>PDBTitle:</b> low-resolution crystal structure of the tiam2 phcccx domain
115	<a href="#">c1xa6A_</a>	Alignment	not modelled	99.2	24 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> beta2-chimaerin; <b>PDBTitle:</b> crystal structure of the human beta2-chimaerin
116	<a href="#">d1u5ea1</a>	Alignment	not modelled	99.2	11 <b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Pleckstrin-homology domain (PH domain)
117	<a href="#">d1wgqa_</a>	Alignment	not modelled	99.2	13 <b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Pleckstrin-homology domain (PH domain)
118	<a href="#">c2dn6A_</a>	Alignment	not modelled	99.1	13 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> kiaa0640 protein; <b>PDBTitle:</b> solution structure of the ph domain of kiaa0640 protein2 from human
119	<a href="#">d1xx0a1</a>	Alignment	not modelled	99.1	12 <b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Pleckstrin-homology domain (PH domain)
120	<a href="#">d2cofa1</a>	Alignment	not modelled	99.1	15 <b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Pleckstrin-homology domain (PH domain)