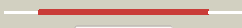
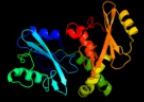


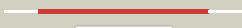























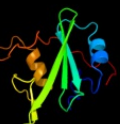




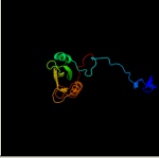
# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q92569
Date	Fri May 25 09:38:24 BST 2012
Unique Job ID	3a30478d3fb3e090

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2oq1A_</a>	 Alignment		100.0	27	<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
2	<a href="#">c2shpA_</a>	 Alignment		100.0	31	<b>PDB header:</b> tyrosine phosphatase <b>Chain:</b> A: <b>PDB Molecule:</b> shp-2; <b>PDBTitle:</b> tyrosine phosphatase shp-2
3	<a href="#">c2b3oA_</a>	 Alignment		100.0	35	<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
4	<a href="#">c3ps5A_</a>	 Alignment		100.0	29	<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
5	<a href="#">c1a81E_</a>	 Alignment		100.0	35	<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
6	<a href="#">c2ozoA_</a>	 Alignment		100.0	27	<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
7	<a href="#">c3gqiB_</a>	 Alignment		100.0	44	<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="#">c2y3aB_</a>	 Alignment		100.0	76	<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
9	<a href="#">c3hizB_</a>	 Alignment		100.0	83	<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
10	<a href="#">d1pica_</a>	 Alignment		99.9	76	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
11	<a href="#">d1qada_</a>	 Alignment		99.9	82	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain

12	<a href="#">c3or8A_</a>	Alignment		99.9	28	<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
13	<a href="#">c2crhA_</a>	Alignment		99.9	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
14	<a href="#">d2oq1a1</a>	Alignment		99.9	25	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
15	<a href="#">c2eo6A_</a>	Alignment		99.9	29	<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 blnk
16	<a href="#">d2oq1a2</a>	Alignment		99.9	25	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
17	<a href="#">d1a81e2</a>	Alignment		99.9	30	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
18	<a href="#">d1a81a1</a>	Alignment		99.9	27	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
19	<a href="#">d1a81a2</a>	Alignment		99.9	30	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
20	<a href="#">c2c9wA_</a>	Alignment		99.9	25	<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
21	<a href="#">c2dlzA_</a>	Alignment	not modelled	99.9	21	<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
22	<a href="#">c2ablA_</a>	Alignment	not modelled	99.9	27	<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
23	<a href="#">c2lctA_</a>	Alignment	not modelled	99.9	32	<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
24	<a href="#">c2vifA_</a>	Alignment	not modelled	99.9	39	<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
25	<a href="#">c2xp1A_</a>	Alignment	not modelled	99.9	15	<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
26	<a href="#">c2dlyA_</a>	Alignment	not modelled	99.8	37	<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
27	<a href="#">d2shpa2</a>	Alignment	not modelled	99.8	31	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
28	<a href="#">d1fu6a_</a>	Alignment	not modelled	99.8	87	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain <b>PDB header:</b> transferase

29	<a href="#">c2fo0A_</a>	Alignment	not modelled	99.8	25	<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
30	<a href="#">d1a81e1</a>	Alignment	not modelled	99.8	27	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
31	<a href="#">d1lopka2</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
32	<a href="#">c1k9aB_</a>	Alignment		99.8	24	<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
33	<a href="#">c2eobA_</a>	Alignment	not modelled	99.8	35	<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
34	<a href="#">d1lkka_</a>	Alignment	not modelled	99.8	39	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
35	<a href="#">c2qe9A_</a>	Alignment	not modelled	99.8	35	<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
36	<a href="#">d1csya_</a>	Alignment	not modelled	99.8	27	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
37	<a href="#">d1k9aa2</a>	Alignment	not modelled	99.8	35	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
38	<a href="#">d1jwoa_</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
39	<a href="#">c2lqnA_</a>	Alignment	not modelled	99.8	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> crk-like protein; <b>PDBTitle:</b> solution structure of crkl
40	<a href="#">d2izva2</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
41	<a href="#">c1oplA_</a>	Alignment	not modelled	99.8	25	<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
42	<a href="#">d1qcfa2</a>	Alignment	not modelled	99.8	39	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
43	<a href="#">d1ayaa_</a>	Alignment	not modelled	99.8	32	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
44	<a href="#">d1rjaa_</a>	Alignment	not modelled	99.8	35	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
45	<a href="#">c2eo3A_</a>	Alignment	not modelled	99.8	27	<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
46	<a href="#">d1luia_</a>	Alignment	not modelled	99.8	31	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
47	<a href="#">c2gsbA_</a>	Alignment	not modelled	99.8	22	<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
48	<a href="#">c2izvA_</a>	Alignment	not modelled	99.8	25	<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
49	<a href="#">c2knoA_</a>	Alignment	not modelled	99.8	30	<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)
50	<a href="#">d1nrva_</a>	Alignment	not modelled	99.8	26	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
51	<a href="#">d2qmsa1</a>	Alignment	not modelled	99.8	25	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
52	<a href="#">d1o48a_</a>	Alignment	not modelled	99.8	36	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
53	<a href="#">d1bjja_</a>	Alignment	not modelled	99.8	35	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
54	<a href="#">c2ysxA_</a>	Alignment	not modelled	99.8	29	<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 shp2 domain
55	<a href="#">c1ka6A</a>	Alignment	not modelled	99.8	28	<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
56	<a href="#">d3c7ia1</a>	Alignment	not modelled	99.8	25	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
57	<a href="#">c3nhnA</a>	Alignment	not modelled	99.8	37	<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
58	<a href="#">c2hnhA</a>	Alignment	not modelled	99.8	28	<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.
59	<a href="#">d2cs0a1</a>	Alignment	not modelled	99.8	28	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
60	<a href="#">d1g83a2</a>	Alignment	not modelled	99.8	32	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
61	<a href="#">d1fhsa</a>	Alignment	not modelled	99.8	32	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
62	<a href="#">c1x6cA</a>	Alignment	not modelled	99.8	30	<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
63	<a href="#">d1f2fa</a>	Alignment	not modelled	99.8	36	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
64	<a href="#">c1x27F</a>	Alignment	not modelled	99.8	33	<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 of p130cas
65	<a href="#">d1bkla</a>	Alignment	not modelled	99.8	37	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
66	<a href="#">c2ekxA</a>	Alignment	not modelled	99.8	33	<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
67	<a href="#">c1y57A</a>	Alignment	not modelled	99.8	30	<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
68	<a href="#">c2ci8A</a>	Alignment	not modelled	99.8	26	<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
69	<a href="#">d2shpa3</a>	Alignment	not modelled	99.8	31	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
70	<a href="#">d1d4ta</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
71	<a href="#">d2eyva1</a>	Alignment	not modelled	99.8	32	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
72	<a href="#">d1i3za</a>	Alignment	not modelled	99.8	30	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
73	<a href="#">d1r1qa</a>	Alignment	not modelled	99.8	34	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
74	<a href="#">d1mila</a>	Alignment	not modelled	99.8	32	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
75	<a href="#">d1xa6a2</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
76	<a href="#">c2dm0A</a>	Alignment	not modelled	99.8	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase btk; <b>PDBTitle:</b> solution structure of the sh2 domain of human tyrosine-2 protein kinase btk
77	<a href="#">d1cwea</a>	Alignment	not modelled	99.8	40	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
78	<a href="#">d2fcia1</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
79	<a href="#">c2kk6A</a>	Alignment	not modelled	99.8	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
80	<a href="#">d2c9wa2</a>	Alignment	not modelled	99.8	34	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain

						<b>Family:</b> SH2 domain
81	<a href="#">c2h8hA</a>	Alignment	not modelled	99.8	30	<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
82	<a href="#">c2dcrA</a>	Alignment	not modelled	99.8	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
83	<a href="#">c1g83A</a>	Alignment	not modelled	99.8	30	<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
84	<a href="#">d1jyra</a>	Alignment	not modelled	99.8	34	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
85	<a href="#">c2c0iA</a>	Alignment	not modelled	99.8	34	<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
86	<a href="#">c3mazA</a>	Alignment	not modelled	99.8	17	<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 ntl ptyr136 peptide
87	<a href="#">c2el8A</a>	Alignment	not modelled	99.8	20	<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
88	<a href="#">d1rpya</a>	Alignment	not modelled	99.7	27	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
89	<a href="#">c2eyzA</a>	Alignment	not modelled	99.7	29	<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
90	<a href="#">c2cr4A</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sh3 domain-binding protein 2; <b>PDBTitle:</b> solution structure of the sh2 domain of human sh3bp2 protein
91	<a href="#">c3gxxB</a>	Alignment	not modelled	99.7	26	<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
92	<a href="#">c1rqcC</a>	Alignment	not modelled	99.7	28	<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
93	<a href="#">c2dx0B</a>	Alignment	not modelled	99.6	39	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phospholipase c, gamma 2; <b>PDBTitle:</b> crystal structure of the n-terminal sh2 domain of mouse2 phospholipase c-gamma 2
94	<a href="#">c3qwxX</a>	Alignment	not modelled	99.6	25	<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
95	<a href="#">c3qwyA</a>	Alignment	not modelled	99.6	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cell death abnormality protein 2; <b>PDBTitle:</b> ced-2
96	<a href="#">c2dvjA</a>	Alignment	not modelled	99.6	29	<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
97	<a href="#">c2eyyA</a>	Alignment	not modelled	99.6	25	<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
98	<a href="#">c1xa6A</a>	Alignment	not modelled	99.5	25	<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
99	<a href="#">c2v1yB</a>	Alignment	not modelled	99.4	79	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit alpha; <b>PDBTitle:</b> structure of a phosphoinositide 3-kinase alpha adaptor-2 binding domain (abd) in a complex with the ish2 domain3 from p85 alpha
100	<a href="#">d1uura3</a>	Alignment	not modelled	99.3	16	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
101	<a href="#">d1bfa3</a>	Alignment	not modelled	99.2	23	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
102	<a href="#">d1bgl1a3</a>	Alignment	not modelled	99.0	23	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
103	<a href="#">c3cblA</a>	Alignment	not modelled	98.7	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase fes/fps; <b>PDBTitle:</b> crystal structure of human feline sarcoma viral oncogene homologue (v-2 fes) in complex with staurosporine and a consensus peptide
104	<a href="#">c4a55B</a>	Alignment	not modelled	98.5	80	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit alpha; <b>PDBTitle:</b> crystal structure of p110alpha in complex with ish2 of p85alpha and2 the inhibitor pik-108
105	<a href="#">c1yvlB</a>	Alignment	not modelled	98.2	11	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> signal transducer and activator of transcription

						<b>PDBTitle:</b> structure of unphosphorylated stat1
106	<a href="#">c3ojaB_</a>	Alignment	not modelled	98.1	8	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> anopheles plasmodium-responsive leucine-rich repeat protein
107	<a href="#">c3na7A_</a>	Alignment	not modelled	98.0	13	<b>PDBTitle:</b> crystal structure of Irim1/apl1c complex <b>PDB header:</b> gene regulation, chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hp0958;
108	<a href="#">c1uusA_</a>	Alignment	not modelled	97.9	14	<b>PDBTitle:</b> 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874 <b>PDB header:</b> signal transduction <b>Chain:</b> A: <b>PDB Molecule:</b> stat protein;
109	<a href="#">c2efrB_</a>	Alignment	not modelled	97.8	17	<b>PDBTitle:</b> structure of an activated dictyostelium stat in its2 dna-unbound form <b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4 and tropomyosin 1 alpha chain;
110	<a href="#">c1bf5A_</a>	Alignment	not modelled	97.8	8	<b>PDBTitle:</b> crystal structure of the c-terminal tropomyosin fragment with n- and 2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution <b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription
111	<a href="#">c2cblA_</a>	Alignment	not modelled	97.7	18	<b>PDBTitle:</b> tyrosine phosphorylated stat-1/dna complex <b>PDB header:</b> complex (proto-oncogene/peptide) <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene cbl;
112	<a href="#">c3bunB_</a>	Alignment	not modelled	97.6	18	<b>PDBTitle:</b> n-terminal domain of cbl in complex with its binding site2 on zap-70 <b>PDB header:</b> ligase/signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase cbl;
113	<a href="#">c1ei3C_</a>	Alignment	not modelled	97.6	10	<b>PDBTitle:</b> crystal structure of c-cbl-tkb domain complexed with its2 binding motif in sprouty4 <b>PDB header:</b> <b>PDB COMPND:</b>
114	<a href="#">c3ghgK_</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> blood clotting <b>Chain:</b> K: <b>PDB Molecule:</b> fibrinogen beta chain; <b>PDBTitle:</b> crystal structure of human fibrinogen
115	<a href="#">c1y1uA_</a>	Alignment	not modelled	97.3	35	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription 5a;
116	<a href="#">c3o0zD_</a>	Alignment	not modelled	97.3	14	<b>PDBTitle:</b> structure of unphosphorylated stat5a <b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> rho-associated protein kinase 1;
117	<a href="#">c2d3eD_</a>	Alignment	not modelled	97.3	13	<b>PDBTitle:</b> crystal structure of a coiled-coil domain from human rock i <b>PDB header:</b> contractile protein <b>Chain:</b> D: <b>PDB Molecule:</b> general control protein gcn4 and tropomyosin 1
118	<a href="#">c3cwgA_</a>	Alignment	not modelled	97.2	8	<b>PDBTitle:</b> crystal structure of the c-terminal fragment of rabbit2 skeletal alpha-tropomyosin <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription
119	<a href="#">c2rd0B_</a>	Alignment	not modelled	97.2	80	<b>PDBTitle:</b> unphosphorylated mouse stat3 core fragment <b>PDB header:</b> transferase/oncoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit alpha;
120	<a href="#">c1ei3E_</a>	Alignment	not modelled	97.1	9	<b>PDBTitle:</b> structure of a human p110alpha/p85alpha complex <b>PDB header:</b> <b>PDB COMPND:</b>