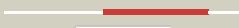



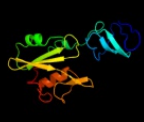


















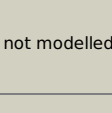


# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q8CG80
Date	Tue Jul 30 13:10:18 BST 2013
Unique Job ID	9dad74adf49bf70a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2eo6A_</a>	 Alignment		100.0	24	<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
2	<a href="#">c2hdxB_</a>	 Alignment		100.0	25	<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 tyr813 phosphopeptide
3	<a href="#">c2y3aB_</a>	 Alignment		100.0	26	<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
4	<a href="#">c2ablA_</a>	 Alignment		100.0	24	<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
5	<a href="#">d2oq1a1</a>	 Alignment		100.0	25	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
6	<a href="#">c2fo0A_</a>	 Alignment		100.0	24	<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
7	<a href="#">c3hizB_</a>	 Alignment		99.9	34	<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
8	<a href="#">d3c7ia1</a>	 Alignment		99.9	29	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
9	<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
10	<a href="#">c2eo3A_</a>	 Alignment		99.9	24	<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
11	<a href="#">c2gsbA_</a>	 Alignment		99.9	30	<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

12	<a href="#">c2crhA_</a>	Alignment		99.9	23	<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
13	<a href="#">d2shpa2</a>	Alignment		99.9	28	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
14	<a href="#">d1fhsa_</a>	Alignment		99.9	28	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
15	<a href="#">d1pica_</a>	Alignment		99.9	26	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
16	<a href="#">c2eobA_</a>	Alignment		99.9	27	<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
17	<a href="#">c2dlyA_</a>	Alignment		99.9	31	<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
18	<a href="#">c1ka6A_</a>	Alignment		99.9	24	<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
19	<a href="#">c2oq1A_</a>	Alignment		99.9	24	<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
20	<a href="#">c2c9wA_</a>	Alignment		99.9	24	<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 and 2 elongin-c at 1.9a resolution
21	<a href="#">c1x6cA_</a>	Alignment	not modelled	99.9	31	<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
22	<a href="#">c2dlzA_</a>	Alignment	not modelled	99.9	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
23	<a href="#">d1ayaa_</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
24	<a href="#">c2b3oA_</a>	Alignment	not modelled	99.9	29	<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
25	<a href="#">c2vifA_</a>	Alignment	not modelled	99.9	27	<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
26	<a href="#">c2lctA_</a>	Alignment	not modelled	99.9	26	<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
27	<a href="#">d1a81e1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
28	<a href="#">c2hmbA_</a>	Alignment	not modelled	99.9	22	<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.

29	<a href="#">d1opka2</a>	Alignment	not modelled	99.9	33	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
30	<a href="#">d1qada</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
31	<a href="#">c2shpA</a>	Alignment	not modelled	99.9	28	<b>PDB header:</b> tyrosine phosphatase <b>Chain:</b> A: <b>PDB Molecule:</b> shp-2; <b>PDBTitle:</b> tyrosine phosphatase shp-2
32	<a href="#">c2kk6A</a>	Alignment	not modelled	99.9	33	<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
33	<a href="#">d1k9aa2</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
34	<a href="#">d1a81e2</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
35	<a href="#">d1blja</a>	Alignment	not modelled	99.9	31	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
36	<a href="#">c2dcrA</a>	Alignment	not modelled	99.9	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
37	<a href="#">d1rjaa</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
38	<a href="#">d2izva2</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
39	<a href="#">c1op1A</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; <b>PDBTitle:</b> structural basis for the auto-inhibition of c-abl tyrosine2 kinase
40	<a href="#">d1a81a1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
41	<a href="#">d1mila</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
42	<a href="#">d2oq1a2</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
43	<a href="#">d1a81a2</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
44	<a href="#">c2ysxA</a>	Alignment	not modelled	99.9	26	<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
45	<a href="#">c2ci8A</a>	Alignment	not modelled	99.9	37	<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
46	<a href="#">d1d4ta</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
47	<a href="#">d1r1qa</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
48	<a href="#">d2shpa3</a>	Alignment	not modelled	99.9	33	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
49	<a href="#">c1y57A</a>	Alignment	not modelled	99.9	19	<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
50	<a href="#">c2izvA</a>	Alignment	not modelled	99.9	22	<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
51	<a href="#">d1lkka</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
52	<a href="#">d1jwoa</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
53	<a href="#">c2knoA</a>	Alignment	not modelled	99.9	24	<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)
54	<a href="#">d2cs0a1</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain

55	<a href="#">c2ozoA</a>	Alignment	not modelled	99.9	24	<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
56	<a href="#">d1luia</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
57	<a href="#">c2augB</a>	Alignment	not modelled	99.9	24	<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
58	<a href="#">c3nhnA</a>	Alignment	not modelled	99.9	23	<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
59	<a href="#">d1csya</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
60	<a href="#">d2eyva1</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
61	<a href="#">d1g83a2</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
62	<a href="#">d1fu6a</a>	Alignment	not modelled	99.9	30	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
63	<a href="#">c1k9aB</a>	Alignment	not modelled	99.9	21	<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
64	<a href="#">d1nrva</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
65	<a href="#">c3ps5A</a>	Alignment	not modelled	99.9	27	<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
66	<a href="#">d1i3za</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
67	<a href="#">c1x27F</a>	Alignment	not modelled	99.9	22	<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
68	<a href="#">c3gqiB</a>	Alignment	not modelled	99.9	21	<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
69	<a href="#">c4f12A</a>	Alignment	not modelled	99.9	21	<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
70	<a href="#">d1jyra</a>	Alignment	not modelled	99.9	31	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
71	<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
72	<a href="#">d2qmsa1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
73	<a href="#">c2ekxA</a>	Alignment	not modelled	99.9	30	<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
74	<a href="#">d1o48a</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
75	<a href="#">c2c0iA</a>	Alignment	not modelled	99.9	22	<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
76	<a href="#">d1qcfa2</a>	Alignment	not modelled	99.9	31	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
77	<a href="#">d2c9wa2</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
78	<a href="#">d1f2fa</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
79	<a href="#">c2ge9A</a>	Alignment	not modelled	99.9	28	<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
80	<a href="#">d1bkla</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
81	<a href="#">d1xa6a2</a>	Alianment	not modelled	99.9	23	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain

					Family:SH2 domain
82	<a href="#">c2e18A_</a>	Alignment	not modelled	99.9	18 <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
83	<a href="#">c1g83A_</a>	Alignment	not modelled	99.9	24 <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="#">c3mazA_</a>	Alignment	not modelled	99.9	11 <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
85	<a href="#">c1a81E_</a>	Alignment	not modelled	99.9	18 <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
86	<a href="#">d2fcia1</a>	Alignment	not modelled	99.9	27 <b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
87	<a href="#">d1rpya_</a>	Alignment	not modelled	99.9	26 <b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
88	<a href="#">c1rqcC_</a>	Alignment	not modelled	99.9	25 <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
89	<a href="#">d1cwea_</a>	Alignment	not modelled	99.9	29 <b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
90	<a href="#">c2cr4A_</a>	Alignment	not modelled	99.9	21 <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="#">c2dm0A_</a>	Alignment	not modelled	99.9	24 <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
92	<a href="#">c2eyzA_</a>	Alignment	not modelled	99.9	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
93	<a href="#">c3gxxB_</a>	Alignment	not modelled	99.9	19 <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
94	<a href="#">c2dviA_</a>	Alignment	not modelled	99.8	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
95	<a href="#">c3qwxX_</a>	Alignment	not modelled	99.8	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
96	<a href="#">c2eyyA_</a>	Alignment	not modelled	99.8	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 i
97	<a href="#">c3qwyA_</a>	Alignment	not modelled	99.8	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
98	<a href="#">c2dx0B_</a>	Alignment	not modelled	99.8	33 <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
99	<a href="#">c3or8A_</a>	Alignment	not modelled	99.7	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
100	<a href="#">c1xa6A_</a>	Alignment	not modelled	99.7	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
101	<a href="#">c2xp1A_</a>	Alignment	not modelled	99.6	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
102	<a href="#">d1uura3</a>	Alignment	not modelled	99.6	11 <b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
103	<a href="#">d1bf5a3</a>	Alignment	not modelled	99.5	21 <b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
104	<a href="#">d1bg1a3</a>	Alignment	not modelled	99.4	20 <b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
105	<a href="#">c3cblA_</a>	Alignment	not modelled	99.2	36 <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
106	<a href="#">c1uusA_</a>	Alignment	not modelled	98.3	16 <b>PDB header:</b> signal transduction <b>Chain:</b> A; <b>PDB Molecule:</b> stat protein; <b>PDBTitle:</b> structure of an activated dictyostelium stat in its2 dna-unbound form
107	<a href="#">c2cblA_</a>	Alignment	not modelled	98.2	17 <b>PDB header:</b> complex (proto-oncogene/peptide) <b>Chain:</b> A; <b>PDB Molecule:</b> proto-oncogene cbl; <b>PDBTitle:</b> n-terminal domain of cbl in complex with its binding site2

					on zap-70
108	<a href="#">c3bunB_</a>	Alignment	not modelled	98.2	17 <b>PDB header:</b> ligase/signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase cbl; <b>PDBTitle:</b> crystal structure of c-cbl-tkb domain complexed with its2 binding motif in sprouty4
109	<a href="#">c1y1uA_</a>	Alignment	not modelled	98.1	18 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription 5a; <b>PDBTitle:</b> structure of unphosphorylated stat5a
110	<a href="#">c1yvlB_</a>	Alignment	not modelled	98.0	27 <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
111	<a href="#">c1bf5A_</a>	Alignment	not modelled	97.8	22 <b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> tyrosine phosphorylated stat-1/dna complex
112	<a href="#">c1bg1A_</a>	Alignment	not modelled	97.6	22 <b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (transcription factor stat3b); <b>PDBTitle:</b> transcription factor stat3b/dna complex
113	<a href="#">c3cwgA_</a>	Alignment	not modelled	96.6	23 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> unphosphorylated mouse stat3 core fragment
114	<a href="#">c1griA_</a>	Alignment	not modelled	94.0	33 <b>PDB header:</b> signal transduction adaptor <b>Chain:</b> A: <b>PDB Molecule:</b> growth factor bound protein 2; <b>PDBTitle:</b> grb2
115	<a href="#">c1fbvA_</a>	Alignment	not modelled	93.0	19 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> signal transduction protein cbl; <b>PDBTitle:</b> structure of a cbl-ubch7 complex: ring domain function in2 ubiquitin-protein ligases
116	<a href="#">d3buxb3</a>	Alignment	not modelled	90.3	19 <b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
117	<a href="#">c3op0B_</a>	Alignment	not modelled	86.4	26 <b>PDB header:</b> signaling protein/signaling protein regu <b>Chain:</b> B: <b>PDB Molecule:</b> signal transduction protein cbl-c; <b>PDBTitle:</b> crystal structure of cbl-c (cbl-3) tkb domain in complex with egfr2 py1069 peptide
118	<a href="#">c2yt6A_</a>	Alignment	not modelled	74.1	19 <b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> adult male urinary bladder cdna, riken full- <b>PDBTitle:</b> solution structure of the sh3_1 domain of yamaguchi sarcoma2 viral (v-yes) oncogene homolog 1
119	<a href="#">d2e9ia1</a>	Alignment	not modelled	65.2	17 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Filamin repeat (rod domain)
120	<a href="#">d1wlha1</a>	Alignment	not modelled	63.8	13 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Filamin repeat (rod domain)