



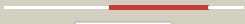








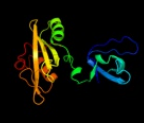










#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1k9aB_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> carboxyl-terminal src kinase; <b>PDBTitle:</b> crystal structure analysis of full-length carboxyl-terminal2 src kinase at 2.5 a resolution
2	<a href="#">c2fo0A_</a>	 Alignment		100.0	31	<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
3	<a href="#">c1op1A_</a>	 Alignment		100.0	34	<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
4	<a href="#">c1y57A_</a>	 Alignment		100.0	31	<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
5	<a href="#">c2ablA_</a>	 Alignment		100.0	33	<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
6	<a href="#">c3nhnA_</a>	 Alignment		100.0	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
7	<a href="#">c2h8hA_</a>	 Alignment		100.0	32	<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
8	<a href="#">c2c0iA_</a>	 Alignment		100.0	39	<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
9	<a href="#">c1x27F_</a>	 Alignment		100.0	35	<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
10	<a href="#">c1griA_</a>	 Alignment		100.0	25	<b>PDB header:</b> signal transduction adaptor <b>Chain:</b> A; <b>PDB Molecule:</b> growth factor bound protein 2; <b>PDBTitle:</b> grb2
11	<a href="#">c1g83A_</a>	 Alignment		100.0	33	<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

12	<a href="#">c2lqnA_</a>	Alignment		100.0	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> crk-like protein; <b>PDBTitle:</b> solution structure of crkl
13	<a href="#">c2l3sA_</a>	Alignment		100.0	22	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> autoinhibited crk protein; <b>PDBTitle:</b> structure of the autoinhibited crk
14	<a href="#">c2b3oA_</a>	Alignment		100.0	23	<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
15	<a href="#">c2eyzA_</a>	Alignment		100.0	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> v-crak sarcoma virus ct10 oncogene homolog <b>PDBTitle:</b> ct10-regulated kinase isoform ii
16	<a href="#">c2ci8A_</a>	Alignment		100.0	100	<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
17	<a href="#">c3ps5A_</a>	Alignment		100.0	24	<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
18	<a href="#">c2shpA_</a>	Alignment		100.0	26	<b>PDB header:</b> tyrosine phosphatase <b>Chain:</b> A: <b>PDB Molecule:</b> shp-2; <b>PDBTitle:</b> tyrosine phosphatase shp-2
19	<a href="#">c2eo6A_</a>	Alignment		100.0	23	<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
20	<a href="#">c1ng2A_</a>	Alignment		100.0	23	<b>PDB header:</b> oxidoreductase activator <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil cytosolic factor 1; <b>PDBTitle:</b> structure of autoinhibited p47phox
21	<a href="#">c2eo3A_</a>	Alignment	not modelled	100.0	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
22	<a href="#">d2shpa2</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
23	<a href="#">c1x6cA_</a>	Alignment	not modelled	99.9	35	<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
24	<a href="#">d1mila_</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
25	<a href="#">c2qsbA_</a>	Alignment	not modelled	99.9	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
26	<a href="#">c2eobA_</a>	Alignment	not modelled	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
27	<a href="#">d3c7ia1</a>	Alignment	not modelled	99.9	35	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
28	<a href="#">c3hizB_</a>	Alignment	not modelled	99.9	26	<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 <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
29	<a href="#">c2hdxB_</a>	Alignment	not modelled	99.9	26
30	<a href="#">d1ayaa_</a>	Alignment	not modelled	99.9	33
31	<a href="#">c3gqiB_</a>	Alignment	not modelled	99.9	31
32	<a href="#">c2kk6A_</a>	Alignment	not modelled	99.9	25
33	<a href="#">d2oq1a1</a>	Alignment	not modelled	99.9	30
34	<a href="#">d1fhsa_</a>	Alignment	not modelled	99.9	35
35	<a href="#">c2dlzA_</a>	Alignment	not modelled	99.9	28
36	<a href="#">c1ov3A_</a>	Alignment	not modelled	99.9	27
37	<a href="#">c2dlyA_</a>	Alignment	not modelled	99.9	30
38	<a href="#">c2vifA_</a>	Alignment	not modelled	99.9	25
39	<a href="#">c2oq1A_</a>	Alignment	not modelled	99.9	29
40	<a href="#">c2crhA_</a>	Alignment	not modelled	99.9	26
41	<a href="#">c2dcrA_</a>	Alignment	not modelled	99.9	21
42	<a href="#">d2izva2</a>	Alignment	not modelled	99.9	27
43	<a href="#">d1a81e1</a>	Alignment	not modelled	99.9	24
44	<a href="#">d1jyra_</a>	Alignment	not modelled	99.9	36
45	<a href="#">d2shpa3</a>	Alignment	not modelled	99.9	38
46	<a href="#">c2y3aB_</a>	Alignment	not modelled	99.9	28
47	<a href="#">c2el8A_</a>	Alignment	not modelled	99.9	22
48	<a href="#">c2c9wA_</a>	Alignment	not modelled	99.9	30
49	<a href="#">d1nrva_</a>	Alignment	not modelled	99.9	26
50	<a href="#">c1ka6A_</a>	Alignment	not modelled	99.9	26
51	<a href="#">d1a81a1</a>	Alignment	not modelled	99.9	24
52	<a href="#">d1rjaa_</a>	Alignment	not modelled	99.9	26
53	<a href="#">d1pica_</a>	Alignment	not modelled	99.9	25
					<b>Fold:</b> SH2-like

54	<a href="#">d1jwoa_</a>	Alignment	not modelled	99.9	25	<b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
55	<a href="#">d2oq1a2</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
56	<a href="#">d1a81e2</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
57	<a href="#">c2ysxA_</a>	Alignment	not modelled	99.9	27	<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
58	<a href="#">d1i3za_</a>	Alignment	not modelled	99.9	30	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
59	<a href="#">d1qada_</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
60	<a href="#">c2lctA_</a>	Alignment	not modelled	99.9	27	<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
61	<a href="#">c2izvA_</a>	Alignment	not modelled	99.9	27	<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
62	<a href="#">d1d4ta_</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
63	<a href="#">d1fu6a_</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
64	<a href="#">d1r1qa_</a>	Alignment	not modelled	99.9	34	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
65	<a href="#">c4fl2A_</a>	Alignment	not modelled	99.9	25	<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
66	<a href="#">d1k9aa2</a>	Alignment	not modelled	99.9	32	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
67	<a href="#">c2ozoA_</a>	Alignment	not modelled	99.9	30	<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
68	<a href="#">d2fcia1</a>	Alignment	not modelled	99.9	31	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
69	<a href="#">c2ekxA_</a>	Alignment	not modelled	99.9	25	<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
70	<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
71	<a href="#">d1a81a2</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
72	<a href="#">d1lkka_</a>	Alignment	not modelled	99.9	32	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
73	<a href="#">c2ge9A_</a>	Alignment	not modelled	99.9	31	<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
74	<a href="#">d1g83a2</a>	Alignment	not modelled	99.9	35	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
75	<a href="#">c2hmhA_</a>	Alignment	not modelled	99.9	27	<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.
76	<a href="#">d1opka2</a>	Alignment	not modelled	99.9	32	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
77	<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
78	<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
79	<a href="#">c2augB_</a>	Alignment	not modelled	99.9	28	<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
80	<a href="#">d1xa6a2</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
81	<a href="#">d1csya_</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain

						<b>Family:</b> SH2 domain
82	<a href="#">c3mazA_</a>	Alignment	not modelled	99.9	20	<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
83	<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
84	<a href="#">d1o48a_</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
85	<a href="#">c1rqgC_</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
86	<a href="#">d2c9wa2</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
87	<a href="#">d1luia_</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
88	<a href="#">d2qmsa1</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
89	<a href="#">d1bkla_</a>	Alignment	not modelled	99.9	32	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
90	<a href="#">d1f2fa_</a>	Alignment	not modelled	99.9	32	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
91	<a href="#">c2cr4A_</a>	Alignment	not modelled	99.9	23	<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
92	<a href="#">d2cs0a1</a>	Alignment	not modelled	99.9	30	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
93	<a href="#">d1qcfa2</a>	Alignment	not modelled	99.9	34	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
94	<a href="#">c2knoA_</a>	Alignment	not modelled	99.9	28	<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)
95	<a href="#">c2dm0A_</a>	Alignment	not modelled	99.9	21	<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
96	<a href="#">d1cwea_</a>	Alignment	not modelled	99.9	36	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
97	<a href="#">c2dviA_</a>	Alignment	not modelled	99.8	26	<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
98	<a href="#">c1mv3A_</a>	Alignment	not modelled	99.8	25	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> myc box dependent interacting protein 1; <b>PDBTitle:</b> nmr structure of the tumor suppressor bin1: alternative2 splicing in melanoma and interaction with c-myc
99	<a href="#">c3qwX_</a>	Alignment	not modelled	99.8	27	<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
100	<a href="#">c3qwY_</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
101	<a href="#">c3gxxB_</a>	Alignment	not modelled	99.8	23	<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
102	<a href="#">c2jw4A_</a>	Alignment	not modelled	99.8	93	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytoplasmic protein nck1; <b>PDBTitle:</b> nmr solution structure of the n-terminal sh3 domain of2 human nckalpha
103	<a href="#">c2yt6A_</a>	Alignment	not modelled	99.8	29	<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
104	<a href="#">c2eyyA_</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> ct10-regulated kinase isoform i
105	<a href="#">d1ng2a2</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
106	<a href="#">c2jxbA_</a>	Alignment	not modelled	99.8	81	<b>PDB header:</b> signaling protein complex <b>Chain:</b> A: <b>PDB Molecule:</b> t-cell surface glycoprotein cd3 epsilon chain, <b>PDBTitle:</b> structure of cd3epsilon-nck2 first sh3 domain complex
107	<a href="#">c2dybA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> neutrophil cytosol factor 4; <b>PDBTitle:</b> the crystal structure of human p40(phox)
						<b>PDB header:</b> protein binding

108	<a href="#">c2rqra_</a>	Alignment	not modelled	99.8	15	<b>Chain:</b> A: <b>PDB Molecule:</b> engulfment and cell motility protein 1, linker, dedicator <b>PDBTitle:</b> the solution structure of human dock2 sh3 domain - elmo1 peptide2 chimera complex
109	<a href="#">c2csqa_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> rim binding protein 2; <b>PDBTitle:</b> solution structure of the second sh3 domain of human rim-2 binding protein 2
110	<a href="#">c2dlpa_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> kiaa1783 protein; <b>PDBTitle:</b> solution structure of the sh3 domain of human kiaa17832 protein
111	<a href="#">c2cuba_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytoplasmic protein nck1; <b>PDBTitle:</b> solution structure of the sh3 domain of the human2 cytoplasmic protein nck1
112	<a href="#">c2k2mA_</a>	Alignment	not modelled	99.7	31	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> eps8-like protein 1; <b>PDBTitle:</b> structural basis of pxxdy motif recognition in sh3 binding
113	<a href="#">c2yuoa_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> run and tbc1 domain containing 3; <b>PDBTitle:</b> solution structure of the sh3 domain of mouse run and tbc12 domain containing 3
114	<a href="#">c2egea_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein kiaa1666; <b>PDBTitle:</b> solution structure of the third sh3 domain from human2 kiaa1666 protein
115	<a href="#">c3or8A_</a>	Alignment	not modelled	99.7	23	<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
116	<a href="#">c2cudA_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> src-like-adapter; <b>PDBTitle:</b> solution structure of the sh3 domain of the human src-like2 adppter protein (slap)
117	<a href="#">c2xp1A_</a>	Alignment	not modelled	99.7	20	<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
118	<a href="#">c2dx0B_</a>	Alignment	not modelled	99.7	27	<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
119	<a href="#">c1wxtA_</a>	Alignment	not modelled	99.7	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein flj21522; <b>PDBTitle:</b> solution structure of the sh3 domain of human hypothetical2 protein flj21522
120	<a href="#">d1uffa_</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain