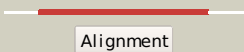

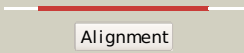

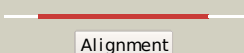

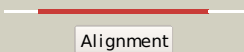

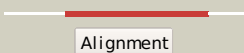

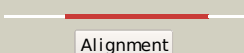





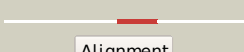

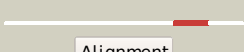

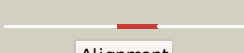






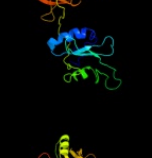


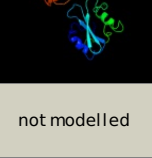


# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q9VXH3
Date	Wed Feb 13 11:23:55 GMT 2013
Unique Job ID	2eb76761bdeaa822

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ohmB</a>	 Alignment		100.0	38	<b>PDB header:</b> signaling protein / hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase <b>PDBTitle:</b> crystal structure of activated g alpha q bound to its effector2 phospholipase c beta 3
2	<a href="#">c3qr0A</a>	 Alignment		100.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase c-beta (plc-beta); <b>PDBTitle:</b> crystal structure of s. officinalis plc21
3	<a href="#">c2fjuB</a>	 Alignment		100.0	36	<b>PDB header:</b> signaling protein,apoptosis/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-phosphatidylinositol-4,5-bisphosphate <b>PDBTitle:</b> activated rac1 bound to its effector phospholipase c beta 2
4	<a href="#">c1djyB</a>	 Alignment		100.0	45	<b>PDB header:</b> lipid degradation <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoinositide-specific phospholipase c, <b>PDBTitle:</b> phosphoinositide-specific phospholipase c-delta1 from rat2 complexed with inositol-2,4,5-trisphosphate
5	<a href="#">d2zkmx4</a>	 Alignment		100.0	59	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLC-like phosphodiesterases <b>Family:</b> Mammalian PLC
6	<a href="#">d1qasa3</a>	 Alignment		100.0	65	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLC-like phosphodiesterases <b>Family:</b> Mammalian PLC
7	<a href="#">c2lqnA</a>	 Alignment		100.0	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> crk-like protein; <b>PDBTitle:</b> solution structure of crkl
8	<a href="#">c2eyzA</a>	 Alignment		100.0	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> v-crkl sarcoma virus ct10 oncogene homolog <b>PDBTitle:</b> ct10-regulated kinase isoform ii
9	<a href="#">c3gqiB</a>	 Alignment		100.0	48	<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
10	<a href="#">d2zkmx2</a>	 Alignment		100.0	26	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
11	<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

12	<a href="#">c2b3oA</a>	Alignment		100.0	30	<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
13	<a href="#">c3ps5A</a>	Alignment		100.0	30	<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
14	<a href="#">d1qasa2</a>	Alignment		100.0	32	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
15	<a href="#">c2eyyA</a>	Alignment		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> ct10-regulated kinase isoform i
16	<a href="#">c2oq1A</a>	Alignment		99.9	26	<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
17	<a href="#">c2dviA</a>	Alignment		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> phosphorylated crk-ii
18	<a href="#">c4fi2A</a>	Alignment		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
19	<a href="#">c3qwyA</a>	Alignment		99.9	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cell death abnormality protein 2; <b>PDBTitle:</b> ced-2
20	<a href="#">c2ozoA</a>	Alignment		99.9	25	<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
21	<a href="#">c3qwxX</a>	Alignment	not modelled	99.9	26	<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
22	<a href="#">d2zkmx3</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> PIleckstrin-homology domain (PH domain)
23	<a href="#">c1a81E</a>	Alignment	not modelled	99.9	25	<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
24	<a href="#">d1dxb1</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> EF-hand modules in multidomain proteins
25	<a href="#">d2zkmx1</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> EF-hand modules in multidomain proteins
26	<a href="#">c3h4wA</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol-specific phospholipase c1; <b>PDBTitle:</b> structure of a ca+2 dependent phosphatidylinositol-specific2 phospholipase c (pi-plc) enzyme from streptomyces antibioticus
27	<a href="#">d1qasa1</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> EF-hand modules in multidomain proteins
28	<a href="#">d1maia</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> PIleckstrin-homology domain (PH domain)

29	<a href="#">c2vszA_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> engulfment and cell motility protein 1; <b>PDBTitle:</b> crystal structure of the elmo1 ph domain
30	<a href="#">c2fj1A_</a>	Alignment	not modelled	99.6	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 split ph domain in phospholipase2 c-gamma1
31	<a href="#">c2xp1A_</a>	Alignment	not modelled	99.5	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
32	<a href="#">c2hdxB_</a>	Alignment	not modelled	99.5	28	<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
33	<a href="#">c3or8A_</a>	Alignment	not modelled	99.5	16	<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
34	<a href="#">c2gsbA_</a>	Alignment	not modelled	99.5	32	<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
35	<a href="#">c2y3aB_</a>	Alignment	not modelled	99.5	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
36	<a href="#">c2dx0B_</a>	Alignment	not modelled	99.5	54	<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
37	<a href="#">c1griA_</a>	Alignment	not modelled	99.5	30	<b>PDB header:</b> signal transduction adaptor <b>Chain:</b> A: <b>PDB Molecule:</b> growth factor bound protein 2; <b>PDBTitle:</b> grb2
38	<a href="#">c3hizB_</a>	Alignment	not modelled	99.4	29	<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
39	<a href="#">d3c7ia1</a>	Alignment	not modelled	99.4	35	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
40	<a href="#">d1gmia_</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
41	<a href="#">c2fo0A_</a>	Alignment	not modelled	99.4	19	<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
42	<a href="#">d2oq1a1</a>	Alignment	not modelled	99.4	24	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
43	<a href="#">d2oq1a2</a>	Alignment	not modelled	99.4	30	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
44	<a href="#">d2eyva1</a>	Alignment	not modelled	99.4	38	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
45	<a href="#">c2q3xA_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulating synaptic membrane exocytosis protein 1; <b>PDBTitle:</b> the rim1alpha c2b domain
46	<a href="#">c2dlzA_</a>	Alignment	not modelled	99.4	28	<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
47	<a href="#">d2qmsa1</a>	Alignment	not modelled	99.4	25	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
48	<a href="#">d1fhsa_</a>	Alignment	not modelled	99.4	33	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
49	<a href="#">c2eo3A_</a>	Alignment	not modelled	99.4	32	<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
50	<a href="#">d1csya_</a>	Alignment	not modelled	99.4	26	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
51	<a href="#">d2shpa2</a>	Alignment	not modelled	99.4	32	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
52	<a href="#">d1a81e2</a>	Alignment	not modelled	99.4	27	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
53	<a href="#">d2izva2</a>	Alignment	not modelled	99.4	25	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
54	<a href="#">c3m7fB_</a>	Alignment	not modelled	99.4	24	<b>PDB header:</b> signaling protein/ligase <b>Chain:</b> B: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase nedd4; <b>PDBTitle:</b> crystal structure of the nedd4 c2/grb10 sh2 complex

55	<a href="#">d1a81a1</a>	Alignment	not modelled	99.4	25	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
56	<a href="#">d2nq3a1</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
57	<a href="#">c2nq3A</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> itchy homolog e3 ubiquitin protein ligase; <b>PDBTitle:</b> crystal structure of the c2 domain of human itchy homolog2 e3 ubiquitin protein ligase
58	<a href="#">d1nrva</a>	Alignment	not modelled	99.4	24	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
59	<a href="#">d1a81a2</a>	Alignment	not modelled	99.4	26	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
60	<a href="#">d2r83a1</a>	Alignment	not modelled	99.4	21	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
61	<a href="#">c2crhA</a>	Alignment	not modelled	99.4	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
62	<a href="#">c1oplA</a>	Alignment	not modelled	99.4	20	<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
63	<a href="#">d1rjaa</a>	Alignment	not modelled	99.4	30	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
64	<a href="#">d1a81e1</a>	Alignment	not modelled	99.4	25	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
65	<a href="#">c2l3sA</a>	Alignment	not modelled	99.4	11	<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
66	<a href="#">c2dlyA</a>	Alignment	not modelled	99.4	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
67	<a href="#">c2augB</a>	Alignment	not modelled	99.4	27	<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
68	<a href="#">c3l9bA</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> otoferlin; <b>PDBTitle:</b> crystal structure of rat otoferlin c2a
69	<a href="#">c2dmhA</a>	Alignment	not modelled	99.3	23	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> myoferlin; <b>PDBTitle:</b> solution structure of the first c2 domain of human myoferlin
70	<a href="#">c3kwtA</a>	Alignment	not modelled	99.3	22	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> munc13-1; <b>PDBTitle:</b> munc13-1 c2b-domain, calcium-free
71	<a href="#">c2ci8A</a>	Alignment	not modelled	99.3	24	<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
72	<a href="#">c2eo6A</a>	Alignment	not modelled	99.3	26	<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
73	<a href="#">d1blja</a>	Alignment	not modelled	99.3	28	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
74	<a href="#">c2chdA</a>	Alignment	not modelled	99.3	24	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> rabphilin-3a; <b>PDBTitle:</b> crystal structure of the c2a domain of rabphilin-3a
75	<a href="#">d1pica</a>	Alignment	not modelled	99.3	28	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
76	<a href="#">c3a98B</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> engulfment and cell motility protein 1; <b>PDBTitle:</b> crystal structure of the complex of the interacting regions of dock22 and elmo1
77	<a href="#">d1rlwa</a>	Alignment	not modelled	99.3	17	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
78	<a href="#">d2cs0a1</a>	Alignment	not modelled	99.3	29	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
79	<a href="#">c1y57A</a>	Alignment	not modelled	99.3	29	<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
80	<a href="#">c2cr4A</a>	Alignment	not modelled	99.3	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
						<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase

81	<a href="#">c2kk6A</a>	Alignment	not modelled	99.3	34	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
82	<a href="#">d1qcfa2</a>	Alignment	not modelled	99.3	25	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
83	<a href="#">d1opka2</a>	Alignment	not modelled	99.3	30	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
84	<a href="#">d1jyra</a>	Alignment	not modelled	99.3	36	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
85	<a href="#">c1ka6A</a>	Alignment	not modelled	99.3	23	<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
86	<a href="#">d1rpya</a>	Alignment	not modelled	99.3	26	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
87	<a href="#">d2fcia1</a>	Alignment	not modelled	99.3	30	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
88	<a href="#">c3nsiA</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> perforin-1; <b>PDBTitle:</b> the x-ray crystal structure of lymphocyte perforin
89	<a href="#">c2dcrA</a>	Alignment	not modelled	99.3	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
90	<a href="#">d2shpa3</a>	Alignment	not modelled	99.3	34	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
91	<a href="#">c2ysxA</a>	Alignment	not modelled	99.3	31	<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
92	<a href="#">c3fbkB</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> regulator of g-protein signaling 3; <b>PDBTitle:</b> crystal structure of the c2 domain of the human regulator2 of g-protein signaling 3 isoform 6 (rgp3), northeast3 structural genomics consortium target hr5550a
93	<a href="#">d1ayaa</a>	Alignment	not modelled	99.2	34	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
94	<a href="#">c2lctA</a>	Alignment	not modelled	99.2	25	<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
95	<a href="#">d1r1qa</a>	Alignment	not modelled	99.2	28	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
96	<a href="#">c1x6cA</a>	Alignment	not modelled	99.2	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
97	<a href="#">c1x27F</a>	Alignment	not modelled	99.2	25	<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 f2 p130cas
98	<a href="#">d1bkla</a>	Alignment	not modelled	99.2	32	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
99	<a href="#">c2ablA</a>	Alignment	not modelled	99.2	31	<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
100	<a href="#">d1dsya</a>	Alignment	not modelled	99.2	20	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
101	<a href="#">c1mv3A</a>	Alignment	not modelled	99.2	12	<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
102	<a href="#">d1d4ta</a>	Alignment	not modelled	99.2	24	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
103	<a href="#">c2nsgA</a>	Alignment	not modelled	99.2	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase nedd4-like protein; <b>PDBTitle:</b> crystal structure of the c2 domain of the human e3 ubiquitin-protein2 ligase nedd4-like protein
104	<a href="#">c2fk9A</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c, eta type; <b>PDBTitle:</b> human protein kinase c, eta
105	<a href="#">c2z0uB</a>	Alignment	not modelled	99.2	20	<b>PDB header:</b> lipid binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> ww domain-containing protein 1; <b>PDBTitle:</b> crystal structure of c2 domain of kibra protein
106	<a href="#">c1rqcC</a>	Alignment	not modelled	99.2	29	<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
107	<a href="#">d1xa6a2</a>	Alignment	not modelled	99.2	29	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
108	<a href="#">d1f2fa_</a>	Alignment	not modelled	99.2	32	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
109	<a href="#">d1lkka_</a>	Alignment	not modelled	99.2	26	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
110	<a href="#">d1a25a_</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
111	<a href="#">c3jzyA_</a>	Alignment	not modelled	99.2	20	<b>PDB header:</b> endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> intersectin 2; <b>PDBTitle:</b> crystal structure of human intersectin 2 c2 domain
112	<a href="#">c1k9aB_</a>	Alignment	not modelled	99.2	30	<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
113	<a href="#">c2h8hA_</a>	Alignment	not modelled	99.2	29	<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
114	<a href="#">c2ge9A_</a>	Alignment	not modelled	99.2	30	<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
115	<a href="#">d1i3za_</a>	Alignment	not modelled	99.2	26	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
116	<a href="#">c3nhnA_</a>	Alignment	not modelled	99.2	25	<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
117	<a href="#">c2c0iA_</a>	Alignment	not modelled	99.2	25	<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
118	<a href="#">c2el8A_</a>	Alignment	not modelled	99.2	21	<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
119	<a href="#">c2hmhA_</a>	Alignment	not modelled	99.2	17	<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.
120	<a href="#">d1k9aa2</a>	Alignment	not modelled	99.2	33	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain