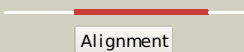

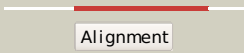

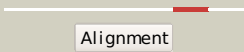

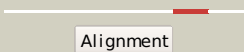

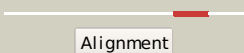

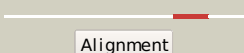



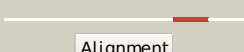

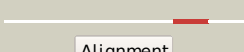

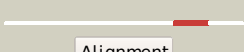

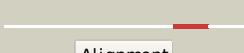







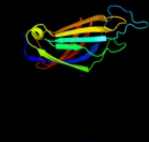




# Phyre2

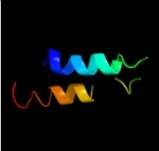

Email	I.a.kelley@imperial.ac.uk
Description	A0FGR9
Date	Thu Apr 26 09:38:06 BST 2012
Unique Job ID	4f054448a9455fdf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2r83B_</a>	 Alignment		100.0	38	<b>PDB header:</b> endocytosis, exocytosis <b>Chain:</b> B: <b>PDB Molecule:</b> synaptotagmin-1; <b>PDBTitle:</b> crystal structure analysis of human synaptotagmin 1 c2a-c2b
2	<a href="#">c1dqvA_</a>	 Alignment		100.0	31	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> synaptotagmin iii; <b>PDBTitle:</b> crystal structure of synaptotagmin iii c2a/c2b
3	<a href="#">c2z0uB_</a>	 Alignment		99.9	22	<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
4	<a href="#">c2dmgA_</a>	 Alignment		99.9	47	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> kiaa1228 protein; <b>PDBTitle:</b> solution structure of the third c2 domain of kiaa12282 protein
5	<a href="#">c2d8kA_</a>	 Alignment		99.9	38	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> synaptotagmin vii; <b>PDBTitle:</b> solution structure of the first c2 domain of synaptotagmin2 vii
6	<a href="#">d1wfmA_</a>	 Alignment		99.9	21	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
7	<a href="#">c2enpA_</a>	 Alignment		99.9	35	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> b/k protein; <b>PDBTitle:</b> solution structure of the first c2 domain from human b/k2 protein
8	<a href="#">c2q3xA_</a>	 Alignment		99.9	31	<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
9	<a href="#">d1v27a_</a>	 Alignment		99.9	26	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
10	<a href="#">d1rsya_</a>	 Alignment		99.9	32	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
11	<a href="#">c2chdA_</a>	 Alignment		99.9	26	<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

12	<a href="#">d2bwqa1</a>	Alignment		99.9	29	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
13	<a href="#">d1gmia_</a>	Alignment		99.9	20	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
14	<a href="#">d1dsya_</a>	Alignment		99.9	31	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
15	<a href="#">c3fbkB_</a>	Alignment		99.9	27	<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
16	<a href="#">d1ugka_</a>	Alignment		99.9	32	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
17	<a href="#">d2r83a1</a>	Alignment		99.9	33	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
18	<a href="#">c2fk9A_</a>	Alignment		99.9	24	<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
19	<a href="#">c3nsiA_</a>	Alignment		99.9	24	<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
20	<a href="#">d1rh8a_</a>	Alignment		99.9	39	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
21	<a href="#">c2b3rA_</a>	Alignment	not modelled	99.9	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol-4-phosphate 3-kinase c2 domain- <b>PDBTitle:</b> crystal structure of the c2 domain of class ii phosphatidylinositide2 3-kinase c2
22	<a href="#">c3m7fB_</a>	Alignment	not modelled	99.9	33	<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
23	<a href="#">d1bdya_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
24	<a href="#">c3jzyA_</a>	Alignment	not modelled	99.9	32	<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
25	<a href="#">d1dqva1</a>	Alignment	not modelled	99.9	36	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
26	<a href="#">c3fdwA_</a>	Alignment	not modelled	99.9	29	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> synaptotagmin-like protein 4; <b>PDBTitle:</b> crystal structure of a c2 domain from human synaptotagmin-2 like protein 4
27	<a href="#">d1rlwa_</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
28	<a href="#">d1dqva2</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
						<b>Fold:</b> C2 domain-like

29	<a href="#">d1uowa_</a>	Alignment	not modelled	99.9	34	<b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
30	<a href="#">c2cm6A_</a>	Alignment	not modelled	99.9	30	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> rabphilin-3a; <b>PDBTitle:</b> crystal structure of the c2b domain of rabphilin3a
31	<a href="#">c2dmhA_</a>	Alignment	not modelled	99.9	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
32	<a href="#">d1byna_</a>	Alignment	not modelled	99.8	32	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
33	<a href="#">d1a25a_</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
34	<a href="#">c3l9bA_</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> otoflerlin; <b>PDBTitle:</b> crystal structure of rat otoferlin c2a
35	<a href="#">c3n5aA_</a>	Alignment	not modelled	99.8	32	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> synaptotagmin-7; <b>PDBTitle:</b> synaptotagmin-7, c2b-domain, calcium bound
36	<a href="#">d2cm5a1</a>	Alignment	not modelled	99.8	31	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
37	<a href="#">c3kwtA_</a>	Alignment	not modelled	99.8	35	<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
38	<a href="#">d1wfja_</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
39	<a href="#">c2nq3A_</a>	Alignment	not modelled	99.8	22	<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
40	<a href="#">d2nq3a1</a>	Alignment	not modelled	99.8	22	<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="#">d2ep6a1</a>	Alignment	not modelled	99.8	33	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
42	<a href="#">d2cjta1</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
43	<a href="#">c2enjA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c theta type; <b>PDBTitle:</b> solution structure of the c2 domain from human protein2 kinase c theta
44	<a href="#">d1w15a_</a>	Alignment	not modelled	99.8	31	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
45	<a href="#">c2nsgA_</a>	Alignment	not modelled	99.8	32	<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
46	<a href="#">d1qasa2</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
47	<a href="#">d2cjsa1</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
48	<a href="#">c1cjbB_</a>	Alignment	not modelled	99.7	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (cytosolic phospholipase a2); <b>PDBTitle:</b> human cytosolic phospholipase a2
49	<a href="#">c2jqzA_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase smurf2; <b>PDBTitle:</b> solution structure of the c2 domain of human smurf2
50	<a href="#">d2zkmx2</a>	Alignment	not modelled	99.6	28	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
51	<a href="#">c1djyB_</a>	Alignment	not modelled	99.5	19	<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
52	<a href="#">c3ohmB_</a>	Alignment	not modelled	99.2	22	<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
53	<a href="#">c3qr0A_</a>	Alignment	not modelled	99.2	21	<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
54	<a href="#">c2fjuB_</a>	Alignment	not modelled	99.0	32	<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
55	<a href="#">c3nfaA_</a>	Alignment	not modelled	98.6	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c beta type;

55	<a href="#">c3p1qA_</a>	Alignment	not modelled	98.8	27	<b>PDBTitle:</b> crystal structure and allosteric activation of protein kinase c beta2 ii
56	<a href="#">d1e7ua2</a>	Alignment	not modelled	97.7	22	<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="#">c2enqA_</a>	Alignment	not modelled	97.5	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol-4,5-bisphosphate 3-kinase <b>PDBTitle:</b> solution structure of the c2 domain from human pi3-kinase2 p110 subunit alpha
58	<a href="#">d1e8ya2</a>	Alignment	not modelled	97.1	22	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
59	<a href="#">c2wxoA_</a>	Alignment	not modelled	96.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic <b>PDBTitle:</b> the crystal structure of the murine class ia pi 3-kinase2 p110delta in complex with as5.
60	<a href="#">c1e8za_</a>	Alignment	not modelled	96.4	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase catalytic subunit; <b>PDBTitle:</b> structure determinants of phosphoinositide 3-kinase2 inhibition by wortmannin, ly294002, quercetin, myricetin3 and staurosporine
61	<a href="#">c2rd0A_</a>	Alignment	not modelled	95.8	13	<b>PDB header:</b> transferase/oncoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic <b>PDBTitle:</b> structure of a human p110alpha/p85alpha complex
62	<a href="#">c3l4cB_</a>	Alignment	not modelled	95.7	15	<b>PDB header:</b> cell adhesion, cell invasion, apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> dedicator of cytokinesis protein 1; <b>PDBTitle:</b> structural basis of membrane-targeting by dock180
63	<a href="#">c2y3aA_</a>	Alignment	not modelled	93.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic <b>PDBTitle:</b> crystal structure of p110beta in complex with icsh2 of p85beta and2 the drug gdc-0941
64	<a href="#">d2yrba1</a>	Alignment	not modelled	81.7	8	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
65	<a href="#">d2iuba2</a>	Alignment		57.3	8	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Magnesium transport protein CorA, transmembrane region <b>Family:</b> Magnesium transport protein CorA, transmembrane region
66	<a href="#">c2v6zM_</a>	Alignment		52.6	21	<b>PDB header:</b> transferase <b>Chain:</b> M: <b>PDB Molecule:</b> dna polymerase epsilon subunit 2; <b>PDBTitle:</b> solution structure of amino terminal domain of human dna2 polymerase epsilon subunit b
67	<a href="#">c2kluA_</a>	Alignment	not modelled	49.9	27	<b>PDB header:</b> immune system, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> t-cell surface glycoprotein cd4; <b>PDBTitle:</b> nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
68	<a href="#">d1ewfa1</a>	Alignment	not modelled	48.8	8	<b>Fold:</b> Aha1/BPI domain-like <b>Superfamily:</b> Bactericidal permeability-increasing protein, BPI <b>Family:</b> Bactericidal permeability-increasing protein, BPI
69	<a href="#">d1d5ra1</a>	Alignment	not modelled	41.9	12	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
70	<a href="#">c3c4mD_</a>	Alignment	not modelled	40.7	35	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> parathyroid hormone; <b>PDBTitle:</b> structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
71	<a href="#">c3c4mC_</a>	Alignment	not modelled	40.7	35	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> parathyroid hormone; <b>PDBTitle:</b> structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
72	<a href="#">c1bp1A_</a>	Alignment	not modelled	37.2	9	<b>PDB header:</b> bactericidal <b>Chain:</b> A: <b>PDB Molecule:</b> bactericidal/permeability-increasing protein; <b>PDBTitle:</b> crystal structure of bpi, the human bactericidal2 permeability-increasing protein
73	<a href="#">c2r2cA_</a>	Alignment	not modelled	34.3	29	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> 28 kda outer membrane protein omp28; <b>PDBTitle:</b> crystal structure of a domain of the outer membrane lipoprotein omp282 from porphyromonas gingivalis
74	<a href="#">c1zwgA_</a>	Alignment	not modelled	23.0	32	<b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> parathyroid hormone; <b>PDBTitle:</b> succinyl human parathyroid hormone 4-37, nmr, 10 structures
75	<a href="#">c3h8mB_</a>	Alignment	not modelled	20.8	37	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 7; <b>PDBTitle:</b> sam domain of human ephrin type-a receptor 7 (epha7)
76	<a href="#">c3snhA_</a>	Alignment	not modelled	18.9	29	<b>PDB header:</b> endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> dynamin-1; <b>PDBTitle:</b> crystal structure of nucleotide-free human dynamin1
77	<a href="#">d1a8ra_</a>	Alignment	not modelled	16.3	19	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> GTP cyclohydrolase I
78	<a href="#">c2bbjB_</a>	Alignment	not modelled	16.0	14	<b>PDB header:</b> metal transport/membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> divalent cation transport-related protein;

						<b>PDBTitle:</b> crystal structure of the cora mg2+ transporter
79	<a href="#">d1g0da2</a>	Alignment	not modelled	15.3	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
80	<a href="#">d1ciya3</a>	Alignment	not modelled	15.2	13	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> delta-Endotoxin (insectocide), N-terminal domain <b>Family:</b> delta-Endotoxin (insectocide), N-terminal domain
81	<a href="#">c1is7F_</a>	Alignment	not modelled	12.2	27	<b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> gtp cyclohydrolase i; <b>PDBTitle:</b> crystal structure of rat gtpchi/grp stimulatory complex
82	<a href="#">d1sdwa2</a>	Alignment	not modelled	12.0	22	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> PHM/PNGase F <b>Family:</b> Peptidylglycine alpha-hydroxylating monooxygenase, PHM
83	<a href="#">c1fvyA_</a>	Alignment	not modelled	11.8	44	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> parathyroid hormone; <b>PDBTitle:</b> solution structure of the osteogenic 1-31 fragment of the2 human parathyroid hormone
84	<a href="#">d1gmea_</a>	Alignment	not modelled	11.8	16	<b>Fold:</b> HSP20-like chaperones <b>Superfamily:</b> HSP20-like chaperones <b>Family:</b> HSP20
85	<a href="#">d1jhna4</a>	Alignment	not modelled	11.7	15	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Calnexin/calreticulin
86	<a href="#">c3kksA_</a>	Alignment	not modelled	11.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> type-2 restriction enzyme pvuii; <b>PDBTitle:</b> crystal structure of single chain pvuii
87	<a href="#">c3zvrA_</a>	Alignment	not modelled	11.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dynamin-1; <b>PDBTitle:</b> crystal structure of dynamin
88	<a href="#">c3lkbB_</a>	Alignment	not modelled	10.7	30	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> nascent polypeptide-associated complex subunit alpha; <b>PDBTitle:</b> human nac dimerization domain
89	<a href="#">d1wpla_</a>	Alignment	not modelled	10.3	25	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> GTP cyclohydrolase I
90	<a href="#">d1dlca3</a>	Alignment	not modelled	10.2	25	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> delta-Endotoxin (insectocide), N-terminal domain <b>Family:</b> delta-Endotoxin (insectocide), N-terminal domain
91	<a href="#">c1wm9D_</a>	Alignment	not modelled	9.9	25	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> gtp cyclohydrolase i; <b>PDBTitle:</b> structure of gtp cyclohydrolase i from thermus thermophilus hb8
92	<a href="#">d1wura1</a>	Alignment	not modelled	9.9	25	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> GTP cyclohydrolase I
93	<a href="#">c4e71A_</a>	Alignment	not modelled	9.5	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> plexin-b2; <b>PDBTitle:</b> crystal structure of the rho gtpase binding domain of plexin b2
94	<a href="#">d2o8ra4</a>	Alignment	not modelled	9.4	17	<b>Fold:</b> Phospholipase D/nuclease <b>Superfamily:</b> Phospholipase D/nuclease <b>Family:</b> Polyphosphate kinase C-terminal domain
95	<a href="#">c2op8A_</a>	Alignment	not modelled	9.2	33	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable tautomerase ywhb; <b>PDBTitle:</b> crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
96	<a href="#">d1gmeb_</a>	Alignment	not modelled	9.2	16	<b>Fold:</b> HSP20-like chaperones <b>Superfamily:</b> HSP20-like chaperones <b>Family:</b> HSP20
97	<a href="#">d1otfa_</a>	Alignment	not modelled	9.1	17	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> 4-oxalocrotonate tautomerase-like
98	<a href="#">d1xdpa4</a>	Alignment	not modelled	8.9	11	<b>Fold:</b> Phospholipase D/nuclease <b>Superfamily:</b> Phospholipase D/nuclease <b>Family:</b> Polyphosphate kinase C-terminal domain
99	<a href="#">c3pjvD_</a>	Alignment	not modelled	8.2	5	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> cyclic dimeric gmp binding protein; <b>PDBTitle:</b> structure of pseudomonas fluorescence lapd periplasmic domain