












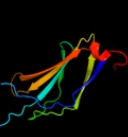











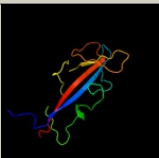
Phyre2

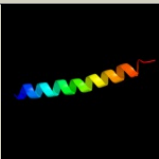
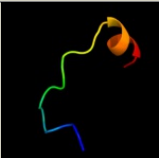

Email	I.a.kelley@imperial.ac.uk
Description	A0AVI2
Date	Wed May 9 17:44:31 BST 2012
Unique Job ID	74f8e09f1a43eb2a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1dqvA_	 Alignment		99.9	27	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: synaptotagmin iii; PDBTitle: crystal structure of synaptotagmin iii c2a/c2b
2	c2r83B_	 Alignment		99.9	26	PDB header: endocytosis, exocytosis Chain: B: PDB Molecule: synaptotagmin-1; PDBTitle: crystal structure analysis of human synaptotagmin 1 c2a-c2b
3	c3l9bA_	 Alignment		99.8	15	PDB header: membrane protein Chain: A: PDB Molecule: otoferlin; PDBTitle: crystal structure of rat otoferlin c2a
4	c3nsjA_	 Alignment		99.7	23	PDB header: immune system Chain: A: PDB Molecule: perforin-1; PDBTitle: the x-ray crystal structure of lymphocyte perforin
5	c2dmhA_	 Alignment		99.6	34	PDB header: lipid binding protein Chain: A: PDB Molecule: myoferlin; PDBTitle: solution structure of the first c2 domain of human myoferlin
6	c3kwtA_	 Alignment		99.6	22	PDB header: metal binding protein Chain: A: PDB Molecule: munc13-1; PDBTitle: munc13-1 c2b-domain, calcium-free
7	d1gmia_	 Alignment		99.6	21	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
8	d2cjta1	 Alignment		99.6	25	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
9	d1bdya_	 Alignment		99.6	15	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
10	d1qasa2	 Alignment		99.5	25	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
11	c3jzyA_	 Alignment		99.5	26	PDB header: endocytosis Chain: A: PDB Molecule: intersectin 2; PDBTitle: crystal structure of human intersectin 2 c2 domain

12	c2fk9A_	Alignment		99.5	17	PDB header: transferase Chain: A: PDB Molecule: protein kinase c, eta type; PDBTitle: human protein kinase c, eta
13	c2nq3A_	Alignment		99.5	23	PDB header: ligase Chain: A: PDB Molecule: itchy homolog e3 ubiquitin protein ligase; PDBTitle: crystal structure of the c2 domain of human itchy homolog2 e3 ubiquitin protein ligase
14	d2nq3a1	Alignment		99.5	23	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
15	d1dsya_	Alignment		99.5	18	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
16	d2cjsa1	Alignment		99.5	20	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
17	c3m7fB_	Alignment		99.5	20	PDB header: signaling protein/ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase nedd4; PDBTitle: crystal structure of the nedd4 c2/grb10 sh2 complex
18	d1rlwa_	Alignment		99.5	27	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
19	c2z0uB_	Alignment		99.4	18	PDB header: lipid binding protein Chain: B: PDB Molecule: ww domain-containing protein 1; PDBTitle: crystal structure of c2 domain of kibra protein
20	d1wfja_	Alignment		99.4	27	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
21	d2ep6a1	Alignment	not modelled	99.4	25	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
22	c2d8kA_	Alignment	not modelled	99.4	30	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: synaptotagmin vii; PDBTitle: solution structure of the first c2 domain of synaptotagmin2 vii
23	c3fbkB_	Alignment	not modelled	99.4	17	PDB header: signaling protein Chain: B: PDB Molecule: regulator of g-protein signaling 3; PDBTitle: crystal structure of the c2 domain of the human regulator2 of g-protein signaling 3 isoform 6 (rgp3), northeast3 structural genomics consortium target hr5550a
24	c2q3xA_	Alignment	not modelled	99.4	27	PDB header: transport protein Chain: A: PDB Molecule: regulating synaptic membrane exocytosis protein 1; PDBTitle: the rim1alpha c2b domain
25	d2r83a1	Alignment	not modelled	99.4	27	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
26	d1a25a_	Alignment	not modelled	99.4	31	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
27	c2jqzA_	Alignment	not modelled	99.4	20	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf2; PDBTitle: solution structure of the c2 domain of human smurf2
28	c2chdA_	Alignment	not modelled	99.4	31	PDB header: protein transport Chain: A: PDB Molecule: rabphilin-3a; PDBTitle: crystal structure of the c2a domain of rabphilin-3a PDB header: ligase

29	c2nsqA	Alignment	not modelled	99.4	25	Chain: A: PDB Molecule: e3 ubiquitin-protein ligase nedd4-like protein; PDBTitle: crystal structure of the c2 domain of the human e3 ubiquitin-protein2 ligase nedd4-like protein
30	d1lugka	Alignment	not modelled	99.3	29	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
31	c1djyB	Alignment	not modelled	99.3	27	PDB header: lipid degradation Chain: B: PDB Molecule: phosphoinositide-specific phospholipase c, PDBTitle: phosphoinositide-specific phospholipase c-delta1 from rat2 complexed with inositol-2,4,5-trisphosphate
32	c2enpA	Alignment	not modelled	99.3	24	PDB header: transport protein Chain: A: PDB Molecule: b/k protein; PDBTitle: solution structure of the first c2 domain from human b/k2 protein
33	d1v27a	Alignment	not modelled	99.3	24	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
34	d2zkmx2	Alignment	not modelled	99.3	26	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
35	d1wfmA	Alignment	not modelled	99.3	19	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
36	d1rsya	Alignment	not modelled	99.3	29	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
37	c2cm6A	Alignment		99.3	25	PDB header: protein transport Chain: A: PDB Molecule: rabphilin-3a; PDBTitle: crystal structure of the c2b domain of rabphilin3a
38	d2cm5a1	Alignment	not modelled	99.3	28	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
39	d1dqva1	Alignment	not modelled	99.2	31	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
40	c2enjA	Alignment	not modelled	99.2	19	PDB header: transferase Chain: A: PDB Molecule: protein kinase c theta type; PDBTitle: solution structure of the c2 domain from human protein2 kinase c theta
41	c2b3rA	Alignment	not modelled	99.2	23	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol-4-phosphate 3-kinase c2 domain- PDBTitle: crystal structure of the c2 domain of class ii phosphatidylinositide 3-kinase c2
42	c2dmgA	Alignment	not modelled	99.2	22	PDB header: lipid binding protein Chain: A: PDB Molecule: kiaa1228 protein; PDBTitle: solution structure of the third c2 domain of kiaa12282 protein
43	d1rh8a	Alignment	not modelled	99.2	29	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
44	d1dqva2	Alignment	not modelled	99.2	26	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
45	d2bwqa1	Alignment	not modelled	99.2	25	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
46	d1uowa	Alignment	not modelled	99.1	25	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
47	c3n5aA	Alignment	not modelled	99.1	28	PDB header: protein transport Chain: A: PDB Molecule: synaptotagmin-7; PDBTitle: synaptotagmin-7, c2b-domain, calcium bound
48	c1cyjB	Alignment	not modelled	99.1	15	PDB header: hydrolase Chain: B: PDB Molecule: protein (cytosolic phospholipase a2); PDBTitle: human cytosolic phospholipase a2
49	d1byna	Alignment	not modelled	99.1	30	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
50	c3fdwA	Alignment	not modelled	99.0	16	PDB header: lipid binding protein Chain: A: PDB Molecule: synaptotagmin-like protein 4; PDBTitle: crystal structure of a c2 domain from human synaptotagmin-2 like protein 4
51	c2k2oA	Alignment		98.9	39	PDB header: membrane protein Chain: A: PDB Molecule: myoferlin; PDBTitle: solution structure of the inner dysf domain of human2 myoferlin
52	c3qr0A	Alignment	not modelled	98.9	28	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase c-beta (plc-beta); PDBTitle: crystal structure of s. officinalis plc21
						Fold: C2 domain-like

53	d1w15a_	Alignment	not modelled	98.9	24	Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
54	c2fjuB_	Alignment	not modelled	98.8	31	PDB header: signaling protein,apoptosis/hydrolase Chain: B: PDB Molecule: 1-phosphatidylinositol-4,5-bisphosphate PDBTitle: activated rac1 bound to its effector phospholipase c beta 2
55	c3ohmB_	Alignment	not modelled	98.7	17	PDB header: signaling protein / hydrolase Chain: B: PDB Molecule: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase PDBTitle: crystal structure of activated g alpha q bound to its effector2.phospholipase c beta 3
56	c2engA_	Alignment	not modelled	97.3	20	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol-4,5-bisphosphate 3-kinase PDBTitle: solution structure of the c2 domain from human pi3-kinase2 p110 subunit alpha
57	c3pfqA_	Alignment	not modelled	97.0	32	PDB header: transferase Chain: A: PDB Molecule: protein kinase c beta type; PDBTitle: crystal structure and allosteric activation of protein kinase c beta2 ii
58	d1e7ua2	Alignment	not modelled	97.0	16	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
59	c2wxoA_	Alignment	not modelled	96.8	20	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic PDBTitle: the crystal structure of the murine class ia pi 3-kinase2 p110delta in complex with as5.
60	d1e8ya2	Alignment	not modelled	96.2	19	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
61	d1whna_	Alignment	not modelled	94.7	23	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
62	c1e8za_	Alignment	not modelled	94.5	22	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol 3-kinase catalytic subunit; PDBTitle: structure determinants of phosphoinositide 3-kinase2 inhibition by wortmannin, ly294002, quercetin, myricetin3 and staurosporine
63	c2rd0A_	Alignment	not modelled	94.5	19	PDB header: transferase/oncoprotein Chain: A: PDB Molecule: phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic PDBTitle: structure of a human p110alpha/p85alpha complex
64	c2y3aA_	Alignment	not modelled	93.4	18	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic PDBTitle: crystal structure of p110beta in complex with icsh2 of p85beta and2 the drug gdc-0941
65	c3hd7A_	Alignment		92.9	16	PDB header: exocytosis Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
66	c3l4cB_	Alignment	not modelled	90.0	16	PDB header: cell adhesion, cell invasion, apoptosis Chain: B: PDB Molecule: dedicator of cytokinesis protein 1; PDBTitle: structural basis of membrane-targeting by dock180
67	c1aabA_	Alignment		59.5	20	PDB header: dna-binding Chain: A: PDB Molecule: high mobility group protein; PDBTitle: nmr structure of rat hmg1 hmga fragment
68	d1aaba_	Alignment		59.5	20	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
69	c3htxA_	Alignment	not modelled	57.3	19	PDB header: transferase/rna Chain: A: PDB Molecule: hen1; PDBTitle: crystal structure of small rna methyltransferase hen1
70	c3adlA_	Alignment	not modelled	52.4	17	PDB header: gene regulation/rna Chain: A: PDB Molecule: risc-loading complex subunit trbp2; PDBTitle: structure of trbp2 and its molecule implications for mirna processing
71	d1di2a_	Alignment	not modelled	51.4	19	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
72	d1q42a_	Alignment	not modelled	50.0	22	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
73	d1d5ra1	Alignment	not modelled	48.9	16	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
74	d1of5b_	Alignment	not modelled	46.3	22	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
						PDB header: translation

75	c1q40C_	Alignment	not modelled	45.2	22	Chain: C: PDB Molecule: mrna transport regulator mtr2; PDBTitle: crystal structure of the c. albicans mtr2-mex67 m domain complex
76	c2zv4O_	Alignment	not modelled	43.6	25	PDB header: structural protein Chain: O: PDB Molecule: major vault protein; PDBTitle: the structure of rat liver vault at 3.5 angstrom resolution
77	d1vf5b_	Alignment	not modelled	42.7	16	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
78	c3nngA_	Alignment	not modelled	39.3	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the f5/8 type c domain of q5lfr2_bacfn protein2 from bacteroides fragilis. northeast structural genomics consortium3 target bfr258e
79	d2g3wa1	Alignment	not modelled	38.3	24	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: YaeQ-like
80	d1q90d_	Alignment	not modelled	38.1	15	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
81	c3ipdB_	Alignment	not modelled	35.8	15	PDB header: exocytosis Chain: B: PDB Molecule: syntaxin-1a; PDBTitle: helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
82	d2dixa1	Alignment	not modelled	33.6	19	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
83	c1j3xA_	Alignment	not modelled	33.0	24	PDB header: dna binding protein Chain: A: PDB Molecule: high mobility group protein 2; PDBTitle: solution structure of the n-terminal domain of the hmgb2
84	d1j3xa_	Alignment	not modelled	33.0	24	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
85	d1ekza_	Alignment	not modelled	32.7	9	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
86	c2yvxD_	Alignment	not modelled	32.3	8	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
87	c3dinD_	Alignment	not modelled	31.4	18	PDB header: membrane protein, protein transport Chain: D: PDB Molecule: preprotein translocase subunit sece; PDBTitle: crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
88	c2yewB_	Alignment	not modelled	31.0	13	PDB header: virus Chain: B: PDB Molecule: e1 envelope glycoprotein; PDBTitle: modeling barmah forest virus structural proteins
89	d2qpva1	Alignment	not modelled	30.6	21	Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like
90	d1uhza_	Alignment	not modelled	30.2	13	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
91	c3adjA_	Alignment	not modelled	30.1	20	PDB header: gene regulation Chain: A: PDB Molecule: f21m12.9 protein; PDBTitle: structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
92	c3oc3B_	Alignment	not modelled	29.4	15	PDB header: hydrolase/transcription Chain: B: PDB Molecule: helicase mot1; PDBTitle: crystal structure of the mot1 n-terminal domain in complex with tbp
93	d2ot9a1	Alignment	not modelled	29.3	21	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: YaeQ-like
94	d2cpna1	Alignment	not modelled	28.7	26	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
95	d2e74b1	Alignment	not modelled	26.3	12	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
96	c3lhb_	Alignment	not modelled	25.6	35	PDB header: rna binding protein Chain: B: PDB Molecule: risc-loading complex subunit tarbp2; PDBTitle: crystal structure of the first dsrbd of tar rna-binding protein 2
97	c3s9jA_	Alignment	not modelled	25.5	24	PDB header: unknown function Chain: A: PDB Molecule: member of duf4221 family; PDBTitle: crystal structure of a member of duf4221 family (bvu_1028) from2 bacteroides vulgatus atcc 8482 at 1.75 a resolution
98	c2yt4A_	Alignment	not modelled	25.1	19	PDB header: rna binding protein Chain: A: PDB Molecule: protein dgcr8; PDBTitle: crystal structure of human dgcr8 core
99	d2yrba1	Alignment	not modelled	24.9	16	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)

100	d1x47a1	Alignment	not modelled	24.8	19	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
101	d1pf4a2	Alignment	not modelled	23.6	15	Fold: ABC transporter transmembrane region Superfamily: ABC transporter transmembrane region Family: ABC transporter transmembrane region
102	c4drvA	Alignment	not modelled	23.4	21	PDB header: viral protein Chain: A: PDB Molecule: outer capsid protein vp4; PDBTitle: cell attachment protein vp8* of a human rotavirus specifically2 interacts with a-type histo-blood group antigen
103	c3n0aA	Alignment	not modelled	23.1	7	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase auxilin; PDBTitle: crystal structure of auxilin (40-400)
104	c2l2nA	Alignment	not modelled	22.5	38	PDB header: rna binding protein, plant protein Chain: A: PDB Molecule: hyponastic leave 1; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for the first2 dsrbd of protein hyl1
105	d1j3da	Alignment	not modelled	22.5	32	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
106	d2aaib1	Alignment	not modelled	22.5	8	Fold: beta-Trefoil Superfamily: Ricin B-like lectins Family: Ricin B-like
107	d1stua	Alignment	not modelled	22.4	5	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
108	c2eqzA	Alignment	not modelled	22.0	11	PDB header: transcription Chain: A: PDB Molecule: high mobility group protein b3; PDBTitle: solution structure of the first hmg-box domain from high2 mobility group protein b3
109	c2yrqA	Alignment	not modelled	20.3	22	PDB header: dna binding protein Chain: A: PDB Molecule: high mobility group protein b1; PDBTitle: solution structure of the tandem hmg box domain from human2 high mobility group protein b1
110	d1z1ba1	Alignment	not modelled	20.3	24	Fold: DNA-binding domain Superfamily: DNA-binding domain Family: lambda integrase N-terminal domain