

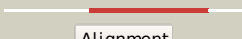

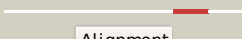








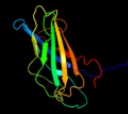


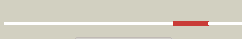

















Phyre2


Email	I.a.kelley@imperial.ac.uk
Description	A0FGR8
Date	Sat Jun 16 10:27:15 BST 2012
Unique Job ID	62d23792cd3259e4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2r83B_	 Alignment		100.0	36	PDB header: endocytosis, exocytosis Chain: B; PDB Molecule: synaptotagmin-1; PDBTitle: crystal structure analysis of human synaptotagmin 1 c2a-c2b
2	c1dqvA_	 Alignment		100.0	34	PDB header: endocytosis/exocytosis Chain: A; PDB Molecule: synaptotagmin iii; PDBTitle: crystal structure of synaptotagmin iii c2a/c2b
3	c2z0uB_	 Alignment		99.9	22	PDB header: lipid binding protein Chain: B; PDB Molecule: ww domain-containing protein 1; PDBTitle: crystal structure of c2 domain of kibra protein
4	c2d8kA_	 Alignment		99.9	32	PDB header: endocytosis/exocytosis Chain: A; PDB Molecule: synaptotagmin vii; PDBTitle: solution structure of the first c2 domain of synaptotagmin2 vii
5	c2enpA_	 Alignment		99.9	34	PDB header: transport protein Chain: A; PDB Molecule: b/k protein; PDBTitle: solution structure of the first c2 domain from human b/k2 protein
6	c2dmgA_	 Alignment		99.9	92	PDB header: lipid binding protein Chain: A; PDB Molecule: kiaa1228 protein; PDBTitle: solution structure of the third c2 domain of kiaa12282 protein
7	d1wfma_	 Alignment		99.9	19	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
8	c2q3xA_	 Alignment		99.9	28	PDB header: transport protein Chain: A; PDB Molecule: regulating synaptic membrane exocytosis protein 1; PDBTitle: the rim1alpha c2b domain
9	d1v27a_	 Alignment		99.9	27	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
10	d1rsya_	 Alignment		99.9	35	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
11	c2chdA_	 Alignment		99.9	22	PDB header: protein transport Chain: A; PDB Molecule: rabphilin-3a; PDBTitle: crystal structure of the c2a domain of rabphilin-3a

12	d2bwqa1	Alignment		99.9	30	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
13	c3fbkB_	Alignment		99.9	28	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
14	d1dsya_	Alignment		99.9	28	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
15	d1ugka_	Alignment		99.9	30	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
16	d2r83a1	Alignment		99.9	32	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
17	d1gmia_	Alignment		99.9	27	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
18	d1rh8a_	Alignment		99.9	37	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
19	c2b3rA_	Alignment		99.9	30	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol-4-phosphate 3-kinase c2 domain- PDBTitle: crystal structure of the c2 domain of class ii phosphatidylinositide2 3-kinase c2
20	c2fk9A_	Alignment		99.9	28	PDB header: transferase Chain: A: PDB Molecule: protein kinase c, eta type; PDBTitle: human protein kinase c, eta
21	c3nsjA_	Alignment		99.9	21	PDB header: immune system Chain: A: PDB Molecule: perforin-1; PDBTitle: the x-ray crystal structure of lymphocyte perforin
22	c3fdwA_	Alignment	not modelled	99.9	31	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
23	d1uowa_	Alignment	not modelled	99.9	32	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
24	d1dqva1	Alignment	not modelled	99.9	37	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
25	d1bdya_	Alignment	not modelled	99.9	17	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
26	d1byna_	Alignment	not modelled	99.8	35	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
27	c3m7fB_	Alignment	not modelled	99.8	31	PDB header: signaling protein/ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase nedd4; PDBTitle: crystal structure of the nedd4 c2/grb10 sh2 complex
						PDB header: endocytosis

28	c3jzyA_	Alignment	not modelled	99.8	34	Chain: A: PDB Molecule: intersectin 2; PDBTitle: crystal structure of human intersectin 2 c2 domain
29	d1dqva2	Alignment	not modelled	99.8	26	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
30	c2cm6A_	Alignment	not modelled	99.8	29	PDB header: protein transport Chain: A: PDB Molecule: rabphilin-3a; PDBTitle: crystal structure of the c2b domain of rabphilin3a
31	d1a25a_	Alignment	not modelled	99.8	29	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
32	d1rlwa_	Alignment	not modelled	99.8	22	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
33	c2dmhA_	Alignment	not modelled	99.8	20	PDB header: lipid binding protein Chain: A: PDB Molecule: myoferlin; PDBTitle: solution structure of the first c2 domain of human myoferlin
34	c3n5aA_	Alignment	not modelled	99.8	30	PDB header: protein transport Chain: A: PDB Molecule: synaptotagmin-7; PDBTitle: synaptotagmin-7, c2b-domain, calcium bound
35	c3l9bA_	Alignment	not modelled	99.8	23	PDB header: membrane protein Chain: A: PDB Molecule: otoferlin; PDBTitle: crystal structure of rat otoferlin c2a
36	d2cm5a1	Alignment	not modelled	99.8	29	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
37	c3kwtA_	Alignment	not modelled	99.8	32	PDB header: metal binding protein Chain: A: PDB Molecule: munc13-1; PDBTitle: munc13-1 c2b-domain, calcium-free
38	d2ep6a1	Alignment	not modelled	99.8	30	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
39	d1wfja_	Alignment	not modelled	99.8	23	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
40	d2nq3a1	Alignment	not modelled	99.8	25	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
41	c2nq3A_	Alignment	not modelled	99.8	25	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
42	d1w15a_	Alignment	not modelled	99.8	31	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
43	d2cjt1	Alignment	not modelled	99.8	17	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
44	d1qasa2	Alignment	not modelled	99.8	23	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
45	c2nsgA_	Alignment	not modelled	99.7	34	PDB header: ligase 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
46	d2cjsa1	Alignment	not modelled	99.7	19	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
47	c2enjA_	Alignment	not modelled	99.7	16	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
48	c1cjbB_	Alignment	not modelled	99.7	24	PDB header: hydrolase Chain: B: PDB Molecule: protein (cytosolic phospholipase a2); PDBTitle: human cytosolic phospholipase a2
49	c2jqzA_	Alignment	not modelled	99.7	23	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf2; PDBTitle: solution structure of the c2 domain of human smurf2
50	d2zkmx2	Alignment	not modelled	99.6	25	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
51	c1djyB_	Alignment	not modelled	99.5	24	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
52	c3ohmB_	Alignment	not modelled	99.2	30	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
53	c3qr0A_	Alignment	not modelled	99.2	17	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase c-beta (plc-beta); PDBTitle: crystal structure of s. officinalis plc21
54	c2fjvB_	Alignment	not modelled	99.0	23	PDB header: signaling protein,apoptosis/hydrolase Chain: B: PDB Molecule: 1-phosphatidylinositol-4,5-bisphosphate

54	c2ijub	Alignment	not modelled	99.0	33	PDBTitle: activated rac1 bound to its effector phospholipase c beta 2 PDB header: transferase
55	c3pfqA	Alignment	not modelled	98.6	30	Chain: A: PDB Molecule: protein kinase c beta type; PDBTitle: crystal structure and allosteric activation of protein kinase c beta2 ii
56	d1e7ua2	Alignment	not modelled	97.4	16	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
57	c2enqA	Alignment	not modelled	97.1	14	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
58	d1e8ya2	Alignment	not modelled	96.7	15	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
59	c2wxoA	Alignment	not modelled	96.5	15	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	c1e8zA	Alignment	not modelled	95.9	15	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
61	c2rd0A	Alignment	not modelled	95.1	13	PDB header: transferase/oncoprotein Chain: A: PDB Molecule: phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic PDBTitle: structure of a human p110alpha/p85alpha complex
62	c3l4cB	Alignment	not modelled	94.2	15	PDB header: cell adhesion, cell invasion, apoptosis Chain: B: PDB Molecule: dedicator of cytokinesis protein 1; PDBTitle: structural basis of membrane-targeting by dock180
63	c2y3aA	Alignment	not modelled	92.4	12	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
64	d2yrba1	Alignment	not modelled	88.5	13	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
65	c2v6zM	Alignment		51.8	16	PDB header: transferase Chain: M: PDB Molecule: dna polymerase epsilon subunit 2; PDBTitle: solution structure of amino terminal domain of human dna2 polymerase epsilon subunit b
66	d1d5ra1	Alignment	not modelled	50.5	15	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
67	d2iuba2	Alignment	not modelled	46.4	8	Fold: Transmembrane helix hairpin Superfamily: Magnesium transport protein CorA, transmembrane region Family: Magnesium transport protein CorA, transmembrane region
68	c3c4mC	Alignment	not modelled	33.9	39	PDB header: membrane protein Chain: C: PDB Molecule: parathyroid hormone; PDBTitle: structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
69	c3c4mD	Alignment	not modelled	33.9	39	PDB header: membrane protein Chain: D: PDB Molecule: parathyroid hormone; PDBTitle: structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
70	c2r2cA	Alignment	not modelled	29.5	32	PDB header: membrane protein Chain: A: PDB Molecule: 28 kda outer membrane protein omp28; PDBTitle: crystal structure of a domain of the outer membrane lipoprotein omp282 from porphyromonas gingivalis
71	c2kluA	Alignment	not modelled	27.9	11	PDB header: immune system, membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd4; PDBTitle: nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
72	c1bp1A	Alignment	not modelled	26.4	8	PDB header: bactericidal Chain: A: PDB Molecule: bactericidal/permeability-increasing protein; PDBTitle: crystal structure of bpi, the human bactericidal2 permeability-increasing protein
73	d1xmeb2	Alignment	not modelled	24.0	27	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
74	c1yewL	Alignment	not modelled	23.1	19	PDB header: oxidoreductase, membrane protein Chain: I: PDB Molecule: particulate methane monooxygenase, b subunit; PDBTitle: crystal structure of particulate methane monooxygenase
75	c3rgbA	Alignment	not modelled	23.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: methane monooxygenase subunit b2; PDBTitle: crystal structure of particulate methane monooxygenase from2 methylcoccus capsulatus (bath)
76	c3h8mB	Alignment	not modelled	20.8	26	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 7; PDBTitle: sam domain of human ephrin type-a receptor 7 (epha7)
77	c1zwgA	Alignment	not modelled	20.2	36	PDB header: hormone Chain: A: PDB Molecule: parathyroid hormone; PDBTitle: succinyl human parathyroid hormone 4-37, nmr, 10 structures

78	c1wazA	Alignment	not modelled	19.5	33	PDB header: transport protein Chain: A: PDB Molecule: merf; PDBTitle: nmr structure determination of the bacterial mercury2 transporter, merf, in micelles
79	c1fvvA	Alignment	not modelled	19.2	50	PDB header: hormone/growth factor Chain: A: PDB Molecule: parathyroid hormone; PDBTitle: solution structure of the osteogenic 1-31 fragment of the2 human parathyroid hormone
80	d1ewfa1	Alignment	not modelled	19.1	8	Fold: Aha1/BPI domain-like Superfamily: Bactericidal permeability-increasing protein, BPI Family: Bactericidal permeability-increasing protein, BPI
81	c2bbjB	Alignment	not modelled	19.0	10	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: parathyroid hormone; PDBTitle: crystal structure of the cora mg2+ transporter
82	c2h3oA	Alignment	not modelled	17.3	37	PDB header: membrane protein Chain: A: PDB Molecule: merf; PDBTitle: structure of merf, a membrane protein with two trans-2 membrane helices
83	d1a8ra	Alignment	not modelled	14.7	19	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
84	d1xg8a	Alignment	not modelled	12.1	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: YuzD-like
85	c1is7F	Alignment	not modelled	12.0	33	PDB header: hydrolase/protein binding Chain: F: PDB Molecule: gtp cyclohydrolase i; PDBTitle: crystal structure of rat gtpchi/grfp stimulatory complex
86	d2diga1	Alignment	not modelled	11.9	42	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
87	d2axtj1	Alignment	not modelled	11.8	12	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein J, Psbj Family: Psbj-like
88	d1ciya3	Alignment	not modelled	10.5	16	Fold: Toxins' membrane translocation domains Superfamily: delta-Endotoxin (insectocide), N-terminal domain Family: delta-Endotoxin (insectocide), N-terminal domain
89	d1jhna4	Alignment	not modelled	10.5	20	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Calnexin/calreticulin
90	d1ppjg	Alignment	not modelled	10.4	19	Fold: Single transmembrane helix Superfamily: Ubiquinone-binding protein QP-C of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: Ubiquinone-binding protein QP-C of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
91	d1bccg	Alignment	not modelled	10.2	19	Fold: Single transmembrane helix Superfamily: Ubiquinone-binding protein QP-C of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: Ubiquinone-binding protein QP-C of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
92	c2l2ta	Alignment	not modelled	9.9	29	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-4; PDBTitle: solution nmr structure of the erbb4 dimeric membrane domain
93	d1wpla	Alignment	not modelled	9.8	32	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
94	c3snhA	Alignment	not modelled	9.5	19	PDB header: endocytosis Chain: A: PDB Molecule: dynamin-1; PDBTitle: crystal structure of nucleotide-free human dynamin1
95	c1wm9D	Alignment	not modelled	9.0	23	PDB header: hydrolase Chain: D: PDB Molecule: gtp cyclohydrolase i; PDBTitle: structure of gtp cyclohydrolase i from thermus thermophilus hb8
96	d1wura1	Alignment	not modelled	9.0	23	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
97	c3cwbT	Alignment	not modelled	8.7	19	PDB header: oxidoreductase Chain: T: PDB Molecule: mitochondrial ubiquinol-cytochrome c reductase ubiquinone- PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
98	d1ehkb2	Alignment	not modelled	8.5	27	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
99	c3h4zC	Alignment	not modelled	8.4	19	PDB header: allergen Chain: C: PDB Molecule: maltose-binding periplasmic protein fused with allergen PDBTitle: crystal structure of an mbp-der p 7 fusion protein