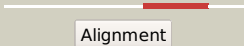

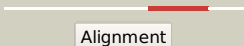

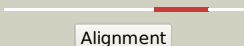

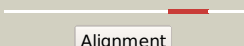

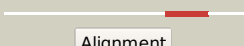

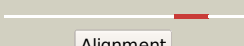

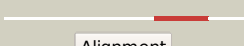




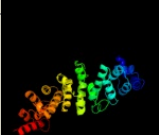




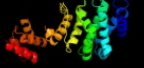


Phyre2

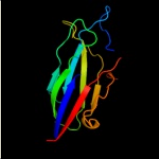
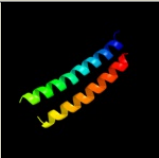

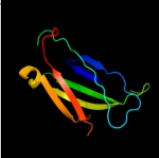
Email	l.a.kelley@imperial.ac.uk
Description	A1L3T7
Date	Tue Jul 30 12:55:19 BST 2013
Unique Job ID	ad7136f74d5492c2


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3l6yE_	 Alignment		98.9	15	PDB header: cell adhesion Chain: E; PDB Molecule: catenin delta-1; PDBTitle: crystal structure of p120 catenin in complex with e-cadherin
2	d1oyza_	 Alignment		98.9	11	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: PBS lyase HEAT-like repeat
3	c3ltjA_	 Alignment		98.8	18	PDB header: protein binding Chain: A; PDB Molecule: alpharep-4; PDBTitle: structure of a new family of artificial alpha helicoidal repeat2 proteins (alpha-rep) based on thermostable heat-like repeats
4	c3l9tA_	 Alignment		98.7	14	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein smu.31; PDBTitle: the crystal structure of smu.31 from streptococcus mutans ua159
5	c3b2aA_	 Alignment		98.6	15	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the archaeal heat-like repeats protein ton_19372 from thermococcus onnurineus na1
6	d1te4a_	 Alignment		98.6	14	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: PBS lyase HEAT-like repeat
7	c2db0B_	 Alignment		98.3	11	PDB header: protein binding Chain: B; PDB Molecule: 253aa long hypothetical protein; PDBTitle: crystal structure of ph0542
8	c3c5wA_	 Alignment		98.3	12	PDB header: hydrolase Chain: A; PDB Molecule: pp2a a subunit; PDBTitle: complex between pp2a-specific methyltransferase pme-1 and pp2a core2 enzyme
9	c3nowA_	 Alignment		98.3	16	PDB header: protein binding Chain: A; PDB Molecule: unc-45 protein, sd10334p; PDBTitle: unc-45 from drosophila melanogaster
10	d1b3ua_	 Alignment		98.2	14	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: HEAT repeat
11	c4adyA_	 Alignment		98.2	12	PDB header: protein binding Chain: A; PDB Molecule: 26s proteasome regulatory subunit rpn2; PDBTitle: crystal structure of 26s proteasome subunit rpn2

12	c3nmwA_	Alignment		98.1	12	PDB header: cell adhesion/cell cycle Chain: A: PDB Molecule: apc variant protein; PDBTitle: crytal structure of armadillo repeats domain of apc
13	c3u0rA_	Alignment		98.1	16	PDB header: apoptosis inhibitor Chain: A: PDB Molecule: apoptosis inhibitor 5; PDBTitle: helical repeat structure of apoptosis inhibitor 5 reveals protein-2 protein interaction modules
14	c2z6hA_	Alignment		97.9	10	PDB header: cell adhesion Chain: A: PDB Molecule: catenin beta-1; PDBTitle: crystal structure of beta-catenin armadillo repeat region2 and its c-terminal domain
15	c1xqrA_	Alignment		97.9	14	PDB header: chaperone Chain: A: PDB Molecule: hspbp1 protein; PDBTitle: crystal structure of the hspbp1 core domain
16	c3v6aA_	Alignment		97.9	16	PDB header: apoptosis inhibitor Chain: A: PDB Molecule: apoptosis inhibitor 5; PDBTitle: helical repeat structure of apoptosis inhibitor 5 reveals protein-2 protein interaction modules
17	d1xqra1	Alignment		97.8	13	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: HspBP1 domain
18	d1gw5b_	Alignment		97.7	10	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Clathrin adaptor core protein
19	c3ifqB_	Alignment		97.7	13	PDB header: cell adhesion Chain: B: PDB Molecule: plakoglobin; PDBTitle: interction of plakoglobin and beta-catenin with desmosomal2 cadherins
20	d1jdha_	Alignment		97.7	13	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
21	c2z6gA_	Alignment	not modelled	97.7	13	PDB header: cell adhesion Chain: A: PDB Molecule: b-catenin; PDBTitle: crystal structure of a full-length zebrafish beta-catenin
22	c4g3aA_	Alignment	not modelled	97.6	18	PDB header: cell cycle Chain: A: PDB Molecule: clip-associating protein; PDBTitle: crystal structure of mast/orbit n-terminal domain
23	d1ee4a_	Alignment	not modelled	97.6	11	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
24	c3sl9G_	Alignment	not modelled	97.5	14	PDB header: signaling protein, protein binding Chain: G: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of beta catenin in complex with bc19
25	c3w3zA_	Alignment	not modelled	97.5	7	PDB header: protein transport/nuclear protein Chain: A: PDB Molecule: importin subunit beta-3; PDBTitle: crystal structure of kap121p bound to rangtp
26	c4k92B_	Alignment	not modelled	97.5	11	PDB header: structural protein Chain: B: PDB Molecule: clip-associating protein 1; PDBTitle: a cryptic tog domain with a distinct architecture underlies clasp-2 dependent bipolar spindle formation
27	c3slaC_	Alignment	not modelled	97.5	13	PDB header: signaling protein Chain: C: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin
28	c3gq2B_	Alignment	not modelled	97.4	16	PDB header: transport protein Chain: B: PDB Molecule: general vesicular transport factor p115; PDBTitle: crystal structure of the dimer of the p115 tether globular head domain
						Fold: alpha-alpha superhelix

29	d1xm9a1	Alignment	not modelled	97.4	14	Superfamily: ARM repeat Family: Plakophilin 1 helical region
30	c3bctA	Alignment	not modelled	97.4	14	PDB header: armadillo repeat Chain: A: PDB Molecule: beta-catenin; PDBTitle: the armadillo repeat region from murine beta-catenin
31	c3sl9A	Alignment	not modelled	97.3	13	PDB header: signaling protein, protein binding Chain: A: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of beta catenin in complex with bcl9
32	c3slaB	Alignment	not modelled	97.3	13	PDB header: signaling protein Chain: B: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin
33	c3l6yA	Alignment	not modelled	97.3	13	PDB header: cell adhesion Chain: A: PDB Molecule: catenin delta-1; PDBTitle: crystal structure of p120 catenin in complex with e-cadherin
34	c3sl9E	Alignment	not modelled	97.2	10	PDB header: signaling protein, protein binding Chain: E: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of beta catenin in complex with bcl9
35	c2of3A	Alignment	not modelled	97.2	11	PDB header: structural protein, cell cycle Chain: A: PDB Molecule: zyg-9; PDBTitle: tog domain structure from c.elegans zyg9
36	c3sl9B	Alignment	not modelled	97.2	10	PDB header: signaling protein, protein binding Chain: B: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of beta catenin in complex with bcl9
37	d1v18a1	Alignment	not modelled	97.2	17	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
38	c3oqsA	Alignment	not modelled	97.2	13	PDB header: protein transport Chain: A: PDB Molecule: importin subunit alpha-2; PDBTitle: crystal structure of importin-alpha bound to a clc4 nls peptide
39	d1q1sc	Alignment	not modelled	97.1	11	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
40	c3slaD	Alignment	not modelled	97.1	13	PDB header: signaling protein Chain: D: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin
41	c3slaA	Alignment	not modelled	97.1	11	PDB header: signaling protein Chain: A: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin
42	c2ynsA	Alignment	not modelled	97.1	9	PDB header: transport protein Chain: A: PDB Molecule: importin subunit alpha-1a; PDBTitle: rimp_alpha_b54nls
43	c3tjzB	Alignment	not modelled	97.0	11	PDB header: protein transport/protein binding Chain: B: PDB Molecule: coatomer subunit gamma; PDBTitle: crystal structure of arf1 bound to the gamma/zeta-cop core complex
44	c3slaE	Alignment	not modelled	97.0	12	PDB header: signaling protein Chain: E: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin
45	d1lrva	Alignment	not modelled	97.0	16	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Leucine-rich repeat variant
46	c2c1tA	Alignment	not modelled	97.0	10	PDB header: protein transport/membrane protein Chain: A: PDB Molecule: importin alpha subunit; PDBTitle: structure of the kap60p:nup2 complex
47	c1pjmB	Alignment	not modelled	96.9	13	PDB header: protein transport Chain: B: PDB Molecule: importin alpha-2 subunit; PDBTitle: mouse importin alpha-bipartite nls from human2 retinoblastoma protein complex
48	c4db8B	Alignment	not modelled	96.9	15	PDB header: de novo protein Chain: B: PDB Molecule: armadillo-repeat protein; PDBTitle: designed armadillo-repeat protein
49	c1w63A	Alignment	not modelled	96.9	11	PDB header: endocytosis Chain: A: PDB Molecule: adapter-related protein complex 1 gamma 1 PDBTitle: ap1 clathrin adaptor core
50	d1u6gc	Alignment	not modelled	96.8	15	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: HEAT repeat
51	c4hxtA	Alignment	not modelled	96.8	16	PDB header: de novo protein Chain: A: PDB Molecule: de novo protein or329; PDBTitle: crystal structure of engineered protein. northeast structural genomics2 consortium target or329
52	c3t7uA	Alignment	not modelled	96.7	14	PDB header: cell adhesion Chain: A: PDB Molecule: adenomatous polyposis coli protein; PDBTitle: a new crytal structure of apc-arm
53	c2w3cA	Alignment	not modelled	96.7	18	PDB header: transport protein Chain: A: PDB Molecule: general vesicular transport factor p115; PDBTitle: globular head region of the human general vesicular2 transport factor p115
54	c4db9A	Alignment	not modelled	96.7	18	PDB header: de novo protein Chain: A: PDB Molecule: armadillo repeat protein, yiiim3aiii; PDBTitle: designed armadillo repeat protein (yiiim3aiii)
55	c4a0cB	Alignment	not modelled	96.6	10	PDB header: cell cycle Chain: B: PDB Molecule: cullin-associated neddb8-dissociated protein 1; PDBTitle: structure of the cand1-cul4b-rbx1 complex PDB header: cell adhesion

56	c3tt9A_	Alignment	not modelled	96.5	11	Chain: A; PDB Molecule: plakophilin-2; PDBTitle: crystal structure of the stable degradation fragment of human2 plakophilin 2 isoform a (pkp2a) c752r variant
57	c3nmzB_	Alignment	not modelled	96.5	13	PDB header: cell adhesion/cell cycle Chain: B; PDB Molecule: apc variant protein; PDBTitle: crystal structure of apc complexed with asef
58	c2jdgB_	Alignment	not modelled	96.4	12	PDB header: protein transport Chain: B; PDB Molecule: importin alpha-1 subunit; PDBTitle: c-terminal domain of influenza a virus polymerase pb22 subunit in complex with human importin alpha5
59	c4ffbC_	Alignment	not modelled	96.0	9	PDB header: hydrolase Chain: C; PDB Molecule: protein stu2; PDBTitle: a tog:alpha/beta-tubulin complex structure reveals conformation-based2 mechanisms for a microtubule polymerase
60	c4i2wA_	Alignment	not modelled	96.0	10	PDB header: chaperone/protein binding Chain: A; PDB Molecule: protein unc-45; PDBTitle: crystal structure of the myosin chaperone unc-45 from c.elegans in2 complex with a hsp70 peptide
61	d1librB_	Alignment	not modelled	95.9	21	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
62	c2ot8B_	Alignment	not modelled	95.9	13	PDB header: transport protein Chain: B; PDB Molecule: transportin-1; PDBTitle: karyopherin beta2/transportin-hnrnp nls complex
63	c1m5nS_	Alignment	not modelled	95.8	10	PDB header: protein transport Chain: S; PDB Molecule: importin beta-1 subunit; PDBTitle: crystal structure of heat repeats (1-11) of importin b2 bound to the non-classical nls(67-94) of pthrp
64	d2ep6a1	Alignment		95.5	24	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
65	c2qnaA_	Alignment	not modelled	95.4	15	PDB header: transport protein Chain: A; PDB Molecule: importin subunit beta-1; PDBTitle: crystal structure of human importin-beta (127-876) in complex with the2 ibb-domain of snurportin1 (1-65)
66	c2qk1A_	Alignment	not modelled	95.3	11	PDB header: protein binding Chain: A; PDB Molecule: protein stu2; PDBTitle: structural basis of microtubule plus end tracking by2 xmap215, clip-170 and eb1
67	d1urfa_	Alignment		94.6	27	Fold: Long alpha-hairpin Superfamily: HR1 repeat Family: HR1 repeat
68	d1gmia_	Alignment	not modelled	94.4	13	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
69	c2qk2A_	Alignment	not modelled	94.4	14	PDB header: protein binding Chain: A; PDB Molecule: lp04448p; PDBTitle: structural basis of microtubule plus end tracking by xmap215, clip-1702 and eb1
70	c2jkrL_	Alignment	not modelled	94.2	17	PDB header: endocytosis Chain: L; PDB Molecule: ap-2 complex subunit alpha-2; PDBTitle: ap2 clathrin adaptor core with dileucine peptide rm(2 phosphos)qikrlise
71	d2bpta1	Alignment	not modelled	94.1	15	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
72	d1wa5b_	Alignment	not modelled	93.9	18	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
73	c1wa5B_	Alignment	not modelled	93.9	18	PDB header: nuclear transport Chain: B; PDB Molecule: importin alpha subunit; PDBTitle: crystal structure of the exportin cse1p complexed with its2 cargo (kap60p) and rangtp
74	c1lshA_	Alignment	not modelled	93.7	11	PDB header: lipid binding protein Chain: A; PDB Molecule: lipovitelin (lv-1n, lv-1c); PDBTitle: lipid-protein interactions in lipovitelin
75	d1cxzb_	Alignment		93.0	22	Fold: Long alpha-hairpin Superfamily: HR1 repeat Family: HR1 repeat
76	c3l9bA_	Alignment		92.8	17	PDB header: membrane protein Chain: A; PDB Molecule: otoferlin; PDBTitle: crystal structure of rat otoferlin c2a
77	d1lsha1	Alignment	not modelled	91.4	11	Fold: alpha-alpha superhelix Superfamily: Lipovitelin-phosvitin complex, superhelical domain Family: Lipovitelin-phosvitin complex, superhelical domain
78	d1qgra_	Alignment	not modelled	90.6	15	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat

79	c3jzyA	Alignment	not modelled	90.5	14	PDB header: endocytosis Chain: A: PDB Molecule: intersectin 2; PDBTitle: crystal structure of human intersectin 2 c2 domain
80	d1qbkB	Alignment	not modelled	90.3	15	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
81	d1wfla	Alignment	not modelled	87.3	21	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
82	d1rlwa	Alignment	not modelled	85.9	18	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
83	c3opbA	Alignment	not modelled	85.7	13	PDB header: protein binding Chain: A: PDB Molecule: swi5-dependent ho expression protein 4; PDBTitle: crystal structure of she4p
84	c2dmhA	Alignment	not modelled	85.5	16	PDB header: lipid binding protein Chain: A: PDB Molecule: myoferlin; PDBTitle: solution structure of the first c2 domain of human myoferlin
85	d2nq3a1	Alignment	not modelled	85.5	20	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
86	c2nq3A	Alignment	not modelled	85.5	20	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
87	d2cjsa1	Alignment	not modelled	78.2	16	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
88	d1sxic1	Alignment		77.7	13	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
89	d2cm5a1	Alignment	not modelled	75.1	20	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
90	c4gmnA	Alignment	not modelled	74.9	22	PDB header: rna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structural basis of rpl5 recognition by syo1
91	c2nsgA	Alignment	not modelled	72.6	18	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
92	c3sqgG	Alignment	not modelled	72.4	58	PDB header: transferase Chain: G: PDB Molecule: methyl coenzyme m reductase, alpha subunit; PDBTitle: crystal structure of a methyl-coenzyme m reductase purified from black2 sea mats
93	c3kwtA	Alignment	not modelled	70.2	16	PDB header: metal binding protein Chain: A: PDB Molecule: munc13-1; PDBTitle: munc13-1 c2b-domain, calcium-free
94	c2raxY	Alignment	not modelled	68.1	25	PDB header: cell cycle Chain: Y: PDB Molecule: borealin; PDBTitle: crystal structure of borealin (20-78) bound to survivin (1-120)
95	c1hbuD	Alignment	not modelled	67.4	75	PDB header: methanogenesis Chain: D: PDB Molecule: methyl-coenzyme m reductase i alpha subunit; PDBTitle: methyl-coenzyme m reductase in the mcr-red1-silent state in2 complex with coenzyme m
96	c1degO	Alignment	not modelled	66.6	9	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
97	c2fk9A	Alignment	not modelled	65.7	18	PDB header: transferase Chain: A: PDB Molecule: protein kinase c, eta type; PDBTitle: human protein kinase c, eta
98	d1wa5c	Alignment	not modelled	65.6	10	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat
99	c2ke4A	Alignment	not modelled	65.0	10	PDB header: membrane protein Chain: A: PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
100	d1hbna1	Alignment	not modelled	64.7	75	Fold: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Superfamily: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Family: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
101	c2l1B	Alignment	not modelled	64.6	10	PDB header: nuclear protein Chain: B: PDB Molecule: exportin-1; PDBTitle: nmr solution structure of the phi0 pki nes peptide in complex with2 crm1-rangtp
102	c1e6yA	Alignment	not modelled	64.5	50	PDB header: oxidoreductase Chain: A: PDB Molecule: methyl-coenzyme m reductase subunit alpha; PDBTitle: methyl-coenzyme m reductase from methanosarcina barkeri

103	d1e6ya1	Alignment	not modelled	64.0	50	Fold: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Superfamily: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Family: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
104	d2vmha1	Alignment	not modelled	60.9	26	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: NPCBM-like
105	d2iuba1	Alignment	not modelled	60.6	21	Fold: CorA soluble domain-like Superfamily: CorA soluble domain-like Family: CorA soluble domain-like
106	c3vwaA	Alignment	not modelled	60.0	17	PDB header: hydrolase Chain: A: PDB Molecule: cytoplasmic export protein 1; PDBTitle: crystal structure of cex1p
107	c2qfaB	Alignment	not modelled	59.7	25	PDB header: cell cycle/cell cycle/cell cycle Chain: B: PDB Molecule: borealin; PDBTitle: crystal structure of a survivin-borealin-incenp core complex
108	c1dvpA	Alignment	not modelled	59.2	16	PDB header: transferase Chain: A: PDB Molecule: hepatocyte growth factor-regulated tyrosine PDBTitle: crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
109	d1euma	Alignment	not modelled	58.5	19	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin
110	c3m7fB	Alignment	not modelled	57.4	16	PDB header: signaling protein/ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase nedd4; PDBTitle: crystal structure of the nedd4 c2/grb10 sh2 complex
111	d1s94a	Alignment	not modelled	56.5	15	Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
112	c1s94A	Alignment	not modelled	56.5	15	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: s-syntaxin; PDBTitle: crystal structure of the habc domain of neuronal syntaxin from the2 squid loligo pealei
113	c3gebC	Alignment	not modelled	55.2	24	PDB header: hydrolase Chain: C: PDB Molecule: eyes absent homolog 2; PDBTitle: crystal structure of edeya2
114	c2vckC	Alignment	not modelled	54.6	10	PDB header: oxidoreductase Chain: C: PDB Molecule: cyanobacterial phycoerythrobilin; PDBTitle: structure of phycoerythrobilin synthase pebs from the2 cyanophage p-ssm2 in complex with the bound substrate3 biliverdin ixa
115	c3ripA	Alignment	not modelled	53.4	16	PDB header: structural protein Chain: A: PDB Molecule: gamma-tubulin complex component 4; PDBTitle: crystal structure of human gamma-tubulin complex protein 4 (gcp4)
116	d1byna	Alignment	not modelled	51.5	15	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
117	d2cjta1	Alignment	not modelled	50.3	14	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
118	c3qx3B	Alignment	not modelled	50.1	39	PDB header: isomerase/dna/isomerase inhibitor Chain: B: PDB Molecule: dna topoisomerase 2-beta; PDBTitle: human topoisomerase iibeta in complex with dna and etoposide
119	c4ev6E	Alignment	not modelled	49.9	14	PDB header: metal transport Chain: E: PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
120	c3rpfC	Alignment	not modelled	49.3	21	PDB header: transferase Chain: C: PDB Molecule: molybdopterin converting factor, subunit 1 (moad); PDBTitle: protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695