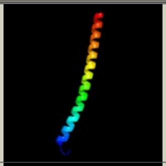
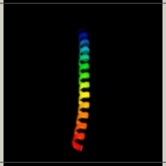
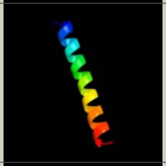
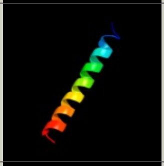
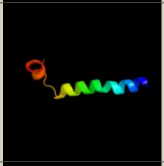
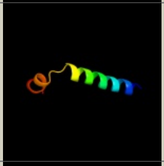
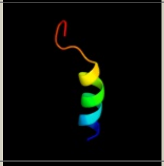
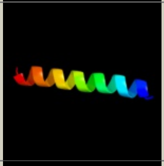
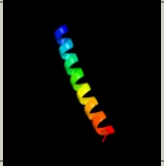
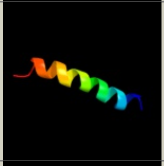
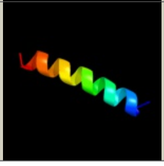
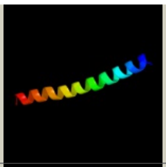
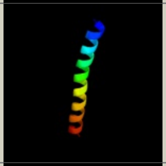
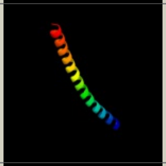
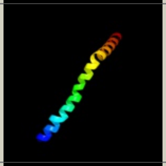
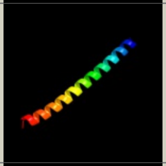
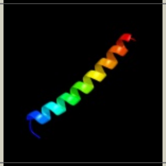
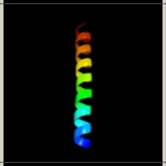
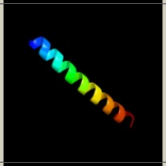
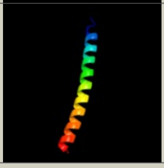
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P65298
Date	Wed Jan 25 15:21:00 GMT 2012
Unique Job ID	cbf4070c793bcc8c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1jccC_	Alignment		99.9	43	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**major outer membrane lipoprotein; **PDBTitle:** crystal structure of a novel alanine-zipper trimer at 1.7 a2 resolution, v13a,l16a,v20a,l23a,v27a,m30a,v34a mutations
2	c1t8zA_	Alignment		99.6	35	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**major outer membrane lipoprotein; **PDBTitle:** atomic structure of a novel tryptophan-zipper pentamer
3	d2gr7a1	Alignment		79.5	21	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
4	c2gr7C_	Alignment		79.5	21	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**adhesin; **PDBTitle:** hia 992-1098
5	c2v7iA_	Alignment		77.1	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**prnb; **PDBTitle:** prnb native
6	d1zeea1	Alignment		76.4	19	**Fold:**Indolic compounds 2,3-dioxygenase-like **Superfamily:**Indolic compounds 2,3-dioxygenase-like **Family:**Indoleamine 2,3-dioxygenase-like
7	c2diuA_	Alignment		66.3	32	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kiaa0430 protein; **PDBTitle:** solution structure of the rrm domain of kiaa0430 protein
8	c3sjbC_	Alignment		61.1	20	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**golgi to er traffic protein 1; **PDBTitle:** crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
9	c1ci6B_	Alignment		55.7	28	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor c/ebp beta; **PDBTitle:** transcription factor atf4-c/ebp beta bzip heterodimer
10	c1by0A_	Alignment		45.7	35	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein (hepatitis delta antigen); **PDBTitle:** n-terminal leucine-repeat region of hepatitis delta antigen
11	c3sjaG_	Alignment		45.6	23	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**golgi to er traffic protein 1; **PDBTitle:** crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain

12	c1fosF_	Alignment		43.3	27	**PDB header:**transcription/dna **Chain:** F: **PDB Molecule:**c-jun proto-oncogene protein; **PDBTitle:** two human c-fos:c-jun:dna complexes
13	c1j1dF_	Alignment		42.2	16	**PDB header:**contractile protein **Chain:** F: **PDB Molecule:**troponin i; **PDBTitle:** crystal structure of the 46kda domain of human cardiac2 troponin in the ca2+ saturated form
14	c2pohA_	Alignment		38.0	17	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**head completion protein; **PDBTitle:** structure of phage p22 tail needle gp26
15	c3na7A_	Alignment		35.5	18	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
16	c2gl2B_	Alignment		35.1	21	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**adhesion a; **PDBTitle:** crystal structure of the tetra muntant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
17	c2akfB_	Alignment		35.0	29	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
18	c2akfA_	Alignment		35.0	29	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
19	c2akfC_	Alignment		35.0	29	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
20	c1avyA_	Alignment		34.4	8	**PDB header:**coiled coil **Chain:** A: **PDB Molecule:**fibritin; **PDBTitle:** fibritin deletion mutant m (bacteriophage t4)
21	c3m9bK_	Alignment	not modelled	33.6	26	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
22	c2ykqC_	Alignment	not modelled	33.2	17	**PDB header:**rna-binding protein **Chain:** C: **PDB Molecule:**line-1 orf1p; **PDBTitle:** structure of the human line-1 orf1p trimer
23	c3ipdB_	Alignment	not modelled	33.1	11	**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
24	c2eqbC_	Alignment	not modelled	32.9	14	**PDB header:**endocytosis/exocytosis **Chain:** C: **PDB Molecule:**rab guanine nucleotide exchange factor sec2; **PDBTitle:** crystal structure of the rab gtpase sec4p, the sec2p gef2 domain, and phosphate complex
25	c3u59C_	Alignment	not modelled	32.4	11	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**tropomyosin beta chain; **PDBTitle:** n-terminal 98-aa fragment of smooth muscle tropomyosin beta
26	c3emoA_	Alignment	not modelled	32.3	19	**PDB header:**membrane protein/cell adhesion **Chain:** A: **PDB Molecule:**hia (adhesin); **PDBTitle:** crystal structure of transmembrane hia 973-1098
27	c1ytzI_	Alignment	not modelled	32.1	9	**PDB header:**contractile protein **Chain:** I: **PDB Molecule:**troponin i; **PDBTitle:** crystal structure of skeletal muscle troponin in the ca2+-2 activated state
28	c2hpcF_	Alignment	not modelled	28.7	14	**PDB header:**blood clotting **Chain:** F: **PDB Molecule:**fibrinogen, gamma polypeptide; **PDBTitle:** crystal structure of fragment d from human fibrinogen

						complexed with2 gly-pro-arg-pro-amide.
29	c2w83C_	Alignment	not modelled	28.3	21	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**c-jun-amino-terminal kinase-interacting protein **PDBTitle:** crystal structure of the arf6 gtpase in complex with a2 specific effector, jip4
30	c1j1eC_	Alignment	not modelled	27.6	16	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**troponin i; **PDBTitle:** crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
31	c1deqO_	Alignment	not modelled	27.3	8	**PDB header:** **PDB COMPND:**
32	c2qa7B_	Alignment	not modelled	26.7	28	**PDB header:**actin binding **Chain:** B: **PDB Molecule:**huntingtin-interacting protein 1; **PDBTitle:** crystal structure of huntingtin-interacting protein 12 (hip1) coiled-coil domain with a basic surface suitable3 for hip-protein interactor (hippi)
33	c1coiA_	Alignment	not modelled	26.6	50	**PDB header:**alpha-helical bundle **Chain:** A: **PDB Molecule:**coil-vald; **PDBTitle:** designed trimeric coiled coil-vald
34	c1bb1B_	Alignment	not modelled	26.3	36	**PDB header:**de novo protein design **Chain:** B: **PDB Molecule:**designed, thermostable heterotrimeric coiled **PDBTitle:** crystal structure of a designed, thermostable2 heterotrimeric coiled coil
35	c1yv0I_	Alignment	not modelled	22.6	9	**PDB header:**contractile protein **Chain:** I: **PDB Molecule:**troponin i, fast skeletal muscle; **PDBTitle:** crystal structure of skeletal muscle troponin in the ca2+-2 free state
36	c1gd2G_	Alignment	not modelled	21.6	19	**PDB header:**transcription/dna **Chain:** G: **PDB Molecule:**transcription factor pap1; **PDBTitle:** crystal structure of bzip transcription factor pap1 bound2 to dna
37	c1ei3E_	Alignment	not modelled	20.7	8	**PDB header:** **PDB COMPND:**
38	c2x7aB_	Alignment	not modelled	19.4	23	**PDB header:**immune system **Chain:** B: **PDB Molecule:**bone marrow stromal antigen 2; **PDBTitle:** structural basis of hiv-1 tethering to membranes by the2 bst2-tetherin ectodomain
39	c2d3eD_	Alignment	not modelled	19.3	19	**PDB header:**contractile protein **Chain:** D: **PDB Molecule:**general control protein gcn4 and tropomyosin 1 **PDBTitle:** crystal structure of the c-terminal fragment of rabbit2 skeletal alpha-tropomyosin
40	c2wt7B_	Alignment	not modelled	19.2	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor mafb; **PDBTitle:** crystal structure of the bzip heterodimeric complex2 mafb:cfos bound to dna
41	c3p8cF_	Alignment	not modelled	18.4	23	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**abl interactor 2; **PDBTitle:** structure and control of the actin regulatory wave complex
42	c2efrB_	Alignment	not modelled	18.1	23	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**general control protein gcn4 and tropomyosin 1 alpha chain; **PDBTitle:** crystal structure of the c-terminal tropomyosin fragment with n- and2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
43	c2ld7B_	Alignment	not modelled	17.5	29	**PDB header:**transcription **Chain:** B: **PDB Molecule:**paired amphipathic helix protein sin3a; **PDBTitle:** solution structure of the msin3a pah3-sap30 sid complex
44	d1cxzb_	Alignment	not modelled	17.4	11	**Fold:**Long alpha-hairpin **Superfamily:**HR1 repeat **Family:**HR1 repeat
45	c2npsD_	Alignment	not modelled	16.7	13	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**syntaxin-6; **PDBTitle:** crystal structure of the early endosomal snare complex
46	c3u1aC_	Alignment	not modelled	16.5	17	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**smooth muscle tropomyosin alpha; **PDBTitle:** n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
47	c1deqD_	Alignment	not modelled	16.4	19	**PDB header:** **PDB COMPND:**
48	d1nkpb_	Alignment	not modelled	16.2	19	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
49	c3bvhE_	Alignment	not modelled	15.2	27	**PDB header:**blood clotting **Chain:** E: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of recombinant gammad364a fibrinogen fragment d with2 the peptide ligand gly-pro-arg-pro-amide
50	c3ghgK_	Alignment	not modelled	15.1	12	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
51	c3gwnA_	Alignment	not modelled	15.1	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable fad-linked sulfhydryl oxidase r596; **PDBTitle:** crystal structure of the fad binding domain from mimivirus sulfhydryl2 oxidase r596
52	c3okqA_	Alignment	not modelled	15.1	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**bud site selection protein 6; **PDBTitle:** crystal structure of a core domain of yeast actin nucleation cofactor2 bud6
						PDB header:de novo protein

53	c2ki0A_	Alignment	not modelled	15.0	38	**Chain:** A: **PDB Molecule:**ds119; **PDBTitle:** nmr structure of a de novo designed beta alpha beta
54	c3b5nF_	Alignment	not modelled	14.8	7	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**protein sso1; **PDBTitle:** structure of the yeast plasma membrane snare complex
55	c2npsB_	Alignment	not modelled	14.6	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**syntaxin 13; **PDBTitle:** crystal structure of the early endosomal snare complex
56	c1ci6A_	Alignment	not modelled	14.4	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor atf-4; **PDBTitle:** transcription factor atf4-c/ebp beta bzip heterodimer
57	c3hizB_	Alignment	not modelled	14.1	14	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit **PDBTitle:** crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha
58	c1a92B_	Alignment	not modelled	14.0	35	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**delta antigen; **PDBTitle:** oligomerization domain of hepatitis delta antigen
59	c2e43A_	Alignment	not modelled	13.9	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**ccaat/enhancer-binding protein beta; **PDBTitle:** crystal structure of c/ebpbeta bzip homodimer k269a mutant2 bound to a high affinity dna fragment
60	c3mkxC_	Alignment	not modelled	13.5	23	**PDB header:**antiviral protein **Chain:** C: **PDB Molecule:**bone marrow stromal antigen 2; **PDBTitle:** crystal structure of bst2/tetherin
61	c1fosE_	Alignment	not modelled	13.1	11	**PDB header:**transcription/dna **Chain:** E: **PDB Molecule:**p55-c-fos proto-oncogene protein; **PDBTitle:** two human c-fos:c-jun:dna complexes
62	c1t3jA_	Alignment	not modelled	12.9	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mitofusin 1; **PDBTitle:** mitofusin domain hr2 v686m/i708m mutant
63	d1fxkc_	Alignment	not modelled	12.7	21	**Fold:**Long alpha-hairpin **Superfamily:**Prefoldin **Family:**Prefoldin
64	c3eukC_	Alignment	not modelled	12.5	17	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**chromosome partition protein mukb, linker; **PDBTitle:** crystal structure of muke-mukf(residues 292-443)-mukb(head2 domain)-atpgammas complex, asymmetric dimer
65	c2qihA_	Alignment	not modelled	12.2	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**protein uspa1; **PDBTitle:** crystal structure of 527-665 fragment of uspa1 protein from2 moraxella catarrhalis
66	c2fxmB_	Alignment	not modelled	12.1	21	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin heavy chain, cardiac muscle beta isoform; **PDBTitle:** structure of the human beta-myosin s2 fragment
67	c2xdjF_	Alignment	not modelled	11.0	22	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein ybgf; **PDBTitle:** crystal structure of the n-terminal domain of e.coli ybgf
68	c2js5B_	Alignment	not modelled	10.7	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of protein q60c73_metca. northeast structural2 genomics consortium target mcr1
69	c1qu7A_	Alignment	not modelled	10.6	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein i; **PDBTitle:** four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
70	c3a5tB_	Alignment	not modelled	10.5	14	**PDB header:**transcription regulator/dna **Chain:** B: **PDB Molecule:**transcription factor mafg; **PDBTitle:** crystal structure of mafg-dna complex
71	d1slqa_	Alignment	not modelled	10.4	29	**Fold:**VP4 membrane interaction domain **Superfamily:**VP4 membrane interaction domain **Family:**VP4 membrane interaction domain
72	c3hnwB_	Alignment	not modelled	10.4	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
73	c1deqF_	Alignment	not modelled	10.3	16	**PDB header:** **PDB COMPND:**
74	d1r05a_	Alignment	not modelled	10.2	26	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
75	d2azeb1	Alignment	not modelled	10.1	13	**Fold:**E2F-DP heterodimerization region **Superfamily:**E2F-DP heterodimerization region **Family:**E2F dimerization segment
76	c3dbzB_	Alignment	not modelled	10.0	21	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**pulmonary surfactant-associated protein d; **PDBTitle:** human surfactant protein d
77	c1ce0B_	Alignment	not modelled	9.9	19	**PDB header:**hiv-1 envelope protein **Chain:** B: **PDB Molecule:**protein (leucine zipper model h38-p1); **PDBTitle:** trimerization specificity in hiv-1 gp41: analysis with a2 gcn4 leucine zipper model
78	d1nlwa_	Alignment	not modelled	9.8	17	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
79	c3layF_	Alignment	not modelled	9.5	16	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**zinc resistance-associated protein; **PDBTitle:** alpha-helical barrel formed by the decamer of the zinc

						resistance-2 associated protein (stm4172) from salmonella enterica subsp. enterica3 serovar typhimurium str. lt2
80	c1gk6B_	Alignment	not modelled	9.3	18	**PDB header:**vimentin **Chain:** B: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment linked to gcn4 leucine2 zipper (z2b)
81	c2wukD_	Alignment	not modelled	9.1	14	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**septum site-determining protein diviva; **PDBTitle:** diviva n-terminal domain, f17a mutant
82	c1rb6C_	Alignment	not modelled	8.9	30	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal form
83	c1swiA_	Alignment	not modelled	8.9	30	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**gcn4p1; **PDBTitle:** gcn4-leucine zipper core mutant as n16a complexed with2 benzene
84	c1ij3B_	Alignment	not modelled	8.4	30	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
85	c1sfcD_	Alignment	not modelled	8.4	17	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**protein (snap-25b); **PDBTitle:** neuronal synaptic fusion complex
86	c1t2kD_	Alignment	not modelled	8.3	19	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**cyclic-amp-dependent transcription factor atf-2; **PDBTitle:** structure of the dna binding domains of irf3, atf-2 and jun2 bound to dna
87	c3g9rF_	Alignment	not modelled	8.3	32	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**fusion complex of hiv-1 envelope glycoprotein **PDBTitle:** structure of the hiv-1 gp41 membrane-proximal ectodomain2 region in a putative prefusion conformation
88	c2d4yA_	Alignment	not modelled	8.3	25	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**flagellar hook-associated protein 1; **PDBTitle:** crystal structure of a 49k fragment of hap1 (flgk)
89	c2xnxM_	Alignment	not modelled	8.3	33	**PDB header:**cell adhesion **Chain:** M: **PDB Molecule:**m protein; **PDBTitle:** bc1 fragment of streptococcal m1 protein in complex with human2 fibrinogen
90	c1g2cN_	Alignment	not modelled	8.2	19	**PDB header:**viral protein **Chain:** N: **PDB Molecule:**fusion protein (f); **PDBTitle:** human respiratory syncytial virus fusion protein core
91	c3gwlB_	Alignment	not modelled	8.2	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**fad-linked sulfhydryl oxidase; **PDBTitle:** crystal structure of asfv pb119l, a viral sulfhydryl oxidase
92	c1n73C_	Alignment	not modelled	8.1	18	**PDB header:**blood clotting **Chain:** C: **PDB Molecule:**fibrin gamma chain; **PDBTitle:** fibrin d-dimer, lamprey complexed with the peptide ligand: gly-his-2 arg-pro-amide
93	c1ij2C_	Alignment	not modelled	8.0	28	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
94	c1l4aD_	Alignment	not modelled	7.9	13	**PDB header:**endocytosis/exocytosis **Chain:** D: **PDB Molecule:**s-snap25 fusion protein; **PDBTitle:** x-ray structure of the neuronal complexin/snare complex2 from the squid loligo pealei
95	c1rb1A_	Alignment	not modelled	7.9	28	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
96	c1rb1B_	Alignment	not modelled	7.9	28	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
97	c3k7zA_	Alignment	not modelled	7.9	28	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
98	c3k7zB_	Alignment	not modelled	7.9	28	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
99	c2ke4A_	Alignment	not modelled	7.8	16	**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