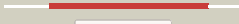


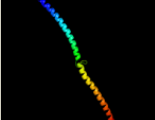
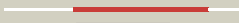
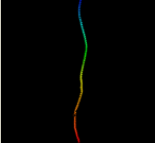



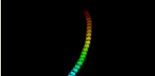

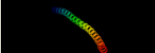

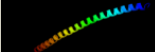

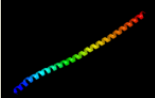



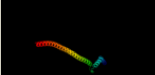


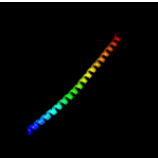
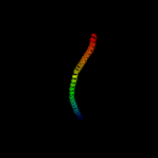

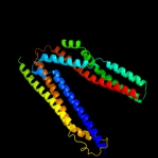

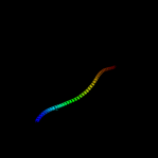
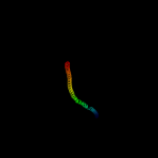


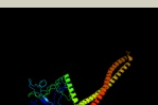


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	A1L317
Date	Tue Jul 30 13:02:37 BST 2013
Unique Job ID	5894ae4ea8d2359b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ciiA_	 Alignment		99.6	7	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
2	c3s4rB_	 Alignment		99.3	34	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1a/1b fragment with a stabilizing2 mutation
3	c1c1gA_	 Alignment		99.3	10	PDB header: contractile protein Chain: A: PDB Molecule: tropomyosin; PDBTitle: crystal structure of tropomyosin at 7 angstroms resolution2 in the spermine-induced crystal form
4	c3tnuA_	 Alignment		99.0	61	PDB header: cytosolic protein Chain: A: PDB Molecule: keratin, type i cytoskeletal 14; PDBTitle: heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
5	c3tnuB_	 Alignment		98.9	31	PDB header: cytosolic protein Chain: B: PDB Molecule: keratin, type ii cytoskeletal 5; PDBTitle: heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
6	c1gk4A_	 Alignment		98.8	31	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 2b fragment (cys2)
7	c1x8yA_	 Alignment		98.8	31	PDB header: structural protein Chain: A: PDB Molecule: lamin a/c; PDBTitle: human lamin coil 2b
8	c3swkB_	 Alignment		98.7	31	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1b fragment
9	c1yvlB_	 Alignment		98.7	10	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1
10	c3ojaB_	 Alignment		98.7	13	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/apl1c complex
11	c2oevA_	 Alignment		98.7	12	PDB header: protein transport Chain: A: PDB Molecule: programmed cell death 6-interacting protein; PDBTitle: crystal structure of alix/aip1

12	c3movB_	Alignment		98.6	27	PDB header: structural protein Chain: B: PDB Molecule: lamin-b1; PDBTitle: crystal structure of human lamin-b1 coil 2 segment
13	c3ol1A_	Alignment		98.6	32	PDB header: structural protein Chain: A: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin (fragment 144-251) from homo sapiens,2 northeast structural genomics consortium target hr4796b
14	c1bf5A_	Alignment		98.5	9	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: tyrosine phosphorylated stat-1/dna complex
15	c4jioA_	Alignment		98.4	10	PDB header: protein binding Chain: A: PDB Molecule: bro1; PDBTitle: bro1 v domain and ubiquitin
16	c2ch7A_	Alignment		98.4	8	PDB header: chemotaxis Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
17	c2efrB_	Alignment		98.4	14	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
18	c2d3eD_	Alignment		98.3	14	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
19	c2xv5A_	Alignment		98.3	35	PDB header: structural protein Chain: A: PDB Molecule: lamin-a/c; PDBTitle: human lamin a coil 2b fragment
20	c2oexB_	Alignment		98.2	12	PDB header: protein transport Chain: B: PDB Molecule: programmed cell death 6-interacting protein; PDBTitle: structure of alix/aip1 v domain
21	c1gk6B_	Alignment	not modelled	98.2	29	PDB header: vimentin Chain: B: PDB Molecule: vimentin; PDBTitle: human vimentin coil 2b fragment linked to gcn4 leucine2 zipper (z2b)
22	c3vkhA_	Alignment	not modelled	98.2	9	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
23	c1ei3C_	Alignment	not modelled	98.2	8	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
24	c3cwgA_	Alignment	not modelled	98.2	10	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
25	c3vkgA_	Alignment	not modelled	98.1	12	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of an mtbd truncation mutant of dynein motor domain
26	c3ghgl_	Alignment	not modelled	98.1	11	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
27	c1gk7A_	Alignment	not modelled	98.1	47	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 1a fragment (1a)
28	c1jchC_	Alignment		98.1	7	PDB header: ribosome inhibitor, hydrolase Chain: C: PDB Molecule: colicin e3; PDBTitle: crystal structure of colicin e3 in complex with its immunity

					protein
29	c2b9cA	Alignment	not modelled	98.1	15 PDB header: contractile protein Chain: A: PDB Molecule: striated-muscle alpha tropomyosin; PDBTitle: structure of tropomyosin's mid-region: bending and binding2 sites for actin
30	c1bg1A	Alignment	not modelled	98.1	11 PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
31	c3vkgB	Alignment	not modelled	98.0	9 PDB header: motor protein Chain: B: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a mtbd truncation mutant of dynein motor domain
32	c3na7A	Alignment	not modelled	98.0	16 PDB header: gene regulation, chaperone Chain: A: PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
33	c3o0zD	Alignment	not modelled	98.0	11 PDB header: transferase Chain: D: PDB Molecule: rho-associated protein kinase 1; PDBTitle: crystal structure of a coiled-coil domain from human rock i
34	c4a7fB	Alignment	not modelled	98.0	14 PDB header: structural protein/hydrolase Chain: B: PDB Molecule: tropomyosin 1 alpha; PDBTitle: structure of the actin-tropomyosin-myosin complex (rigor atm 3)
35	c2v71A	Alignment	not modelled	98.0	8 PDB header: nuclear protein Chain: A: PDB Molecule: nuclear distribution protein nude-like 1; PDBTitle: coiled-coil region of nudel
36	c1hciB	Alignment	not modelled	97.9	8 PDB header: triple-helix coiled coil Chain: B: PDB Molecule: alpha-actinin 2; PDBTitle: crystal structure of the rod domain of alpha-actinin
37	c3ojaA	Alignment	not modelled	97.9	11 PDB header: protein binding Chain: A: PDB Molecule: leucine-rich immune molecule 1; PDBTitle: crystal structure of lrim1/apl1c complex
38	c2i1kA	Alignment	not modelled	97.8	10 PDB header: cell adhesion, membrane protein Chain: A: PDB Molecule: moesin; PDBTitle: moesin from spodoptera frugiperda reveals the coiled-coil domain at2 3.0 angstrom resolution
39	c2fxmB	Alignment	not modelled	97.8	16 PDB header: contractile protein Chain: B: PDB Molecule: myosin heavy chain, cardiac muscle beta isoform; PDBTitle: structure of the human beta-myosin s2 fragment
40	c1deqF	Alignment	not modelled	97.8	6 PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
41	c3dtpA	Alignment	not modelled	97.8	12 PDB header: contractile protein Chain: A: PDB Molecule: myosin 2 heavy chain chimera of smooth and PDBTitle: tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map
42	c1ei3E	Alignment	not modelled	97.7	12 PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
43	c1sijB	Alignment	not modelled	97.7	8 PDB header: contractile protein Chain: B: PDB Molecule: actinin; PDBTitle: cryo-em structure of chicken gizzard smooth muscle alpha-2 actinin
44	c2ocyB	Alignment	not modelled	97.5	16 PDB header: endocytosis/exocytosis Chain: B: PDB Molecule: rab guanine nucleotide exchange factor sec2; PDBTitle: complex of the guanine exchange factor sec2p and the rab2 gtpase sec4p
45	c4a55B	Alignment	not modelled	97.5	13 PDB header: transferase Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: crystal structure of p110alpha in complex with ish2 of p85alpha and2 the inhibitor pik-108
46	c3ghgK	Alignment	not modelled	97.5	8 PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
47	c1u4qB	Alignment	not modelled	97.5	11 PDB header: structural protein Chain: B: PDB Molecule: spectrin alpha chain, brain; PDBTitle: crystal structure of repeats 15, 16 and 17 of chicken brain2 alpha spectrin
48	c3q8tB	Alignment	not modelled	97.5	13 PDB header: apoptosis Chain: B: PDB Molecule: beclin-1; PDBTitle: crystal structure of the coiled coil domain of beclin 1, an essential2 autophagy protein
49	c1deqO	Alignment	not modelled	97.5	9 PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
50	c3hizB	Alignment	not modelled	97.4	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
51	c2v66C	Alignment	not modelled	97.4	13 PDB header: structural protein Chain: C: PDB Molecule: nuclear distribution protein nude-like 1; PDBTitle: crystal structure of the coiled-coil domain of ndel1 (a.a.258 to 169)c
52	c2y3aB	Alignment	not modelled	97.3	9 PDB header: transferase Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit beta; PDBTitle: crystal structure of p110beta in complex with icsh2 of p85beta and2 the drug gdc-0941 PDB header: blood clotting

53	c1deqD_	Alignment	not modelled	97.2	9	Chain: D: PDB Molecule: fibrinogen (alpha chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
54	c3u59C_	Alignment	not modelled	97.2	9	PDB header: contractile protein Chain: C: PDB Molecule: tropomyosin beta chain; PDBTitle: n-terminal 98-aa fragment of smooth muscle tropomyosin beta
55	c1f5nA_	Alignment	not modelled	97.0	9	PDB header: signaling protein Chain: A: PDB Molecule: interferon-induced guanylate-binding protein 1; PDBTitle: human guanylate binding protein-1 in complex with the gtp2 analogue, gmppnp.
56	c2rd0B_	Alignment	not modelled	97.0	9	PDB header: transferase/oncoprotein Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: structure of a human p110alpha/p85alpha complex
57	c3kltB_	Alignment	not modelled	96.8	35	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of a vimentin fragment
58	c4gkwB_	Alignment	not modelled	96.7	11	PDB header: structural protein Chain: B: PDB Molecule: spindle assembly abnormal protein 6; PDBTitle: crystal structure of the coiled-coil domain of c. elegans sas-6
59	c3l9oA_	Alignment	not modelled	96.4	10	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dob1; PDBTitle: crystal structure of mtr4, a co-factor of the nuclear exosome
60	c3r6nA_	Alignment	not modelled	96.4	11	PDB header: cell adhesion Chain: A: PDB Molecule: desmoplakin; PDBTitle: crystal structure of a rigid four spectrin repeat fragment of the2 human desmoplakin plakin domain
61	c3ipkA_	Alignment	not modelled	96.3	11	PDB header: cell adhesion Chain: A: PDB Molecule: agi/ii; PDBTitle: crystal structure of a3vp1 of agi/ii of streptococcus mutans
62	c4l6yB_	Alignment	not modelled	96.1	6	PDB header: structural protein Chain: B: PDB Molecule: protein regulator of cytokinesis 1; PDBTitle: structure of the microtubule associated protein prc1 (protein2 regulator of cytokinesis 1)
63	c4hpgC_	Alignment	not modelled	96.1	13	PDB header: protein transport Chain: C: PDB Molecule: atg17; PDBTitle: crystal structure of the atg17-atg31-atg29 complex
64	c4dylA_	Alignment	not modelled	95.7	11	PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase fes/fps; PDBTitle: f-bar domain of human fes tyrosine kinase
65	c2gl2B_	Alignment	not modelled	95.6	10	PDB header: cell adhesion Chain: B: PDB Molecule: adhesion a; PDBTitle: crystal structure of the tetra mutant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
66	c3hnwB_	Alignment	not modelled	95.2	13	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
67	c2qa7C_	Alignment	not modelled	95.0	13	PDB header: actin binding Chain: C: 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)
68	c1y4cA_	Alignment	not modelled	94.7	10	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
69	c2no2A_	Alignment	not modelled	94.7	16	PDB header: cell adhesion Chain: A: PDB Molecule: huntingtin-interacting protein 1; PDBTitle: crystal structure of the dllrkn-containing coiled-coil2 domain of huntingtin-interacting protein 1
70	c2nrjA_	Alignment	not modelled	94.0	11	PDB header: toxin Chain: A: PDB Molecule: hbl b protein; PDBTitle: crystal structure of hemolysin binding component from2 bacillus cereus
71	c3vkhD_	Alignment	not modelled	93.9	6	PDB header: motor protein Chain: D: PDB Molecule: PDBTitle: x-ray structure of a functional full-length dynein motor domain
72	c3g67A_	Alignment	not modelled	93.9	6	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
73	c1quuA_	Alignment	not modelled	93.3	7	PDB header: contractile protein Chain: A: PDB Molecule: human skeletal muscle alpha-actinin 2; PDBTitle: crystal structure of two central spectrin-like repeats from2 alpha-actinin
74	c2v1yB_	Alignment	not modelled	93.3	9	PDB header: transferase Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: structure of a phosphoinositide 3-kinase alpha adaptor-2 binding domain (abd) in a complex with the ish2 domain3 from p85 alpha
75	c1l8dB_	Alignment	not modelled	92.3	13	PDB header: replication Chain: B: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: rad50 coiled-coil zn hook
76	c3kbtA_	Alignment	not modelled	92.0	8	PDB header: structural protein Chain: A: PDB Molecule: spectrin beta chain, erythrocyte; PDBTitle: crystal structure of the ankyrin binding domain of human erythroid2 beta spectrin (repeats 13-15) in complex with the spectrin binding3 domain of human erythroid ankyrin (zu5-ank)
77	c2l1jA_	Alignment	not modelled	92.0	7	PDB header: cell adhesion, membrane protein Chain: A: PDB Molecule: moesin; PDBTitle: moesin from spodoptera frugiperda at 2.1 angstroms resolution

78	c2dq3A	Alignment	not modelled	92.0	15	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of aq_298
79	c3lssA	Alignment	not modelled	91.9	8	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: trypanosoma brucei seryl-trna synthetase in complex with atp
80	c2lemA	Alignment	not modelled	91.8	5	PDB header: lipid transport Chain: A: PDB Molecule: apolipoprotein a-i; PDBTitle: monomeric mouse apoai(1-216)
81	c3edvB	Alignment	not modelled	91.7	10	PDB header: structural protein Chain: B: PDB Molecule: spectrin beta chain, brain 1; PDBTitle: crystal structure of repeats 14-16 of beta2-spectrin
82	c2dfsA	Alignment	not modelled	91.4	10	PDB header: contractile protein/transport protein Chain: A: PDB Molecule: myosin-5a; PDBTitle: 3-d structure of myosin-v inhibited state
83	c2jeeA	Alignment	not modelled	91.4	16	PDB header: cell cycle Chain: A: PDB Molecule: yjiu; PDBTitle: xray structure of e. coli yjiu
84	c1m1jA	Alignment	not modelled	91.3	8	PDB header: blood clotting Chain: A: PDB Molecule: fibrinogen alpha subunit; PDBTitle: crystal structure of native chicken fibrinogen with two different2 bound ligands
85	c2yo3C	Alignment	not modelled	90.9	13	PDB header: membrane protein Chain: C: PDB Molecule: general control protein gcn4, putative inner membrane PDBTitle: salmonella enterica sada 1185-1386 fused to gcn4 adaptors (sadak14)
86	c2v4hA	Alignment	not modelled	90.1	21	PDB header: transcription Chain: A: PDB Molecule: nf-kappa-b essential modulator; PDBTitle: nemo cc2-lz domain - 1d5 darpin complex
87	c4etpA	Alignment	not modelled	89.8	22	PDB header: motor protein Chain: A: PDB Molecule: skinesin-like protein kar3; PDBTitle: c-terminal motor and motor homology domain of kar3vik1 fused to a2 synthetic heterodimeric coiled coil
88	c1g8xB	Alignment	not modelled	89.3	9	PDB header: structural protein Chain: B: PDB Molecule: myosin ii heavy chain fused to alpha-actinin 3; PDBTitle: structure of a genetically engineered molecular motor
89	c2j69D	Alignment	not modelled	89.0	7	PDB header: hydrolase Chain: D: PDB Molecule: bacterial dynamin-like protein; PDBTitle: bacterial dynamin-like protein bdlp
90	c2qihA	Alignment	not modelled	88.9	10	PDB header: cell adhesion Chain: A: PDB Molecule: protein uspa1; PDBTitle: crystal structure of 527-665 fragment of uspa1 protein from2 moraxella catarrhalis
91	c1u5pA	Alignment	not modelled	88.7	10	PDB header: structural protein Chain: A: PDB Molecule: spectrin alpha chain, brain; PDBTitle: crystal structure of repeats 15 and 16 of chicken brain2 alpha spectrin
92	c2e7sM	Alignment	not modelled	88.7	15	PDB header: endocytosis/exocytosis Chain: M: PDB Molecule: rab guanine nucleotide exchange factor sec2; PDBTitle: crystal structure of the yeast sec2p gef domain
93	c1qu7A	Alignment	not modelled	88.5	10	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
94	c4dvzA	Alignment	not modelled	88.2	9	PDB header: oncoprotein Chain: A: PDB Molecule: cytotoxicity-associated immunodominant antigen; PDBTitle: crystal structure of the helicobacter pylori caga oncoprotein
95	c2wpgA	Alignment	not modelled	88.1	13	PDB header: membrane protein Chain: A: PDB Molecule: trimeric autotransporter adhesin fragment; PDBTitle: salmonella enterica sada 479-519 fused to gcn4 adaptors (2 sadak3, in-register fusion)
96	c2yy0D	Alignment	not modelled	87.6	25	PDB header: transcription Chain: D: PDB Molecule: c-myc-binding protein; PDBTitle: crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
97	c3q0xA	Alignment	not modelled	86.8	12	PDB header: structural protein Chain: A: PDB Molecule: centriole protein; PDBTitle: n-terminal coiled-coil dimer domain of c. reinhardtii sas-6 homolog2 bld12p
98	c3a7pB	Alignment	not modelled	86.6	12	PDB header: protein transport Chain: B: PDB Molecule: autophagy protein 16; PDBTitle: the crystal structure of saccharomyces cerevisiae atg16
99	d2ap3a1	Alignment	not modelled	86.2	6	Fold: Four-helical up-and-down bundle Superfamily: MW0975(SA0943)-like Family: MW0975(SA0943)-like
100	c2xzfA	Alignment	not modelled	86.2	15	PDB header: cell adhesion Chain: A: PDB Molecule: immunoglobulin-binding protein eibd; PDBTitle: escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
101	c3u1aC	Alignment	not modelled	85.6	19	PDB header: contractile protein Chain: C: PDB Molecule: smooth muscle tropomyosin alpha; PDBTitle: n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
102	c3cvfA	Alignment	not modelled	84.3	14	PDB header: signaling protein Chain: A: PDB Molecule: homer protein homolog 3; PDBTitle: crystal structure of the carboxy terminus of homer3
103	c2eqbC	Alignment	not modelled	83.6	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
104	c1cz7C_	Alignment	not modelled	83.3	10	PDB header: contractile protein Chain: C; PDB Molecule: microtubule motor protein ncd; PDBTitle: the crystal structure of a minus-end directed microtubule2 motor protein ncd reveals variable dimer conformations
105	c2xgjA_	Alignment	not modelled	83.1	11	PDB header: hydrolase/rna Chain: A; PDB Molecule: atp-dependent rna helicase dob1; PDBTitle: structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance
106	c2odvA_	Alignment	not modelled	82.3	8	PDB header: structural protein Chain: A; PDB Molecule: plectin 1; PDBTitle: crystal structure of a fragment of the plakin domain of plectin, cys2 to ala mutant.
107	c1junB_	Alignment	not modelled	82.2	22	PDB header: transcription regulation Chain: B; PDB Molecule: c-jun homodimer; PDBTitle: nmr study of c-jun homodimer
108	c2zvnF_	Alignment	not modelled	81.9	15	PDB header: signaling protein/transcription Chain: F; PDB Molecule: nf-kappa-b essential modulator; PDBTitle: nemo cozi domain incomplex with diubiquitin in p2121212 space group
109	c1wt6B_	Alignment	not modelled	81.3	15	PDB header: transferase Chain: B; PDB Molecule: myotonin-protein kinase; PDBTitle: coiled-coil domain of dmpk
110	d1ykhb1	Alignment	not modelled	81.2	12	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like
111	c3r2pA_	Alignment	not modelled	79.4	14	PDB header: lipid transport Chain: A; PDB Molecule: apolipoprotein a-i; PDBTitle: 2.2 angstrom crystal structure of c terminal truncated human2 apolipoprotein a-i reveals the assembly of hdl by dimerization.
112	c3ghgD_	Alignment	not modelled	79.3	13	PDB header: blood clotting Chain: D; PDB Molecule: fibrinogen alpha chain; PDBTitle: crystal structure of human fibrinogen
113	c3ajwA_	Alignment	not modelled	79.1	15	PDB header: protein transport Chain: A; PDB Molecule: flagellar fljij protein; PDBTitle: structure of fljij, a soluble component of flagellar type iii export2 apparatus
114	c1i84V_	Alignment	not modelled	78.9	15	PDB header: contractile protein Chain: V; PDB Molecule: smooth muscle myosin heavy chain; PDBTitle: cryo-em structure of the heavy meromyosin subfragment of2 chicken gizzard smooth muscle myosin with regulatory light3 chain in the dephosphorylated state. only c alphas4 provided for regulatory light chain. only backbone atoms5 provided for s2 fragment.
115	c3pe0B_	Alignment	not modelled	76.8	7	PDB header: structural protein Chain: B; PDB Molecule: plectin; PDBTitle: structure of the central region of the plakin domain of plectin
116	c3cveC_	Alignment	not modelled	75.8	19	PDB header: signaling protein Chain: C; PDB Molecule: homer protein homolog 1; PDBTitle: crystal structure of the carboxy terminus of homer1
117	c2q6qB_	Alignment	not modelled	75.2	30	PDB header: cell cycle Chain: B; PDB Molecule: spindle pole body component spc42; PDBTitle: crystal structure of spc42p, a critical component of spindle pole body2 in budding yeast
118	c3a6mB_	Alignment	not modelled	74.6	12	PDB header: chaperone Chain: B; PDB Molecule: protein grpe; PDBTitle: crystal structure of grpe from thermus thermophilus hb8
119	c4aniA_	Alignment	not modelled	74.6	17	PDB header: chaperone Chain: A; PDB Molecule: protein grpe; PDBTitle: structural basis for the intermolecular communication between2 dnak and grpe in the dnak chaperone system from3 geobacillus kaustophilus hta426
120	c1ik9B_	Alignment	not modelled	73.8	16	PDB header: gene regulation/ligase Chain: B; PDB Molecule: dna repair protein xrcc4; PDBTitle: crystal structure of a xrcc4-dna ligase iv complex