
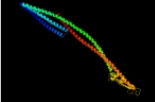

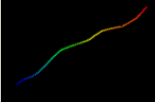

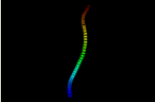



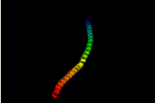

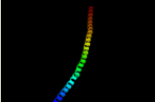

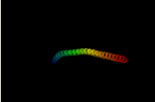

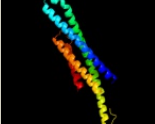

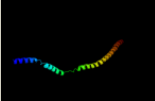



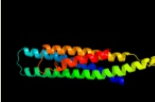
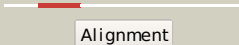
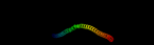
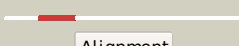










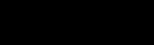
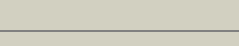
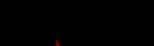
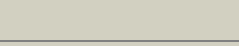


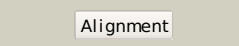


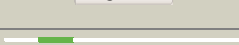

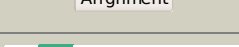

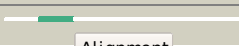


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A0MZ66
Date	Sat Jun 16 10:26:01 BST 2012
Unique Job ID	9a279396d7ab0d93

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ciiA_	 Alignment		97.4	8	PDB header: transmembrane protein Chain: A; PDB Molecule: colicin ia; PDBTitle: colicin ia
2	c1c1gA_	 Alignment		95.9	12	PDB header: contractile protein Chain: A; PDB Molecule: tropomyosin; PDBTitle: crystal structure of tropomyosin at 7 angstroms resolution ² in the spermine-induced crystal form
3	c2efrB_	 Alignment		95.4	7	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- and 2 c-terminal extensions of the leucine zipper at 1.8 angstroms ³ resolution
4	c2fxmB_	 Alignment		95.3	8	PDB header: contractile protein Chain: B; PDB Molecule: myosin heavy chain, cardiac muscle beta isoform; PDBTitle: structure of the human beta-myosin s2 fragment
5	c3ol1A_	 Alignment		94.8	13	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
6	c3u59C_	 Alignment		94.7	24	PDB header: contractile protein Chain: C; PDB Molecule: tropomyosin beta chain; PDBTitle: n-terminal 98-aa fragment of smooth muscle tropomyosin beta
7	c3q8tB_	 Alignment		94.5	10	PDB header: apoptosis Chain: B; PDB Molecule: beclin-1; PDBTitle: crystal structure of the coiled coil domain of beclin 1, an essential ² autophagy protein
8	c1bg1A_	 Alignment		94.0	7	PDB header: transcription/dna Chain: A; PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
9	c1deaF_	 Alignment		93.6	8	PDB header: PDB COMPND:
10	c3ghgK_	 Alignment		92.8	11	PDB header: blood clotting Chain: K; PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
11	c1bf5A_	 Alignment		92.7	6	PDB header: gene regulation/dna Chain: A; PDB Molecule: signal transducer and activator of transcription PDBTitle: tyrosine phosphorylated stat-1/dna complex

12	c2d3eD_	 Alignment		92.2	9	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
13	c2gl2B_	 Alignment		92.2	7	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
14	c1deqO_	 Alignment		92.1	8	PDB header: PDB COMPND:
15	c3ojaB_	 Alignment		91.9	11	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of Irim1/apl1c complex
16	c3r6nA_	 Alignment		89.7	6	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
17	c2oevA_	 Alignment		89.1	8	PDB header: protein transport Chain: A: PDB Molecule: programmed cell death 6-interacting protein; PDBTitle: crystal structure of alix/aip1
18	c1ei3E_	 Alignment		86.9	8	PDB header: PDB COMPND:
19	c3o0zD_	 Alignment		84.6	13	PDB header: transferase Chain: D: PDB Molecule: rho-associated protein kinase 1; PDBTitle: crystal structure of a coiled-coil domain from human rock i
20	c3na7A_	 Alignment		84.3	5	PDB header: gene regulation, chaperone Chain: A: PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
21	c2b9cA_	 Alignment	not modelled	84.1	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
22	c1ei3C_	 Alignment	not modelled	80.6	6	PDB header: PDB COMPND:
23	c3hnwB_	 Alignment	not modelled	79.4	17	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
24	c2v71A_	 Alignment	not modelled	78.7	13	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear distribution protein nude-like 1; PDBTitle: coiled-coil region of nudel
25	c3dtpA_	 Alignment	not modelled	69.3	11	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
26	c2jeeA_	 Alignment	not modelled	63.9	24	PDB header: cell cycle Chain: A: PDB Molecule: yiiu; PDBTitle: xray structure of e. coli yiiu
27	c3ipkA_	 Alignment	not modelled	63.1	9	PDB header: cell adhesion Chain: A: PDB Molecule: agi/ii; PDBTitle: crystal structure of a3vp1 of agi/ii of streptococcus mutans
28	c3vkhD_	 Alignment	not modelled	53.7	11	PDB header: motor protein Chain: D: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: crystal structure of an motor protein
29	c2v66C_	 Alignment	not modelled	49.3	13	PDB header: structural protein Chain: C: PDB Molecule: nuclear distribution protein nude-like 1;

29	c2v00C	Alignment	not modelled	49.3	13	PDB header: crystal structure of the coiled-coil domain of nde1 (a.a.2 58 to 169)c PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
30	c3cwgA	Alignment	not modelled	46.3	9	PDB header: ribosome inhibitor, hydrolase Chain: C: PDB Molecule: colicin e3; PDBTitle: crystal structure of colicin e3 in complex with its immunity protein
31	c1jchC	Alignment	not modelled	45.5	9	PDB header: replication Chain: B: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: rad50 coiled-coil zn hook
32	c1f8dB	Alignment	not modelled	44.9	15	PDB header: protein transport Chain: B: PDB Molecule: autophagy protein 16; PDBTitle: the crystal structure of saccharomyces cerevisiae atg16
33	c3a7pB	Alignment	not modelled	43.4	8	PDB header: contractile protein Chain: C: PDB Molecule: smooth muscle tropomyosin alpha; PDBTitle: n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
34	c3u1aC	Alignment	not modelled	40.0	18	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
35	c3hizB	Alignment	not modelled	39.7	10	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
36	c4a55B	Alignment	not modelled	39.4	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)
37	c2wpgA	Alignment	not modelled	32.6	6	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
38	c2y3aB	Alignment	not modelled	28.6	11	PDB header: protein transport Chain: B: PDB Molecule: programmed cell death 6-interacting protein; PDBTitle: structure of alix/aipl1 v domain
39	c2oexB	Alignment	not modelled	25.1	7	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 2b fragment (cys2)
40	c1gk4A	Alignment	not modelled	20.6	12	PDB header: transcription Chain: A: PDB Molecule: nf-kappa-b essential modulator; PDBTitle: nemo cc2-lz domain - 1d5 darpin complex
41	c2v4hA	Alignment	not modelled	18.6	18	PDB header: protein binding Chain: A: PDB Molecule: leucine-rich immune molecule 1; PDBTitle: crystal structure of lrim1/apl1c complex
42	c3ojaA	Alignment	not modelled	18.2	10	PDB header: cell adhesion Chain: A: PDB Molecule: huntingtin-interacting protein 1; PDBTitle: crystal structure of the dl1rkn-containing coiled-coil2 domain of huntingtin-interacting protein 1
43	c1deqD	Alignment	not modelled	17.8	12	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
44	c2no2A	Alignment	not modelled	17.2	20	PDB header: structural protein Chain: A: PDB Molecule: liprin-beta-2; PDBTitle: human liprin-beta2 coiled-coil
45	c2zvnF	Alignment	not modelled	15.8	17	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 1a fragment (1a)
46	c3qh9A	Alignment	not modelled	15.3	21	PDB header: structural protein Chain: A: PDB Molecule: head morphogenesis protein, chaotic nuclear migration PDBTitle: structure of the c-terminal domain of cnm67, a core component of the2 spindle pole body of saccharomyces cerevisiae
47	c1gk7A	Alignment	not modelled	14.9	18	PDB header: contractile protein Chain: B: PDB Molecule: tropomyosin alpha chain, skeletal muscle; PDBTitle: deciphering the design of the tropomyosin molecule
48	c3oa7A	Alignment	not modelled	14.2	18	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
49	c1ic2B	Alignment	not modelled	13.8	23	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dob1; PDBTitle: crystal structure of mtr4, a co-factor of the nuclear exosome
50	c3m9bK	Alignment	not modelled	13.1	15	PDB header: structural protein Chain: A: PDB Molecule: centriole protein; PDBTitle: n-terminal coiled-coil dimer domain of c. reinhardtii sas-6 homolog2 bld12p
51	c3l9oA	Alignment	not modelled	12.9	20	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
52	c3q0xA	Alignment	not modelled	12.8	12	PDB header: transcription
53	c1y4cA	Alignment	not modelled	12.5	12	

54	c1ci6A_	Alignment	not modelled	12.2	26	Chain: A: PDB Molecule: transcription factor atf-4; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
55	c3tnfB_	Alignment	not modelled	12.2	10	PDB header: protein transport Chain: B: PDB Molecule: lida; PDBTitle: lida from legionella in complex with active rab8a
56	c3movB_	Alignment	not modelled	11.9	16	PDB header: structural protein Chain: B: PDB Molecule: lamin-b1; PDBTitle: crystal structure of human lamin-b1 coil 2 segment
57	c1x8yA_	Alignment	not modelled	11.6	15	PDB header: structural protein Chain: A: PDB Molecule: lamin a/c; PDBTitle: human lamin coil 2b
58	c1cz7C_	Alignment	not modelled	11.4	12	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
59	c1yvlB_	Alignment	not modelled	10.9	7	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1
60	c1fosF_	Alignment	not modelled	10.6	13	PDB header: transcription/dna Chain: F: PDB Molecule: c-jun proto-oncogene protein; PDBTitle: two human c-fos:c-jun:dna complexes
61	c2w83C_	Alignment	not modelled	10.6	16	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
62	c4e61A_	Alignment	not modelled	10.1	18	PDB header: cell cycle Chain: A: PDB Molecule: protein bim1; PDBTitle: crystal structure of the eb1-like motif of bim1p
63	c2wt7B_	Alignment	not modelled	10.1	21	PDB header: transcription Chain: B: PDB Molecule: transcription factor mafb; PDBTitle: crystal structure of the bzip heterodimeric complex2 mafb:cfos bound to dna
64	c3n4xB_	Alignment	not modelled	9.9	11	PDB header: replication Chain: B: PDB Molecule: monopolin complex subunit csm1; PDBTitle: structure of csm1 full-length
65	c2yy0D_	Alignment	not modelled	9.8	36	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
66	c3mudA_	Alignment	not modelled	8.4	12	PDB header: contractile protein Chain: A: PDB Molecule: dna repair protein xrcc4, tropomyosin alpha-1 chain; PDBTitle: structure of the tropomyosin overlap complex from chicken smooth2 muscle
67	c2rd0B_	Alignment	not modelled	7.9	16	PDB header: transferase/oncoprotein Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: structure of a human p110alpha/p85alpha complex
68	c2e7sM_	Alignment	not modelled	7.9	19	PDB header: endocytosis/exocytosis Chain: M: PDB Molecule: rab guanine nucleotide exchange factor sec2; PDBTitle: crystal structure of the yeast sec2p gef domain
69	c1gk6B_	Alignment	not modelled	7.9	14	PDB header: vimentin Chain: B: PDB Molecule: vimentin; PDBTitle: human vimentin coil 2b fragment linked to gcn4 leucine2 zipper (z2b)
70	c1t2kD_	Alignment	not modelled	7.6	18	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
71	c2v1yB_	Alignment	not modelled	7.6	13	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
72	c1fosE_	Alignment	not modelled	7.2	15	PDB header: transcription/dna Chain: E: PDB Molecule: p55-c-fos proto-oncogene protein; PDBTitle: two human c-fos:c-jun:dna complexes
73	c1wt6B_	Alignment	not modelled	7.2	11	PDB header: transferase Chain: B: PDB Molecule: myotoniin-protein kinase; PDBTitle: coiled-coil domain of dmpk
74	c1gd2G_	Alignment	not modelled	6.8	15	PDB header: transcription/dna Chain: G: PDB Molecule: transcription factor pap1; PDBTitle: crystal structure of bzip transcription factor pap1 bound2 to dna
75	c3vkhB_	Alignment	not modelled	6.5	10	PDB header: motor protein Chain: B: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: crystal structure of an motor protein
76	c2xdjF_	Alignment	not modelled	6.2	11	PDB header: unknown function Chain: F: PDB Molecule: uncharacterized protein ybgf; PDBTitle: crystal structure of the n-terminal domain of e.coli ybgf
77	c2eqbC_	Alignment	not modelled	6.1	19	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
78	c1n73C_	Alignment	not modelled	6.0	16	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 PDB header: chaperone

79	c2zdiA_	Alignment	not modelled	5.8	20	Chain: A: PDB Molecule: prefoldin subunit beta; PDBTitle: crystal structure of prefoldin from pyrococcus horikoshii2 ot3
80	c2xv5A_	Alignment	not modelled	5.8	15	PDB header: structural protein Chain: A: PDB Molecule: lamin-a/c; PDBTitle: human lamin a coil 2b fragment
81	dlivsa1	Alignment	not modelled	5.7	11	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Valyl-tRNA synthetase (ValRS) C-terminal domain
82	c1debA_	Alignment	not modelled	5.4	10	PDB header: structural protein Chain: A: PDB Molecule: adenomatous polyposis coli protein; PDBTitle: crystal structure of the n-terminal coiled coil domain from2 apc
83	c1junB_	Alignment	not modelled	5.3	14	PDB header: transcription regulation Chain: B: PDB Molecule: c-jun homodimer; PDBTitle: nmr study of c-jun homodimer
84	d1nkpa_	Alignment	not modelled	5.2	27	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain