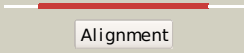
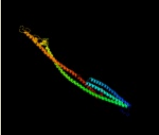
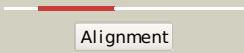
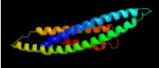

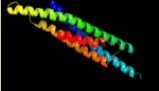
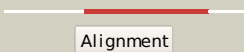
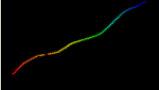
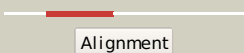
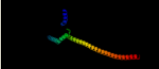



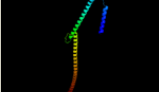


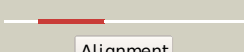
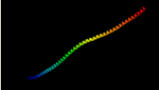
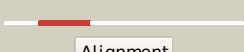
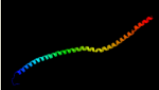
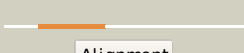












Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A1A5D9
Date	Fri May 25 10:16:11 BST 2012
Unique Job ID	0c8c41615101a198

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ciiA_	 Alignment		98.9	10	PDB header: transmembrane protein Chain: A; PDB Molecule: colicin ia; PDBTitle: colicin ia
2	c1bg1A_	 Alignment		96.6	9	PDB header: transcription/dna Chain: A; PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
3	c1bf5A_	 Alignment		96.2	12	PDB header: gene regulation/dna Chain: A; PDB Molecule: signal transducer and activator of transcription PDBTitle: tyrosine phosphorylated stat-1/dna complex
4	c1c1gA_	 Alignment		95.3	13	PDB header: contractile protein Chain: A; PDB Molecule: tropomyosin; PDBTitle: crystal structure of tropomyosin at 7 angstroms resolution2 in the spermine-induced crystal form
5	c3ojaB_	 Alignment		94.6	16	PDB header: protein binding Chain: B; PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of Irim1/apl1c complex
6	c3cwgA_	 Alignment		94.4	15	PDB header: transcription Chain: A; PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
7	c3ojaA_	 Alignment		94.4	16	PDB header: protein binding Chain: A; PDB Molecule: leucine-rich immune molecule 1; PDBTitle: crystal structure of Irim1/apl1c complex
8	c1jchC_	 Alignment		93.3	10	PDB header: ribosome inhibitor, hydrolase Chain: C; PDB Molecule: colicin e3; PDBTitle: crystal structure of colicin e3 in complex with its immunity protein
9	c2v71A_	 Alignment		91.1	15	PDB header: nuclear protein Chain: A; PDB Molecule: nuclear distribution protein nude-like 1; PDBTitle: coiled-coil region of nudel
10	c1ei3C_	 Alignment		90.5	8	PDB header: PDB COMPND:
11	c3hizB_	 Alignment		89.9	10	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

12	c3ghgK_	Alignment		89.6	9	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
13	c1degF_	Alignment		89.5	10	PDB header: PDB COMPND:
14	c3ipkA_	Alignment		85.4	14	PDB header: cell adhesion Chain: A: PDB Molecule: agi/ii; PDBTitle: crystal structure of a3vp1 of agi/ii of streptococcus mutans
15	c1ei3E_	Alignment		83.2	11	PDB header: PDB COMPND:
16	c1yvlB_	Alignment		80.9	11	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1
17	c3ol1A_	Alignment		78.6	22	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
18	c3na7A_	Alignment		78.5	13	PDB header: gene regulation, chaperone Chain: A: PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
19	c2fxmB_	Alignment		75.8	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
20	c2d3eD_	Alignment		75.0	12	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
21	c1degO_	Alignment	not modelled	74.8	6	PDB header: PDB COMPND:
22	c2oevA_	Alignment	not modelled	72.5	9	PDB header: protein transport Chain: A: PDB Molecule: programmed cell death 6-interacting protein; PDBTitle: crystal structure of alix/aip1
23	c3r6nA_	Alignment	not modelled	70.9	10	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
24	c3dtpA_	Alignment	not modelled	70.2	15	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
25	c1degD_	Alignment	not modelled	65.8	8	PDB header: PDB COMPND:
26	c3o0zD_	Alignment	not modelled	64.6	12	PDB header: transferase Chain: D: PDB Molecule: rho-associated protein kinase 1; PDBTitle: crystal structure of a coiled-coil domain from human rock i
27	c4a55B_	Alignment	not modelled	63.9	14	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
28	c3l9oA_	Alignment	not modelled	61.0	10	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dob1; PDBTitle: crystal structure of ntr4, a co-factor of the nuclear

						exosome
29	c3q8tB_	Alignment	not modelled	59.7	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
30	c1wt6B_	Alignment		59.4	16	PDB header: transferase Chain: B: PDB Molecule: myotoni n-protein kinase; PDBTitle: coiled-coil domain of dmpk
31	c3u59C_	Alignment	not modelled	56.7	7	PDB header: contractile protein Chain: C: PDB Molecule: tropomyosin beta chain; PDBTitle: n-terminal 98-aa fragment of smooth muscle tropomyosin beta
32	c2efrB_	Alignment	not modelled	55.0	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
33	c2b9cA_	Alignment	not modelled	52.1	12	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
34	c2gl2B_	Alignment	not modelled	49.4	11	PDB header: cell adhesion Chain: B: PDB Molecule: adhesion a; PDBTitle: crystal structure of the burkholderia glumae lipase-2 y69g) of bacterial adhesin fada
35	c1gk4A_	Alignment	not modelled	47.7	14	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 2b fragment (cys2)
36	c3hnwB_	Alignment	not modelled	47.1	8	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
37	c1y4cA_	Alignment	not modelled	45.7	16	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
38	d1sa0e_	Alignment	not modelled	43.5	27	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Stathmin Family: Stathmin
39	c2oexB_	Alignment	not modelled	43.5	9	PDB header: protein transport Chain: B: PDB Molecule: programmed cell death 6-interacting protein; PDBTitle: structure of alix/aip1 v domain
40	c2es4D_	Alignment	not modelled	43.2	13	PDB header: hydrolase Chain: D: PDB Molecule: lipase chaperone; PDBTitle: crystal structure of the burkholderia glumae lipase-2 specific foldase in complex with its cognate lipase
41	d2es4d1	Alignment	not modelled	43.2	13	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Lipase chaperone-like Family: Lipase chaperone Lifo-like
42	c2rd0B_	Alignment	not modelled	42.2	14	PDB header: transferase/oncoprotein Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: structure of a human p110alpha/p85alpha complex
43	c3vkgB_	Alignment	not modelled	40.7	12	PDB header: motor protein Chain: B: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: crystal structure of an motor protein
44	c2jeeA_	Alignment	not modelled	31.2	19	PDB header: cell cycle Chain: A: PDB Molecule: yiu; PDBTitle: xray structure of e. coli yiu
45	c3lx4B_	Alignment	not modelled	31.1	50	PDB header: oxidoreductase Chain: B: PDB Molecule: fe-hydrogenase; PDBTitle: stepwise [fefe]-hydrogenase h-cluster assembly revealed in the2 structure of hyda(delta tae f g)
46	d1d2ta_	Alignment	not modelled	30.4	40	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Type 2 phosphatidic acid phosphatase, PAP2
47	c3nfgG_	Alignment	not modelled	30.0	20	PDB header: transcription Chain: G: PDB Molecule: dna-directed rna polymerase i subunit rpa49; PDBTitle: crystal structure of dimerization module of rna polymerase i2 subcomplex a49/a34.5
48	c1x8yA_	Alignment	not modelled	29.5	17	PDB header: structural protein Chain: A: PDB Molecule: lamin a/c; PDBTitle: human lamin coil 2b
49	d3c8ya1	Alignment	not modelled	29.1	33	Fold: Fe-only hydrogenase Superfamily: Fe-only hydrogenase Family: Fe-only hydrogenase
50	c2v66C_	Alignment	not modelled	27.7	14	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.2 58 to 169)c
51	d1r5sa_	Alignment	not modelled	27.5	33	Fold: Connexin43 Superfamily: Connexin43 Family: Connexin43
52	c2qa7B_	Alignment	not modelled	27.5	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)

53	c3a5tB_	Alignment	not modelled	26.8	9	PDB header: transcription regulator/dna Chain: B: PDB Molecule: transcription factor mafg; PDBTitle: crystal structure of mafg-dna complex
54	d1h2vc2	Alignment	not modelled	26.2	31	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
55	c2p22C_	Alignment	not modelled	24.7	14	PDB header: transport protein Chain: C: PDB Molecule: protein srn2; PDBTitle: structure of the yeast escrt-i heterotetramer core
56	d1ezsa_	Alignment	not modelled	23.2	57	Fold: Ecotin, trypsin inhibitor Superfamily: Ecotin, trypsin inhibitor Family: Ecotin, trypsin inhibitor
57	d1slua_	Alignment	not modelled	23.0	43	Fold: Ecotin, trypsin inhibitor Superfamily: Ecotin, trypsin inhibitor Family: Ecotin, trypsin inhibitor
58	c2akcC_	Alignment	not modelled	22.9	44	PDB header: hydrolase Chain: C: PDB Molecule: class a nonspecific acid phosphatase phon; PDBTitle: crystal structure of tungstate complex of the phon protein2 from s. typhimurium
59	d1v7mv_	Alignment	not modelled	22.8	15	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Short-chain cytokines
60	d1xxfc_	Alignment	not modelled	20.6	43	Fold: Ecotin, trypsin inhibitor Superfamily: Ecotin, trypsin inhibitor Family: Ecotin, trypsin inhibitor
61	c3movB_	Alignment	not modelled	20.6	16	PDB header: structural protein Chain: B: PDB Molecule: lamin-b1; PDBTitle: crystal structure of human lamin-b1 coil 2 segment
62	c3qh9A_	Alignment	not modelled	19.1	16	PDB header: structural protein Chain: A: PDB Molecule: liprin-beta-2; PDBTitle: human liprin-beta2 coiled-coil
63	c2ktlA_	Alignment	not modelled	15.9	32	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: structure of c-terminal domain from mttyrfs of a. nidulans
64	c1l8dB_	Alignment	not modelled	15.4	21	PDB header: replication Chain: B: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: rad50 coiled-coil zn hook
65	c1c4cA_	Alignment	not modelled	15.4	33	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (fe-only hydrogenase); PDBTitle: binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum
66	c3mv2A_	Alignment	not modelled	13.2	14	PDB header: protein transport Chain: A: PDB Molecule: coatomer subunit alpha; PDBTitle: crystal structure of a-cop in complex with e-cop
67	c2pmsD_	Alignment	not modelled	12.6	17	PDB header: metal transport, hydrolase Chain: D: PDB Molecule: pneumococcal surface protein a (pspa); PDBTitle: crystal structure of the complex of human lactoferrin n-lobe and2 lactoferrin-binding domain of pneumococcal surface protein a
68	c2v1yB_	Alignment	not modelled	12.5	11	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
69	d1eera_	Alignment	not modelled	12.5	6	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Short-chain cytokines
70	c2e7sM_	Alignment	not modelled	11.8	14	PDB header: endocytosis/exocytosis Chain: M: PDB Molecule: rab guanine nucleotide exchange factor sec2; PDBTitle: crystal structure of the yeast sec2p gef domain
71	c2no2A_	Alignment	not modelled	11.7	22	PDB header: cell adhesion Chain: A: PDB Molecule: huntingtin-interacting protein 1; PDBTitle: crystal structure of the dlIrkn-containing coiled-coil2 domain of huntingtin-interacting protein 1
72	c2rmsB_	Alignment	not modelled	11.4	32	PDB header: transcription Chain: B: PDB Molecule: msin3a-binding protein; PDBTitle: solution structure of the msin3a pah1-sap25 sid complex
73	c3if4C_	Alignment	not modelled	11.3	38	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: integron cassette protein hfx_cass5; PDBTitle: structure from the mobile metagenome of north west arm2 sewage outfall: integron cassette protein hfx_cass5
74	c1fo0H_	Alignment	not modelled	10.9	23	PDB header: immune system Chain: H: PDB Molecule: protein (allogeneic h-2kb mhc class i molecule); PDBTitle: murine alloreactive scfv tcr-peptide-mhc class i molecule2 complex
75	c3bewD_	Alignment	not modelled	10.8	36	PDB header: immune system Chain: D: PDB Molecule: major histocompatibility complex class i PDBTitle: 10mer crystal structure of chicken mhc class i haplotype b21
76	c1wbzA_	Alignment	not modelled	10.4	23	PDB header: immune system Chain: A: PDB Molecule: h-2 class i histocompatibility antigen, k-b PDBTitle: crystal structures of murine mhc class i h-2 db and kb2 molecules in complex with ct epitopes from influenza a3 virus: implications for tcr repertoire selection and4 immunodominance
77	c1namH_	Alignment	not modelled	10.4	23	PDB header: immune system Chain: H: PDB Molecule: h-2 class i histocompatibility antigen, k-b alpha chain PDBTitle: murine alloreactive scfv tcr-peptide-mhc class i

						molecule complex
78	c2kw3A_	Alignment	not modelled	10.3	50	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein rfx5; PDBTitle: heterotrimeric interaction between rfx5 and rfxap
79	c2y3aB_	Alignment	not modelled	10.2	15	PDB header: transferase Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit beta; PDBTitle: crystal structure of p110beta in complex with ics2 of p85beta and2 the drug gdc-0941
80	d2ap3a1	Alignment	not modelled	10.1	8	Fold: Four-helical up-and-down bundle Superfamily: MW0975(SA0943)-like Family: MW0975(SA0943)-like
81	c3cm8A_	Alignment	not modelled	10.1	46	PDB header: rna binding protein/transferase Chain: A: PDB Molecule: polymerase acidic protein; PDBTitle: a rna polymerase subunit structure from virus
82	d1t3ta3	Alignment	not modelled	10.0	33	Fold: PurS-like Superfamily: PurS-like Family: FGAM synthase PurL, PurS-like domain
83	d1xbpg2	Alignment	not modelled	9.9	26	Fold: Ribosomal L11/L12e N-terminal domain Superfamily: Ribosomal L11/L12e N-terminal domain Family: Ribosomal L11/L12e N-terminal domain
84	c3rooA_	Alignment	not modelled	9.9	23	PDB header: immune system Chain: A: PDB Molecule: murine class i major histocompatibility complex h-2kb; PDBTitle: murine class i major histocompatibility complex h-2kb in complex with2 immunodominant lcmv-derived gp34-41 peptide
85	c1qhhA_	Alignment	not modelled	9.9	18	PDB header: hydrolase Chain: A: PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
86	d2gycg2	Alignment	not modelled	9.6	26	Fold: Ribosomal L11/L12e N-terminal domain Superfamily: Ribosomal L11/L12e N-terminal domain Family: Ribosomal L11/L12e N-terminal domain
87	c4dylA_	Alignment	not modelled	9.4	14	PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase fes/fps; PDBTitle: f-bar domain of human fes tyrosine kinase
88	c1ypzA_	Alignment	not modelled	9.4	23	PDB header: immune system Chain: A: PDB Molecule: h2-t22 protein; PDBTitle: immune receptor
89	d2qqba1	Alignment	not modelled	9.3	30	Fold: RPA2825-like Superfamily: RPA2825-like Family: RPA2825-like
90	d1h16a_	Alignment	not modelled	9.3	35	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: PFL-like
91	c2adzA_	Alignment	not modelled	9.3	23	PDB header: protein binding Chain: A: PDB Molecule: alpha-1-syntrophin; PDBTitle: solution structure of the joined ph domain of alpha1-2 syntrophin
92	c2k53A_	Alignment	not modelled	9.2	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: a3dk08 protein; PDBTitle: nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
93	c2jq5A_	Alignment	not modelled	9.0	20	PDB header: structural genomics Chain: A: PDB Molecule: sec-c motif; PDBTitle: solution structure of rpa3114, a sec-c motif containing protein from2 rhodospseudomonas palustris; northeast structural genomics consortium3 target rpt5 / ontario center for structural proteomics target rp3097
94	c3n4xB_	Alignment	not modelled	8.9	18	PDB header: replication Chain: B: PDB Molecule: monopolin complex subunit csm1; PDBTitle: structure of csm1 full-length
95	c2zswG_	Alignment	not modelled	8.9	23	PDB header: immune system Chain: G: PDB Molecule: h-2 class i histocompatibility antigen, k-b alpha chain; PDBTitle: crystal structure of h-2kb in complex with the q600y variant of jhmv2 epitope s598
96	c2zswC_	Alignment	not modelled	8.9	23	PDB header: immune system Chain: C: PDB Molecule: h-2 class i histocompatibility antigen, k-b alpha chain; PDBTitle: crystal structure of h-2kb in complex with the q600y variant of jhmv2 epitope s598
97	c2zswA_	Alignment	not modelled	8.9	23	PDB header: immune system Chain: A: PDB Molecule: h-2 class i histocompatibility antigen, k-b alpha chain; PDBTitle: crystal structure of h-2kb in complex with the q600y variant of jhmv2 epitope s598
98	d1mmsa2	Alignment	not modelled	8.9	26	Fold: Ribosomal L11/L12e N-terminal domain Superfamily: Ribosomal L11/L12e N-terminal domain Family: Ribosomal L11/L12e N-terminal domain
99	c2iljA_	Alignment	not modelled	8.9	11	PDB header: cell adhesion, membrane protein Chain: A: PDB Molecule: moesin; PDBTitle: moesin from spodoptera frugiperda at 2.1 angstroms resolution