
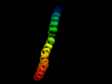
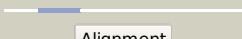
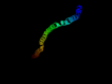
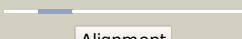
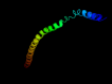

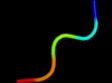



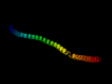



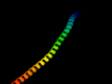
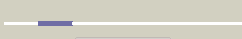
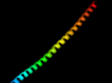

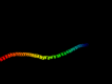

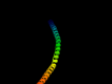


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	A0JLY1
Date	Wed Jul 10 14:04:55 BST 2013
Unique Job ID	eff52b4a6f8e5f27

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1deqO_	 Alignment		27.4	4	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
2	c3ghgK_	 Alignment		25.3	9	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
3	c1deqF_	 Alignment		23.6	3	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
4	c2ktaA_	 Alignment		22.4	60	PDB header: hydrolase Chain: A: PDB Molecule: putative helicase; PDBTitle: solution nmr structure of a domain of protein a6ky75 from bacteroides2 vulgatus, northeast structural genomics target bvr106a
5	c3euhF_	 Alignment		17.7	71	PDB header: cell cycle Chain: F: PDB Molecule: muke; PDBTitle: crystal structure of the muke-mukf complex
6	c1ei3E_	 Alignment		17.6	10	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
7	d1lgha_	 Alignment		16.4	60	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
8	c3q8tB_	 Alignment		16.1	14	PDB header: apoptosis Chain: B: PDB Molecule: beclin-1; PDBTitle: crystal structure of the coiled coil domain of beclin 1, an essential2 autophagy protein
9	c3swkB_	 Alignment		12.2	10	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1b fragment
10	c4gkB_	 Alignment		11.8	14	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
11	c3ol1A_	 Alignment		11.5	12	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

12	c3tnuB_	Alignment		11.5	7	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)
13	c2jeeA_	Alignment		11.1	13	PDB header: cell cycle Chain: A; PDB Molecule: yiiu; PDBTitle: xray structure of e. coli yiiu
14	d2euta1	Alignment		11.0	20	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
15	c2gl2B_	Alignment		10.7	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
16	c1y4cA_	Alignment		10.7	11	PDB header: de novo protein Chain: A; PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
17	c2qa7C_	Alignment		10.6	8	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)
18	c4avcA_	Alignment		10.5	43	PDB header: transferase Chain: A; PDB Molecule: lysine acetyltransferase; PDBTitle: crystal structure of protein lysine acetyltransferase rv09982 in complex with acetyl coa and camp
19	c2i1kA_	Alignment		10.5	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
20	c2v66C_	Alignment		9.8	8	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
21	c4g7wB_	Alignment	not modelled	9.4	44	PDB header: protein binding Chain: B; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the n-terminal domain of the minor coat protein2 piii from ctxphi
22	c1hkgA_	Alignment	not modelled	9.2	80	PDB header: transferase Chain: A; PDB Molecule: hexokinase a; PDBTitle: structural dynamics of yeast hexokinase during catalysis
23	d2arha1	Alignment	not modelled	9.1	50	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: Aq 1966-like
24	c3lfcC_	Alignment	not modelled	9.0	31	PDB header: unknown function Chain: C; PDB Molecule: marr like protein, tvq0766549; PDBTitle: a reported archaeal mechanosensitive channel is a structural2 homolog of marr-like transcriptional regulators
25	c2fxmB_	Alignment	not modelled	8.8	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
26	d1mxaa3	Alignment	not modelled	8.3	25	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
27	d2p02a3	Alignment	not modelled	8.2	25	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
28	c2o0hA_	Alignment	not modelled	8.0	57	PDB header: hydrolase Chain: A; PDB Molecule: dna packaging protein gp17; PDBTitle: t4 gp17 atpase domain mutant complexed with atp
29	c2imlB_	Alignment	not modelled	7.8	22	PDB header: transferase Chain: B; PDB Molecule: s-adenosylmethionine synthetase;

29	c3mmb_	Alignment	not modelled	7.8	42	PDBTitle: crystal structure of s-adenosylmethionine synthetase from burkholderia2 pseudomallei PDB header: transferase
30	c3so4C_	Alignment	not modelled	7.8	17	Chain: C: PDB Molecule: methionine-adenosyltransferase; PDBTitle: methionine-adenosyltransferase from entamoeba histolytica
31	c2y3aB_	Alignment	not modelled	7.7	11	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
32	c3a7pB_	Alignment	not modelled	7.7	16	PDB header: protein transport Chain: B: PDB Molecule: autophagy protein 16; PDBTitle: the crystal structure of saccharomyces cerevisiae atg16
33	c3v32B_	Alignment	not modelled	7.7	22	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpi1 n-terminal conserved domain
34	d1qm4a3	Alignment	not modelled	7.6	36	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
35	c4g7xA_	Alignment	not modelled	7.5	44	PDB header: protein binding/protein binding Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a complex between the ctxphi piiii n-terminal2 domain and the vibrio cholerae tola c-terminal domain
36	c3rv2B_	Alignment	not modelled	7.5	17	PDB header: transferase Chain: B: PDB Molecule: s-adenosylmethionine synthase; PDBTitle: crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum
37	c1x4qA_	Alignment	not modelled	7.5	71	PDB header: rna binding protein Chain: A: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp3; PDBTitle: solution structure of pwi domain in u4/u6 small nuclear2 ribonucleoprotein prp3(hprp3)
38	d1ig8a1	Alignment	not modelled	7.4	80	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
39	d1czan3	Alignment	not modelled	7.4	31	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
40	c3q4nA_	Alignment	not modelled	7.3	12	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein mj0754; PDBTitle: crystal structure of hypothetical protein mj0754 from methanococcus2 jannaschii dsm 2661
41	d1sbqa_	Alignment	not modelled	7.2	60	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: Methenyltetrahydrofolate synthetase
42	c1u3fA_	Alignment	not modelled	7.2	60	PDB header: ligase Chain: A: PDB Molecule: 5,10-methenyltetrahydrofolate synthetase; PDBTitle: structural and functional characterization of a 5,10-2 methenyltetrahydrofolate synthetase from mycoplasma3 pneumoniae (gi: 13508087)
43	c2d7gD_	Alignment	not modelled	7.2	33	PDB header: hydrolase Chain: D: PDB Molecule: primosomal protein n; PDBTitle: crystal structure of the aa complex of the n-terminal2 domain of pria
44	c3dluA_	Alignment	not modelled	7.2	14	PDB header: rna binding protein Chain: A: PDB Molecule: signal recognition particle 19 kda protein; PDBTitle: structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
45	d1bg3a3	Alignment	not modelled	7.1	31	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
46	c2ppwA_	Alignment	not modelled	6.8	60	PDB header: isomerase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
47	c3hnwB_	Alignment	not modelled	6.8	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
48	c3tnuA_	Alignment	not modelled	6.8	12	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)
49	d2b5ga1	Alignment	not modelled	6.7	29	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
50	c3b0dB_	Alignment	not modelled	6.5	50	PDB header: dna binding protein Chain: B: PDB Molecule: centromere protein t; PDBTitle: crystal structure of the chicken cenp-t histone fold/cenp-w complex,2 crystal form ii
51	c3n4xB_	Alignment	not modelled	6.5	10	PDB header: replication Chain: B: PDB Molecule: monopolin complex subunit csm1; PDBTitle: structure of csm1 full-length
52	d1qhdA1	Alignment	not modelled	6.3	22	Fold: A virus capsid protein alpha-helical domain Superfamily: A virus capsid protein alpha-helical domain Family: vp6, the major capsid protein of group A rotavirus
53	d1czan1	Alignment	not modelled	6.3	31	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
54	c3u59C_	Alignment	not modelled	6.2	6	PDB header: contractile protein Chain: C: PDB Molecule: tropomyosin beta chain; PDBTitle: n-terminal 98-aa fragment of smooth muscle

						tropomyosin beta
55	d1bg3a1	Alignment	not modelled	6.2	60	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
56	c2vo9C	Alignment	not modelled	6.2	43	PDB header: hydrolase Chain: C: PDB Molecule: l-alanyl-d-glutamate peptidase; PDBTitle: crystal structure of the enzymatically active domain of the2 listeria monocytogenes bacteriophage 500 endolysin ply500
57	c2li5B	Alignment	not modelled	6.2	33	PDB header: protein transport Chain: B: PDB Molecule: ubiquitin-like modifier-activating enzyme atg7; PDBTitle: nmr structure of atg8-atg7c30 complex
58	c3vkhD	Alignment	not modelled	6.2	7	PDB header: motor protein Chain: D: PDB Molecule: PDBTitle: x-ray structure of a functional full-length dynein motor domain
59	c3v33A	Alignment	not modelled	6.1	22	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 conserved domain with zinc-finger motif
60	d1lapxa	Alignment	not modelled	6.1	13	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
61	c3c5yD	Alignment	not modelled	6.0	60	PDB header: isomerase Chain: D: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
62	c1rg9D	Alignment	not modelled	6.0	25	PDB header: transferase Chain: D: PDB Molecule: s-adenosylmethionine synthetase; PDBTitle: s-adenosylmethionine synthetase complexed with sam and pppp
63	d1dqua	Alignment	not modelled	6.0	50	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
64	c1ig8A	Alignment	not modelled	5.9	80	PDB header: transferase Chain: A: PDB Molecule: hexokinase pii; PDBTitle: crystal structure of yeast hexokinase pii with the correct2 amino acid sequence
65	c3c0mB	Alignment	not modelled	5.9	60	PDB header: toxin Chain: B: PDB Molecule: aerolysin; PDBTitle: crystal structure of the proaerolysin mutant y221g
66	d1v4sa1	Alignment	not modelled	5.9	36	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
67	c2jx3A	Alignment	not modelled	5.9	50	PDB header: dna binding protein Chain: A: PDB Molecule: protein dek; PDBTitle: nmr solution structure of the n-terminal domain of dek
68	d1bdga1	Alignment	not modelled	5.9	43	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
69	c1ci6B	Alignment	not modelled	5.7	24	PDB header: transcription Chain: B: PDB Molecule: transcription factor c/ebp beta; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
70	c2obvA	Alignment	not modelled	5.6	36	PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine synthetase isoform type-1; PDBTitle: crystal structure of the human s-adenosylmethionine synthetase 1 in2 complex with the product
71	d1erpa	Alignment	not modelled	5.4	60	Fold: Protozoan pheromone-like Superfamily: Protozoan pheromone proteins Family: Protozoan pheromone proteins
72	c4f4mA	Alignment	not modelled	5.4	28	PDB header: hydrolase regulator Chain: A: PDB Molecule: papain peptidoglycan amidase effector tse1; PDBTitle: structure of the type vi peptidoglycan amidase effector tse1 (c30a)2 from pseudomonas aeruginosa
73	c1wd6B	Alignment	not modelled	5.4	60	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ydhr; PDBTitle: crystal structure of jw1657 from escherichia coli
74	c3ef5A	Alignment	not modelled	5.3	19	PDB header: hydrolase Chain: A: PDB Molecule: probable pyrophosphohydrolase; PDBTitle: structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
75	c2lkgA	Alignment	not modelled	5.3	44	PDB header: signaling protein Chain: A: PDB Molecule: acetylcholine receptor; PDBTitle: wsa major conformation
76	c3ey5A	Alignment	not modelled	5.2	57	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase-like, gnat family; PDBTitle: putative acetyltransferase from gnat family from bacteroides2 thetaiotaomicron.
77	c1v4sA	Alignment	not modelled	5.1	36	PDB header: transferase Chain: A: PDB Molecule: glucokinase isoform 2; PDBTitle: crystal structure of human glucokinase
78	c3hy4A	Alignment	not modelled	5.1	50	PDB header: ligase Chain: A: PDB Molecule: 5-formyltetrahydrofolate cyclo-ligase; PDBTitle: structure of human mthfs with n5-iminium phosphate
79	c2wuhD	Alignment	not modelled	5.1	50	PDB header: receptor/peptide Chain: D: PDB Molecule: collagen peptide; PDBTitle: crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
80	d2vo9a1	Alignment	not modelled	5.0	43	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: VanY-like

