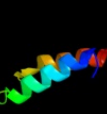
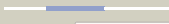
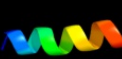
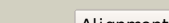
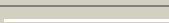


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	O75012
Date	Mon Jul 2 19:10:23 BST 2012
Unique Job ID	1312447d8ae6db08

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ei0A_	 Alignment		90.9	22	PDB header: cell cycle Chain: A: PDB Molecule: p8mtcp1; PDBTitle: nmr structure of the alpha-helical hairpin of p8mtcp1
2	d2hp8a_	 Alignment		85.9	24	Fold: Cysteine alpha-hairpin motif Superfamily: Cysteine alpha-hairpin motif Family: p8-MTCP1
3	c2k3jA_	 Alignment		78.3	10	PDB header: oxidoreductase Chain: A: PDB Molecule: mitochondrial intermembrane space import and PDBTitle: the solution structure of human mia40
4	d1u97a_	 Alignment		76.8	23	Fold: Cysteine alpha-hairpin motif Superfamily: Cysteine alpha-hairpin motif Family: COX17-like
5	c2rnbA_	 Alignment		58.2	21	PDB header: metal transport Chain: A: PDB Molecule: cytochrome c oxidase copper chaperone; PDBTitle: solution structure of human cu(i)cox17
6	d2db7a1	 Alignment		44.1	23	Fold: Orange domain-like Superfamily: Orange domain-like Family: Hairy Orange domain
7	c3qp5C_	 Alignment		36.1	13	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
8	d1yioa1	 Alignment		29.4	2	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
9	c1h0mD_	 Alignment		28.5	6	PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
10	c1zljE_	 Alignment		28.2	14	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
11	c2q0oA_	 Alignment		26.5	0	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing

12	d1ppjh_	 Alignment		24.4	18	Fold: Non-heme 11 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: Non-heme 11 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: Non-heme 11 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
13	d1fsea_	 Alignment		23.1	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
14	d1a04a1	 Alignment		21.6	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
15	d1l0lh_	 Alignment		20.6	18	Fold: Non-heme 11 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: Non-heme 11 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: Non-heme 11 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
16	c3sztB_	 Alignment		20.6	6	PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
17	c2jpcA_	 Alignment		19.9	3	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
18	d1p4wa_	 Alignment		18.2	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
19	c3u1dA_	 Alignment		17.2	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the structure of a protein with a gntR superfamily winged-helix-turn-2 helix domain from halomicrobium mukohataei.
20	c3cloC_	 Alignment		16.8	13	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
21	c3c3wB_	 Alignment	not modelled	15.4	13	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
22	c2krfB_	 Alignment	not modelled	14.8	19	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
23	c2km4A_	 Alignment	not modelled	14.7	7	PDB header: transcription regulator Chain: A: PDB Molecule: regulator of ty1 transposition protein 103; PDBTitle: solution structure of rtt103 ctd interacting domain
24	c3kmpA_	 Alignment	not modelled	14.2	19	PDB header: transcription regulator/dna Chain: A: PDB Molecule: smad1-mh1; PDBTitle: crystal structure of smad1-mh1/dna complex
25	c3qsvD_	 Alignment	not modelled	14.1	21	PDB header: transcription/dna Chain: D: PDB Molecule: mothers against decapentaplegic homolog 4; PDBTitle: structural basis for dna recognition by constitutive smad4 mh1 dimers
26	c1x3uA_	 Alignment	not modelled	14.1	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein fixj; PDBTitle: solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
27	c3ck4K_	 Alignment	not modelled	11.8	50	PDB header: protein binding Chain: K: PDB Molecule: gcn4 leucine zipper; PDBTitle: a heterospecific leucine zipper tetramer
28	c2of5A_	 Alignment	not modelled	11.4	11	PDB header: apoptosis Chain: A: PDB Molecule: death domain-containing protein cradd; PDBTitle: oligomeric death domain complex

29	d1l3la1	Alignment	not modelled	9.6	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
30	c1zn2A	Alignment	not modelled	9.5	6	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
31	c3klnC	Alignment	not modelled	9.4	16	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
32	c3qqmD	Alignment	not modelled	9.3	63	PDB header: transferase Chain: D: PDB Molecule: mlr3007 protein; PDBTitle: crystal structure of a putative amino-acid aminotransferase2 (np_104211.1) from mesorhizobium loti at 2.30 a resolution
33	c2rniA	Alignment	not modelled	9.0	5	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
34	d2p4wa1	Alignment	not modelled	8.6	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF1790-like
35	c2yqfA	Alignment	not modelled	8.5	25	PDB header: protein binding Chain: A: PDB Molecule: ankyrin-1; PDBTitle: solution structure of the death domain of ankyrin-1
36	d1fada	Alignment	not modelled	8.1	30	Fold: DEATH domain Superfamily: DEATH domain Family: DEATH domain, DD
37	d2yt9a2	Alignment	not modelled	7.9	60	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
38	d1rlua	Alignment	not modelled	7.8	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
39	d2cazc1	Alignment	not modelled	7.5	60	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS37 C-terminal domain-like
40	d2f66c1	Alignment	not modelled	7.4	60	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS37 C-terminal domain-like
41	c1l6nA	Alignment	not modelled	6.9	20	PDB header: viral protein Chain: A: PDB Molecule: gag polyprotein; PDBTitle: structure of the n-terminal 283-residue fragment of the hiv-2 1 gag polyprotein
42	c3jthA	Alignment	not modelled	6.8	33	PDB header: transcription Chain: A: PDB Molecule: transcription activator hlyu; PDBTitle: crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
43	c2zkzC	Alignment	not modelled	6.7	13	PDB header: transcription Chain: C: PDB Molecule: transcriptional repressor pagr; PDBTitle: crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
44	c1rnlA	Alignment	not modelled	6.7	13	PDB header: signal transduction protein Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narl; PDBTitle: the nitrate/nitrite response regulator protein narl from narl
45	d1sg7a1	Alignment	not modelled	6.6	30	Fold: ChaB-like Superfamily: ChaB-like Family: ChaB-like
46	c1sg7A	Alignment	not modelled	6.6	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative cation transport regulator chab; PDBTitle: nmr solution structure of the putative cation transport2 regulator chab
47	c2z5hB	Alignment	not modelled	6.5	36	PDB header: contractile protein Chain: B: PDB Molecule: general control protein gcn4 and tropomyosin PDBTitle: crystal structure of the head-to-tail junction of2 tropomyosin complexed with a fragment of tnt
48	c2jscB	Alignment	not modelled	6.5	33	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator rv1994c/mt2050; PDBTitle: nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
49	c2ipzD	Alignment	not modelled	6.3	75	PDB header: biosynthetic protein Chain: D: PDB Molecule: general control protein gcn4; PDBTitle: a parallel coiled-coil tetramer with offset helices
50	c2qufB	Alignment	not modelled	6.2	8	PDB header: transcription Chain: B: PDB Molecule: transcription factor pf0095; PDBTitle: crystal structure of transcription factor axxa-pf0095 from pyrococcus2 furiosus
51	c1ld4E	Alignment	not modelled	6.0	75	PDB header: virus Chain: E: PDB Molecule: general control protein gcn4; PDBTitle: placement of the structural proteins in sindbis virus
52	d1rl1ta	Alignment	not modelled	5.8	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
53	c1r22B	Alignment	not modelled	5.7	17	PDB header: transcription repressor Chain: B: PDB Molecule: transcriptional repressor smtb; PDBTitle: crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
54	c2ahpB	Alignment	not modelled	5.6	75	PDB header: de novo protein Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4 leucine zipper, mutation of lys15 to epsilon-azido-

						lys
55	c2ztaB_	Alignment	not modelled	5.6	75	PDB header: leucine zipper Chain: B: PDB Molecule: gcn4 leucine zipper; PDBTitle: x-ray structure of the gcn4 leucine zipper, a two-stranded,2 parallel coiled coil
56	c2ztaA_	Alignment	not modelled	5.6	75	PDB header: leucine zipper Chain: A: PDB Molecule: gcn4 leucine zipper; PDBTitle: x-ray structure of the gcn4 leucine zipper, a two-stranded,2 parallel coiled coil
57	c3f6oB_	Alignment	not modelled	5.6	17	PDB header: transcription regulator Chain: B: PDB Molecule: probable transcriptional regulator, arsr family PDBTitle: crystal structure of arsr family transcriptional regulator,2 rha00566
58	c2ahpA_	Alignment	not modelled	5.5	75	PDB header: de novo protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4 leucine zipper, mutation of lys15 to epsilon-azido-lys
59	c2g9jA_	Alignment	not modelled	5.5	75	PDB header: structural protein Chain: A: PDB Molecule: tropomyosin 1 alpha chain/general control protein PDBTitle: complex of tm1a(1-14)zip with tm9a(251-284): a model for the2 polymerization domain ("overlap region") of tropomyosin,3 northeast structural genomics target or9
60	c3jrnA_	Alignment	not modelled	5.5	13	PDB header: plant protein Chain: A: PDB Molecule: at1g72930 protein; PDBTitle: crystal structure of tir domain from arabidopsis thaliana
61	d1v54h_	Alignment	not modelled	5.4	17	Fold: Cytochrome c oxidase subunit h Superfamily: Cytochrome c oxidase subunit h Family: Cytochrome c oxidase subunit h
62	c1d5yD_	Alignment	not modelled	5.4	21	PDB header: transcription/dna Chain: D: PDB Molecule: rob transcription factor; PDBTitle: crystal structure of the e. coli rob transcription factor2 in complex with dna
63	c1ce9A_	Alignment	not modelled	5.3	75	PDB header: helix capping Chain: A: PDB Molecule: protein (gcn4-pmse); PDBTitle: helix capping in the gcn4 leucine zipper
64	c1ce9C_	Alignment	not modelled	5.3	75	PDB header: helix capping Chain: C: PDB Molecule: protein (gcn4-pmse); PDBTitle: helix capping in the gcn4 leucine zipper
65	c1ce9D_	Alignment	not modelled	5.3	75	PDB header: helix capping Chain: D: PDB Molecule: protein (gcn4-pmse); PDBTitle: helix capping in the gcn4 leucine zipper
66	c1ce9B_	Alignment	not modelled	5.3	75	PDB header: helix capping Chain: B: PDB Molecule: protein (gcn4-pmse); PDBTitle: helix capping in the gcn4 leucine zipper
67	c3cuoB_	Alignment	not modelled	5.3	36	PDB header: transcription regulator Chain: B: PDB Molecule: uncharacterized hth-type transcriptional regulator ygav; PDBTitle: crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
68	c1ihqA_	Alignment	not modelled	5.1	75	PDB header: de novo protein Chain: A: PDB Molecule: chimeric peptide glytm1bzip: tropomyosin alpha PDBTitle: glytm1bzip: a chimeric peptide model of the n-terminus of a2 rat short alpha tropomyosin with the n-terminus encoded by3 exon 1b
69	c2xusA_	Alignment	not modelled	5.0	38	PDB header: protein binding Chain: A: PDB Molecule: breast cancer metastasis-suppressor 1; PDBTitle: crystal structure of the brms1 n-terminal region