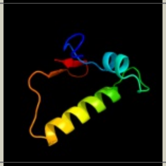
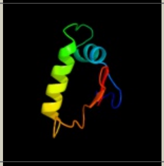
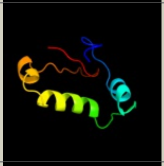
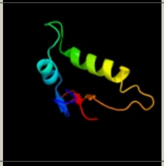
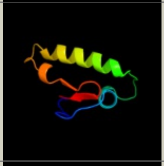
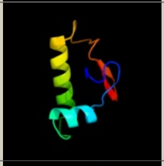
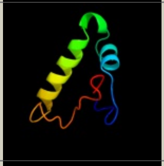
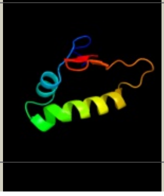
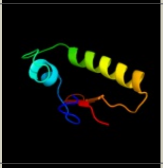
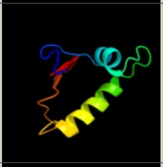
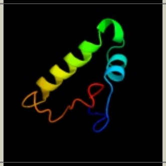
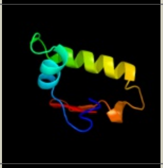
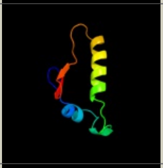
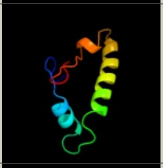
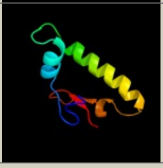
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P39901
Date	Thu Jan 5 12:01:08 GMT 2012
Unique Job ID	56c1867131a0bccc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1opca_	Alignment		99.7	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
2	c2k4jA_	Alignment		99.7	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** arsr dna binding domain
3	c2hwvA_	Alignment		99.7	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-binding response regulator vicr; **PDBTitle:** crystal structure of an essential response regulator dna binding2 domain, vicrc in enterococcus faecalis, a member of the yycf3 subfamily.
4	c2zxjB_	Alignment		99.7	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein walr; **PDBTitle:** crystal structure of yycf dna-binding domain from staphylococcus2 aureus
5	c2jzyA_	Alignment		99.7	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein pcor; **PDBTitle:** solution structure of c-terminal effector domain of2 putative two-component-system response regulator involved3 in copper resistance from klebsiella pneumoniae
6	c2hqnA_	Alignment		99.7	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
7	d1gxqa_	Alignment		99.7	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
8	c2oqrA_	Alignment		99.7	26	**PDB header:**transcription,signaling protein **Chain:** A: **PDB Molecule:**sensory transduction protein regx3; **PDBTitle:** the structure of the response regulator regx3 from mycobacterium2 tuberculosis
9	d1p2fa1	Alignment		99.7	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
10	c1ys7B_	Alignment		99.6	22	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulatory protein prra; **PDBTitle:** crystal structure of the response regulator protein prra comlexed with2 mg2+
11	c2pmuD_	Alignment		99.6	18	**PDB header:**transcription regulation **Chain:** D: **PDB Molecule:**response regulator phop; **PDBTitle:** crystal structure of the dna-binding domain of phop

12	c2hqrA_	Alignment		99.6	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
13	d1ys7a1	Alignment		99.5	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
14	c2gwrA_	Alignment		99.5	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dna-binding response regulator mtra; **PDBTitle:** crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
15	c1p2fA_	Alignment		99.5	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure analysis of response regulator drrb, a2 thermotoga maritima ompr/phob homolog
16	c3r0jA_	Alignment		99.4	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**possible two component system response transcriptional **PDBTitle:** structure of phop from mycobacterium tuberculosis
17	d1kgsa1	Alignment		99.4	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
18	d2ff4a1	Alignment		99.4	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
19	c1kgsA_	Alignment		99.2	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna binding response regulator d; **PDBTitle:** crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
20	c2ff4B_	Alignment		98.1	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable regulatory protein embr; **PDBTitle:** mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
21	d1biaa1	Alignment	not modelled	90.0	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
22	c3klnC_	Alignment	not modelled	81.8	7	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional regulator, luxr family; **PDBTitle:** vibrio cholerae vpst
23	c1rnlA_	Alignment	not modelled	79.5	12	**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
24	c1zn2A_	Alignment	not modelled	70.9	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulatory protein; **PDBTitle:** low resolution structure of response regulator styr
25	c3c3wB_	Alignment	not modelled	69.4	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
26	d1j5ya1	Alignment	not modelled	69.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
27	c1h0mD_	Alignment	not modelled	48.1	12	**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
28	c2q0oA_	Alignment	not modelled	46.5	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar; **PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing

29	c3qp5C_	Alignment	not modelled	46.0	12	**PDB header:**transcription **Chain:** C: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl)
30	c3sztB_	Alignment	not modelled	43.6	12	**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
31	c2jpcA_	Alignment	not modelled	43.0	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
32	c2ewnA_	Alignment	not modelled	42.0	24	**PDB header:**ligase, transcription **Chain:** A: **PDB Molecule:**bira bifunctional protein; **PDBTitle:** ecoli biotin repressor with co-repressor analog
33	c1zljE_	Alignment	not modelled	36.3	29	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
34	d1yioa1	Alignment	not modelled	36.2	18	**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)
35	d1l3la1	Alignment	not modelled	36.2	12	**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)
36	d1p4wa_	Alignment	not modelled	34.6	12	**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)
37	d1t6sa1	Alignment	not modelled	33.3	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ScpB/YpuH-like
38	c1x3uA_	Alignment	not modelled	30.0	6	**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
39	d1fsea_	Alignment	not modelled	29.9	29	**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)
40	d1a04a1	Alignment	not modelled	28.4	12	**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)
41	c2rnjA_	Alignment	not modelled	23.4	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
42	c1j5yA_	Alignment	not modelled	23.1	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, biotin repressor family; **PDBTitle:** crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
43	d2q07a2	Alignment	not modelled	22.0	20	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**AF0587 domain-like
44	c3kz4A_	Alignment	not modelled	20.1	15	**PDB header:**virus **Chain:** A: **PDB Molecule:**inner capsid protein vp2; **PDBTitle:** crystal structure of the rotavirus double layered particle
45	c3gzuB_	Alignment	not modelled	19.6	13	**PDB header:**virus **Chain:** B: **PDB Molecule:**inner capsid protein vp2; **PDBTitle:** vp7 recoated rotavirus dlp
46	c3cloC_	Alignment	not modelled	18.8	18	**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
47	c2krfB_	Alignment	not modelled	18.8	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
48	c1debA_	Alignment	not modelled	18.5	29	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**adenomatous polyposis coli protein; **PDBTitle:** crystal structure of the n-terminal coiled coil domain from2 apc
49	c3he5A_	Alignment	not modelled	18.0	43	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synzip1; **PDBTitle:** heterospecific coiled-coil pair synzip2:synzip1
50	d1pg5b2	Alignment	not modelled	16.3	25	**Fold:**Rubredoxin-like **Superfamily:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain **Family:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain
51	d1ud0a_	Alignment	not modelled	15.7	18	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Heat shock protein 70kD (HSP70), C-terminal subdomain **Family:**Heat shock protein 70kD (HSP70), C-terminal subdomain
52	d1fcda2	Alignment	not modelled	13.2	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
53	c3mzyA_	Alignment	not modelled	11.9	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna polymerase sigma-h factor; **PDBTitle:** the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
54	d1vqoo1	Alignment	not modelled	11.7	13	**Fold:**Ribosomal proteins L15p and L18e **Superfamily:**Ribosomal proteins L15p and L18e

						Family: Ribosomal proteins L15p and L18e
55	d1xsva_	Alignment	not modelled	11.7	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
56	c1ud0B_	Alignment	not modelled	11.5	18	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**70 kda heat-shock-like protein; **PDBTitle:** crystal structure of the c-terminal 10-kda subdomain of hsc70
57	d1or7a1	Alignment	not modelled	11.0	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
58	c2l5gB_	Alignment	not modelled	10.9	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative uncharacterized protein ncor2; **PDBTitle:** co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
59	c2o8xA_	Alignment	not modelled	10.2	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable rna polymerase sigma-c factor; **PDBTitle:** crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
60	d1o57a1	Alignment	not modelled	9.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**N-terminal domain of Bacillus PurR
61	c2p32B_	Alignment	not modelled	9.3	28	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**heat shock 70 kda protein a; **PDBTitle:** crystal structure of the c-terminal 10 kda subdomain from c. elegans2 hsp70
62	c3ocmB_	Alignment	not modelled	8.5	15	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**putative membrane protein; **PDBTitle:** the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
63	c2q07A_	Alignment	not modelled	7.9	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af0587; **PDBTitle:** crystal structure of af0587, a protein of unknown function
64	c3k69A_	Alignment	not modelled	7.7	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcription regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution
65	c2k5cA_	Alignment	not modelled	7.6	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
66	d1jhfa1	Alignment	not modelled	7.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
67	c3hugA_	Alignment	not modelled	6.4	5	**PDB header:**transcription/membrane protein **Chain:** A: **PDB Molecule:**rna polymerase sigma factor; **PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
68	d1klva_	Alignment	not modelled	6.1	7	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**GABARAP-like
69	d1rrqa1	Alignment	not modelled	5.8	16	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
70	d1zela1	Alignment	not modelled	5.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Rv2827c N-terminal domain-like
71	c3kblA_	Alignment	not modelled	5.2	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**female germline-specific tumor suppressor gld-1; **PDBTitle:** crystal structure of the gld-1 homodimerization domain from2 caenorhabditis elegans n169a mutant at 2.28 a resolution
72	c2gv1A_	Alignment	not modelled	5.1	43	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable acylphosphatase; **PDBTitle:** nmr solution structure of the acylphosphatase from2 eschaerichia coli
73	d2cz4a1	Alignment	not modelled	5.1	20	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
74	c3c4mD_	Alignment	not modelled	5.1	40	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**parathyroid hormone; **PDBTitle:** structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
75	c3c4mC_	Alignment	not modelled	5.1	40	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**parathyroid hormone; **PDBTitle:** structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)