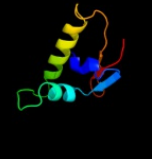
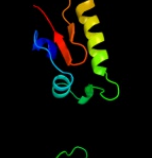
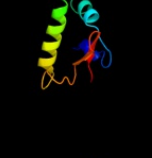
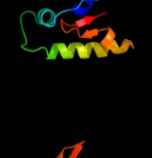
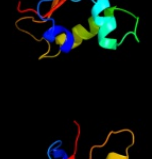
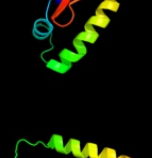
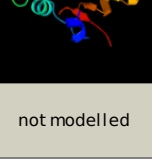


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1opca_	 Alignment		99.8	34	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
2	c2hwwA_	 Alignment		99.8	31	PDB header: transcription Chain: 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.
3	c2zxbB_	 Alignment		99.8	36	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein walr; PDBTitle: crystal structure of yycf dna-binding domain from staphylococcus2 aureus
4	c2k4jA_	 Alignment		99.8	23	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: arsr dna binding domain
5	c2jzyA_	 Alignment		99.8	21	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	c2hqnaA_	 Alignment		99.8	24	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	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
8	d1p2fa1	 Alignment		99.7	42	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
9	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
10	c2pmuD_	 Alignment		99.7	17	PDB header: transcription regulation Chain: D: PDB Molecule: response regulator phop; PDBTitle: crystal structure of the dna-binding domain of phop
11	c1ys7B_	 Alignment		99.7	26	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed with2 mg2+

12	dlys7a1	Alignment		99.7	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
13	c2hqrA_	Alignment		99.7	24	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
14	c2gwrA_	Alignment		99.6	26	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	d1kgsa1	Alignment		99.6	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
16	c1p2fA_	Alignment		99.6	42	PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure analysis of response regulator drrb, a2 thermotoga maritima ompR/phob homolog
17	d2ff4a1	Alignment		99.6	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
18	c3r0jA_	Alignment		99.5	17	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
19	c1kgsA_	Alignment		99.3	20	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		98.9	12	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	95.9	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
22	c3k69A_	Alignment	not modelled	95.5	19	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
23	c2ewnA_	Alignment	not modelled	94.4	20	PDB header: ligase, transcription Chain: A: PDB Molecule: bira bifunctional protein; PDBTitle: ecoli biotin repressor with co-repressor analog
24	d1j5ya1	Alignment	not modelled	93.0	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
25	d1ylfa1	Alignment	not modelled	90.8	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator Rrf2
26	d1o57a1	Alignment	not modelled	88.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: N-terminal domain of Bacillus PurR
27	c3lwFD_	Alignment	not modelled	87.0	21	PDB header: transcription regulator Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
28	c2y75F_	Alignment	not modelled	84.4	14	PDB header: transcription Chain: F: PDB Molecule: hth-type transcriptional regulator cymr; PDBTitle: the structure of cymr (yrzc) the global cysteine regulator2 of b. subtilis
						PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, biotin

29	c1j5yA_	Alignment	not modelled	83.9	22	repressor family; PDBTitle: crystal structure of transcriptional regulator (tm1602) from <i>Thermotoga maritima</i> at 2.3 Å resolution
30	d1t6sa1	Alignment	not modelled	82.4	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ScpB/YpuH-like
31	c3klnC_	Alignment	not modelled	70.2	15	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxR family; PDBTitle: vibrio cholerae vpst
32	c1rnlA_	Alignment	not modelled	69.9	13	PDB header: signal transduction protein Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narI; PDBTitle: the nitrate/nitrite response regulator protein narI from narI
33	c3c3wB_	Alignment	not modelled	68.9	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
34	d1xd7a_	Alignment	not modelled	56.2	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator Rrf2
35	c1zn2A_	Alignment	not modelled	52.2	25	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styR
36	c1t6sB_	Alignment	not modelled	41.6	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of a conserved hypothetical protein from <i>Chlorobium tepidum</i>
37	c2z99A_	Alignment	not modelled	41.0	11	PDB header: cell cycle Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of scpB from mycobacterium tuberculosis
38	c2q0oA_	Alignment	not modelled	39.7	17	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
39	c2fu4B_	Alignment	not modelled	37.7	15	PDB header: dna binding protein Chain: B: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
40	c1o57A_	Alignment	not modelled	33.1	13	PDB header: dna binding protein Chain: A: PDB Molecule: pur operon repressor; PDBTitle: crystal structure of the purine operon repressor of <i>Bacillus subtilis</i>
41	c3sztB_	Alignment	not modelled	33.0	17	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
42	c1h0mD_	Alignment	not modelled	32.7	29	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
43	c3qp5C_	Alignment	not modelled	32.7	18	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
44	c2jpcA_	Alignment	not modelled	31.5	12	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
45	d1l3la1	Alignment	not modelled	27.1	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)
46	c3kfwX_	Alignment	not modelled	26.2	15	PDB header: structural genomics, unknown function Chain: X: PDB Molecule: uncharacterized protein; PDBTitle: uncharacterized protein rv0674 from mycobacterium tuberculosis
47	c3kevA_	Alignment	not modelled	25.4	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: gallieria sulfuraria dcun1 domain-containing protein; PDBTitle: x-ray crystal structure of a dcun1 domain-containing protein from <i>Gallidieria sulfuraria</i>
48	c1zljE_	Alignment	not modelled	25.3	10	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
49	c2w57A_	Alignment	not modelled	24.3	18	PDB header: metal transport Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of the vibrio cholerae ferric uptake2 regulator (fur) reveals structural rearrangement of the3 dna-binding domains
50	d1yioa1	Alignment	not modelled	22.9	24	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)
51	d1p4wa_	Alignment	not modelled	21.6	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)
52	c3r0aB_	Alignment	not modelled	20.8	21	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
53	d1fsea_	Alignment	not modelled	20.3	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)

54	c1x3uA	Alignment	not modelled	19.6	24	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
55	d1a04a1	Alignment	not modelled	18.7	24	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)
56	c2is9A	Alignment	not modelled	17.0	9	PDB header: transcription Chain: A: PDB Molecule: defective in cullin neddylation protein 1; PDBTitle: structure of yeast dcn-1
57	c2o03A	Alignment	not modelled	15.1	22	PDB header: gene regulation Chain: A: PDB Molecule: probable zinc uptake regulation protein furb; PDBTitle: crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
58	c3mzyA	Alignment	not modelled	14.7	37	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
59	c2l5gB	Alignment	not modelled	13.5	21	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
60	c3bq3A	Alignment	not modelled	13.5	9	PDB header: cell cycle, ligase Chain: A: PDB Molecule: defective in cullin neddylation protein 1; PDBTitle: crystal structure of s. cerevisiae dcn1
61	c3sqnB	Alignment	not modelled	13.1	13	PDB header: transcription regulator Chain: B: PDB Molecule: conserved domain protein; PDBTitle: putative mga family transcriptional regulator from enterococcus2 faecalis
62	d1xsva	Alignment	not modelled	12.4	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
63	c2rnjA	Alignment	not modelled	12.2	22	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
64	d1jhfa1	Alignment	not modelled	11.7	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
65	d1mzba	Alignment	not modelled	11.5	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FUR-like
66	c2krfB	Alignment	not modelled	11.1	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
67	c3edpB	Alignment	not modelled	11.1	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lin2111 protein; PDBTitle: the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
68	c2o8xA	Alignment	not modelled	11.0	17	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
69	c3mwmA	Alignment	not modelled	10.8	17	PDB header: transcription Chain: A: PDB Molecule: putative metal uptake regulation protein; PDBTitle: graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
70	d1hwua	Alignment	not modelled	10.5	19	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
71	d1ud0a	Alignment	not modelled	9.7	6	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Heat shock protein 70kD (HSP70), C-terminal subdomain Family: Heat shock protein 70kD (HSP70), C-terminal subdomain
72	d1p6ra	Alignment	not modelled	9.3	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
73	d1hw1a1	Alignment	not modelled	9.3	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
74	c3cloC	Alignment	not modelled	9.0	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
75	c3d0wD	Alignment	not modelled	8.5	5	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: yflh protein; PDBTitle: crystal structure of yflh protein from bacillus subtilis.2 northeast structural genomics consortium target sr326
76	d3bwga1	Alignment	not modelled	8.5	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
77	c3ctzA	Alignment	not modelled	8.1	11	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro aminopeptidase 1; PDBTitle: structure of human cytosolic x-prolyl aminopeptidase
78	c2xigA	Alignment	not modelled	7.9	8	PDB header: transcription Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites
79	c3kz4A	Alignment	not modelled	7.9	17	PDB header: virus Chain: A: PDB Molecule: inner capsid protein vp2; PDBTitle: crystal structure of the rotavirus double layered particle

80	c2k4bA_	Alignment	not modelled	7.9	20	PDB header: dna binding protein Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: copr repressor structure
81	d1fcda2	Alignment	not modelled	7.9	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
82	d1or7a1	Alignment	not modelled	7.8	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
83	d1rrqa1	Alignment	not modelled	7.8	20	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
84	d2ieaa2	Alignment	not modelled	7.6	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
85	c3bwgA_	Alignment	not modelled	7.2	17	PDB header: transcription regulator Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator yydk; PDBTitle: the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
86	d1o98a1	Alignment	not modelled	7.2	22	Fold: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Superfamily: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
87	c3by6C_	Alignment	not modelled	7.1	19	PDB header: transcription regulator Chain: C: PDB Molecule: predicted transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator from oenococcus oeni
88	c2fe3B_	Alignment	not modelled	7.1	13	PDB header: dna binding protein Chain: B: PDB Molecule: peroxide operon regulator; PDBTitle: the crystal structure of bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch
89	d2fb1a1	Alignment	not modelled	6.9	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Nudix-associated domain
90	c1ud0B_	Alignment	not modelled	6.9	6	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
91	c3nw0B_	Alignment	not modelled	6.8	18	PDB header: metal binding protein Chain: B: PDB Molecule: melanoma-associated antigen g1; PDBTitle: crystal structure of mage1 and nse1 complex
92	c2wa0A_	Alignment	not modelled	6.7	11	PDB header: immune system Chain: A: PDB Molecule: melanoma-associated antigen 4; PDBTitle: crystal structure of the human magea4
93	d2saka_	Alignment	not modelled	6.5	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Staphylokinase/streptokinase Family: Staphylokinase/streptokinase
94	c2p32B_	Alignment	not modelled	6.2	6	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
95	d1ssna_	Alignment	not modelled	6.0	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Staphylokinase/streptokinase Family: Staphylokinase/streptokinase
96	c3hugA_	Alignment	not modelled	5.7	17	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
97	c3neuA_	Alignment	not modelled	5.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1836 protein; PDBTitle: the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
98	c3ketA_	Alignment	not modelled	5.6	16	PDB header: transcription/dna Chain: A: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
99	d2g9wa1	Alignment	not modelled	5.6	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor