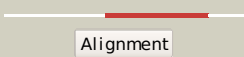
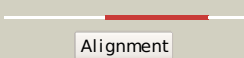
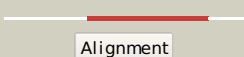
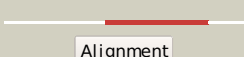
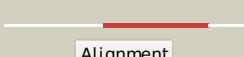
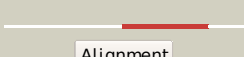
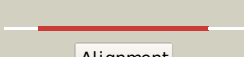


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0CF11
Date	Thu Jan 5 11:30:43 GMT 2012
Unique Job ID	bdab2f238d4cb464

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2jn6a1	 Alignment		98.0	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
2	d1k78a1	 Alignment		98.0	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
3	d6paxa1	 Alignment		97.9	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
4	d1pdnc	 Alignment		97.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
5	c1u78A	 Alignment		97.8	15	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposable element tc3 transposase; PDBTitle: structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
6	c6paxA	 Alignment		97.7	20	PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
7	c2rn7A	 Alignment		97.6	17	PDB header: unknown function Chain: A: PDB Molecule: is629 orfa; PDBTitle: nmr solution structure of tmpe protein from shigella2 flexneri. northeast structural genomics target sfr125
8	c2r0qF	 Alignment		97.2	16	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
9	c3gn5B	 Alignment		97.2	21	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
10	c2k27A	 Alignment		97.0	20	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
11	c3hefB	 Alignment		96.8	17	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small2 subunit

12	c2gm4B_	Alignment		96.5	13	PDB header: recombination, dna Chain: B: PDB Molecule: transposon gamma-delta resolvase; PDBTitle: an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
13	c3mzyA_	Alignment		96.5	14	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
14	d1xsva_	Alignment		96.4	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
15	c3hugA_	Alignment		96.4	16	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
16	c2elhA_	Alignment		96.4	23	PDB header: dna binding protein Chain: A: PDB Molecule: cg11849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
17	d1or7a1	Alignment		96.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
18	c1zljE_	Alignment		96.3	8	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
19	c3sztB_	Alignment		96.2	16	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
20	c2q0oA_	Alignment		96.1	19	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
21	d1a04a1	Alignment	not modelled	96.1	19	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)
22	d1p4wa_	Alignment	not modelled	96.0	14	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)
23	c2o8xA_	Alignment	not modelled	96.0	11	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
24	c2vbzA_	Alignment	not modelled	96.0	7	PDB header: dna-binding protein Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
25	c2cg4B_	Alignment	not modelled	96.0	17	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
26	c1x3uA_	Alignment	not modelled	95.9	14	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	c2e7xA_	Alignment	not modelled	95.9	12	PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the Lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
28	d1rp3a2	Alignment	not modelled	95.9	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain

29	d1fsea	Alignment	not modelled	95.9	11	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	d1yioa1	Alignment	not modelled	95.9	19	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)
31	c1or7A	Alignment	not modelled	95.8	14	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma-e factor; PDBTitle: crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
32	c2jpcA	Alignment	not modelled	95.8	14	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
33	d2cg4a1	Alignment	not modelled	95.8	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
34	d1s7oa	Alignment	not modelled	95.8	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
35	d1l3la1	Alignment	not modelled	95.8	16	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	c2krfB	Alignment	not modelled	95.8	14	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
37	c3qp5C	Alignment	not modelled	95.8	22	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
38	c1hlvA	Alignment	not modelled	95.7	20	PDB header: dna binding protein/dna Chain: A: PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
39	c1h0mD	Alignment	not modelled	95.7	16	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
40	c3i4pA	Alignment	not modelled	95.7	12	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
41	c2ia0A	Alignment	not modelled	95.7	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hth-type transcriptional regulator pf0864; PDBTitle: transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
42	c2cfxD	Alignment	not modelled	95.6	10	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
43	c2rnjA	Alignment	not modelled	95.6	16	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
44	d1hlva1	Alignment	not modelled	95.5	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
45	c2p6tH	Alignment	not modelled	95.5	20	PDB header: transcription Chain: H: PDB Molecule: transcriptional regulator, lrp/asnc family; PDBTitle: crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
46	d2coba1	Alignment	not modelled	95.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
47	c1rn1A	Alignment	not modelled	95.3	19	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
48	c1rp3G	Alignment	not modelled	95.3	7	PDB header: transcription Chain: G: PDB Molecule: rna polymerase sigma factor sigma-28 (fliA); PDBTitle: cocrystal structure of the flagellar sigma/anti-sigma2 complex, sigma-28/flgm
49	d2cfxa1	Alignment	not modelled	95.2	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
50	c2e1cA	Alignment	not modelled	95.2	27	PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
51	c2dbbA	Alignment	not modelled	95.2	12	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
52	c3c3wB	Alignment	not modelled	95.1	11	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
53	c1i1gA	Alignment	not modelled	95.1	10	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpA; PDBTitle: crystal structure of the lrp-like transcriptional regulator

					from the2 archaeon pyrococcus furiosus 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
54	c3cloC_	Alignment	not modelled	95.0	22
55	dli1ga1	Alignment	not modelled	95.0	10
56	d2cyya1	Alignment	not modelled	94.9	24
57	d1bw6a_	Alignment	not modelled	94.9	20
58	d1biaa1	Alignment	not modelled	94.9	14
59	c2w48D_	Alignment	not modelled	94.8	21
60	c2gqgB_	Alignment	not modelled	94.8	12
61	c3hosA_	Alignment	not modelled	94.7	12
62	c2l4aA_	Alignment	not modelled	94.7	10
63	d1twfi2	Alignment	not modelled	94.7	13
64	c2ewnA_	Alignment	not modelled	94.6	17
65	d1wiia_	Alignment	not modelled	94.4	19
66	c2q1zA_	Alignment	not modelled	94.2	16
67	dlijwc_	Alignment	not modelled	94.2	23
68	c3frwF_	Alignment	not modelled	94.2	12
69	c3klnC_	Alignment	not modelled	94.0	30
70	d1hcra_	Alignment	not modelled	94.0	23
71	c3korD_	Alignment	not modelled	93.8	15
72	c3iwfA_	Alignment	not modelled	93.7	20
73	d1qypa_	Alignment	not modelled	93.7	27
74	d1g2ha_	Alignment	not modelled	93.7	25
75	c1zn2A_	Alignment	not modelled	93.6	19
76	c3h0gl_	Alignment	not modelled	93.6	26
77	d1fipa_	Alignment	not modelled	93.5	28
78	d1ntca_	Alignment	not modelled	93.4	22
79	c1i3ql_	Alignment	not modelled	93.3	14
					Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding

80	d1ttya_	Alignment	not modelled	93.1	9	Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
81	c3e7lD_	Alignment	not modelled	93.1	19	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
82	c2qa4Z_	Alignment	not modelled	93.0	36	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
83	d1j5ya1	Alignment	not modelled	92.9	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
84	d1etob_	Alignment	not modelled	92.8	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
85	d1etxa_	Alignment	not modelled	92.7	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
86	c3cc4Z_	Alignment	not modelled	92.6	36	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: co-crystal structure of anisomycin bound to the 50s ribosomal subunit
87	d2hsqa1	Alignment	not modelled	92.6	27	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
88	d1ffkw_	Alignment	not modelled	92.4	30	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
89	d1vqoz1	Alignment	not modelled	92.4	36	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
90	d2isya1	Alignment	not modelled	92.4	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
91	c2zkrz_	Alignment	not modelled	92.4	25	PDB header: ribosomal protein/rna Chain: Z: PDB Molecule: e site t-rna; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
92	d1umqa_	Alignment	not modelled	92.3	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
93	c1umqa_	Alignment	not modelled	92.3	18	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
94	c4a17Y_	Alignment	not modelled	92.3	30	PDB header: ribosome Chain: Y: PDB Molecule: rpl37a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
95	c1yshD_	Alignment	not modelled	92.3	25	PDB header: structural protein/rna Chain: D: PDB Molecule: ribosomal protein l37a; PDBTitle: localization and dynamic behavior of ribosomal protein l30e
96	c1r7lB_	Alignment	not modelled	92.3	16	PDB header: transcription/dna Chain: B: PDB Molecule: transcriptional repressor protein korb; PDBTitle: crystal structure of the dna binding domain of korb in2 complex with the operator dna
97	d1tra_	Alignment	not modelled	92.3	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
98	d1jhga_	Alignment	not modelled	92.2	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
99	d1mkma1	Alignment	not modelled	92.2	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator lclR, N-terminal domain
100	d1jj2y_	Alignment	not modelled	92.1	31	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
101	c2l0kA_	Alignment	not modelled	92.0	18	PDB header: transcription Chain: A: PDB Molecule: stage iii sporulation protein d; PDBTitle: nmr solution structure of a transcription factor spoiiiid in complex2 with dna
102	c1rr7A_	Alignment	not modelled	91.5	15	PDB header: transcription Chain: A: PDB Molecule: middle operon regulator; PDBTitle: crystal structure of the middle operon regulator protein of2 bacteriophage mu
103	d1rr7a_	Alignment	not modelled	91.5	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Middle operon regulator, Mor
104	d1g3wa1	Alignment	not modelled	91.5	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
105	d1ku3a_	Alignment	not modelled	91.5	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain

106	d1tfia_	Alignment	not modelled	91.4	14	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
107	d1r71a_	Alignment	not modelled	91.4	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
108	d1jhfa1	Alignment	not modelled	91.4	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
109	c2oqgA_	Alignment	not modelled	91.3	16	PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. rha1
110	d2bjca1	Alignment	not modelled	91.3	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
111	c3cngC_	Alignment	not modelled	91.2	19	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
112	d1luxa_	Alignment	not modelled	91.2	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
113	d2ev0a1	Alignment	not modelled	91.2	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
114	d1lcda_	Alignment	not modelled	91.0	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
115	d1luxda_	Alignment	not modelled	90.9	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
116	d2ao9a1	Alignment	not modelled	90.8	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
117	d1rlua_	Alignment	not modelled	90.8	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
118	d1vz0a1	Alignment	not modelled	90.6	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
119	c2kpiA_	Alignment	not modelled	90.6	15	PDB header: transcription regulator Chain: A: PDB Molecule: sos-response transcriptional repressor, lexa; PDBTitle: solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
120	c3m1eA_	Alignment	not modelled	90.4	7	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of benm_dbd