








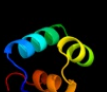























# Phyre2

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Description	P0CF10
Date	Thu Jan 5 11:30:42 GMT 2012
Unique Job ID	2748ecd6cf9bfd66

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">dlk78a1</a>	 Alignment		98.0	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
2	<a href="#">d6paxa1</a>	 Alignment		97.9	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
3	<a href="#">d2jn6a1</a>	 Alignment		97.8	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
4	<a href="#">d1pdnc</a>	 Alignment		97.8	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
5	<a href="#">c1u78A</a>	 Alignment		97.7	16	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element tc3 transposase; <b>PDBTitle:</b> structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
6	<a href="#">c6paxA</a>	 Alignment		97.7	20	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein pax-6; <b>PDBTitle:</b> crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
7	<a href="#">c2rn7A</a>	 Alignment		97.4	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> is629 orfa; <b>PDBTitle:</b> nmr solution structure of tpe protein from shigella2 flexneri. northeast structural genomics target sfr125
8	<a href="#">c3gn5B</a>	 Alignment		97.2	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa (ygit/b3021); <b>PDBTitle:</b> structure of the e. coli protein mqsa (ygit/b3021)
9	<a href="#">c2r0qF</a>	 Alignment		97.1	16	<b>PDB header:</b> recombination/dna <b>Chain:</b> F: <b>PDB Molecule:</b> putative transposon tn552 dna-invertase bin3; <b>PDBTitle:</b> crystal structure of a serine recombinase- dna regulatory2 complex
10	<a href="#">c2k27A</a>	 Alignment		96.9	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> paired box protein pax-8; <b>PDBTitle:</b> solution structure of human pax8 paired box domain
11	<a href="#">c3hefB</a>	 Alignment		96.5	20	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gene 1 protein; <b>PDBTitle:</b> crystal structure of the bacteriophage sf6 terminase small2 subunit

12	<a href="#">c2gm4B_</a>	Alignment		96.4	13	<b>PDB header:</b> recombination, dna <b>Chain:</b> B: <b>PDB Molecule:</b> transposon gamma-delta resolvase; <b>PDBTitle:</b> an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
13	<a href="#">c3mzyA_</a>	Alignment		96.3	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-h factor; <b>PDBTitle:</b> the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
14	<a href="#">c3sztB_</a>	Alignment		96.2	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> quorum-sensing control repressor; <b>PDBTitle:</b> quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
15	<a href="#">c1zljE_</a>	Alignment		96.2	8	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> dormancy survival regulator; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
16	<a href="#">c2elhA_</a>	Alignment		96.2	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cg11849-pa; <b>PDBTitle:</b> solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
17	<a href="#">c2q0oA_</a>	Alignment		96.2	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional activator protein trar; <b>PDBTitle:</b> crystal structure of an anti-activation complex in bacterial quorum2 sensing
18	<a href="#">dlxsva_</a>	Alignment		96.2	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
19	<a href="#">c3hugA_</a>	Alignment		96.2	16	<b>PDB header:</b> transcription/membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
20	<a href="#">dlor7a1</a>	Alignment		96.1	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
21	<a href="#">d1a04a1</a>	Alignment	not modelled	95.9	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
22	<a href="#">d1p4wa_</a>	Alignment	not modelled	95.9	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
23	<a href="#">c3qp5C_</a>	Alignment	not modelled	95.9	22	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> cvir transcriptional regulator; <b>PDBTitle:</b> crystal structure of cvir bound to antagonist chlorolactone (cl)
24	<a href="#">c1x3uA_</a>	Alignment	not modelled	95.9	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein fixj; <b>PDBTitle:</b> solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
25	<a href="#">d1yioa1</a>	Alignment	not modelled	95.8	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
26	<a href="#">c2o8xA_</a>	Alignment	not modelled	95.8	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-c factor; <b>PDBTitle:</b> crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
27	<a href="#">c1h0mD_</a>	Alignment	not modelled	95.8	16	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional activator protein trar; <b>PDBTitle:</b> three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
28	<a href="#">d1fsea_</a>	Alignment	not modelled	95.7	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)

29	<a href="#">c2cg4B_</a>	Alignment	not modelled	95.7	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
30	<a href="#">c1or7A_</a>	Alignment	not modelled	95.7	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-e factor; <b>PDBTitle:</b> crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
31	<a href="#">d1l3la1</a>	Alignment	not modelled	95.7	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
32	<a href="#">c2vbzA_</a>	Alignment	not modelled	95.7	8	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
33	<a href="#">d1rp3a2</a>	Alignment	not modelled	95.7	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
34	<a href="#">c2e7xA_</a>	Alignment	not modelled	95.6	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> 150aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> structure of the Lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
35	<a href="#">c2jpcA_</a>	Alignment	not modelled	95.6	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ssrb; <b>PDBTitle:</b> ssrb dna binding protein
36	<a href="#">c2krfB_</a>	Alignment	not modelled	95.6	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein coma; <b>PDBTitle:</b> nmr solution structure of the dna binding domain of competence protein2 a
37	<a href="#">d1s7oa_</a>	Alignment	not modelled	95.5	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
38	<a href="#">d2cg4a1</a>	Alignment	not modelled	95.5	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
39	<a href="#">c3i4pA_</a>	Alignment	not modelled	95.4	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, asnc family; <b>PDBTitle:</b> crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
40	<a href="#">c1hlvA_</a>	Alignment	not modelled	95.4	20	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> major centromere autoantigen b; <b>PDBTitle:</b> crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
41	<a href="#">c2rnjA_</a>	Alignment	not modelled	95.3	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein vvar; <b>PDBTitle:</b> nmr structure of the s. aureus vvar dna binding domain
42	<a href="#">c2ia0A_</a>	Alignment	not modelled	95.3	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator pf0864; <b>PDBTitle:</b> transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
43	<a href="#">c1rn1A_</a>	Alignment	not modelled	95.3	19	<b>PDB header:</b> signal transduction protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate/nitrite response regulator protein narl; <b>PDBTitle:</b> the nitrate/nitrite response regulator protein narl from narl
44	<a href="#">d1hlva1</a>	Alignment	not modelled	95.2	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
45	<a href="#">c2cfxD_</a>	Alignment	not modelled	95.2	10	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional regulator lrpc; <b>PDBTitle:</b> structure of b.subtilis lrpc
46	<a href="#">c3c3wB_</a>	Alignment	not modelled	95.2	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> two component transcriptional regulatory protein devr; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
47	<a href="#">d2coba1</a>	Alignment	not modelled	95.1	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Psq domain
48	<a href="#">c2p6tH_</a>	Alignment	not modelled	95.1	18	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> transcriptional regulator, lrp/asnc family; <b>PDBTitle:</b> crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
49	<a href="#">c1rp3G_</a>	Alignment	not modelled	95.1	7	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> rna polymerase sigma factor sigma-28 (fliA); <b>PDBTitle:</b> cocrystal structure of the flagellar sigma/anti-sigma2 complex, sigma-28/flgM
50	<a href="#">c3hosA_</a>	Alignment	not modelled	95.0	12	<b>PDB header:</b> transferase, dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element mariner, complete cds; <b>PDBTitle:</b> crystal structure of the mariner mos1 paired end complex with mg
51	<a href="#">d1bw6a_</a>	Alignment	not modelled	94.9	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
52	<a href="#">c3cloC_</a>	Alignment	not modelled	94.8	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> 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
						<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional

53	<a href="#">c2e1cA_</a>	Alignment	not modelled	94.7	28	regulator ph1519; <b>PDBTitle:</b> structure of putative hth-type transcriptional regulator ph1519/dna2 complex
54	<a href="#">c2dbbA_</a>	Alignment	not modelled	94.7	13	<b>PDB header:</b> transcriptional regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph0061; <b>PDBTitle:</b> crystal structure of ph0061
55	<a href="#">c1ilgA_</a>	Alignment	not modelled	94.7	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lrpA; <b>PDBTitle:</b> crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
56	<a href="#">c2w48D_</a>	Alignment	not modelled	94.6	24	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> sorbitol operon regulator; <b>PDBTitle:</b> crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
57	<a href="#">d2cyya1</a>	Alignment	not modelled	94.6	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
58	<a href="#">d1twfi2</a>	Alignment	not modelled	94.6	13	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
59	<a href="#">d2cfxa1</a>	Alignment	not modelled	94.5	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
60	<a href="#">d1biaa1</a>	Alignment	not modelled	94.5	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
61	<a href="#">c3frwF_</a>	Alignment	not modelled	94.2	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> putative trp repressor protein; <b>PDBTitle:</b> crystal structure of putative trp protein from ruminococcus obeum
62	<a href="#">d1wiia_</a>	Alignment	not modelled	94.2	19	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Putative zinc binding domain
63	<a href="#">d1iiga1</a>	Alignment	not modelled	94.2	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
64	<a href="#">c2ewnA_</a>	Alignment	not modelled	94.1	17	<b>PDB header:</b> ligase, transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bira bifunctional protein; <b>PDBTitle:</b> ecoli biotin repressor with co-repressor analog
65	<a href="#">c2gqQB_</a>	Alignment	not modelled	94.1	10	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> leucine-responsive regulatory protein; <b>PDBTitle:</b> crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
66	<a href="#">c3klnC_</a>	Alignment	not modelled	94.0	30	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, luxr family; <b>PDBTitle:</b> vibrio cholerae vpst
67	<a href="#">c3h0gl_</a>	Alignment	not modelled	93.8	26	<b>PDB header:</b> transcription <b>Chain:</b> I: <b>PDB Molecule:</b> dna-directed rna polymerase ii subunit rpb9; <b>PDBTitle:</b> rna polymerase ii from schizosaccharomyces pombe
68	<a href="#">d1qypa_</a>	Alignment	not modelled	93.8	27	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
69	<a href="#">c3korD_</a>	Alignment	not modelled	93.8	15	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> possible trp repressor; <b>PDBTitle:</b> crystal structure of a putative trp repressor from staphylococcus2 aureus
70	<a href="#">c1zn2A_</a>	Alignment	not modelled	93.7	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> response regulatory protein; <b>PDBTitle:</b> low resolution structure of response regulator styr
71	<a href="#">c2l4aA_</a>	Alignment	not modelled	93.7	8	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> leucine responsive regulatory protein; <b>PDBTitle:</b> nmr structure of the dna-binding domain of e.coli lrp
72	<a href="#">d1g2ha_</a>	Alignment	not modelled	93.6	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
73	<a href="#">c2q1zA_</a>	Alignment	not modelled	93.6	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rpoe, ecf sigE; <b>PDBTitle:</b> crystal structure of rhodobacter sphaeroides sigE in complex with the2 anti-sigma chrr
74	<a href="#">d1fipa_</a>	Alignment	not modelled	93.4	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
75	<a href="#">c1i3ql_</a>	Alignment	not modelled	93.4	15	<b>PDB header:</b> transcription <b>Chain:</b> I: <b>PDB Molecule:</b> dna-directed rna polymerase ii 14.2kd <b>PDBTitle:</b> rna polymerase ii crystal form i at 3.1 a resolution
76	<a href="#">c2qa4Z_</a>	Alignment	not modelled	93.3	34	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 50s ribosomal protein l37ae; <b>PDBTitle:</b> a more complete structure of the the 17/12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
77	<a href="#">c3cc4Z_</a>	Alignment	not modelled	93.1	34	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 50s ribosomal protein l37ae; <b>PDBTitle:</b> co-crystal structure of anisomycin bound to the 50s ribosomal subunit
78	<a href="#">d1ijwc_</a>	Alignment	not modelled	93.1	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
79	<a href="#">d1vqoz1</a>	Alignment	not modelled	92.9	34	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37ae

80	<a href="#">d2hsga1</a>	Alignment	not modelled	92.8	27	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
81	<a href="#">d1ffkw</a>	Alignment	not modelled	92.8	28	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37ae
82	<a href="#">c2zkrz</a>	Alignment	not modelled	92.8	24	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> Z: <b>PDB Molecule:</b> e site t-rna; <b>PDBTitle:</b> 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
83	<a href="#">c1yshD</a>	Alignment	not modelled	92.7	24	<b>PDB header:</b> structural protein/rna <b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal protein l37a; <b>PDBTitle:</b> localization and dynamic behavior of ribosomal protein l30e
84	<a href="#">c4a17Y</a>	Alignment	not modelled	92.7	28	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> rpl37a; <b>PDBTitle:</b> 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.
85	<a href="#">d1ttya</a>	Alignment	not modelled	92.6	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
86	<a href="#">d1ntca</a>	Alignment	not modelled	92.6	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
87	<a href="#">d1etxa</a>	Alignment	not modelled	92.6	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
88	<a href="#">d1hcra</a>	Alignment	not modelled	92.6	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
89	<a href="#">d1jj2y</a>	Alignment	not modelled	92.5	28	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37ae
90	<a href="#">d1etob</a>	Alignment	not modelled	92.3	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
91	<a href="#">d1jhga</a>	Alignment	not modelled	92.2	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
92	<a href="#">d1trra</a>	Alignment	not modelled	92.2	30	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> Trp repressor, TrpR
93	<a href="#">c3e7ID</a>	Alignment	not modelled	92.2	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4's dna binding2 domain
94	<a href="#">d1jhfa1</a>	Alignment	not modelled	92.0	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LexA repressor, N-terminal DNA-binding domain
95	<a href="#">c1umqA</a>	Alignment	not modelled	92.0	18	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> photosynthetic apparatus regulatory protein; <b>PDBTitle:</b> solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
96	<a href="#">d1umqa</a>	Alignment	not modelled	92.0	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
97	<a href="#">c1r71B</a>	Alignment	not modelled	91.9	16	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor protein korb; <b>PDBTitle:</b> crystal structure of the dna binding domain of korb in2 complex with the operator dna
98	<a href="#">c3iwfA</a>	Alignment	not modelled	91.9	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator rpir family; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
99	<a href="#">d1j5ya1</a>	Alignment	not modelled	91.8	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
100	<a href="#">d1tfia</a>	Alignment	not modelled	91.8	14	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Transcriptional factor domain
101	<a href="#">d1uxca</a>	Alignment	not modelled	91.8	24	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
102	<a href="#">d2isya1</a>	Alignment	not modelled	91.7	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
103	<a href="#">c2i0kA</a>	Alignment	not modelled	91.7	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> stage iii sporulation protein d; <b>PDBTitle:</b> nmr solution structure of a transcription factor spoiiiid in complex2 with dna
104	<a href="#">d2bjca1</a>	Alignment	not modelled	91.6	26	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
105	<a href="#">d1lcda</a>	Alignment	not modelled	91.5	26	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator

106	<a href="#">c3h5tA_</a>	Alignment	not modelled	91.3	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, laci family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
107	<a href="#">d1uxda_</a>	Alignment	not modelled	91.3	24	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
108	<a href="#">d1r71a_</a>	Alignment	not modelled	91.0	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> KorB DNA-binding domain-like <b>Family:</b> KorB DNA-binding domain-like
109	<a href="#">d1g3wa1</a>	Alignment	not modelled	91.0	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
110	<a href="#">d1qpza1</a>	Alignment	not modelled	90.6	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
111	<a href="#">c3cngC_</a>	Alignment	not modelled	90.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> nudix hydrolase; <b>PDBTitle:</b> crystal structure of nudix hydrolase from nitrosomonas europaea
112	<a href="#">d1efaa1</a>	Alignment	not modelled	90.5	26	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
113	<a href="#">d1mkma1</a>	Alignment	not modelled	90.5	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator IclR, N-terminal domain
114	<a href="#">d1vz0a1</a>	Alignment	not modelled	90.4	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> KorB DNA-binding domain-like <b>Family:</b> KorB DNA-binding domain-like
115	<a href="#">d1b9ma1</a>	Alignment	not modelled	90.3	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> N-terminal domain of molybdate-dependent transcriptional regulator ModE
116	<a href="#">c2oqgA_</a>	Alignment	not modelled	90.2	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein; <b>PDBTitle:</b> arsr-like transcriptional regulator from rhodococcus sp. rha1
117	<a href="#">d1ku3a_</a>	Alignment	not modelled	90.2	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
118	<a href="#">d1r1ua_</a>	Alignment	not modelled	90.1	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
119	<a href="#">d2ev0a1</a>	Alignment	not modelled	90.1	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
120	<a href="#">c3kxD_</a>	Alignment	not modelled	90.1	26	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, laci family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi