Phyre2

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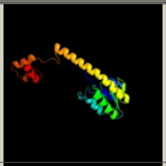
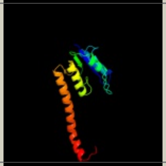
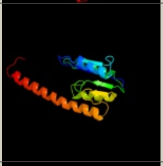
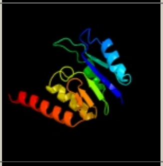
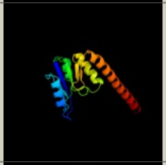
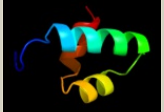
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gm4B_	Alignment		100.0	94	**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
2	c2r0qF_	Alignment		100.0	31	**PDB header:**recombination/dna **Chain:** F: **PDB Molecule:**putative transposon tn552 dna-invertase bin3; **PDBTitle:** crystal structure of a serine recombinase- dna regulatory2 complex
3	d1gdta2	Alignment		100.0	100	**Fold:**Resolvase-like **Superfamily:**Resolvase-like **Family:**gamma,delta resolvase, catalytic domain
4	d2gm4a2	Alignment		100.0	96	**Fold:**Resolvase-like **Superfamily:**Resolvase-like **Family:**gamma,delta resolvase, catalytic domain
5	d2rsla_	Alignment		99.9	99	**Fold:**Resolvase-like **Superfamily:**Resolvase-like **Family:**gamma,delta resolvase, catalytic domain
6	c3ploX_	Alignment		99.9	42	**PDB header:**recombination **Chain:** X: **PDB Molecule:**dna-invertase; **PDBTitle:** crystal structure of the fis-independent mutant of gin
7	d1hx7a_	Alignment		99.9	100	**Fold:**Resolvase-like **Superfamily:**Resolvase-like **Family:**gamma,delta resolvase, catalytic domain
8	c3g13B_	Alignment		99.9	27	**PDB header:**recombination **Chain:** B: **PDB Molecule:**putative conjugative transposon recombinase; **PDBTitle:** crystal structure of putative conjugative transposon recombinase from2 clostridium difficile
9	c3guvA_	Alignment		99.9	31	**PDB header:**recombination **Chain:** A: **PDB Molecule:**site-specific recombinase, resolvase family protein; **PDBTitle:** crystal structure of a resolvase family site-specific recombinase from2 streptococcus pneumoniae
10	c3pkzK_	Alignment		99.9	34	**PDB header:**recombination **Chain:** K: **PDB Molecule:**recombinase sin; **PDBTitle:** structural basis for catalytic activation of a serine recombinase
11	c3lhfC_	Alignment		99.9	26	**PDB header:**recombination **Chain:** C: **PDB Molecule:**serine recombinase; **PDBTitle:** the crystal structure of a serine recombinase from2 sulfolobus solfataricus to 2.3a

12	c3bvpB_	Alignment		99.8	35	**PDB header:**recombination **Chain:** B: **PDB Molecule:**tp901-1 integrase; **PDBTitle:** crystal structure of the n-terminal catalytic domain of tp901-12 integrase
13	c3lhkA_	Alignment		99.8	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna binding protein mj0014; **PDBTitle:** crystal structure of putative dna binding protein from2 methanocaldococcus jannaschii.
14	d1gdta1	Alignment		97.5	100	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
15	c1u78A_	Alignment		97.3	9	**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
16	d1pdnc_	Alignment		97.1	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
17	c6paxA_	Alignment		97.1	18	**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
18	d1k78a1	Alignment		97.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
19	d6paxa1	Alignment		96.7	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
20	c3sztB_	Alignment		96.1	15	**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
21	d2jn6a1	Alignment	not modelled	96.0	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
22	c2elhA_	Alignment	not modelled	95.8	9	**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
23	c2k27A_	Alignment	not modelled	95.4	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**paired box protein pax-8; **PDBTitle:** solution structure of human pax8 paired box domain
24	c3mzyA_	Alignment	not modelled	95.3	13	**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
25	c3hefB_	Alignment	not modelled	95.3	18	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
26	c1zljE_	Alignment	not modelled	95.2	22	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
27	d1a04a1	Alignment	not modelled	95.1	28	**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)
28	d1xsva_	Alignment	not modelled	95.1	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
						PDB header:structural genomics, unknown function

29	c3frwF_	Alignment	not modelled	95.1	16	**Chain:** F: **PDB Molecule:**putative trp repressor protein; **PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum
30	c2krfB_	Alignment	not modelled	95.0	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
31	c1x3uA_	Alignment	not modelled	94.9	25	**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
32	d1hlva1	Alignment	not modelled	94.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
33	c3hugA_	Alignment	not modelled	94.9	22	**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
34	c3korD_	Alignment	not modelled	94.8	19	**PDB header:**transcription **Chain:** D: **PDB Molecule:**possible trp repressor; **PDBTitle:** crystal structure of a putative trp repressor from staphylococcus2 aureus
35	d1yioa1	Alignment	not modelled	94.8	27	**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	c2jpcA_	Alignment	not modelled	94.7	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
37	d1p4wa_	Alignment	not modelled	94.7	21	**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)
38	d1l3la1	Alignment	not modelled	94.6	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)
39	d1ijwc_	Alignment	not modelled	94.6	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
40	d1fsea_	Alignment	not modelled	94.6	21	**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	c2q0oA_	Alignment	not modelled	94.5	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar; **PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing
42	c2rnjA_	Alignment	not modelled	94.5	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
43	d1hcra_	Alignment	not modelled	94.4	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
44	c1h0mD_	Alignment	not modelled	94.3	8	**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
45	c3qp5C_	Alignment	not modelled	94.3	15	**PDB header:**transcription **Chain:** C: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl)
46	d1rp3a2	Alignment	not modelled	94.2	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
47	d1bw6a_	Alignment	not modelled	94.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
48	d1or7a1	Alignment	not modelled	94.0	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
49	c2o8xA_	Alignment	not modelled	93.9	14	**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
50	c1hlvA_	Alignment	not modelled	93.8	19	**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
51	c2rn7A_	Alignment	not modelled	93.8	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**is629 orfa; **PDBTitle:** nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
52	d1s7oa_	Alignment	not modelled	93.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
53	d1qpza1	Alignment	not modelled	93.6	29	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
54	d1umqa_	Alignment	not modelled	93.5	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like

55	c1umqA_	Alignment	not modelled	93.5	12	**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
56	d1efaa1	Alignment	not modelled	93.5	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
57	c1r71B_	Alignment	not modelled	93.5	13	**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
58	c1or7A_	Alignment	not modelled	93.5	24	**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
59	c3c3wB_	Alignment	not modelled	93.5	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
60	d1uxca_	Alignment	not modelled	93.5	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
61	d2bjca1	Alignment	not modelled	93.4	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
62	d1biaa1	Alignment	not modelled	93.3	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
63	d2hsga1	Alignment	not modelled	93.3	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
64	c3cloC_	Alignment	not modelled	93.3	24	**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
65	c1rp3G_	Alignment	not modelled	93.3	16	**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
66	d1nera_	Alignment	not modelled	93.3	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
67	d1lcda_	Alignment	not modelled	93.1	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
68	d1ttya_	Alignment	not modelled	93.0	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
69	d1r71a_	Alignment	not modelled	93.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
70	d1g2ha_	Alignment	not modelled	92.9	0	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
71	d1jhga_	Alignment	not modelled	92.9	4	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
72	c2lcvA_	Alignment	not modelled	92.9	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr; **PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation
73	d1uxda_	Alignment	not modelled	92.8	27	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
74	d1vz0a1	Alignment	not modelled	92.6	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
75	d1j5ya1	Alignment	not modelled	92.5	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
76	d2cg4a1	Alignment	not modelled	92.5	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
77	c3hosA_	Alignment	not modelled	92.3	4	**PDB header:**transferase, dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element mariner, complete cds; **PDBTitle:** crystal structure of the mariner mos1 paired end complex with mg
78	c3e7lD_	Alignment	not modelled	92.3	15	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
79	c2l8nA_	Alignment	not modelled	92.2	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional repressor cytr; **PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
						Fold:DNA/RNA-binding 3-helical bundle

80	d1mkma1	Alignment	not modelled	92.2	19	**Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
81	d1trra_	Alignment	not modelled	92.1	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
82	d2p7vb1	Alignment	not modelled	92.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
83	c1rnlA_	Alignment	not modelled	92.0	27	**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
84	c2l4aA_	Alignment	not modelled	92.0	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**leucine responsive regulatory protein; **PDBTitle:** nmr structure of the dna-binding domain of e.coli lrp
85	c2kpjA_	Alignment	not modelled	92.0	9	**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
86	d1fipa_	Alignment	not modelled	91.9	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
87	c3klnC_	Alignment	not modelled	91.9	12	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional regulator, luxr family; **PDBTitle:** vibrio cholerae vpst
88	d1ku3a_	Alignment	not modelled	91.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
89	d1smyf2	Alignment	not modelled	91.5	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
90	d2cfxa1	Alignment	not modelled	91.5	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
91	d1ku7a_	Alignment	not modelled	91.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
92	d1etxa_	Alignment	not modelled	91.4	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
93	d1i1ga1	Alignment	not modelled	91.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
94	d1etob_	Alignment	not modelled	91.2	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
95	c3t76A_	Alignment	not modelled	91.1	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
96	d1rr7a_	Alignment	not modelled	91.0	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Middle operon regulator, Mor
97	c1rr7A_	Alignment	not modelled	91.0	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**middle operon regulator; **PDBTitle:** crystal structure of the middle operon regulator protein of2 bacteriophage mu
98	c3b7hA_	Alignment	not modelled	91.0	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
99	c2oqgA_	Alignment	not modelled	90.9	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
100	c3fmyA_	Alignment	not modelled	90.8	6	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator mqsa **PDBTitle:** structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
101	d2cyya1	Alignment	not modelled	90.7	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
102	d2coba1	Alignment	not modelled	90.7	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
103	d2isya1	Alignment	not modelled	90.3	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
104	d1r69a_	Alignment	not modelled	90.1	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
105	c3omtA_	Alignment	not modelled	89.8	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
						Fold:DNA/RNA-binding 3-helical bundle

106	d1r1ta_	Alignment	not modelled	89.8	13	**Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
107	c1r22B_	Alignment	not modelled	89.7	13	**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
108	d1ntca_	Alignment	not modelled	89.6	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
109	c2jscB_	Alignment	not modelled	89.5	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator rv1994c/mt2050; **PDBTitle:** nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
110	d1z05a1	Alignment	not modelled	89.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
111	c3op9A_	Alignment	not modelled	89.3	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
112	d1adra_	Alignment	not modelled	89.3	3	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
113	d1r1ua_	Alignment	not modelled	89.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
114	d1jt6a1	Alignment	not modelled	89.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
115	c2l0kA_	Alignment	not modelled	89.0	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stage iii sporulation protein d; **PDBTitle:** nmr solution structure of a transcription factor spoiiid in complex2 with dna
116	d1g3wa1	Alignment	not modelled	88.8	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
117	c3bs3A_	Alignment	not modelled	88.7	3	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of a putative dna-binding protein from bacteroides2 fragilis
118	c2x48B_	Alignment	not modelled	88.6	10	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
119	c1f5tA_	Alignment	not modelled	88.6	12	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
120	c3pqkD_	Alignment	not modelled	88.5	9	**PDB header:**transcription **Chain:** D: **PDB Molecule:**biofilm growth-associated repressor; **PDBTitle:** crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa