Phyre2

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Description	P76546
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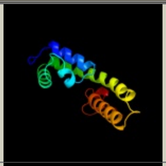
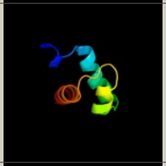
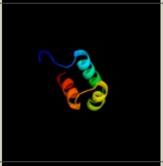
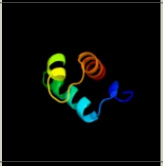
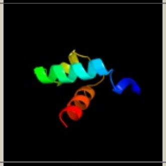
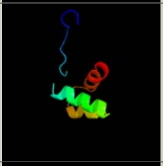
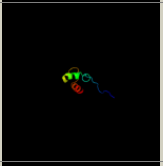
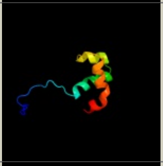
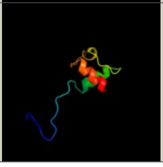
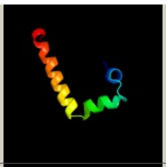
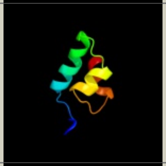
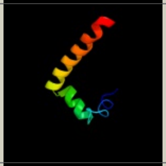
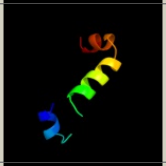
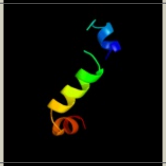
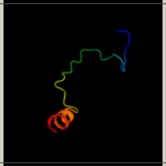
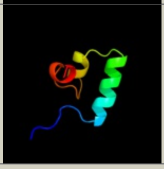
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hefB_	Alignment		99.9	26	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
2	c6paxA_	Alignment		93.7	22	**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
3	d1pdnc_	Alignment		93.5	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
4	c2rn7A_	Alignment		93.4	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
5	d6paxa1	Alignment		92.1	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
6	d2jn6a1	Alignment		91.4	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
7	d1k78a1	Alignment		90.4	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
8	c2r0qF_	Alignment		89.9	25	**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	c2gm4B_	Alignment		88.9	15	**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
10	c2elhA_	Alignment		87.8	14	**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
11	c1u78A_	Alignment		87.3	14	**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

12	d2ao9a1	Alignment		77.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Nanomeric phage protein-like
13	d2coba1	Alignment		76.8	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
14	c2ao9H_	Alignment		76.1	13	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**phage protein; **PDBTitle:** structural genomics, the crystal structure of a phage protein2 (phbc6a51) from bacillus cereus atcc 14579
15	d2ezia_	Alignment		72.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
16	d2ezha_	Alignment		71.6	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
17	c2l5aA_	Alignment		69.4	26	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**histone h3-like centromeric protein cse4, protein scm3, **PDBTitle:** structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3
18	d1hlva1	Alignment		69.0	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
19	c2k27A_	Alignment		68.7	27	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**paired box protein pax-8; **PDBTitle:** solution structure of human pax8 paired box domain
20	d1ijwc_	Alignment		66.1	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
21	d1hcra_	Alignment	not modelled	65.6	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
22	c3gziA_	Alignment	not modelled	64.9	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of a transcriptional regulator of the tetr family2 (shew_3567) from shewanella loihica pv-4 at 2.05 a resolution
23	c1hlvA_	Alignment	not modelled	63.5	13	**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
24	d1jhfa1	Alignment	not modelled	63.1	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
25	c2xroE_	Alignment	not modelled	52.6	29	**PDB header:**dna-binding protein/dna **Chain:** E: **PDB Molecule:**hth-type transcriptional regulator ttgv; **PDBTitle:** crystal structure of ttgv in complex with its dna operator
26	d2v0ea1	Alignment	not modelled	51.9	19	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
27	d2ckaa1	Alignment	not modelled	49.9	25	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
28	c2ckaA_	Alignment	not modelled	49.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 8; **PDBTitle:** solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3

						with gyf domain suggesting a role in protein interaction
29	c3nrgA_	Alignment	not modelled	49.9	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tetr family transcriptional regulator; **PDBTitle:** crystal structure of a tetr family transcriptional regulator2 (caur_2714) from chloroflexus aurantiacus j-10-fl at 2.56 a3 resolution
30	d2ckca1	Alignment	not modelled	47.8	19	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
31	c2ckcA_	Alignment	not modelled	47.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 7; **PDBTitle:** solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
32	d2hkua1	Alignment	not modelled	46.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
33	d1rkta1	Alignment	not modelled	44.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
34	c1z4hA_	Alignment	not modelled	42.8	14	**PDB header:**protein binding, dna binding protein **Chain:** A: **PDB Molecule:**tor inhibition protein; **PDBTitle:** the response regulator tori belongs to a new family of2 atypical excisionase
35	d1sh0a_	Alignment	not modelled	42.7	24	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
36	d1yioa1	Alignment	not modelled	40.7	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)
37	d1y9qa1	Alignment	not modelled	40.0	21	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
38	d2qzga1	Alignment	not modelled	39.9	35	**Fold:**Bromodomain-like **Superfamily:**Ta0600-like **Family:**Ta0600-like
39	d1a04a1	Alignment	not modelled	39.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
40	d2qsba1	Alignment	not modelled	39.6	20	**Fold:**Bromodomain-like **Superfamily:**Ta0600-like **Family:**Ta0600-like
41	c3hosA_	Alignment	not modelled	38.3	15	**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
42	d3c07a1	Alignment	not modelled	38.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
43	c2g7uB_	Alignment	not modelled	36.6	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
44	d2dl6a1	Alignment	not modelled	36.5	25	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
45	c1zljE_	Alignment	not modelled	35.7	16	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
46	c2jpcA_	Alignment	not modelled	35.1	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
47	c2nx4A_	Alignment	not modelled	32.8	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family protein; **PDBTitle:** the crystal structure of athe putative tetr-family transcriptional2 regulator rha06780 from rhodococcus sp. rha1.
48	c2krfB_	Alignment	not modelled	30.5	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
49	d1bw6a_	Alignment	not modelled	30.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
50	c2b43D_	Alignment	not modelled	30.3	24	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**non-structural polyprotein; **PDBTitle:** crystal structure of the norwalk virus rna dependent rna polymerase2 from strain hu/nlv/dresden174/1997/ge
51	c1x3uA_	Alignment	not modelled	28.7	19	**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
52	d1zk8a1	Alignment	not modelled	28.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
53	d2g7la1	Alignment	not modelled	27.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
						Fold:DNA/RNA-binding 3-helical bundle

54	d1j1va_	Alignment	not modelled	27.2	21	**Superfamily:**TrpR-like **Family:**Chromosomal replication initiation factor DnaA C-terminal domain IV
55	d1adra_	Alignment	not modelled	26.9	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
56	d1p4wa_	Alignment	not modelled	26.6	15	**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)
57	c2y31A_	Alignment	not modelled	26.6	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative repressor simreg2; **PDBTitle:** simocyclinone c4 bound form of tetr-like repressor simr
58	d2v0fa1	Alignment	not modelled	26.2	23	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
59	d2fq4a1	Alignment	not modelled	25.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
60	d1vi0a1	Alignment	not modelled	25.8	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
61	c2q0oA_	Alignment	not modelled	25.3	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar; **PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing
62	d1utxa_	Alignment	not modelled	25.0	7	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
63	d2g3ba1	Alignment	not modelled	25.0	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
64	c3fiwB_	Alignment	not modelled	24.8	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** structure of sco0253, a tetr-family transcriptional regulator from2 streptomyces coelicolor
65	c3r4kD_	Alignment	not modelled	24.6	13	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**transcriptional regulator, iclr family; **PDBTitle:** crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
66	d1nera_	Alignment	not modelled	24.2	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
67	c2id3A_	Alignment	not modelled	23.8	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of transcriptional regulator sco5951 from2 streptomyces coelicolor a3(2)
68	d1l3la1	Alignment	not modelled	23.7	13	**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)
69	c3omtA_	Alignment	not modelled	23.2	9	**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.
70	c3g7rB_	Alignment	not modelled	22.9	7	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of sco4454, a tetr-family transcriptional2 regulator from streptomyces coelicolor
71	d2fd5a1	Alignment	not modelled	22.7	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
72	c2o0yB_	Alignment	not modelled	22.4	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
73	c3b7hA_	Alignment	not modelled	22.0	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
74	d1stza1	Alignment	not modelled	21.7	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
75	d1l8qa1	Alignment	not modelled	21.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Chromosomal replication initiation factor DnaA C-terminal domain IV
76	d2o7ta1	Alignment	not modelled	20.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
77	d2id3a1	Alignment	not modelled	20.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
78	d1u5ta1	Alignment	not modelled	19.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
79	d1fsea_	Alignment	not modelled	19.5	9	**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)
						Fold:DNA/RNA-binding 3-helical bundle

80	d2gena1	Alignment	not modelled	19.2	8	**Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
81	d1joga_	Alignment	not modelled	19.1	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nucleotidyltransferase substrate binding subunit/domain **Family:**Family 1 bi-partite nucleotidyltransferase subunit
82	d2gfna1	Alignment	not modelled	19.1	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
83	d2i10a1	Alignment	not modelled	18.7	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
84	c2rnjA_	Alignment	not modelled	18.5	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
85	c1mkmA_	Alignment	not modelled	18.4	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**iclr transcriptional regulator; **PDBTitle:** crystal structure of the thermotoga maritima iclr
86	c3bs3A_	Alignment	not modelled	18.3	16	**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
87	c2zcxA_	Alignment	not modelled	18.0	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tetr-family transcriptional regulator; **PDBTitle:** crystal structure of tetr family transcriptional regulator2 sco7815
88	d1v7ba1	Alignment	not modelled	17.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
89	d1qtma2	Alignment	not modelled	17.7	21	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I
90	c3pvpA_	Alignment	not modelled	17.5	22	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
91	c2g7gA_	Alignment	not modelled	17.4	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rha04620, putative transcriptional regulator; **PDBTitle:** the crystal structure of the putative transcriptional regulator2 rha04620 from rhodococcus sp. rha1
92	c2ia2D_	Alignment	not modelled	17.2	8	**PDB header:**transcription **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
93	c1h0mD_	Alignment	not modelled	16.6	10	**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
94	c2g7lA_	Alignment	not modelled	15.7	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tetr-family transcriptional regulator; **PDBTitle:** crystal structure of putative transcription regulator sco7704 from2 streptomyces coelicor
95	c3tqnC_	Alignment	not modelled	15.6	31	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** structure of the transcriptional regulator of the gntr family, from2 coxiella burnetii.
96	d1t56a1	Alignment	not modelled	15.5	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
97	c4a4zA_	Alignment	not modelled	15.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**antiviral helicase ski2; **PDBTitle:** crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp
98	d1mkma1	Alignment	not modelled	15.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
99	c2wuiA_	Alignment	not modelled	14.9	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of mexz, a key repressor responsible for2 antibiotic resistance in pseudomonas aeruginosa.