Phyre2

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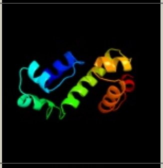
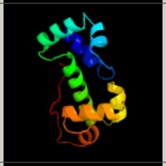
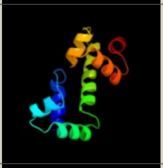
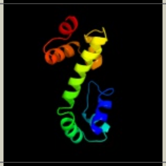
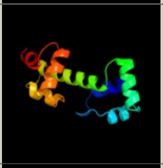
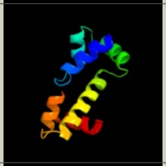
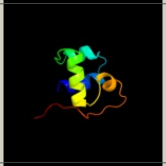
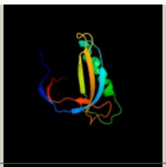
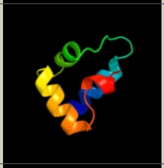
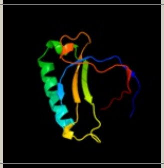
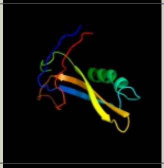
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1d5yD_	Alignment		100.0	29	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**rob transcription factor; **PDBTitle:** crystal structure of the e. coli rob transcription factor2 in complex with dna
2	c3gbgA_	Alignment		99.9	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tcp pilus virulence regulatory protein; **PDBTitle:** crystal structure of toxt from vibrio cholerae o395
3	c1bl0A_	Alignment		99.9	32	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (multiple antibiotic resistance protein); **PDBTitle:** multiple antibiotic resistance protein (mara)/dna complex
4	c3oouA_	Alignment		99.9	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2118 protein; **PDBTitle:** the structure of a protein with unkown function from listeria innocua
5	c3oioA_	Alignment		99.9	34	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (arac-type dna-binding domain- **PDBTitle:** crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum
6	c2k9sA_	Alignment		99.9	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arabinose operon regulatory protein; **PDBTitle:** solution structure of dna binding domain of e. coli arac
7	c3mklB_	Alignment		99.9	22	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator gadx; **PDBTitle:** crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
8	c3mn2B_	Alignment		99.9	29	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable arac family transcriptional regulator; **PDBTitle:** the crystal structure of a probable arac family transcriptional2 regulator from rhodopseudomonas palustris cga009
9	c3lsgD_	Alignment		99.8	20	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**two-component response regulator yesn; **PDBTitle:** the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
10	d1d5ya2	Alignment		99.5	47	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
11	d1bl0a2	Alignment		99.5	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator

12	d1d5ya3	Alignment		99.1	16	**Fold:**Probable bacterial effector-binding domain **Superfamily:**Probable bacterial effector-binding domain **Family:**Rob transcription factor, C-terminal domain
13	d1d5ya1	Alignment		99.1	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
14	d1bl0a1	Alignment		99.1	40	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
15	c1zgwA_	Alignment		98.9	17	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**ada polyprotein; **PDBTitle:** nmr structure of e. coli ada protein in complex with dna
16	d1jyha_	Alignment		98.6	11	**Fold:**Probable bacterial effector-binding domain **Superfamily:**Probable bacterial effector-binding domain **Family:**Gyrase inhibitory protein GyrI (SbmC, YeeB)
17	c3gk6A_	Alignment		98.5	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**integron cassette protein vch_cass2; **PDBTitle:** crystal structure from the mobile metagenome of vibrio cholerae.2 integron cassette protein vch_cass2.
18	c3lurB_	Alignment		98.2	10	**PDB header:**transcription activator **Chain:** B: **PDB Molecule:**putative bacterial transcription regulation protein; **PDBTitle:** crystal structure of putative bacterial transcription regulation2 protein (np_372959.1) from staphylococcus aureus mu50 at 1.81 a3 resolution
19	c2kcuA_	Alignment		97.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ctr107; **PDBTitle:** nmr solution structure of an uncharacterized protein from2 chlorobium tepidum. northeast structural genomics target3 ctr107
20	c3d6zA_	Alignment		95.7	9	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**multidrug-efflux transporter 1 regulator; **PDBTitle:** crystal structure of r275e mutant of bmrr bound to dna and rhodamine
21	d1r8ea2	Alignment	not modelled	95.5	15	**Fold:**Probable bacterial effector-binding domain **Superfamily:**Probable bacterial effector-binding domain **Family:**Multidrug-binding domain of transcription activator BmrR
22	c3iwfA_	Alignment	not modelled	95.1	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator rpir family; **PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
23	c3b49A_	Alignment	not modelled	95.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2189 protein; **PDBTitle:** crystal structure of an uncharacterized conserved protein from2 listeria innocua
24	c2gfnA_	Alignment	not modelled	95.0	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator pksa related protein; **PDBTitle:** crystal structure of hth-type transcriptional regulator pksa related2 protein from rhodococcus sp. rha1
25	d1jt6a1	Alignment	not modelled	93.7	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
26	d2id3a1	Alignment	not modelled	93.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
27	d2fbqa1	Alignment	not modelled	93.5	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
28	d2gfna1	Alignment	not modelled	93.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain

29	d2fq4a1	Alignment	not modelled	93.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
30	c3geuC_	Alignment	not modelled	93.2	10	**PDB header:**cell adhesion **Chain:** C: **PDB Molecule:**intercellular adhesion protein r; **PDBTitle:** crystal structure of icar from staphylococcus aureus, a member of the2 tetracycline repressor protein family
31	d1sgma1	Alignment	not modelled	93.2	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
32	d3c07a1	Alignment	not modelled	93.1	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
33	d2hyja1	Alignment	not modelled	93.1	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
34	d1t56a1	Alignment	not modelled	93.0	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
35	c1vi0B_	Alignment	not modelled	93.0	26	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator
36	c2nx4A_	Alignment	not modelled	92.9	20	**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.
37	d2g7sa1	Alignment	not modelled	92.9	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
38	c3bhqB_	Alignment	not modelled	92.9	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a putative tetr-family transcriptional regulator2 (mlr_4833) from mesorhizobium loti maff303099 at 1.54 a resolution
39	c3on4D_	Alignment	not modelled	92.7	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of tetr transcriptional regulator from legionella2 pneumophila
40	d2fx0a1	Alignment	not modelled	92.6	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
41	d1pb6a1	Alignment	not modelled	92.6	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
42	c3bcgA_	Alignment	not modelled	92.5	28	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator acrr; **PDBTitle:** conformational changes of the acrr regulator reveal a2 mechanism of induction
43	c2f07A_	Alignment	not modelled	92.4	34	**PDB header:**transcription **Chain:** A: **PDB Molecule:**yvdt; **PDBTitle:** crystal structure of yvdt from bacillus subtilis
44	c2rasB_	Alignment	not modelled	92.4	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of a putative tetr/acrr family transcriptional2 regulator (saro_0558) from novosphingobium aromaticivorans dsm at3 1.80 a resolution
45	d2i10a1	Alignment	not modelled	92.4	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
46	c3b81A_	Alignment	not modelled	92.4	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, acrr family; **PDBTitle:** crystal structure of predicted dna-binding transcriptional regulator2 of tetr/acrr family (np_350189.1) from clostridium acetobutylicum at3 2.10 a resolution
47	c3lwjA_	Alignment	not modelled	92.3	28	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of putative tetr-family transcriptional regulator2 (yp_752756.1) from syntrophomonas wolfei str. goettingen at 2.07 a3 resolution
48	c2o3fC_	Alignment	not modelled	92.3	13	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative hth-type transcriptional regulator ybbh; **PDBTitle:** structural genomics, the crystal structure of the n-2 terminal domain of the putative transcriptional regulator3 ybbh from bacillus subtilis subsp. subtilis str. 168.
49	c2fq4A_	Alignment	not modelled	92.3	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** the crystal structure of the transcriptional regulator (tetr family)2 from bacillus cereus
50	d1ui5a1	Alignment	not modelled	92.3	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
51	d2vkea1	Alignment	not modelled	92.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
52	d2o3fa1	Alignment	not modelled	92.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**RpiR-like
53	d1qpza1	Alignment	not modelled	92.2	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator

54	c1sgmA_	Alignment	not modelled	92.2	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator yxaf; **PDBTitle:** crystal structure of hypothetical protein yxaf
55	d1j5ya1	Alignment	not modelled	92.1	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
56	c1jumB_	Alignment	not modelled	92.0	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hypothetical transcriptional regulator in qaca **PDBTitle:** crystal structure of the multidrug binding transcriptional2 repressor qacr bound to the natural drug berberine
57	c3f1bA_	Alignment	not modelled	92.0	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tetr-like transcriptional regulator; **PDBTitle:** the crystal structure of a tetr-like transcriptional regulator from2 rhodococcus sp. rha1.
58	c2g3bB_	Alignment	not modelled	92.0	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of putative tetr-family transcriptional regulator2 from rhodococcus sp.
59	c3bniA_	Alignment	not modelled	92.0	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor
60	c2eh3A_	Alignment	not modelled	91.9	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of aq_1058, a transcriptional regulator (terr/acrr2 family) from aquifex aeolicus vf5
61	d2g3ba1	Alignment	not modelled	91.9	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
62	d2gena1	Alignment	not modelled	91.9	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
63	c2id3A_	Alignment	not modelled	91.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of transcriptional regulator sco5951 from2 streptomyces coelicolor a3(2)
64	d1rkta1	Alignment	not modelled	91.8	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
65	d2d6ya1	Alignment	not modelled	91.8	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
66	c3qbmA_	Alignment	not modelled	91.8	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tetr transcriptional regulator; **PDBTitle:** crystal structure of a tetr transcriptional regulator (caur_2221) from2 chloroflexus aurantiacus j-10-fl at 1.80 a resolution
67	c3ljlB_	Alignment	not modelled	91.7	24	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator luxt; **PDBTitle:** the crystal structure of the full-length transcriptional regulator2 luxt from vibrio parahaemolyticus rimd 2210633.
68	c2of7A_	Alignment	not modelled	91.7	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** structural genomics, the crystal structure of a tetr-family2 transcriptional regulator from streptomyces coelicolor a3
69	c3e7qB_	Alignment	not modelled	91.7	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** the crystal structure of the putative transcriptional regulator from2 pseudomonas aeruginosa pao1
70	c2pbxB_	Alignment	not modelled	91.7	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hemagglutinin/protease regulatory protein; **PDBTitle:** vibrio cholerae hapr
71	d2hsga1	Alignment	not modelled	91.6	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
72	d1v7ba1	Alignment	not modelled	91.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
73	c3anpD_	Alignment	not modelled	91.6	17	**PDB header:**transcription **Chain:** D: **PDB Molecule:**transcriptional repressor, tetr family; **PDBTitle:** crystal structure of thermus thermophilus fadr, a tetr familly2 transcriptional repressor, in complex with lauroyl-coa.
74	c3cwrA_	Alignment	not modelled	91.5	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of transcriptional regulator of tetr2 family (yp_425770.1) from rhodospirillum rubrum atcc 111703 at 1.50 a resolution
75	d2np5a1	Alignment	not modelled	91.5	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
76	c3cdlA_	Alignment	not modelled	91.4	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator aefr; **PDBTitle:** crystal structure of a tetr family transcriptional regulator from2 pseudomonas syringae pv. tomato str. dc3000
77	d2o7ta1	Alignment	not modelled	91.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
78	c2wuiA_	Alignment	not modelled	91.3	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of mexz, a key repressor responsible for2 antibiotic resistance in pseudomonas aeruginosa.

79	c3c07B_	Alignment	not modelled	91.3	25	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of a tetr family transcriptional regulator from2 streptomyces coelicolor a3(2)
80	c3ppbB_	Alignment	not modelled	91.3	24	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative tetr family transcription regulator; **PDBTitle:** crystal structure of a putative tetr family transcription regulator2 (shew_3104) from shewanella sp. pv-4 at 2.10 a resolution
81	c1ui6B_	Alignment	not modelled	91.3	14	**PDB header:**antibiotic **Chain:** B: **PDB Molecule:**a-factor receptor homolog; **PDBTitle:** crystal structure of gamma-butyrolactone receptor (arpa-like protein)
82	c2fbqA_	Alignment	not modelled	91.2	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** the crystal structure of transcriptional regulator pa3006
83	c2ibdB_	Alignment	not modelled	91.2	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**possible transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulatory protein2 rha5900
84	c3bruA_	Alignment	not modelled	91.2	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein, tetr family; **PDBTitle:** crystal structure of regulatory protein tetr from rhodobacter2 sphaeroides
85	c3bjbE_	Alignment	not modelled	91.2	13	**PDB header:**transcription regulator **Chain:** E: **PDB Molecule:**probable transcriptional regulator, tetr family protein; **PDBTitle:** crystal structure of a tetr transcriptional regulator from rhodococcus2 sp. rha1
86	c3dcfB_	Alignment	not modelled	91.1	24	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator of the tetr/acrr **PDBTitle:** crystal structure of transcriptional regulator of the2 tetr/acrr family (yp_290855.1) from thermobifida fusca yx-3 er1 at 2.50 a resolution
87	c3dewA_	Alignment	not modelled	91.1	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** the structure of a putative tetr family transcriptional regulator from2 geobacter sulfurreducens pca.
88	c3mvpA_	Alignment	not modelled	91.1	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tetr/acrr transcriptional regulator; **PDBTitle:** the crystal structure of a tetr/acrr transcriptional regulator from2 streptococcus mutans to 1.85a
89	c2hytA_	Alignment	not modelled	91.1	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tetr-family transcriptional regulator; **PDBTitle:** crystal structure of a tetr-family transcriptional regulator (eca1819)2 from pectobacterium atrosepticum at 1.64 a resolution
90	c3qkxB_	Alignment	not modelled	91.0	14	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**uncharacterized hth-type transcriptional regulator hi_0893; **PDBTitle:** crystal structure of a tetr-family transcriptional regulator (hi0893)2 from haemophilus influenzae rd at 2.35 a resolution
91	c3f0cA_	Alignment	not modelled	91.0	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of transcriptional regulator from cytophaga2 hutchinsonii atcc 33406
92	c2genA_	Alignment	not modelled	91.0	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** structural genomics, the crystal structure of a probable2 transcriptional regulator from pseudomonas aeruginosa pao1
93	c1rktA_	Alignment	not modelled	91.0	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein yfir; **PDBTitle:** crystal structure of yfir, a putative transcriptional regulator from2 bacillus subtilis
94	c2dg7A_	Alignment	not modelled	90.9	24	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
95	c3cjdB_	Alignment	not modelled	90.9	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of putative tetr transcriptional regulator2 (yp_510936.1) from jannaschia sp. ccs1 at 1.79 a resolution
96	c2zb9A_	Alignment	not modelled	90.8	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of tetr family transcription regulator2 sco0332
97	c3kjxD_	Alignment	not modelled	90.8	26	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from silicibacter pomeroyi
98	c2jk3A_	Alignment	not modelled	90.8	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hemolysin ii regulatory protein; **PDBTitle:** crystal structure of the hlyiir mutant protein with2 residues 169-186 substituted by gssgssg linker
99	d1vi0a1	Alignment	not modelled	90.8	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
100	c2raeA_	Alignment	not modelled	90.7	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, acrr family protein; **PDBTitle:** crystal structure of a tetr/acrr family transcriptional regulator from2 rhodococcus sp. rha1
101	d2vkva1	Alignment	not modelled	90.7	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
102	d2id6a1	Alignment	not modelled	90.7	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain

103	c3c2bA_	Alignment	not modelled	90.6	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of tetr transcriptional regulator from agrobacterium2 tumefaciens
104	c3he0A_	Alignment	not modelled	90.6	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** the structure of a putative transcriptional regulator tetr family2 protein from vibrio parahaemolyticus.
105	c2yvhA_	Alignment	not modelled	90.6	19	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of the operator-binding form of the multi-drug2 binding transcriptional repressor cgmr
106	d2oi8a1	Alignment	not modelled	90.6	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
107	c3eupA_	Alignment		90.4	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** the crystal structure of the transcriptional regulator, tetr family2 from cytophaga hutchinsonii
108	c3kkcB_	Alignment	not modelled	90.4	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**tetr family transcriptional regulator; **PDBTitle:** the crystal structure of tetr transcriptional regulator from2 streptococcus agalactiae 2603v
109	c2guhA_	Alignment	not modelled	90.3	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of the putative tetr-family transcriptional2 regulator from rhodococcus sp. rha1
110	d2bjca1	Alignment	not modelled	90.3	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
111	c2qwtA_	Alignment	not modelled	90.3	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of the tetr transcription regulatory2 protein from mycobacterium vanbaalenii
112	c2hyjA_	Alignment	not modelled	90.2	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** the crystal structure of a tetr-family transcriptional regulator from2 streptomyces coelicolor
113	d2fd5a1	Alignment	not modelled	90.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
114	c1bdhA_	Alignment	not modelled	90.2	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (purine repressor); **PDBTitle:** purine repressor mutant-hypoxanthine-palindromic operator2 complex
115	c3g7rB_	Alignment	not modelled	90.2	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of sco4454, a tetr-family transcriptional2 regulator from streptomyces coelicolor
116	c3iuvA_	Alignment	not modelled	90.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized tetr family protein; **PDBTitle:** the structure of a member of tetr family (sco1917) from2 streptomyces coelicolor a3
117	c2np5A_	Alignment	not modelled	90.2	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator (rha1_ro04179) from2 rhodococcus sp. rha1.
118	c3dpjB_	Alignment	not modelled	90.1	18	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**transcription regulator, tetr family; **PDBTitle:** the crystal structure of a tetr transcription regulator2 from silicibacter pomeroyi dss
119	c3s5rA_	Alignment	not modelled	90.0	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**transcriptional regulator tetr family; **PDBTitle:** crystal structure of a putative transcriptional regulator of the tetr2 family (syn_02108) from syntrophus aciditrophicus at 2.60 a3 resolution
120	d1t33a1	Alignment	not modelled	90.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain