Phyre2

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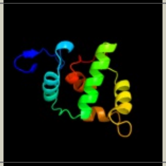
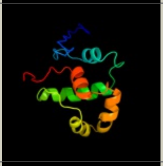
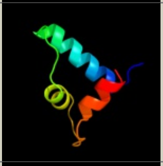
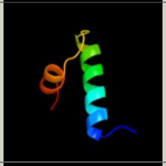
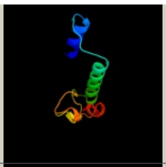
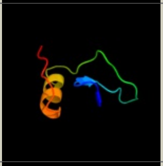
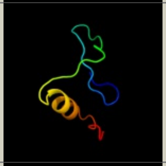
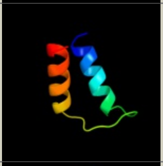
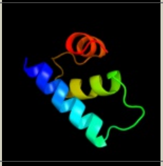
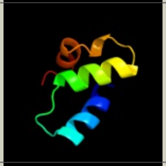
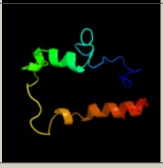
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yx3A_	Alignment		100.0	47	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dsrc; **PDBTitle:** nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
2	c2a5wC_	Alignment		100.0	40	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**sulfite reductase, desulfoviridin-type subunit gamma **PDBTitle:** crystal structure of the oxidized gamma-subunit of the dissimilatory2 sulfite reductase (dsrc) from archaeoglobus fulgidus
3	d2v4jc1	Alignment		100.0	38	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
4	d1ji8a_	Alignment		100.0	36	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
5	d1jhfa1	Alignment		96.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
6	c3k2zA_	Alignment		93.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lexa repressor; **PDBTitle:** crystal structure of a lexa protein from thermotoga maritima
7	d1stza1	Alignment		90.9	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
8	d2hkua1	Alignment		63.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
9	c2wgbB_	Alignment		59.2	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tetr family transcriptional repressor lfrr; **PDBTitle:** crystal structure of the tetr-like transcriptional2 regulator lfrr from mycobacterium smegmatis
10	d1pbya1	Alignment		57.3	28	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
11	d1jmxa1	Alignment		57.2	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2

12	d1fi4a2	Alignment		55.8	18	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Mevalonate 5-diphosphate decarboxylase
13	d1tf5a1	Alignment		50.3	27	**Fold:**Pre-protein crosslinking domain of SecA **Superfamily:**Pre-protein crosslinking domain of SecA **Family:**Pre-protein crosslinking domain of SecA
14	c3on4D_	Alignment		47.2	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of tetr transcriptional regulator from legionella2 pneumophila
15	d1nkta1	Alignment		47.0	17	**Fold:**Pre-protein crosslinking domain of SecA **Superfamily:**Pre-protein crosslinking domain of SecA **Family:**Pre-protein crosslinking domain of SecA
16	c2bpbB_	Alignment		46.2	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit b; **PDBTitle:** sulfite dehydrogenase from starkeya novella
17	d3c07a1	Alignment		44.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
18	c2g3bB_	Alignment		43.7	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of putative tetr-family transcriptional regulator2 from rhodococcus sp.
19	c2q24A_	Alignment		43.2	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr family transcriptional regulator; **PDBTitle:** crystal structure of tetr transcriptional regulator sco0520 from2 streptomyces coelicolor
20	d1bg6a1	Alignment		43.1	24	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**N-(1-D-carboxylethyl)-L-norvaline dehydrogenase
21	d1jt6a1	Alignment	not modelled	42.4	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
22	d2d6ya1	Alignment	not modelled	42.1	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
23	d2gfna1	Alignment	not modelled	40.6	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
24	d2fbqa1	Alignment	not modelled	40.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
25	d1vi0a1	Alignment	not modelled	39.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
26	d1pb6a1	Alignment	not modelled	39.3	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
27	c2nsaA_	Alignment	not modelled	38.2	27	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** structures of and interactions between domains of trigger factor from2 themotoga maritim
28	d2g7sa1	Alignment	not modelled	37.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
29	d1t33a1	Alignment	not modelled	37.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like

						Family: Tetracyclin repressor-like, N-terminal domain
30	d1t56a1	Alignment	not modelled	36.3	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
31	d2g3ba1	Alignment	not modelled	35.3	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
32	c2x9oA_	Alignment	not modelled	35.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**15,16- dihydrobiliverdin-ferredoxin oxidoreductase; **PDBTitle:** structure of 15, 16- dihydrobiliverdin:ferredoxin2 oxidoreductase (peba)
33	d2id6a1	Alignment	not modelled	34.1	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
34	d2ezia_	Alignment	not modelled	33.6	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
35	d2gena1	Alignment	not modelled	31.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
36	c3cdlA_	Alignment	not modelled	31.2	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
37	d2g7ga1	Alignment	not modelled	30.8	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
38	d2np5a1	Alignment	not modelled	30.7	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
39	d2vkva1	Alignment	not modelled	30.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
40	d1ui5a1	Alignment	not modelled	29.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
41	d2id3a1	Alignment	not modelled	29.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
42	d1sgma1	Alignment	not modelled	29.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
43	d1v7ba1	Alignment	not modelled	29.2	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
44	c3e7qB_	Alignment	not modelled	29.1	5	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** the crystal structure of the putative transcriptional regulator from2 pseudomonas aeruginosa pao1
45	d2fd5a1	Alignment	not modelled	28.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
46	d2fq4a1	Alignment	not modelled	28.8	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
47	c2rekA_	Alignment	not modelled	28.4	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of tetr-family transcriptional regulator
48	c2g7lA_	Alignment	not modelled	28.2	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tetr-family transcriptional regulator; **PDBTitle:** crystal structure of putative transcription regulator sco7704 from2 streptomyces coelicor
49	c2qwtA_	Alignment	not modelled	28.1	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of the tetr transcription regulatory2 protein from mycobacterium vanbaalenii
50	d2vkea1	Alignment	not modelled	27.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
51	d2ezha_	Alignment	not modelled	27.4	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
52	c2i10A_	Alignment	not modelled	26.8	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr transcriptional regulator; **PDBTitle:** putative tetr transcriptional regulator from rhodococcus sp. rha1
53	c3bjbE_	Alignment	not modelled	26.7	21	**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
54	c3he0A_	Alignment	not modelled	26.6	15	**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.
55	c1sgmA_	Alignment	not modelled	26.5	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator yxaf; **PDBTitle:** crystal structure of hypothetical protein yxaf

56	c2g7gA_	Alignment	not modelled	25.9	8	**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
57	c3lwjA_	Alignment	not modelled	25.2	18	**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
58	c1l0oC_	Alignment	not modelled	25.2	6	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**sigma factor; **PDBTitle:** crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
59	d1l0oc_	Alignment	not modelled	25.2	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
60	c3geuC_	Alignment	not modelled	25.1	15	**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
61	d2o7ta1	Alignment	not modelled	25.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
62	d1xpua3	Alignment	not modelled	24.9	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
63	c1t33B_	Alignment	not modelled	24.9	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative transcriptional repressor (tetr/acrr family); **PDBTitle:** structural genomics, the crystal structure of a putative2 transcriptional repressor (tetr/acrr family) from salmonella3 typhimurim lt2
64	d2oi8a1	Alignment	not modelled	24.6	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
65	c3gziA_	Alignment	not modelled	24.5	14	**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
66	d1ku2a1	Alignment	not modelled	24.3	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
67	c2vdaA_	Alignment	not modelled	24.1	24	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**translocase subunit seca; **PDBTitle:** solution structure of the seca-signal peptide complex
68	d2iu5a1	Alignment	not modelled	24.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
69	c3nnrA_	Alignment	not modelled	23.9	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of a tetr-family transcriptional regulator2 (maqu_3571) from marinobacter aquaeolei vt8 at 2.49 a resolution
70	c3jsjC_	Alignment	not modelled	23.9	21	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of a putative tetr-transcriptional regulator2 (sav143) from streptomyces avermitilis ma-4680 at 2.10 a resolution
71	c2hkuB_	Alignment	not modelled	23.4	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**a putative transcriptional regulator; **PDBTitle:** structural genomics, the crystal structure of a putative2 transcriptional regulator from rhodococcus sp. rha1
72	c2qtqB_	Alignment	not modelled	23.0	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of a predicted dna-binding transcriptional regulator2 (saro_1072) from novosphingobium aromaticivorans dsm at 1.85 a3 resolution
73	c2fbqA_	Alignment	not modelled	22.9	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** the crystal structure of transcriptional regulator pa3006
74	c3egqB_	Alignment	not modelled	22.8	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tetr family transcriptional regulator; **PDBTitle:** crystal structure of a tetr-family transcriptional regulator (af_1817)2 from archaeoglobus fulgidus at 2.55 a resolution
75	c1jumB_	Alignment	not modelled	22.8	18	**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
76	c2rasB_	Alignment	not modelled	22.3	17	**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
77	c3hq2A_	Alignment	not modelled	21.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bacillus subtilis m32 carboxypeptidase; **PDBTitle:** bsucp crystal structure
78	c1zkgB_	Alignment	not modelled	21.0	5	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of transcriptional regulator, tetr family (tm1030)2 from thermotoga maritima at 2.30 a resolution
						PDB header:gene regulation

79	c3npiB_	Alignment	not modelled	20.9	18	**Chain:** B: **PDB Molecule:**tetr family regulatory protein; **PDBTitle:** crystal structure of a tetr family regulatory protein (dip1788) from2 corynebacterium diphtheriae at 2.96 a resolution
80	c2dg8D_	Alignment	not modelled	20.8	13	**PDB header:**gene regulation **Chain:** D: **PDB Molecule:**putative tetr-family transcriptional regulatory protein; **PDBTitle:** crystal structure of the putative trasncriptional regulator sco75182 from streptomyces coelicolor a3(2)
81	c3bcgA_	Alignment	not modelled	20.6	15	**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
82	d2gxba1	Alignment	not modelled	20.5	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
83	c2id3A_	Alignment	not modelled	20.5	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of transcriptional regulator sco5951 from2 streptomyces coelicolor a3(2)
84	c3rh2A_	Alignment	not modelled	20.4	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hypothetical tetr-like transcriptional regulator; **PDBTitle:** crystal structure of a hypothetical tetr-like transcriptional2 regulator (sama_0099) from shewanella amazonensis sb2b at 2.42 a3 resolution
85	c3ccyA_	Alignment	not modelled	20.4	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of a tetr-family transcriptional regulator from2 bordetella parapertussis 12822
86	d1zk8a1	Alignment	not modelled	20.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
87	c2vn2B_	Alignment	not modelled	20.3	17	**PDB header:**replication **Chain:** B: **PDB Molecule:**chromosome replication initiation protein; **PDBTitle:** crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
88	c2fq4A_	Alignment	not modelled	20.0	14	**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
89	d1bl0a1	Alignment	not modelled	19.7	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
90	c1vi0B_	Alignment	not modelled	19.7	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator
91	c3dewA_	Alignment	not modelled	19.6	14	**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.
92	d1qgpa_	Alignment	not modelled	19.3	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
93	d1d5ya1	Alignment	not modelled	19.3	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
94	c2fd5A_	Alignment	not modelled	18.8	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** the crystal structure of a transcriptional regulator from pseudomonas2 aeruginosa pao1
95	c2pbxB_	Alignment	not modelled	18.7	5	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hemagglutinin/protease regulatory protein; **PDBTitle:** vibrio cholerae hapr
96	c1tygG_	Alignment	not modelled	18.4	27	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
97	c3fiwB_	Alignment	not modelled	18.4	26	**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
98	d2a0sa1	Alignment	not modelled	18.1	24	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**6-pyruvoyl tetrahydropterin synthase
99	c3bqyA_	Alignment	not modelled	18.0	26	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative tetr family transcriptional regulator; **PDBTitle:** crystal structure of a possible tetr family transcriptional regulator2 from streptomyces coelicolor a3(2).