Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	A1A4V9
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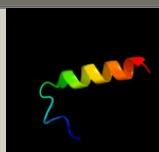
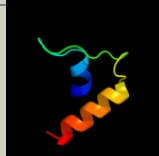
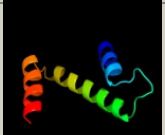
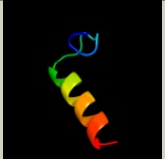
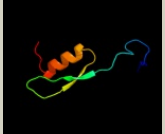
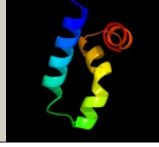
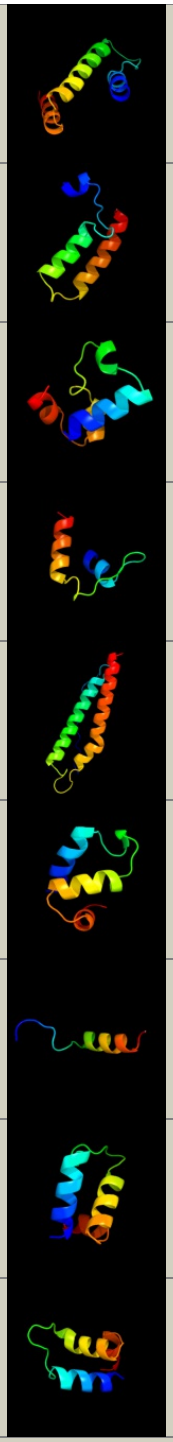
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gksa_	Alignment		60.1	22	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
2	c3cu4A_	Alignment		51.9	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** omcf, outer membrance cytochrome f from geobacter2 sulfurreducens
3	c2azqA_	Alignment		47.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 1,2-dioxygenase; **PDBTitle:** crystal structure of catechol 1,2-dioxygenase from pseudomonas arvilla2 c-1
4	c2zonG_	Alignment		42.4	26	**PDB header:**oxidoreductase/electron transport **Chain:** G: **PDB Molecule:**cytochrome c551; **PDBTitle:** crystal structure of electron transfer complex of nitrite2 reductase with cytochrome c
5	d2np5a2	Alignment		31.6	13	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
6	d1a9xa1	Alignment		23.9	17	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
7	d1xjca_	Alignment		23.6	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
8	c2is9A_	Alignment		22.6	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**defective in cullin neddylation protein 1; **PDBTitle:** structure of yeast dcn-1
9	d1f2ri_	Alignment		22.4	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**CAD domain
10	c3tbiB_	Alignment		21.2	28	**PDB header:**transcription **Chain:** B: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** crystal structure of t4 gp33 bound to e. coli rnap beta-flap domain
11	d2np5a1	Alignment		20.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain

12	d1dmha_	Alignment		16.5	14	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
13	d1w53a_	Alignment		15.3	11	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Phosphoserine phosphatase RsbU, N-terminal domain
14	d1ui5a1	Alignment		15.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
15	d1wvec1	Alignment		15.2	17	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
16	d1lb3a_	Alignment		14.0	13	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
17	c1vi0B_	Alignment		12.7	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator
18	d1qksa1	Alignment		12.5	17	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
19	d2d6ya1	Alignment		11.7	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
20	d1vi0a1	Alignment		11.6	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
21	d3c07a1	Alignment	not modelled	11.5	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
22	c2zxyA_	Alignment	not modelled	11.4	27	**PDB header:**oxygen binding, transport protein **Chain:** A: **PDB Molecule:**cytochrome c552; **PDBTitle:** crystal structure of cytochrome c555 from aquifex aeolicus
23	d2g3ba1	Alignment	not modelled	11.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
24	d1puga_	Alignment	not modelled	11.1	22	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
25	c2bpbB_	Alignment	not modelled	10.9	38	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit b; **PDBTitle:** sulfite dehydrogenase from starkeya novella
26	c3o60A_	Alignment	not modelled	10.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin0861 protein; **PDBTitle:** the crystal structure of lin0861 from listeria innocua to 2.8a
27	c2q24A_	Alignment	not modelled	10.7	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr family transcriptional regulator; **PDBTitle:** crystal structure of tetr transcriptional regulator sco0520 from2 streptomyces coelicolor
28	d2oi8a1	Alignment	not modelled	10.5	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain

29	d2id3a1	Alignment	not modelled	10.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
30	c3cqdB_	Alignment	not modelled	10.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructokinase isozyme 2; **PDBTitle:** structure of the tetrameric inhibited form of2 phosphofructokinase-2 from escherichia coli
31	c3bq3A_	Alignment	not modelled	10.0	22	**PDB header:**cell cycle, ligase **Chain:** A: **PDB Molecule:**defective in cullin neddylation protein 1; **PDBTitle:** crystal structure of s. cerevisiae dcn1
32	d2fq4a1	Alignment	not modelled	9.9	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
33	c1jn5B_	Alignment	not modelled	9.7	25	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tap; **PDBTitle:** structural basis for the recognition of a nucleoporin fg-2 repeat by the ntf2-like domain of tap-p15 mrna export3 factor
34	d1jt6a1	Alignment	not modelled	9.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
35	d2id6a1	Alignment	not modelled	9.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
36	c1zdbA_	Alignment	not modelled	9.6	21	**PDB header:**igg binding domain **Chain:** A: **PDB Molecule:**mini protein a domain, z38; **PDBTitle:** phage-selected mini protein a domain, z38, nmr, minimized2 mean structure
37	d2fbqa1	Alignment	not modelled	9.5	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
38	d2iu5a1	Alignment	not modelled	9.3	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
39	c3f1bA_	Alignment	not modelled	9.2	8	**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.
40	c2kj8A_	Alignment	not modelled	9.0	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative prophage cps-53 integrase; **PDBTitle:** nmr structure of fragment 87-196 from the putative phage2 integrase ints of e. coli: northeast structural genomics3 consortium target er652a, psi-2
41	c2eh3A_	Alignment	not modelled	8.9	19	**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
42	d2hyja1	Alignment	not modelled	8.7	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
43	c2dl1A_	Alignment	not modelled	8.6	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**spartin; **PDBTitle:** solution structure of the mit domain from human spartin
44	c3fiwB_	Alignment	not modelled	8.4	14	**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
45	c2g7sA_	Alignment	not modelled	8.4	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** the crystal structure of transcriptional regulator, tetr family, from2 agrobacterium tumefaciens
46	c2nx4A_	Alignment	not modelled	8.3	8	**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.
47	c2jk3A_	Alignment	not modelled	8.3	10	**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
48	c2d0sA_	Alignment	not modelled	8.1	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus
49	d1ls9a_	Alignment	not modelled	8.1	26	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
50	c2gfnA_	Alignment	not modelled	8.0	5	**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
51	d1z0xa2	Alignment	not modelled	8.0	32	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
52	d2ceia1	Alignment	not modelled	8.0	16	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
53	d1jkgb_	Alignment	not modelled	7.9	25	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**NTF2-like
54	c2rasB_	Alignment	not modelled	7.9	13	**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
55	d1yrnb_	Alignment	not modelled	7.9	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
56	c2wjyA_	Alignment	not modelled	7.7	41	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of nonsense transcripts 1; **PDBTitle:** crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 orthorhombic form
57	d1cora_	Alignment	not modelled	7.4	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
58	c2o7tA_	Alignment	not modelled	7.3	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a tetr family transcriptional regulator2 (ncgl1578, cgl1640) from corynebacterium glutamicum at 2.10 a3 resolution
59	c3f0cA_	Alignment	not modelled	7.3	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of transcriptional regulator from cytophaga2 hutchinsonii atcc 33406
60	c3anpD_	Alignment	not modelled	7.3	13	**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.
61	c3qbmA_	Alignment	not modelled	7.0	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
62	c1jumB_	Alignment	not modelled	6.9	12	**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
63	c3m66A_	Alignment	not modelled	6.9	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mterf domain-containing protein 1, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial transcription termination2 factor 3
64	c2be6F_	Alignment	not modelled	6.8	38	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**voltage-dependent l-type calcium channel alpha-1c subunit; **PDBTitle:** 2.0 a crystal structure of the cav1.2 iq domain-ca/cam complex
65	c2dg8D_	Alignment	not modelled	6.8	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)
66	c2dg7A_	Alignment	not modelled	6.8	18	**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)
67	d2vkea1	Alignment	not modelled	6.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
68	c3kkcB_	Alignment	not modelled	6.7	18	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**tetr family transcriptional regulator; **PDBTitle:** the crystal structure of tetr transcriptional regulator from2 streptococcus agalactiae 2603v
69	c2jonA_	Alignment	not modelled	6.6	32	**PDB header:**allergen **Chain:** A: **PDB Molecule:**beta-1,3-glucanase; **PDBTitle:** solution structure of the c-terminal domain ole e 9
70	c2uxoB_	Alignment	not modelled	6.6	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator ttgr; **PDBTitle:** ttgr in complex with tetracycline
71	d2vkva1	Alignment	not modelled	6.5	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
72	d1zk8a1	Alignment	not modelled	6.4	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
73	c3n8uB_	Alignment	not modelled	6.4	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**imelysin peptidase; **PDBTitle:** crystal structure of an imelysin peptidase (bacova_03801) from2 bacteroides ovatus at 1.44 a resolution
74	c3iuvA_	Alignment	not modelled	6.4	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
75	d2fd5a1	Alignment	not modelled	6.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
76	d1pbya1	Alignment	not modelled	6.3	19	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
77	d2i10a1	Alignment	not modelled	6.3	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
78	d1jmxa1	Alignment	not modelled	6.3	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
						PDB header:dna binding protein

79	c3g56A_	Alignment	not modelled	6.2	18	**Chain:** A: **PDB Molecule:**regulator of macrolide 2'-phosphotransferase i; **PDBTitle:** structure of the macrolide biosensor protein, mphr(a)
80	d1v7ba1	Alignment	not modelled	6.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
81	c3hjlA_	Alignment	not modelled	6.2	14	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**flagellar motor switch protein flig; **PDBTitle:** the structure of full-length flig from aquifex aeolicus
82	c3cjdB_	Alignment	not modelled	6.2	20	**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
83	c3qkxB_	Alignment	not modelled	6.1	15	**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
84	d1rkta1	Alignment	not modelled	6.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
85	c2i10A_	Alignment	not modelled	5.9	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr transcriptional regulator; **PDBTitle:** putative tetr transcriptional regulator from rhodococcus sp. rha1
86	c2xtsD_	Alignment	not modelled	5.8	14	**PDB header:**oxidoreductase/electron transport **Chain:** D: **PDB Molecule:**cytochrome; **PDBTitle:** crystal structure of the sulfane dehydrogenase soxcd from paracoccus2 pantotrophus
87	d351ca_	Alignment	not modelled	5.8	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
88	c2xzlA_	Alignment	not modelled	5.8	37	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent helicase nam7; **PDBTitle:** upf1-rna complex
89	c3b81A_	Alignment	not modelled	5.8	8	**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
90	c2np5A_	Alignment	not modelled	5.7	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator (rha1_ro04179) from2 rhodococcus sp. rha1.
91	c3rd3B_	Alignment	not modelled	5.6	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** structure of pseudomonas aeruginosa transcriptional regulator pa2196
92	d2o7ta1	Alignment	not modelled	5.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
93	d2fx0a1	Alignment	not modelled	5.5	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
94	d1fi3a_	Alignment	not modelled	5.5	27	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
95	c2of7A_	Alignment	not modelled	5.5	18	**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
96	d1gdva_	Alignment	not modelled	5.4	16	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
97	c2x43S_	Alignment	not modelled	5.4	15	**PDB header:**membrane protein **Chain:** S: **PDB Molecule:**sherp; **PDBTitle:** structural basis of molecular recognition by sherp at membrane2 surfaces
98	d2g7la1	Alignment	not modelled	5.3	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
99	c3dpjB_	Alignment	not modelled	5.3	13	**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