Phyre^2

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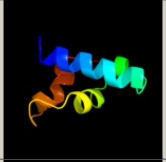
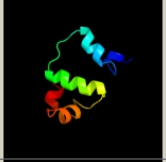
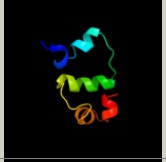
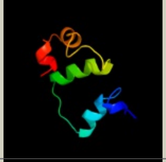
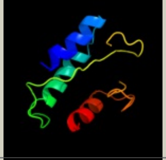
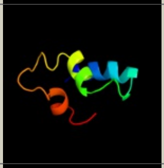
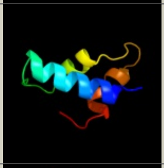
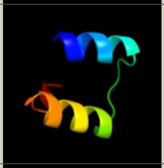
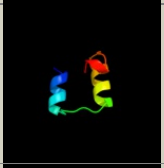
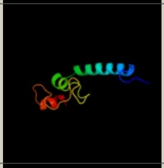
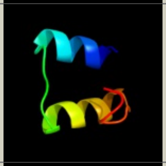
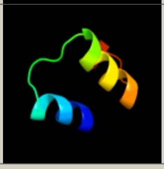
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fug21	Alignment		100.0	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**NQO2-like
2	c2auvA_	Alignment		99.9	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**potential nad-reducing hydrogenase subunit; **PDBTitle:** solution structure of hndac : a thioredoxin-like [2fe-2s]2 ferredoxin involved in the nadp-reducing hydrogenase3 complex
3	d1f37b_	Alignment		99.6	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioredoxin-like 2Fe-2S ferredoxin
4	d1m2da_	Alignment		99.6	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioredoxin-like 2Fe-2S ferredoxin
5	c2q24A_	Alignment		80.9	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr family transcriptional regulator; **PDBTitle:** crystal structure of tetr transcriptional regulator sco0520 from2 streptomyces coelicolor
6	c3iuvA_	Alignment		80.9	20	**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
7	c3m6zA_	Alignment		79.8	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase v; **PDBTitle:** crystal structure of an n-terminal 44 kda fragment of topoisomerase v2 in the presence of guanidium hydrochloride
8	d2csba5	Alignment		76.2	27	**Fold:**Topoisomerase V catalytic domain-like **Superfamily:**Topoisomerase V catalytic domain-like **Family:**Topoisomerase V catalytic domain-like
9	c2csdB_	Alignment		71.9	27	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**topoisomerase v; **PDBTitle:** crystal structure of topoisomerase v (61 kda fragment)
10	d1aopa4	Alignment		70.8	16	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
11	d1t33a1	Alignment		69.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain

12	c3jsjC_	Alignment		69.4	19	**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
13	c2qwtA_	Alignment		65.8	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of the tetr transcription regulatory2 protein from mycobacterium vanbaalenii
14	c2dg8D_	Alignment		65.1	17	**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)
15	c2rekA_	Alignment		64.9	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of tetr-family transcriptional regulator
16	d1p7ia_	Alignment		62.0	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
17	d1au7a1	Alignment		61.7	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
18	d1smyf2	Alignment		61.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
19	d2craa1	Alignment		61.0	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
20	d1nk3p_	Alignment		60.3	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
21	c2xsdC_	Alignment	not modelled	58.4	18	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**pou domain, class 3, transcription factor 1; **PDBTitle:** crystal structure of the dimeric oct-6 (pou3f1) pou domain2 bound to palindromic more dna
22	c2dmsA_	Alignment	not modelled	58.0	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein otx2; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein otx2
23	d1jhfa1	Alignment	not modelled	57.2	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
24	d1r7ha_	Alignment	not modelled	57.2	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
25	c2da2A_	Alignment	not modelled	57.0	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the second homeobox domain of at-2 binding transcription factor 1 (atbf1)
26	d1du0a_	Alignment	not modelled	56.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
27	c3a01A_	Alignment	not modelled	56.4	15	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeodomain-containing protein; **PDBTitle:** crystal structure of aristaless and clawless homeodomains bound to dna
28	c2da1A_	Alignment	not modelled	56.0	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein;

						PDBTitle: solution structure of the first homeobox domain of at-2 binding transcription factor 1 (atbf1)
29	d1fjla_	Alignment	not modelled	55.6	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
30	c3ccyA_	Alignment	not modelled	55.6	23	**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
31	c3nauA_	Alignment	not modelled	55.4	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 2; **PDBTitle:** crystal structure of zhx2 hd2 (zinc-fingers and homeoboxes protein 2,2 homeodomain 2)
32	d1jt6a1	Alignment	not modelled	55.0	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
33	c3ic4A_	Alignment	not modelled	55.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin (grx-1); **PDBTitle:** the crystal structure of the glutaredoxin(grx-1) from archaeoglobus2 fulgidus
34	d1fjlb_	Alignment	not modelled	54.5	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
35	d2e1oa1	Alignment	not modelled	54.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
36	d2cuea1	Alignment	not modelled	54.1	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
37	d1zq3p1	Alignment	not modelled	54.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
38	c3a03A_	Alignment	not modelled	53.5	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**t-cell leukemia homeobox protein 2; **PDBTitle:** crystal structure of hox11l1 homeodomain
39	d1gt0c1	Alignment	not modelled	53.3	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
40	c2dmuA_	Alignment	not modelled	52.8	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein goosecoid; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein goosecoid
41	d2hddb_	Alignment	not modelled	52.3	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
42	c3anpD_	Alignment	not modelled	52.2	21	**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.
43	d1dg9a_	Alignment	not modelled	52.1	13	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
44	c2ibdB_	Alignment	not modelled	51.9	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**possible transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulatory protein2 rha5900
45	d1bw5a_	Alignment	not modelled	51.8	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
46	d1ocpa_	Alignment	not modelled	51.2	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
47	c2dg7A_	Alignment	not modelled	51.1	11	**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)
48	d1ig7a_	Alignment	not modelled	50.8	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
49	d1ahdp_	Alignment	not modelled	50.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
50	d1sana_	Alignment	not modelled	50.3	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
51	d2fd5a1	Alignment	not modelled	50.1	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
52	d1jgga_	Alignment	not modelled	49.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
53	d1b8ia_	Alignment	not modelled	49.6	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
54	d1octc1	Alignment	not modelled	49.5	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
						PDB header:transcription regulator

55	c3fiwB_	Alignment	not modelled	49.4	16	**Chain:** B: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** structure of sco0253, a tetr-family transcriptional regulator from2 streptomyces coelicolor
56	c3gziA_	Alignment	not modelled	49.3	19	**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
57	c2wgbB_	Alignment	not modelled	49.2	23	**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
58	d1j5ya1	Alignment	not modelled	49.0	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
59	d1le8a_	Alignment	not modelled	49.0	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
60	d1hdpa_	Alignment	not modelled	48.7	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
61	d2ecba1	Alignment	not modelled	48.1	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
62	d1b72a_	Alignment	not modelled	47.9	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
63	c2hkuB_	Alignment	not modelled	47.8	17	**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
64	d1zk8a1	Alignment	not modelled	47.4	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
65	c1sgmA_	Alignment	not modelled	47.4	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator yxaf; **PDBTitle:** crystal structure of hypothetical protein yxaf
66	d1p7jb_	Alignment	not modelled	47.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
67	c3he0A_	Alignment	not modelled	47.3	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of a putative transcriptional regulator tetr family2 protein from vibrio parahaemolyticus.
68	d1z6ma1	Alignment	not modelled	47.3	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
69	c2k9mA_	Alignment	not modelled	47.1	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** the structure of the core binding domain of sigma54
70	c2g3bB_	Alignment	not modelled	46.9	26	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of putative tetr-family transcriptional regulator2 from rhodococcus sp.
71	c2gi4A_	Alignment	not modelled	46.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible phosphotyrosine protein phosphatase; **PDBTitle:** solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.
72	d1ztra1	Alignment	not modelled	46.5	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
73	c2vi6F_	Alignment	not modelled	46.3	15	**PDB header:**transcription **Chain:** F: **PDB Molecule:**homeobox protein nanog; **PDBTitle:** crystal structure of the nanog homeodomain
74	d1vnda_	Alignment	not modelled	45.9	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
75	c2yvhA_	Alignment	not modelled	45.3	7	**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
76	d2v4jb3	Alignment	not modelled	45.2	16	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
77	c3bniA_	Alignment	not modelled	45.1	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor
78	d1ftza_	Alignment	not modelled	44.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
79	c2eh3A_	Alignment	not modelled	44.6	16	**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
80	d2id3a1	Alignment	not modelled	43.9	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain

81	d1mh3a1	Alignment	not modelled	43.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
82	c1or7A_	Alignment	not modelled	43.7	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma-e factor; **PDBTitle:** crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
83	c2akjA_	Alignment	not modelled	43.6	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nitrite reductase, chloroplast; **PDBTitle:** structure of spinach nitrite reductase
84	c2nx4A_	Alignment	not modelled	43.4	19	**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.
85	c3narA_	Alignment	not modelled	43.2	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 1; **PDBTitle:** crystal structure of zhx1 hd4 (zinc-fingers and homeoboxes protein 1,2 homeodomain 4)
86	c2da5A_	Alignment	not modelled	43.1	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 3; **PDBTitle:** solution structure of the second homeobox domain of zinc2 fingers and homeoboxes protein 3 (triple homeobox 13 protein)
87	c3f1bA_	Alignment	not modelled	42.9	21	**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.
88	c1au7B_	Alignment	not modelled	42.8	18	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**protein pit-1; **PDBTitle:** pit-1 mutant/dna complex
89	d1pufa_	Alignment	not modelled	42.5	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
90	d9anta_	Alignment	not modelled	42.3	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
91	c2qkoA_	Alignment	not modelled	42.2	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, tetr family protein; **PDBTitle:** crystal structure of transcriptional regulator rha06399 from2 rhodococcus sp. rha1
92	c2da7A_	Alignment	not modelled	42.2	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc finger homeobox protein 1b; **PDBTitle:** solution structure of the homeobox domain of zinc finger2 homeobox protein 1b (smad interacting protein 1)
93	d1e3oc1	Alignment	not modelled	42.0	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
94	c2of7A_	Alignment	not modelled	41.9	21	**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
95	c1vi0B_	Alignment	not modelled	41.9	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator
96	c3ppbB_	Alignment	not modelled	41.6	17	**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
97	c2raeA_	Alignment	not modelled	41.3	12	**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
98	d1ftta_	Alignment	not modelled	41.2	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
99	d1rr7a_	Alignment	not modelled	41.1	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Middle operon regulator, Mor
100	c1rr7A_	Alignment	not modelled	41.1	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**middle operon regulator; **PDBTitle:** crystal structure of the middle operon regulator protein of2 bacteriophage mu
101	c2fbqA_	Alignment	not modelled	41.0	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** the crystal structure of transcriptional regulator pa3006
102	d1ui5a1	Alignment	not modelled	40.8	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
103	c2g7gA_	Alignment	not modelled	40.8	22	**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
104	c2l9rA_	Alignment	not modelled	40.5	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein nkx-3.1; **PDBTitle:** solution nmr structure of homeobox domain of homeobox protein nkx-3.12 from homo sapiens, northeast structural genomics consortium target3 hr6470a
						PDB header:transcription

105	c2zcxA_	Alignment	not modelled	40.5	19	**Chain:** A: **PDB Molecule:**tetr-family transcriptional regulator; **PDBTitle:** crystal structure of tetr family transcriptional regulator2 sco7815
106	d1f43a_	Alignment	not modelled	40.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
107	d3c7bb3	Alignment	not modelled	40.3	18	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
108	d2ecca1	Alignment	not modelled	40.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
109	c3ni7A_	Alignment	not modelled	40.1	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**bacterial regulatory proteins, tetr family; **PDBTitle:** crystal structure of the tetr transcriptional regulator from2 nitrosomonas europaea atcc 19718
110	c2k9lA_	Alignment	not modelled	40.0	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** structure of the core binding domain of sigma54
111	c3bjbE_	Alignment	not modelled	40.0	19	**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
112	c3hugA_	Alignment	not modelled	39.9	19	**PDB header:**transcription/membrane protein **Chain:** A: **PDB Molecule:**rna polymerase sigma factor; **PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
113	c2dmtA_	Alignment	not modelled	39.7	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein barh-like 1; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein barh-like 1
114	c2djnA_	Alignment	not modelled	39.4	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein dlx-5; **PDBTitle:** the solution structure of the homeobox domain of human2 homeobox protein dlx-5
115	c2kgrA_	Alignment	not modelled	39.3	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intersectin-1; **PDBTitle:** solution structure of protein itsn1 from homo sapiens.2 northeast structural genomics consortium target hr5524a
116	c3kkcB_	Alignment	not modelled	39.1	16	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**tetr family transcriptional regulator; **PDBTitle:** the crystal structure of tetr transcriptional regulator from2 streptococcus agalactiae 2603v
117	d1t56a1	Alignment	not modelled	38.7	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
118	c2i10A_	Alignment	not modelled	38.7	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr transcriptional regulator; **PDBTitle:** putative tetr transcriptional regulator from rhodococcus sp. rha1
119	c1u2pA_	Alignment	not modelled	38.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine- **PDBTitle:** crystal structure of mycobacterium tuberculosis low2 molecular protein tyrosine phosphatase (mptpa) at 1.9a3 resolution
120	c2dn0A_	Alignment	not modelled	38.0	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 3; **PDBTitle:** solution structure of the second homeobox domain of human2 zinc fingers and homeoboxes protein 3