Phyre2

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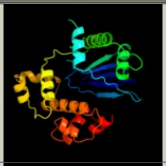
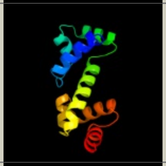
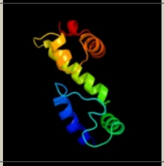
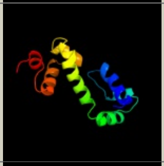
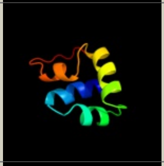
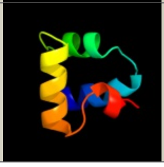
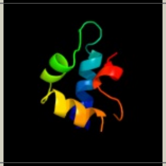
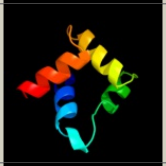
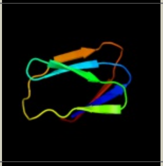
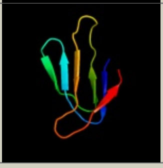
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gbgA_	Alignment		100.0	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tcp pilus virulence regulatory protein; **PDBTitle:** crystal structure of toxt from vibrio cholerae o395
2	c3oouA_	Alignment		99.9	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2118 protein; **PDBTitle:** the structure of a protein with unkown function from listeria innocua
3	c3mklB_	Alignment		99.9	38	**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
4	c1d5yD_	Alignment		99.9	17	**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
5	c3oioA_	Alignment		99.9	22	**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	c1bl0A_	Alignment		99.9	13	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (multiple antibiotic resistance protein); **PDBTitle:** multiple antibiotic resistance protein (mara)/dna complex
7	c3mn2B_	Alignment		99.9	21	**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
8	c2k9sA_	Alignment		99.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arabinose operon regulatory protein; **PDBTitle:** solution structure of dna binding domain of e. coli arac
9	c3lsgD_	Alignment		99.7	28	**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		99.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
11	d1bl0a2	Alignment		99.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator

12	d1d5ya1	Alignment		98.7	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
13	d1bl0a1	Alignment		98.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
14	c1zgwA_	Alignment		98.5	15	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**ada polyprotein; **PDBTitle:** nmr structure of e. coli ada protein in complex with dna
15	d2arca_	Alignment		97.9	12	**Fold:**Double-stranded beta-helix **Superfamily:**Regulatory protein AraC **Family:**Regulatory protein AraC
16	c3fjsC_	Alignment		96.3	4	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**uncharacterized protein with rmlc-like cupin fold; **PDBTitle:** crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
17	c3ibmB_	Alignment		96.1	4	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of cupin 2 domain-containing protein hhal_0468 from2 halorhodospira halophila
18	d1y9qa2	Alignment		96.0	4	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
19	c3kgzA_	Alignment		95.9	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2 conserved barrel domain protein; **PDBTitle:** crystal structure of a cupin 2 conserved barrel domain protein from2 rhodopseudomonas palustris
20	c3cewA_	Alignment		95.9	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized cupin protein; **PDBTitle:** crystal structure of a cupin protein (bf4112) from bacteroides2 fragilis. northeast structural genomics consortium target bfr205
21	c2vpvA_	Alignment	not modelled	95.8	6	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p
22	c3h7yA_	Alignment	not modelled	95.8	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**bacilysin biosynthesis protein bacb; **PDBTitle:** crystal structure of bacb, an enzyme involved in bacilysin synthesis,2 in tetragonal form
23	c3jzvA_	Alignment	not modelled	95.8	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein rru_a2000; **PDBTitle:** crystal structure of rru_a2000 from rhodospirillum rubrum: a cupin-22 domain.
24	d1y3ta1	Alignment	not modelled	95.7	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
25	c2pfwB_	Alignment	not modelled	95.6	12	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of a rmlc-like cupin (sfri_3105) from shewanella2 frigidimarina ncimb 400 at 1.90 a resolution
26	c2opkC_	Alignment	not modelled	95.5	11	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
27	c2gu9B_	Alignment	not modelled	95.5	8	**PDB header:**immune system **Chain:** B: **PDB Molecule:**tetracenomycin polyketide synthesis protein; **PDBTitle:** crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
						PDB header:oxidoreductase

28	c2d40C_	Alignment	not modelled	95.4	11	**Chain:** C: **PDB Molecule:**putative gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure of z3393 from escherichia coli o157:h7
29	c3lwcA_	Alignment	not modelled	95.4	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of structural genomics, unknown function2 (yp_766765.1) from rhizobium leguminosarum bv. viciae 3841 at 1.40 a3 resolution
30	d1sfna_	Alignment	not modelled	95.4	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
31	c3iwfA_	Alignment	not modelled	95.4	13	**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
32	d1yhfa1	Alignment	not modelled	95.3	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
33	d1o4ta_	Alignment	not modelled	95.3	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
34	c2o8qA_	Alignment	not modelled	95.3	6	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a protein with a cupin-like fold and unknown2 function (bxe_c0505) from burkholderia xenovorans lb400 at 1.55 a3 resolution
35	d1sq4a_	Alignment	not modelled	95.2	4	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
36	d2d40a1	Alignment	not modelled	95.2	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
37	d3bu7a1	Alignment	not modelled	95.2	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
38	c3bu7A_	Alignment	not modelled	95.2	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure and biochemical characterization of gdosp,2 a gentisate 1,2-dioxygenase from silicibacter pomeroyi
39	d1v70a_	Alignment	not modelled	95.1	2	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
40	d1vj2a_	Alignment	not modelled	95.0	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
41	c2ozjB_	Alignment	not modelled	94.9	8	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel; **PDBTitle:** crystal structure of a cupin superfamily protein (dsy2733) from2 desulfitobacterium hafniense dcb-2 at 1.60 a resolution
42	d2phda1	Alignment	not modelled	94.8	7	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
43	c3d82A_	Alignment	not modelled	94.6	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of a cupin-2 domain containing protein (sfri_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution
44	c2i45C_	Alignment	not modelled	94.3	10	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
45	c3l2hD_	Alignment	not modelled	94.3	8	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative sugar phosphate isomerase; **PDBTitle:** crystal structure of putative sugar phosphate isomerase (afe_0303)2 from acidithiobacillus ferrooxidans atcc 23270 at 1.85 a resolution
46	d1rc6a_	Alignment	not modelled	94.3	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
47	c2q30C_	Alignment	not modelled	94.3	6	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a rmlc-like cupin protein (dde_2303) from2 desulfovibrio desulfuricans subsp. at 1.94 a resolution
48	d2b8ma1	Alignment	not modelled	94.1	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**MJ0764-like
49	d1sefa_	Alignment	not modelled	94.0	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
50	c1sefA_	Alignment	not modelled	94.0	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
51	c3i7dB_	Alignment	not modelled	93.6	8	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**sugar phosphate isomerase; **PDBTitle:** crystal structure of sugar phosphate isomerase from a cupin2 superfamily spo2919 from silicibacter pomeroyi (yp_168127.1) from3 silicibacter pomeroyi dss-3 at 2.30 a resolution
52	d2bnma2	Alignment	not modelled	93.5	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like

53	d1lr5a_	Alignment	not modelled	93.5	2	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
54	c3ht2A_	Alignment	not modelled	93.4	6	**PDB header:**lyase **Chain:** A: **PDB Molecule:**remf protein; **PDBTitle:** zinc containing polyketide cyclase remf from streptomyces2 resistomycificus
55	d1efaa1	Alignment	not modelled	93.3	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
56	d1yfua1	Alignment	not modelled	93.3	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
57	c3kjxD_	Alignment	not modelled	93.1	24	**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
58	d2bjca1	Alignment	not modelled	93.1	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
59	c2o3fC_	Alignment	not modelled	93.1	12	**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.
60	d2o3fa1	Alignment	not modelled	93.1	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**RpiR-like
61	c1bdhA_	Alignment	not modelled	93.0	16	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (purine repressor); **PDBTitle:** purine repressor mutant-hypoxanthine-palindromic operator2 complex
62	c3h8uA_	Alignment	not modelled	93.0	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein with double-stranded **PDBTitle:** crystal structure of uncharacterized conserved protein with double-2 stranded beta-helix domain (yp_001338853.1) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.80 a resolution
63	d1juha_	Alignment	not modelled	92.9	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
64	c3rnsA_	Alignment	not modelled	92.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2 conserved barrel domain protein; **PDBTitle:** cupin 2 conserved barrel domain protein from leptotrichia buccalis
65	c3h5tA_	Alignment	not modelled	92.7	29	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from corynebacterium glutamicum
66	d1qpza1	Alignment	not modelled	92.3	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
67	c2oa2A_	Alignment	not modelled	92.2	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh2720 protein; **PDBTitle:** crystal structure of bh2720 (10175341) from bacillus halodurans at2 1.41 a resolution
68	c3f0cA_	Alignment	not modelled	92.0	4	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of transcriptional regulator from cytophaga2 hutchinsonii atcc 33406
69	d2pyta1	Alignment	not modelled	91.8	5	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**EutQ-like
70	d1j5ya1	Alignment	not modelled	91.6	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
71	d2f4pa1	Alignment	not modelled	91.3	7	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
72	d1o5ua_	Alignment	not modelled	91.3	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112
73	c3dcfB_	Alignment	not modelled	91.3	11	**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
74	c1vi0B_	Alignment	not modelled	90.8	5	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator
75	d1uika1	Alignment	not modelled	90.8	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
76	d2hsga1	Alignment	not modelled	90.5	7	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
77	c1jumB_	Alignment	not modelled	90.5	11	**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
						PDB header:recombination/dna

78	c2r0qF_	Alignment	not modelled	90.4	7	**Chain:** F: **PDB Molecule:**putative transposon tn552 dna-invertase bin3; **PDBTitle:** crystal structure of a serine recombinase- dna regulatory2 complex
79	d1mkma1	Alignment	not modelled	90.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
80	c3myxA_	Alignment	not modelled	90.3	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pspto_0244; **PDBTitle:** crystal structure of a pspto_0244 (protein with unknown function which2 belongs to pfam duf861 family) from pseudomonas syringae pv. tomato3 str. dc3000 at 1.30 a resolution
81	c2f07A_	Alignment	not modelled	90.2	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**yvdt; **PDBTitle:** crystal structure of yvdt from bacillus subtilis
82	d1jt6a1	Alignment	not modelled	90.0	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
83	d1zvfa1	Alignment	not modelled	89.9	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
84	c1u78A_	Alignment	not modelled	89.9	10	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element tc3 transposase; **PDBTitle:** structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
85	c2ibdB_	Alignment	not modelled	89.9	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**possible transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulatory protein2 rha5900
86	c3bcwB_	Alignment	not modelled	89.7	11	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a duf861 family protein with a rmlc-like cupin2 fold (bb1179) from bordetella bronchiseptica rb50 at 1.60 a3 resolution
87	d2i10a1	Alignment	not modelled	89.4	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
88	d1dgwa_	Alignment	not modelled	89.4	8	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
89	d2gfna1	Alignment	not modelled	89.4	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
90	d1biaa1	Alignment	not modelled	89.2	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
91	c3iuvA_	Alignment	not modelled	89.1	5	**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
92	d2fq4a1	Alignment	not modelled	89.1	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
93	c2pbxB_	Alignment	not modelled	89.0	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hemagglutinin/protease regulatory protein; **PDBTitle:** vibrio cholerae hapr
94	c3ppbB_	Alignment	not modelled	88.9	10	**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
95	c3e7lD_	Alignment	not modelled	88.9	21	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
96	c2genA_	Alignment	not modelled	88.9	8	**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
97	d1uxca_	Alignment	not modelled	88.6	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
98	c2dg7A_	Alignment	not modelled	88.5	4	**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)
99	d1lcda_	Alignment	not modelled	88.5	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
100	c2eh3A_	Alignment	not modelled	88.5	9	**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
101	d2cg4a1	Alignment	not modelled	88.3	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
102	d2fbqa1	Alignment	not modelled	88.3	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
103	c3he0A_	Alignment	not modelled	88.3	1	**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.
104	c3f1bA_	Alignment	not modelled	88.2	12	**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.
105	d1fipa_	Alignment	not modelled	88.2	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
106	d1g2ha_	Alignment	not modelled	88.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
107	c2yvhA_	Alignment	not modelled	88.2	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
108	d1v7ba1	Alignment	not modelled	88.1	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
109	d1ui5a1	Alignment	not modelled	87.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
110	d3c07a1	Alignment	not modelled	87.8	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
111	d1etxa_	Alignment	not modelled	87.8	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
112	d2d6ya1	Alignment	not modelled	87.6	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
113	d1t56a1	Alignment	not modelled	87.6	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
114	c3r0aB_	Alignment	not modelled	87.6	14	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
115	c3b81A_	Alignment	not modelled	87.5	15	**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
116	c2qtqB_	Alignment	not modelled	87.4	12	**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
117	c3qbmA_	Alignment	not modelled	87.4	7	**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
118	d1pb6a1	Alignment	not modelled	87.3	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
119	c2hytA_	Alignment	not modelled	87.2	6	**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
120	d2g3ba1	Alignment	not modelled	87.2	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain