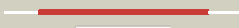





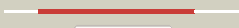














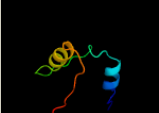

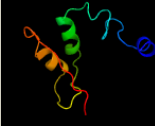



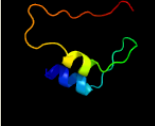
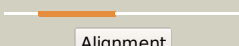

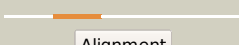

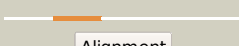

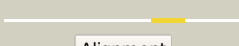





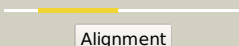


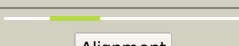

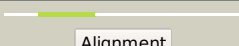
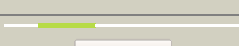



# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3149\_(nuoE)\_3514654\_3515412  
 Date Thu Aug 8 16:20:33 BST 2019  
 Unique Job ID 8d360be7972d63e5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5lnk2_</a>	 Alignment		100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> 2: <b>PDB Molecule:</b> mitochondrial complex i, 24 kda subunit; <b>PDBTitle:</b> entire ovine respiratory complex i
2	<a href="#">c5xf9E_</a>	 Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> nad-reducing hydrogenase; <b>PDBTitle:</b> crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
3	<a href="#">c5lc5E_</a>	 Alignment		100.0	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] flavoprotein 2, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
4	<a href="#">c6gcsH_</a>	 Alignment		100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> 24-kda subunit (nuhm); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
5	<a href="#">d2fug21</a>	 Alignment		100.0	36	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> NQO2-like
6	<a href="#">c6hl2C_</a>	 Alignment		100.0	31	<b>PDB header:</b> electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit e; <b>PDBTitle:</b> wild-type nuoef from aquifex aeolicus - oxidized form
7	<a href="#">c2auvA_</a>	 Alignment		99.9	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> potential nad-reducing hydrogenase subunit; <b>PDBTitle:</b> solution structure of hndac : a thioredoxin-like [2fe-2s]2 ferredoxin involved in the nadp-reducing hydrogenase3 complex
8	<a href="#">c5abrB_</a>	 Alignment		99.5	18	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin, 2fe-2s; <b>PDBTitle:</b> structure of fesi protein from azotobacter vinelandii
9	<a href="#">d1m2da_</a>	 Alignment		99.4	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioredoxin-like 2Fe-2S ferredoxin
10	<a href="#">d1f37b_</a>	 Alignment		99.4	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioredoxin-like 2Fe-2S ferredoxin
11	<a href="#">c6q9gD_</a>	 Alignment		97.1	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit f; <b>PDBTitle:</b> crystal structure of reduced aquifex aeolicus nadh-quinone2 oxidoreductase subunits nuoef g129d and nuof bound to nadh

12	<a href="#">c5lc5F_</a>	 Alignment		96.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] flavoprotein 1, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
13	<a href="#">c2fugA_</a>	 Alignment		96.4	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh-quinone oxidoreductase chain 1; <b>PDBTitle:</b> crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
14	<a href="#">d2fug12</a>	 Alignment		96.3	25	<b>Fold:</b> Nqo1 FMN-binding domain-like <b>Superfamily:</b> Nqo1 FMN-binding domain-like <b>Family:</b> Nqo1 FMN-binding domain-like
15	<a href="#">c5u7zA_</a>	 Alignment		88.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acid ceramidase; <b>PDBTitle:</b> human acid ceramidase (asah1, acdase) self-activated
16	<a href="#">c3iuvA_</a>	 Alignment		82.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized tetr family protein; <b>PDBTitle:</b> the structure of a member of tetr family (sco1917) from2 streptomyces coelicolor a3
17	<a href="#">c2dg8D_</a>	 Alignment		80.5	18	<b>PDB header:</b> gene regulation <b>Chain:</b> D: <b>PDB Molecule:</b> putative tetr-family transcriptional regulatory protein; <b>PDBTitle:</b> crystal structure of the putative trasncriptional regulator sco75182 from streptomyces coelicolor a3(2)
18	<a href="#">c5kbcA_</a>	 Alignment		77.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dsba; <b>PDBTitle:</b> crystal structure of chlamydia trachomatis dsba
19	<a href="#">c5x5iC_</a>	 Alignment		77.3	19	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> hth-type transcriptional regulator rcda; <b>PDBTitle:</b> the x-ray crystal structure of a tetr family transcription regulator2 rcda involved in the regulation of biofilm formation in escherichia3 coli
20	<a href="#">c2q24A_</a>	 Alignment		77.1	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr family transcriptional regulator; <b>PDBTitle:</b> crystal structure of tetr transcriptional regulator sco0520 from2 streptomyces coelicolor
21	<a href="#">c5u84A_</a>	 Alignment	not modelled	75.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acid ceramidase; <b>PDBTitle:</b> acid ceramidase (asah1, acdase) from common minke whale, cys143ala,2 uncleaved
22	<a href="#">c3jsjC_</a>	 Alignment	not modelled	69.5	19	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a putative tetr-transcriptional regulator2 (sav143) from streptomyces avermitilis ma-4680 at 2.10 a resolution
23	<a href="#">c6dy1A_</a>	 Alignment	not modelled	69.1	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acylethanolamine acid amidase alpha-subunit; <b>PDBTitle:</b> rabbit n-acylethanolamine-hydrolyzing acid amidase (naaa) with fatty2 acid (myristate), in presence of triton x-100
24	<a href="#">d1t33a1</a>	 Alignment	not modelled	68.0	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
25	<a href="#">c2k9lA_</a>	 Alignment	not modelled	68.0	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor rpon; <b>PDBTitle:</b> structure of the core binding domain of sigma54
26	<a href="#">c1rr7A_</a>	 Alignment	not modelled	67.9	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> middle operon regulator; <b>PDBTitle:</b> crystal structure of the middle operon regulator protein of2 bacteriophage mu
27	<a href="#">d1rr7a_</a>	 Alignment	not modelled	67.9	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Middle operon regulator, Mor
28	<a href="#">c5ovvA_</a>	 Alignment	not modelled	66.7	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator, tetr

28	<a href="#">c3vvyA</a>	Alignment	not modelled	66.7	19	family; <b>PDBTitle:</b> crystal structure of mab_4384 tet
29	<a href="#">c2rekA</a>	Alignment	not modelled	66.1	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of tetr-family transcriptional regulator
30	<a href="#">c2k9mA</a>	Alignment	not modelled	66.0	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor rpon; <b>PDBTitle:</b> structure of the core binding domain of sigma54
31	<a href="#">c2qwtA</a>	Alignment	not modelled	65.9	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of the tetr transcription regulatory protein from2 mycobacterium vanbaalenii
32	<a href="#">c3ccyA</a>	Alignment	not modelled	64.7	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a tetr-family transcriptional regulator from2 bordetella parapertussis 12822
33	<a href="#">c3vw0D</a>	Alignment	not modelled	64.1	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> putative regulatory protein; <b>PDBTitle:</b> crystal structure of the dequalinum-bound form of ramr2 (transcriptional regulator of tetr family) from salmonella3 typhimurium
34	<a href="#">c4nn1A</a>	Alignment	not modelled	64.0	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of transcriptional regulator rv1219c of2 mycobacterium tuberculosis
35	<a href="#">d2dt5a1</a>	Alignment	not modelled	63.5	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional repressor Rex, N-terminal domain
36	<a href="#">c4me9B</a>	Alignment	not modelled	60.1	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, tetr family2 (bce_2991) from bacillus cereus atcc 10987 at 2.50 a resolution
37	<a href="#">c3anpD</a>	Alignment	not modelled	59.6	11	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional repressor, tetr family; <b>PDBTitle:</b> crystal structure of thermus thermophilus fadr, a tetr family2 transcriptional repressor, in complex with lauroyl-coa.
38	<a href="#">c5k7fA</a>	Alignment	not modelled	59.5	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of apo aibr
39	<a href="#">c2da2A</a>	Alignment	not modelled	59.3	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-fetoprotein enhancer binding protein; <b>PDBTitle:</b> solution structure of the second homeobox domain of at-2 binding transcription factor 1 (atbf1)
40	<a href="#">c1nw3A</a>	Alignment	not modelled	58.5	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone methyltransferase dot11; <b>PDBTitle:</b> structure of the catalytic domain of human dot11, a non-set domain2 nucleosomal histone methyltransferase
41	<a href="#">d1nw3a</a>	Alignment	not modelled	58.5	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Catalytic, N-terminal domain of histone methyltransferase Dot11
42	<a href="#">d2craa1</a>	Alignment	not modelled	58.2	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
43	<a href="#">d1nk3p</a>	Alignment	not modelled	58.1	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
44	<a href="#">d1b8ia</a>	Alignment	not modelled	58.0	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
45	<a href="#">d2fd5a1</a>	Alignment	not modelled	57.9	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
46	<a href="#">c5ydpC</a>	Alignment	not modelled	57.6	16	<b>PDB header:</b> gene regulation <b>Chain:</b> C: <b>PDB Molecule:</b> tetr transcriptional regulatory protein; <b>PDBTitle:</b> crystal structure of tetr family repressor alkx from dietzia sp.2 strain dq12-45-1b implicated in biodegradation of n-alkanes
47	<a href="#">c2dmsA</a>	Alignment	not modelled	57.5	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein otx2; <b>PDBTitle:</b> solution structure of the homeobox domain of homeobox2 protein otx2
48	<a href="#">c2da1A</a>	Alignment	not modelled	57.3	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-fetoprotein enhancer binding protein; <b>PDBTitle:</b> solution structure of the first homeobox domain of at-2 binding transcription factor 1 (atbf1)
49	<a href="#">c2dg7A</a>	Alignment	not modelled	57.0	17	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
50	<a href="#">c1sgmA</a>	Alignment	not modelled	56.6	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator yxaf; <b>PDBTitle:</b> crystal structure of hypothetical protein yxaf
51	<a href="#">d1p7ia</a>	Alignment	not modelled	56.5	30	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
52	<a href="#">c2mgqA</a>	Alignment	not modelled	56.0	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein ceh-37; <b>PDBTitle:</b> structure of ceh37 homeodomain
						<b>PDB header:</b> calcium-binding protein

53	<a href="#">c1vzmB_</a>	Alignment	not modelled	55.8	27	<b>Chain:</b> B: <b>PDB Molecule:</b> osteocalcin; <b>PDBTitle:</b> osteocalcin from fish argyrosomus regius
54	<a href="#">d1au7a1</a>	Alignment	not modelled	55.4	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
55	<a href="#">d1jt6a1</a>	Alignment	not modelled	55.3	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
56	<a href="#">c3v6gA_</a>	Alignment	not modelled	54.9	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulatory protein (probably deor- <b>PDBTitle:</b> crystal structure of transcriptional regulator
57	<a href="#">c2dmuA_</a>	Alignment	not modelled	54.5	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein gooseoid; <b>PDBTitle:</b> solution structure of the homeobox domain of homeobox2 protein gooseoid
58	<a href="#">c3a01A_</a>	Alignment	not modelled	54.4	27	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> homeodomain-containing protein; <b>PDBTitle:</b> crystal structure of aristaless and clawless homeodomains bound to dna
59	<a href="#">c2qkoA_</a>	Alignment	not modelled	53.6	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, tetr family protein; <b>PDBTitle:</b> crystal structure of transcriptional regulator rha06399 from2 rhodococcus sp. rha1
60	<a href="#">c4cgrA_</a>	Alignment	not modelled	52.9	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> structure of regulator protein sco3201 from streptomyces coelicolor
61	<a href="#">d2e1oa1</a>	Alignment	not modelled	52.8	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
62	<a href="#">c5z2tC_</a>	Alignment	not modelled	52.7	21	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> double homeobox protein 4; <b>PDBTitle:</b> crystal structure of dna-bound dux4-hd2
63	<a href="#">c2ibdB_</a>	Alignment	not modelled	52.0	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> possible transcriptional regulator; <b>PDBTitle:</b> crystal structure of probable transcriptional regulatory protein2 rha5900
64	<a href="#">d1zq3p1</a>	Alignment	not modelled	51.8	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
65	<a href="#">d1fjla_</a>	Alignment	not modelled	51.5	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
66	<a href="#">d2cuea1</a>	Alignment	not modelled	51.3	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
67	<a href="#">d1zk8a1</a>	Alignment	not modelled	50.7	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
68	<a href="#">c4g12A_</a>	Alignment	not modelled	50.5	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulatory protein (probably tetr- <b>PDBTitle:</b> crystal structure of putative tetr family transcriptional regulator,2 fad35r, from mycobacterium tuberculosis
69	<a href="#">c3nauA_</a>	Alignment	not modelled	50.5	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc fingers and homeoboxes protein 2; <b>PDBTitle:</b> crystal structure of zhx2 hd2 (zinc-fingers and homeoboxes protein 2,2 homeodomain 2)
70	<a href="#">d1du0a_</a>	Alignment	not modelled	50.3	30	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
71	<a href="#">c3voxD_</a>	Alignment	not modelled	50.1	15	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> x-ray crystal structure of wild type hrtr in the apo form
72	<a href="#">d1gt0c1</a>	Alignment	not modelled	50.0	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
73	<a href="#">c5dxzA_</a>	Alignment	not modelled	49.9	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tetr family transcriptional regulator; <b>PDBTitle:</b> crystal of amtr from corynebacterium glutamicum
74	<a href="#">d1r7ha_</a>	Alignment	not modelled	49.8	38	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
75	<a href="#">c5hodD_</a>	Alignment	not modelled	49.5	15	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> lim/homeobox protein lhx4; <b>PDBTitle:</b> structure of lhx4 transcription factor complexed with dna
76	<a href="#">c5dajB_</a>	Alignment	not modelled	49.5	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> nald; <b>PDBTitle:</b> crystal structure of nald, the secondary repressor of mexab-oprm2 multidrug efflux pump in pseudomonas aeruginosa
77	<a href="#">d1fjlb_</a>	Alignment	not modelled	49.5	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
78	<a href="#">d1j5ya1</a>	Alignment	not modelled	49.0	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
79	<a href="#">c2fa4A_</a>	Alignment	not modelled	49.0	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family;

79	<a href="#">c2iq4A</a>	Alignment	not modelled	49.0	22	<b>PDBTitle:</b> the crystal structure of the transcriptional regulator (tetr family)2 from bacillus cereus <b>PDB header:</b> transcription
80	<a href="#">c3gziA</a>	Alignment	not modelled	48.9	16	<b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator of the tetr family2 (shew_3567) from shewanella loihica pv-4 at 2.05 a resolution
81	<a href="#">d1ahdp</a>	Alignment	not modelled	48.9	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
82	<a href="#">c2g3bB</a>	Alignment	not modelled	48.7	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative tetr-family transcriptional regulator2 from rhodococcus sp.
83	<a href="#">d1bw5a</a>	Alignment	not modelled	48.6	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
84	<a href="#">c4jl3B</a>	Alignment	not modelled	48.5	16	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of ms6564-dna complex
85	<a href="#">c3a03A</a>	Alignment	not modelled	48.4	27	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> t-cell leukemia homeobox protein 2; <b>PDBTitle:</b> crystal structure of hox11l1 homeodomain
86	<a href="#">c3vprA</a>	Alignment	not modelled	48.4	26	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of a tetr family transcriptional regulator pfmr from2 thermus thermophilus hb8
87	<a href="#">d2hddb</a>	Alignment	not modelled	48.3	30	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
88	<a href="#">c3he0A</a>	Alignment	not modelled	48.3	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> the structure of a putative transcriptional regulator tetr family2 protein from vibrio parahaemolyticus.
89	<a href="#">d1octc1</a>	Alignment	not modelled	48.0	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
90	<a href="#">c3zizA</a>	Alignment	not modelled	48.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of the thioredoxin-like protein bc3987
91	<a href="#">d1sana</a>	Alignment	not modelled	47.6	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
92	<a href="#">d1u2za</a>	Alignment	not modelled	47.5	9	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Catalytic, N-terminal domain of histone methyltransferase Dot1l
93	<a href="#">c4er3A</a>	Alignment	not modelled	47.2	15	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> histone-lysine n-methyltransferase, h3 lysine-79 specific; <b>PDBTitle:</b> crystal structure of human dot1l in complex with inhibitor epz004777
94	<a href="#">d1ztra1</a>	Alignment	not modelled	47.1	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
95	<a href="#">c6g8hC</a>	Alignment	not modelled	47.0	16	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> tetr/acrr family transcriptional regulator; <b>PDBTitle:</b> flavonoid-responsive regulator frra in complex with naringenin
96	<a href="#">d1k61a</a>	Alignment	not modelled	46.9	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
97	<a href="#">c5gpcC</a>	Alignment	not modelled	46.6	19	<b>PDB header:</b> transcription, dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator (tetr/acrr family); <b>PDBTitle:</b> structural analysis of fatty acid degradation regulator fadr from2 bacillus halodurans
98	<a href="#">c3b81A</a>	Alignment	not modelled	46.5	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, acrr family; <b>PDBTitle:</b> crystal structure of predicted dna-binding transcriptional regulator2 of tetr/acrr family (np_350189.1) from clostridium acetobutylicum at3 2.10 a resolution
99	<a href="#">c3fiwB</a>	Alignment	not modelled	46.5	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> structure of sco0253, a tetr-family transcriptional regulator from2 streptomyces coelicolor
100	<a href="#">c3vuqD</a>	Alignment	not modelled	45.6	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator (tetr/acrr family); <b>PDBTitle:</b> crystal structure of ttha0167, a transcriptional regulator, tetr/acrr2 family from thermus thermophilus hb8
101	<a href="#">c2yvha</a>	Alignment	not modelled	45.5	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of the operator-binding form of the multi-drug2 binding transcriptional repressor cgmr
102	<a href="#">d1hdpa</a>	Alignment	not modelled	45.4	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
103	<a href="#">d1le8a</a>	Alignment	not modelled	45.4	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
104	<a href="#">d1le8b</a>	Alignment	not modelled	45.2	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like

						<b>Family:</b> Homeodomain
105	<a href="#">c3ni7A_</a>	Alignment	not modelled	45.1	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> bacterial regulatory proteins, tetr family; <b>PDBTitle:</b> crystal structure of the tetr transcriptional regulator from2 nitrosomonas europaea atcc 19718
106	<a href="#">c4ichA_</a>	Alignment	not modelled	45.1	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of a putative tetr family transcriptional regulator2 from saccharomonospora viridis dsm 43017
107	<a href="#">c3bniA_</a>	Alignment	not modelled	45.1	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor
108	<a href="#">d1v7ba1</a>	Alignment	not modelled	45.1	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
109	<a href="#">c1vi0B_</a>	Alignment	not modelled	44.9	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of a transcriptional regulator
110	<a href="#">d1t56a1</a>	Alignment	not modelled	44.8	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
111	<a href="#">d1jgga_</a>	Alignment	not modelled	44.7	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
112	<a href="#">d1ocpa_</a>	Alignment	not modelled	44.6	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
113	<a href="#">d2ecba1</a>	Alignment	not modelled	44.5	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
114	<a href="#">d1yrnb_</a>	Alignment	not modelled	44.3	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
115	<a href="#">d1pufa_</a>	Alignment	not modelled	44.3	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
116	<a href="#">c3bjbE_</a>	Alignment	not modelled	44.3	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> E: <b>PDB Molecule:</b> probable transcriptional regulator, tetr family protein; <b>PDBTitle:</b> crystal structure of a tetr transcriptional regulator from rhodococcus2 sp. rha1
117	<a href="#">c2raeA_</a>	Alignment	not modelled	44.2	8	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, acrr family protein; <b>PDBTitle:</b> crystal structure of a tetr/acrr family transcriptional regulator from2 rhodococcus sp. rha1
118	<a href="#">d1ig7a_</a>	Alignment	not modelled	44.2	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
119	<a href="#">c2djnA_</a>	Alignment	not modelled	44.1	30	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein dlx-5; <b>PDBTitle:</b> the solution structure of the homeobox domain of human2 homeobox protein dlx-5
120	<a href="#">d1b72a_</a>	Alignment	not modelled	44.0	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain