



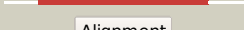

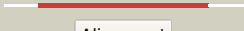









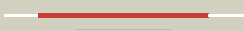







# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3557c (- )_3997208_3997810
Date	Fri Aug 9 18:20:23 BST 2019
Unique Job ID	9cdcf67b5a59a9c

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4w97A_</a>	 Alignment		100.0	100	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor kstr2; <b>PDBTitle:</b> structure of ketosteroid transcriptional regulator kstr2 of2 mycobacterium tuberculosis
2	<a href="#">c3himA_</a>	 Alignment		99.9	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a bacterial regulatory protein in the tetr2 family from rhodococcus rha1 to 2.2a
3	<a href="#">c2ibdB_</a>	 Alignment		99.9	58	<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
4	<a href="#">c3dcfB_</a>	 Alignment		99.9	25	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator of the tetr/acrr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator of the tetr/acrr family2 (yp_290855.1) from thermobifida fusca yx-er1 at 2.50 a resolution
5	<a href="#">c5gpcC_</a>	 Alignment		99.9	21	<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
6	<a href="#">c3vprA_</a>	 Alignment		99.9	30	<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
7	<a href="#">c2iaiA_</a>	 Alignment		99.9	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator sco3833; <b>PDBTitle:</b> crystal structure of sco3833, a member of the tetr transcriptional2 regulator family from streptomyces coelicolor a3
8	<a href="#">c2pbxB_</a>	 Alignment		99.9	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin/protease regulatory protein; <b>PDBTitle:</b> vibrio cholerae hapr
9	<a href="#">c6azhA_</a>	 Alignment		99.9	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tetr family transcriptional regulator; <b>PDBTitle:</b> clostridium perfringens putative fatty acid metabolism regulator
10	<a href="#">c2genA_</a>	 Alignment		99.9	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> structural genomics, the crystal structure of a probable2 transcriptional regulator from pseudomonas aeruginosa pao1
11	<a href="#">c1vi0B_</a>	 Alignment		99.9	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of a transcriptional regulator

12	<a href="#">c3ccyA_</a>	Alignment		99.9	20	<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
13	<a href="#">c2f07A_</a>	Alignment		99.9	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> yvdt; <b>PDBTitle:</b> crystal structure of yvdt from bacillus subtilis
14	<a href="#">c5k7fA_</a>	Alignment		99.9	22	<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
15	<a href="#">c3pasA_</a>	Alignment		99.9	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tetr family transcription regulator; <b>PDBTitle:</b> crystal structure of a tetr family transcription regulator (maqu_1417)2 from marinobacter aquaeolei vt8 at 1.90 a resolution
16	<a href="#">c3lwjA_</a>	Alignment		99.9	19	<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 putative tetr-family transcriptional regulator2 (yp_752756.1) from syntrophomonas wolfei str. goettingen at 2.07 a3 resolution
17	<a href="#">c3anpD_</a>	Alignment		99.9	20	<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.
18	<a href="#">c4ichA_</a>	Alignment		99.9	18	<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
19	<a href="#">c3eupA_</a>	Alignment		99.9	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> the crystal structure of the transcriptional regulator, tetr family2 from cytophaga hutchinsonii
20	<a href="#">c3qbmA_</a>	Alignment		99.9	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tetr transcriptional regulator; <b>PDBTitle:</b> crystal structure of a tetr transcriptional regulator (caur_2221) from2 chloroflexus aurantiacus j-10-fl at 1.80 a resolution
21	<a href="#">c1jumB_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical transcriptional regulator in qaca 5' region; <b>PDBTitle:</b> crystal structure of the multidrug binding transcriptional repressor2 qacr bound to the natural drug berberine
22	<a href="#">c2hyjA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a tetr-family transcriptional regulator from2 streptomyces coelicolor
23	<a href="#">c3nrgA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tetr family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a tetr family transcriptional regulator2 (caur_2714) from chloroflexus aurantiacus j-10-fl at 2.56 a3 resolution
24	<a href="#">c3ppbB_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative tetr family transcription regulator; <b>PDBTitle:</b> crystal structure of a putative tetr family transcription regulator2 (shew_3104) from shewanella sp. pv-4 at 2.10 a resolution
25	<a href="#">c4me9B_</a>	Alignment	not modelled	99.9	17	<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
26	<a href="#">c5ztcA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lmo2088 protein; <b>PDBTitle:</b> apo structure of tetr family transcription regulator lmo2088 of2 listeria monocytogenes egde
27	<a href="#">c5dajB_</a>	Alignment	not modelled	99.9	13	<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 <b>PDB header:</b> transcription

28	<a href="#">c2g7sA_</a>	Alignment	not modelled	99.9	18	<b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> the crystal structure of transcriptional regulator, tetr family, from2 agrobacterium tumefaciens
29	<a href="#">c1u9nA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional repressor ethr; <b>PDBTitle:</b> crystal structure of the transcriptional regulator ethr in2 a ligand bound conformation opens therapeutic perspectives3 against tuberculosis and leprosy
30	<a href="#">c2zb9A_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of tetr family transcription regulator2 sco0332
31	<a href="#">c3on2C_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> structure of a protein with unknown function from rhodococcus sp. rha1
32	<a href="#">c3e7qB_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> the crystal structure of the putative transcriptional regulator from2 pseudomonas aeruginosa pao1
33	<a href="#">c3f1bA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tetr-like transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a tetr-like transcriptional regulator from2 rhodococcus sp. rha1.
34	<a href="#">c3s5rA_</a>	Alignment	not modelled	99.9	17	<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 putative transcriptional regulator of the tetr2 family (syn_02108) from syntrophus aciditrophicus at 2.60 a3 resolution
35	<a href="#">c2nx4A_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family protein; <b>PDBTitle:</b> the crystal structure of a the putative tetr-family transcriptional2 regulator rha06780 from rhodococcus sp. rha1.
36	<a href="#">c3vuqD_</a>	Alignment	not modelled	99.9	16	<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
37	<a href="#">c3gziA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transcription <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
38	<a href="#">c2uxoB_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator ttgr; <b>PDBTitle:</b> ttgr in complex with tetracycline
39	<a href="#">c2rasB_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of a putative tetr/acrr family transcriptional2 regulator (saro_0558) from novosphingobium aromaticivorans dsm at3 1.80 a resolution
40	<a href="#">c1pb6D_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical transcriptional regulator ycdc; <b>PDBTitle:</b> crystal structure of hypothetical transcriptional regulator ycdc
41	<a href="#">c3bcgA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator acrr; <b>PDBTitle:</b> conformational changes of the acrr regulator reveal a2 mechanism of induction
42	<a href="#">c3dewA_</a>	Alignment	not modelled	99.9	18	<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 tetr family transcriptional regulator from2 geobacter sulfurreducens pca.
43	<a href="#">c2fq4A_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> the crystal structure of the transcriptional regulator (tetr family)2 from bacillus cereus
44	<a href="#">c2qtqB_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of a predicted dna-binding transcriptional regulator2 (saro_1072) from novosphingobium aromaticivorans dsm at 1.85 a3 resolution
45	<a href="#">c3vibD_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> mtrr; <b>PDBTitle:</b> structural basis for multidrug recognition and antimicrobial2 resistance by mtrr, an efflux pump regulator from neisseria3 gonorrhoeae
46	<a href="#">c1zkgB_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator, tetr family (tm1030)2 from thermotoga maritima at 2.30 a resolution
47	<a href="#">c2hytA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a tetr-family transcriptional regulator (eca1819)2 from pectobacterium atrosepticum at 1.64 a resolution
48	<a href="#">c5mwrB_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> tetr family transcriptional regulator; <b>PDBTitle:</b> the fadr transcription regulator from sulfolobus acidocaldarius
49	<a href="#">c1rktA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> protein yfir; <b>PDBTitle:</b> crystal structure of yfir, a putative transcriptional regulator from2 bacillus subtilis
50	<a href="#">c4gctA_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoid occlusion factor slma; <b>PDBTitle:</b> structure of no factor protein-dna complex
51	<a href="#">c6ayhA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tetr family transcriptional regulator; <b>PDBTitle:</b> salmonella enterica gusr
						<b>PDB header:</b> transcription

52	<a href="#">c2id3A_</a>	Alignment	not modelled	99.9	16	<b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of transcriptional regulator sco5951 from2 streptomyces coelicolor a3(2)
53	<a href="#">c2g3bB_</a>	Alignment	not modelled	99.9	17	<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.
54	<a href="#">c4udsA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> mbdr regulator; <b>PDBTitle:</b> crystal structure of mbdr regulator from azoarcus sp. cib
55	<a href="#">c2raeA_</a>	Alignment	not modelled	99.9	14	<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
56	<a href="#">c3he0A_</a>	Alignment	not modelled	99.9	18	<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 parahemolyticus.
57	<a href="#">c3brvA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein, tetr family; <b>PDBTitle:</b> crystal structure of regulatory protein tetr from rhodobacter2 sphaeroides
58	<a href="#">c5vl9D_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein tetr; <b>PDBTitle:</b> crystal structure of eilr in complex with eilo dna element
59	<a href="#">c3npiB_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> tetr family regulatory protein; <b>PDBTitle:</b> crystal structure of a tetr family regulatory protein (dip1788) from2 corynebacterium diphtheriae at 2.96 a resolution
60	<a href="#">c3bhqB_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of a putative tetr-family transcriptional regulator2 (mlr_4833) from mesorhizobium loti maff303099 at 1.54 a resolution
61	<a href="#">c1ui6B_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> a-factor receptor homolog; <b>PDBTitle:</b> crystal structure of gamma-butyrolactone receptor (arpa-like protein)
62	<a href="#">c2gfnA_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator pksa related protein; <b>PDBTitle:</b> crystal structure of hth-type transcriptional regulator pksa related2 protein from rhodococcus sp. rha1
63	<a href="#">c6ayiA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator uidr; <b>PDBTitle:</b> escherichia coli gusr
64	<a href="#">c6g8hC_</a>	Alignment	not modelled	99.9	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
65	<a href="#">c3c07B_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a tetr family transcriptional regulator from2 streptomyces coelicolor a3(2)
66	<a href="#">c3f0cA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of transcriptional regulator from cytophaga2 hutchinsonii atcc 33406
67	<a href="#">c3qkxB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator hi_0893; <b>PDBTitle:</b> crystal structure of a tetr-family transcriptional regulator (hi0893)2 from haemophilus influenzae rd at 2.35 a resolution
68	<a href="#">c2rekA_</a>	Alignment	not modelled	99.9	20	<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
69	<a href="#">c4za6A_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tetr family transcriptional regulator; <b>PDBTitle:</b> structure of the r. erythropolis transcriptional repressor qsdr from2 tetr family
70	<a href="#">c2qibA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor
71	<a href="#">c2wuiA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of mexz, a key repressor responsible for2 antibiotic resistance in pseudomonas aeruginosa.
72	<a href="#">c3rh2A_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical tetr-like transcriptional regulator; <b>PDBTitle:</b> crystal structure of a tetr-like transcriptional regulator (sama_0099)2 from shewanella amazonensis sb2b at 2.42 a resolution
73	<a href="#">c3colB_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcription regulator; <b>PDBTitle:</b> crystal structure of putative transcription regulator from2 lactobacillus plantarum
74	<a href="#">c2fbqA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> the crystal structure of transcriptional regulator pa3006
75	<a href="#">c5ovyA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of mab_4384 tetr
						<b>PDB header:</b> transcription

76	<a href="#">c3lsjA_</a>	Alignment	not modelled	99.9	14	<b>Chain:</b> A: <b>PDB Molecule:</b> dest; <b>PDBTitle:</b> crystal structure of dest in complex with palmitoyl-coa
77	<a href="#">c4yzeD_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional repressor nemr; <b>PDBTitle:</b> crystal structure of e.coli nemr reduced form
78	<a href="#">c3q7rB_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of sco4454, a tet-family transcriptional regulator2 from streptomyces coelicolor
79	<a href="#">c2o7tA_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of a tet family transcriptional regulator2 (ncgl1578, cgl1640) from corynebacterium glutamicum at 2.10 a3 resolution
80	<a href="#">c2q24A_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tet family transcriptional regulator; <b>PDBTitle:</b> crystal structure of tet transcriptional regulator sco0520 from2 streptomyces coelicolor
81	<a href="#">c5d19A_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tetr family transcriptional regulator; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis rv0302, form ii
82	<a href="#">c4nn1A_</a>	Alignment	not modelled	99.9	17	<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
83	<a href="#">c3c2bA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tet family; <b>PDBTitle:</b> crystal structure of tet transcriptional regulator from agrobacterium2 tumefaciens
84	<a href="#">c3vw0D_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> putative regulatory protein; <b>PDBTitle:</b> crystal structure of the dequalinium-bound form of ramr2 (transcriptional regulator of tet family) from salmonella3 typhimurium
85	<a href="#">c4jl3B_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, tet family; <b>PDBTitle:</b> crystal structure of ms6564-dna complex
86	<a href="#">c2hkuB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> a putative transcriptional regulator; <b>PDBTitle:</b> structural genomics, the crystal structure of a putative2 transcriptional regulator from rhodococcus sp. rha1
87	<a href="#">c5xazD_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> gamma-butyrolactone receptor protein; <b>PDBTitle:</b> crystal structure of full length native tylp, a tet regulator from2 streptomyces fradiae
88	<a href="#">c3mn1A_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein (probably tet-family); <b>PDBTitle:</b> the crystal structure of kstr (rv3574) from mycobacterium tuberculosis2 h37rv
89	<a href="#">c3b81A_</a>	Alignment	not modelled	99.9	19	<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 tet/acrr family (np_350189.1) from clostridium acetobutylicum at3 2.10 a resolution
90	<a href="#">c5d1wD_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> rv3249c transcriptional regulator; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis rv3249c2 transcriptional regulator.
91	<a href="#">c2zcxA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of tet family transcriptional regulator2 sco7815
92	<a href="#">c3rd3B_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> structure of pseudomonas aeruginosa transcriptional regulator pa2196
93	<a href="#">c3nnrA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tet family; <b>PDBTitle:</b> crystal structure of a tet-family transcriptional regulator2 (maqu_3571) from marinobacter aquaeolei vt8 at 2.49 a resolution
94	<a href="#">c6mj1A_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable hth-type transcriptional regulator yttp; <b>PDBTitle:</b> crystal structure of refz (regulator of ftsz) from bacillus subtilis
95	<a href="#">c4ac6A_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor acnr; <b>PDBTitle:</b> corynebacterium glutamicum acnr au derivative structure
96	<a href="#">c5d1rA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rv1816 transcriptional regulator; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis rv1816 transcriptional2 regulator.
97	<a href="#">c5n1cA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulatory protein; <b>PDBTitle:</b> iodinated form of the mycobacterium tuberculosis repressor ethr2
98	<a href="#">c4cgrA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tet-family transcriptional regulator; <b>PDBTitle:</b> structure of regulator protein sco3201 from streptomyces coelicolor
99	<a href="#">c2qwtA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tet family; <b>PDBTitle:</b> crystal structure of the tet transcription regulatory protein from2 mycobacterium vanbaalenii
						<b>PDB header:</b> transcription regulator

100	<a href="#">c1zk8A_</a>	Alignment	not modelled	99.9	16	<b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator from bacillus cereus2 atcc 14579
101	<a href="#">c1t33B_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional repressor (tetr/acrr family); <b>PDBTitle:</b> structural genomics, the crystal structure of a putative2 transcriptional repressor (tetr/acrr family) from salmonella3 typhimurim lt2
102	<a href="#">c4g12A_</a>	Alignment	not modelled	99.8	23	<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
103	<a href="#">c3knwB_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator (tetr/acrr family); <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator (tetr/acrr2 family member) from putative transcriptional regulator (tetr/acrr3 family)
104	<a href="#">c3cwrA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator of tetr family2 (yp_425770.1) from rhodospirillum rubrum atcc 11170 at 1.50 a3 resolution
105	<a href="#">c5xs9B_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> tetr family transcriptional regulator; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis bioq
106	<a href="#">c2i10A_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr transcriptional regulator; <b>PDBTitle:</b> putative tetr transcriptional regulator from rhodococcus sp. rha1
107	<a href="#">c3mvpA_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tetr/acrr transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a tetr/acrr transcriptional regulator from2 streptococcus mutans to 1.85a
108	<a href="#">c3cjdB_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of putative tetr transcriptional regulator2 (yp_510936.1) from jannaschia sp. ccs1 at 1.79 a resolution
109	<a href="#">c2dg7A_</a>	Alignment	not modelled	99.8	14	<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)
110	<a href="#">c2dg8D_</a>	Alignment	not modelled	99.8	19	<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 trascriptional regulator sco75182 from streptomyces coelicolor a3(2)
111	<a href="#">c2of7A_</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> structural genomics, the crystal structure of a tetr-family2 transcriptional regulator from streptomyces coelicolor a3
112	<a href="#">c2qcoA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> cmer; <b>PDBTitle:</b> crystal structure of the transcriptional regulator cmer from2 campylobacter jejuni
113	<a href="#">c2np5A_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of a transcriptional regulator (rha1_ro04179) from2 rhodococcus sp. rha1.
114	<a href="#">c3djpB_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> transcription regulator, tetr family; <b>PDBTitle:</b> the crystal structure of a tetr transcription regulator2 from silicibacter pomeroyi dss
115	<a href="#">c3on4D_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of tetr transcriptional regulator from legionella2 pneumophila
116	<a href="#">c3aqsD_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> bacterial regulatory proteins, tetr family; <b>PDBTitle:</b> crystal structure of rolr (ncgl1110) without ligand
117	<a href="#">c2oi8A_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative regulatory protein sco4313; <b>PDBTitle:</b> crystal structure of putative regulatory protein sco4313
118	<a href="#">c3nxcA_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type protein slma; <b>PDBTitle:</b> molecular mechanism by which the escherichia coli nucleoid occlusion2 factor, slma, keeps cytokinesis in check
119	<a href="#">c3bjbE_</a>	Alignment	not modelled	99.8	13	<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
120	<a href="#">c3v6gA_</a>	Alignment	not modelled	99.8	12	<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