



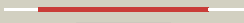




















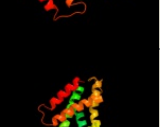







| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|--|---|------------|--------|--|
| 1  | <a href="#">c3qbmA_</a> | <br>Alignment   |    | 99.9       | 20     | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> tetr transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of a tetr transcriptional regulator (caur_2221) from2 chloroflexus aurantiacus j-10-fl at 1.80 a resolution                  |
| 2  | <a href="#">c3bruA_</a> | <br>Alignment   |    | 99.9       | 17     | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein, tetr family;<br><b>PDBTitle:</b> crystal structure of regulatory protein tetr from rhodobacter2 sphaeroides  |
| 3  | <a href="#">c2pbxB_</a> | <br>Alignment   |    | 99.9       | 13     | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin/protease regulatory protein;<br><b>PDBTitle:</b> vibrio cholerae hapr  |
| 4  | <a href="#">c2g7sA_</a> | <br>Alignment   |   | 99.9       | 16     | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family;<br><b>PDBTitle:</b> the crystal structure of transcriptional regulator, tetr family, from2 agrobacterium tumefaciens   |
| 5  | <a href="#">c2hyjA_</a> | <br>Alignment |  | 99.9       | 15     | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator;<br><b>PDBTitle:</b> the crystal structure of a tetr-family transcriptional regulator from2 streptomyces coelicolor   |
| 6  | <a href="#">c3e7gB_</a> | <br>Alignment |  | 99.9       | 11     | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> the crystal structure of the putative transcriptional regulator from2 pseudomonas aeruginosa pao1   |
| 7  | <a href="#">c2i10A_</a> | <br>Alignment |  | 99.9       | 30     | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr transcriptional regulator;<br><b>PDBTitle:</b> putative tetr transcriptional regulator from rhodococcus sp. rha1   |
| 8  | <a href="#">c3eupA_</a> | <br>Alignment |  | 99.9       | 19     | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family;<br><b>PDBTitle:</b> the crystal structure of the transcriptional regulator, tetr family2 from cytophaga hutchinsonii                                       |
| 9  | <a href="#">c2zb9A_</a> | <br>Alignment |  | 99.9       | 19     | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of tetr family transcription regulator2 sco0332  |
| 10 | <a href="#">c2iaiA_</a> | <br>Alignment |  | 99.9       | 15     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator sco3833;<br><b>PDBTitle:</b> crystal structure of sco3833, a member of the tetr transcriptional2 regulator family from streptomyces coelicolor a3 |
| 11 | <a href="#">c1rktA_</a> | <br>Alignment |  | 99.9       | 17     | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein yfir;<br><b>PDBTitle:</b> crystal structure of yfir, a putative transcriptional regulator from2 bacillus subtilis  |

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| 12 | <a href="#">c3nrgA_</a> | Alignment |     | 99.9 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> tetr family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of a tetr family transcriptional regulator2 (caur_2714) from chloroflexus aurantiacus j-10-fl at 2.56 a3 resolution                                      |
| 13 | <a href="#">c2uxoB_</a> | Alignment |    | 99.9 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator ttgr;<br><b>PDBTitle:</b> ttgr in complex with tetracycline  |
| 14 | <a href="#">c2f07A_</a> | Alignment |    | 99.9 | 11 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> yvdt;<br><b>PDBTitle:</b> crystal structure of yvdt from bacillus subtilis  |
| 15 | <a href="#">c3on2C_</a> | Alignment |    | 99.9 | 15 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> C: <b>PDB Molecule:</b> probable transcriptional regulator;<br><b>PDBTitle:</b> structure of a protein with unknown function from rhodococcus sp. rha1  |
| 16 | <a href="#">c2nx4A_</a> | Alignment |    | 99.9 | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family protein;<br><b>PDBTitle:</b> the crystal structure of athe putative tetr-family transcriptional2 regulator rha06780 from rhodococcus sp. rha1.                         |
| 17 | <a href="#">c3knwB_</a> | Alignment |    | 99.9 | 18 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator (tetr/acrr family);<br><b>PDBTitle:</b> crystal structure of a putative transcriptional regulator (tetr/acrr2 family member) from putative transcriptional regulator (tetr/acrr3 family) |
| 18 | <a href="#">c3bcgA_</a> | Alignment |   | 99.9 | 16 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator acrr;<br><b>PDBTitle:</b> conformational changes of the acrr regulator reveal a2 mechanism of induction  |
| 19 | <a href="#">c1vi0B_</a> | Alignment |  | 99.9 | 16 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of a transcriptional regulator   |
| 20 | <a href="#">c2gfnA_</a> | Alignment |  | 99.9 | 16 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator pksa related protein;<br><b>PDBTitle:</b> crystal structure of hth-type transcriptional regulator pksa related2 protein from rhodococcus sp. rha1  |
| 21 | <a href="#">c2id3A_</a> | Alignment | not modelled  | 99.9 | 15 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of transcriptional regulator sco5951 from2 streptomyces coelicolor a3(2)  |
| 22 | <a href="#">c3bhbB_</a> | Alignment | not modelled  | 99.9 | 18 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of a putative tetr-family transcriptional regulator2 (mlr_4833) from mesorhizobium loti maff303099 at 1.54 a resolution  |
| 23 | <a href="#">c3lwjA_</a> | Alignment | not modelled  | 99.9 | 16 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of putative tetr-family transcriptional regulator2 (yp_752756.1) from syntrophomonas wolfei str. goettingen at 2.07 a3 resolution     |
| 24 | <a href="#">c2g3bB_</a> | Alignment | not modelled  | 99.9 | 20 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of putative tetr-family transcriptional regulator2 from rhodococcus sp.   |
| 25 | <a href="#">c1u9nA_</a> | Alignment | not modelled  | 99.9 | 18 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional repressor ethr;<br><b>PDBTitle:</b> crystal structure of the transcriptional regulator ethr in2 a ligand bound conformation opens therapeutic perspectives3   |
| 26 | <a href="#">c3himA_</a> | Alignment | not modelled  | 99.9 | 14 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator;<br><b>PDBTitle:</b> the crystal structure of a bacterial regulatory protein in the tetr2 family from rhodococcus rha1 to 2.2a   |
| 27 | <a href="#">c3gziA_</a> | Alignment | not modelled  | 99.9 | 16 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family;<br><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  |

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| 28 | <a href="#">c3g7rB_</a> | Alignment | not modelled | 99.9 | 13 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of sco4454, a tetr-family transcriptional2 regulator from streptomyces coelicolor   |
| 29 | <a href="#">c3cwrA_</a> | Alignment | not modelled | 99.9 | 16 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family;<br><b>PDBTitle:</b> crystal structure of transcriptional regulator of tetr2 family (yp_425770.1) from rhodospirillum rubrum atcc 111703 at 1.50 a resolution          |
| 30 | <a href="#">c3anpD_</a> | Alignment | not modelled | 99.9 | 12 | <b>PDB header:</b> transcription<br><b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional repressor, tetr family;<br><b>PDBTitle:</b> crystal structure of thermus thermophilus fadr, a tetr family2 transcriptional repressor, in complex with lauroyl-coa.                                      |
| 31 | <a href="#">c2genA_</a> | Alignment | not modelled | 99.9 | 18 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator;<br><b>PDBTitle:</b> structural genomics, the crystal structure of a probable2 transcriptional regulator from pseudomonas aeruginosa pao1  |
| 32 | <a href="#">c3mvpA_</a> | Alignment | not modelled | 99.9 | 17 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> tetr/acrr transcriptional regulator;<br><b>PDBTitle:</b> the crystal structure of a tetr/acrr transcriptional regulator from2 streptococcus mutans to 1.85a   |
| 33 | <a href="#">c2hkuB_</a> | Alignment | not modelled | 99.9 | 18 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> a putative transcriptional regulator;<br><b>PDBTitle:</b> structural genomics, the crystal structure of a putative2 transcriptional regulator from rhodococcus sp. rha1                                       |
| 34 | <a href="#">c2rasB_</a> | Alignment | not modelled | 99.9 | 16 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, tetr family;<br><b>PDBTitle:</b> crystal structure of a putative tetr/acrr family transcriptional2 regulator (saro_0558) from novosphingobium aromaticivorans dsm at3 1.80 a resolution      |
| 35 | <a href="#">c1jumB_</a> | Alignment | not modelled | 99.9 | 15 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical transcriptional regulator in qaca<br><b>PDBTitle:</b> crystal structure of the multidrug binding transcriptional2 repressor qacr bound to the natural drug berberine                                       |
| 36 | <a href="#">c2qtqB_</a> | Alignment | not modelled | 99.9 | 15 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, tetr family;<br><b>PDBTitle:</b> crystal structure of a predicted dna-binding transcriptional regulator2 (saro_1072) from novosphingobium aromaticivorans dsm at 1.85 a3 resolution          |
| 37 | <a href="#">c3dpjB_</a> | Alignment | not modelled | 99.9 | 20 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcription regulator, tetr family;<br><b>PDBTitle:</b> the crystal structure of a tetr transcription regulator2 from silicibacter pomeroyi dss   |
| 38 | <a href="#">c1zkgB_</a> | Alignment | not modelled | 99.9 | 15 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, tetr family;<br><b>PDBTitle:</b> crystal structure of transcriptional regulator, tetr family (tm1030)2 from thermotoga maritima at 2.30 a resolution                               |
| 39 | <a href="#">c3f0cA_</a> | Alignment | not modelled | 99.9 | 16 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of transcriptional regulator from cytophaga2 hutchinsonii atcc 33406   |
| 40 | <a href="#">c1pb6D_</a> | Alignment | not modelled | 99.9 | 20 | <b>PDB header:</b> transcription<br><b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical transcriptional regulator ycdc;<br><b>PDBTitle:</b> crystal structure of hypothetical transcriptional regulator ycdc   |
| 41 | <a href="#">c2wuiA_</a> | Alignment | not modelled | 99.9 | 18 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of mexz, a key repressor responsible for2 antibiotic resistance in pseudomonas aeruginosa.   |
| 42 | <a href="#">c3dcfB_</a> | Alignment | not modelled | 99.9 | 19 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator of the tetr/acrr<br><b>PDBTitle:</b> crystal structure of transcriptional regulator of the2 tetr/acrr family (yp_290855.1) from thermobifida fusca yx-3 er1 at 2.50 a resolution    |
| 43 | <a href="#">c3dewA_</a> | Alignment | not modelled | 99.9 | 18 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family;<br><b>PDBTitle:</b> the structure of a putative tetr family transcriptional regulator from2 geobacter sulfurreducens pca.   |
| 44 | <a href="#">c3ppbB_</a> | Alignment | not modelled | 99.9 | 15 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative tetr family transcription regulator;<br><b>PDBTitle:</b> crystal structure of a putative tetr family transcription regulator2 (shew_3104) from shewanella sp. pv-4 at 2.10 a resolution              |
| 45 | <a href="#">c3rh2A_</a> | Alignment | not modelled | 99.9 | 17 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical tetr-like transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of a hypothetical tetr-like transcriptional2 regulator (sama_0099) from shewanella amazonensis sb2b at 2.42 a3 resolution |
| 46 | <a href="#">c3s5rA_</a> | Alignment | not modelled | 99.9 | 16 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator tetr family;<br><b>PDBTitle:</b> crystal structure of a putative transcriptional regulator of the tetr2 family (syn_02108) from syntrophus aciditrophicus at 2.60 a3 resolution         |
| 47 | <a href="#">c2fq4A_</a> | Alignment | not modelled | 99.9 | 14 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family;<br><b>PDBTitle:</b> the crystal structure of the transcriptional regulator (tetr family)2 from bacillus cereus  |
| 48 | <a href="#">c1sgmA_</a> | Alignment | not modelled | 99.9 | 20 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator yxaf;<br><b>PDBTitle:</b> crystal structure of hypothetical protein yxaf  |
| 49 | <a href="#">c3pasA_</a> | Alignment | not modelled | 99.9 | 19 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> tetr family transcription regulator;<br><b>PDBTitle:</b> crystal structure of a tetr family transcription regulator (maqu_1417)2 from marinobacter aquaeolei vt8 at 1.90 a resolution                         |
| 50 | <a href="#">c3on4D_</a> | Alignment | not modelled | 99.9 | 19 | <b>PDB header:</b> transcription<br><b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, tetr family;<br><b>PDBTitle:</b> crystal structure of tetr transcriptional regulator from legionella2 pneumophila  |

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|----|------------------------|-----------|--------------|------|----|---|
| 51 | <a href="#">c2o7tA</a> | Alignment | not modelled | 99.8 | 12 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of a tet family transcriptional regulator2 (ncgl1578, cgl1640) from corynebacterium glutamicum at 2.10 a3 resolution                           |
| 52 | <a href="#">c2ibdB</a> | Alignment | not modelled | 99.8 | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> possible transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of probable transcriptional regulatory protein2 rha5900   |
| 53 | <a href="#">c2raeA</a> | Alignment | not modelled | 99.8 | 15 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, acrr family protein;<br><b>PDBTitle:</b> crystal structure of a tet/acrr family transcriptional regulator from2 rhodococcus sp. rha1   |
| 54 | <a href="#">c2hytA</a> | Alignment | not modelled | 99.8 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> tetr-family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of a tet-family transcriptional regulator (eca1819)2 from pectobacterium atrosepticum at 1.64 a resolution                         |
| 55 | <a href="#">c1ui6B</a> | Alignment | not modelled | 99.8 | 18 | <b>PDB header:</b> antibiotic<br><b>Chain:</b> B: <b>PDB Molecule:</b> a-factor receptor homolog;<br><b>PDBTitle:</b> crystal structure of gamma-butyrolactone receptor (arpa-like protein)   |
| 56 | <a href="#">c3npiB</a> | Alignment | not modelled | 99.8 | 13 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> B: <b>PDB Molecule:</b> tetr family regulatory protein;<br><b>PDBTitle:</b> crystal structure of a tet family regulatory protein (dip1788) from2 corynebacterium diphtheriae at 2.96 a resolution                                     |
| 57 | <a href="#">c3he0A</a> | Alignment | not modelled | 99.8 | 17 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tet family;<br><b>PDBTitle:</b> the structure of a putative transcriptional regulator tet family2 protein from vibrio parahaemolyticus.                                    |
| 58 | <a href="#">c3ccyA</a> | Alignment | not modelled | 99.8 | 15 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative tet-family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of a tet-family transcriptional regulator from2 bordetella parapertussis 12822                                   |
| 59 | <a href="#">c2q24A</a> | Alignment | not modelled | 99.8 | 19 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative tet family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of tet transcriptional regulator sco0520 from2 streptomyces coelicolor   |
| 60 | <a href="#">c3jsjC</a> | Alignment | not modelled | 99.8 | 20 | <b>PDB header:</b> transcription<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative tet-family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of a putative tet-transcriptional regulator2 (sav143) from streptomyces avermitilis ma-4680 at 2.10 a resolution           |
| 61 | <a href="#">c2oi8A</a> | Alignment | not modelled | 99.8 | 14 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative regulatory protein sco4313;<br><b>PDBTitle:</b> crystal structure of putative regulatory protein sco4313   |
| 62 | <a href="#">c2fbqA</a> | Alignment | not modelled | 99.8 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator;<br><b>PDBTitle:</b> the crystal structure of transcriptional regulator pa3006   |
| 63 | <a href="#">c2qibA</a> | Alignment | not modelled | 99.8 | 13 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> tetr-family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of tet-family transcriptional regulator from2 streptomyces coelicolor  |
| 64 | <a href="#">c3f1bA</a> | Alignment | not modelled | 99.8 | 16 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> tetr-like transcriptional regulator;<br><b>PDBTitle:</b> the crystal structure of a tet-like transcriptional regulator from2 rhodococcus sp. rha1.  |
| 65 | <a href="#">c2np5A</a> | Alignment | not modelled | 99.8 | 13 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of a transcriptional regulator (rha1_ro04179) from2 rhodococcus sp. rha1.  |
| 66 | <a href="#">c3c2bA</a> | Alignment | not modelled | 99.8 | 14 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tet family;<br><b>PDBTitle:</b> crystal structure of tet transcriptional regulator from agrobacterium2 tumefaciens   |
| 67 | <a href="#">c2rekA</a> | Alignment | not modelled | 99.8 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative tet-family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of tet-family transcriptional regulator  |
| 68 | <a href="#">c1t33B</a> | Alignment | not modelled | 99.8 | 12 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional repressor (tet/acrr family);<br><b>PDBTitle:</b> structural genomics, the crystal structure of a putative2 transcriptional repressor (tet/acrr family) from salmonella3 typhimurim lt2 |
| 69 | <a href="#">c2d6yA</a> | Alignment | not modelled | 99.8 | 12 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative tet family regulatory protein;<br><b>PDBTitle:</b> crystal structure of transcriptional factor sco4008 from streptomyces2 coelicolor a3(2)   |
| 70 | <a href="#">c3lsjA</a> | Alignment | not modelled | 99.8 | 15 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> dest;<br><b>PDBTitle:</b> crystal structure of dest in complex with palmitoyl-coa   |
| 71 | <a href="#">c3nnrA</a> | Alignment | not modelled | 99.8 | 14 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tet family;<br><b>PDBTitle:</b> crystal structure of a tet-family transcriptional regulator2 (maqu_3571) from marinobacter aquaeolei vt8 at 2.49 a resolution                        |
| 72 | <a href="#">c3bjbE</a> | Alignment | not modelled | 99.8 | 16 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> E: <b>PDB Molecule:</b> probable transcriptional regulator, tet family protein;<br><b>PDBTitle:</b> crystal structure of a tet transcriptional regulator from rhodococcus2 sp. rha1   |
| 73 | <a href="#">c2qwtA</a> | Alignment | not modelled | 99.8 | 20 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tet family;<br><b>PDBTitle:</b> crystal structure of the tet transcription regulatory2 protein from mycobacterium vanbaalenii  |
|    |                        |           |              |      |    | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative tet-family transcriptional   |

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|----|--------------------------|-----------|--------------|------|----|---|
| 74 | <a href="#">c3c07B_</a>  | Alignment | not modelled | 99.8 | 20 | regulator;<br><b>PDBTitle:</b> crystal structure of a tetr family transcriptional regulator from2 streptomyces coelicolor a3(2)   |
| 75 | <a href="#">c3b81A_</a>  | Alignment | not modelled | 99.8 | 16 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, acrr family;<br><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 |
| 76 | <a href="#">c3mnlA_</a>  | Alignment | not modelled | 99.8 | 16 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein (probably tetr-family);<br><b>PDBTitle:</b> the crystal structure of kstr (rv3574) from mycobacterium tuberculosis2 h37rv  |
| 77 | <a href="#">c1zk8A_</a>  | Alignment | not modelled | 99.8 | 14 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family;<br><b>PDBTitle:</b> crystal structure of transcriptional regulator from bacillus cereus2 atcc 14579   |
| 78 | <a href="#">c3aqsD_</a>  | Alignment | not modelled | 99.8 | 14 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> D: <b>PDB Molecule:</b> bacterial regulatory proteins, tetr family;<br><b>PDBTitle:</b> crystal structure of rolr (ncgl1110) without ligand   |
| 79 | <a href="#">c3cdlA_</a>  | Alignment | not modelled | 99.8 | 17 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator aefr;<br><b>PDBTitle:</b> crystal structure of a tetr family transcriptional regulator from2 pseudomonas syringae pv. tomato str. dc3000  |
| 80 | <a href="#">c2qcoA_</a>  | Alignment | not modelled | 99.8 | 15 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> cmer;<br><b>PDBTitle:</b> crystal structure of the transcriptional regulator cmer from2 campylobacter jejuni  |
| 81 | <a href="#">c2zcxA_</a>  | Alignment | not modelled | 99.8 | 16 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> tetr-family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of tetr family transcriptional regulator2 sco7815  |
| 82 | <a href="#">c2of7A_</a>  | Alignment | not modelled | 99.8 | 15 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator;<br><b>PDBTitle:</b> structural genomics, the crystal structure of a tetr-family2 transcriptional regulator from streptomyces coelicolor a3  |
| 83 | <a href="#">c3g56A_</a>  | Alignment | not modelled | 99.8 | 12 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> regulator of macrolide 2'-phosphotransferase i;<br><b>PDBTitle:</b> structure of the macrolide biosensor protein, mphr(a)   |
| 84 | <a href="#">c2dgd8D_</a> | Alignment | not modelled | 99.8 | 15 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative tetr-family transcriptional regulatory protein;<br><b>PDBTitle:</b> crystal structure of the putative trasncriptional regulator sco75182 from streptomyces coelicolor a3(2)  |
| 85 | <a href="#">c2fd5A_</a>  | Alignment | not modelled | 99.8 | 14 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> the crystal structure of a transcriptional regulator from pseudomonas2 aeruginosa pa01   |
| 86 | <a href="#">c3cjdB_</a>  | Alignment | not modelled | 99.8 | 13 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, tetr family;<br><b>PDBTitle:</b> crystal structure of putative tetr transcriptional regulator2 (yp_510936.1) from jannaschia sp. ccs1 at 1.79 a resolution                                     |
| 87 | <a href="#">c3qkxB_</a>  | Alignment | not modelled | 99.8 | 18 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator hi_0893;<br><b>PDBTitle:</b> crystal structure of a tetr-family transcriptional regulator (hi0893)2 from haemophilus influenzae rd at 2.35 a resolution                |
| 88 | <a href="#">c2dg7A_</a>  | Alignment | not modelled | 99.8 | 13 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)   |
| 89 | <a href="#">c3colB_</a>  | Alignment | not modelled | 99.8 | 14 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative transcription regulator;<br><b>PDBTitle:</b> crystal structure of putative transcription regulator from2 lactobacillus plantarum   |
| 90 | <a href="#">c2eh3A_</a>  | Alignment | not modelled | 99.8 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of aq_1058, a transcriptional regulator (terr/acrr2 family) from aquifex aeolicus vf5  |
| 91 | <a href="#">c3iuvA_</a>  | Alignment | not modelled | 99.8 | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized tetr family protein;<br><b>PDBTitle:</b> the structure of a member of tetr family (sco1917) from2 streptomyces coelicolor a3  |
| 92 | <a href="#">c3geuC_</a>  | Alignment | not modelled | 99.8 | 18 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> C: <b>PDB Molecule:</b> intercellular adhesion protein r;<br><b>PDBTitle:</b> crystal structure of icar from staphylococcus aureus, a member of the2 tetracycline repressor protein family  |
| 93 | <a href="#">c3crjC_</a>  | Alignment | not modelled | 99.8 | 14 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> C: <b>PDB Molecule:</b> transcription regulator;<br><b>PDBTitle:</b> crystal structure of a tetr transcription regulator from haloarcula2 marismortui atcc 43049  |
| 94 | <a href="#">c2y31A_</a>  | Alignment | not modelled | 99.8 | 16 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative repressor simreg2;<br><b>PDBTitle:</b> simocyclinone c4 bound form of tetr-like repressor simr   |
| 95 | <a href="#">c2zcmB_</a>  | Alignment | not modelled | 99.8 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> biofilm operon icaabdc hth-type negative transcriptional<br><b>PDBTitle:</b> crystal structure of icar, a repressor of the tetr family  |
| 96 | <a href="#">c2jk3A_</a>  | Alignment | not modelled | 99.8 | 13 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> hemolysin ii regulatory protein;<br><b>PDBTitle:</b> crystal structure of the hlyiir mutant protein with2 residues 169-186 substituted by gssgssg linker  |
| 97 | <a href="#">c3kkdA_</a>  | Alignment | not modelled | 99.8 | 12 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> structure of a putative tetr transcriptional regulator (pa3699) from2 pseudomonas aeruginosa pa01  |
| 98 | <a href="#">c2yvvhA_</a> | Alignment | not modelled | 99.8 | 16 | <b>PDB header:</b> transcription/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of the operator-binding form of the  |



|     |                         |           |              |      |    |  |
|-----|-------------------------|-----------|--------------|------|----|--|
|     |                         |           |              |      |    | multi-drug2 binding transcriptional repressor cgmR   |
| 99  | <a href="#">c3nxC_A</a> | Alignment | not modelled | 99.8 | 17 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> hth-type protein slma;<br><b>PDBTitle:</b> molecular mechanism by which the escherichia coli nucleoid occlusion2 factor, slma, keeps cytokinesis in check                          |
| 100 | <a href="#">c3o60A</a>  | Alignment | not modelled | 99.8 | 9  | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> lin0861 protein;<br><b>PDBTitle:</b> the crystal structure of lin0861 from listeria innocua to 2.8a  |
| 101 | <a href="#">c2pz9A</a>  | Alignment | not modelled | 99.8 | 16 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative regulatory protein;<br><b>PDBTitle:</b> crystal structure of putative transcriptional regulator sco4942 from2 streptomyces coelicolor   |
| 102 | <a href="#">c3bniA</a>  | Alignment | not modelled | 99.7 | 15 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor                   |
| 103 | <a href="#">c1z0xA</a>  | Alignment | not modelled | 99.7 | 11 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family;<br><b>PDBTitle:</b> crystal structure of transcriptional regulator, tetr family from2 enterococcus faecalis v583                                 |
| 104 | <a href="#">c3bqyA</a>  | Alignment | not modelled | 99.7 | 15 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of a possible tetr family transcriptional regulator2 from streptomyces coelicolor a3(2). |
| 105 | <a href="#">c3fiwB</a>  | Alignment | not modelled | 99.7 | 15 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator;<br><b>PDBTitle:</b> structure of sco0253, a tetr-family transcriptional regulator from2 streptomyces coelicolor                |
| 106 | <a href="#">c3ni7A</a>  | Alignment | not modelled | 99.7 | 15 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> bacterial regulatory proteins, tetr family;<br><b>PDBTitle:</b> crystal structure of the tetr transcriptional regulator from2 nitrosomonas europaea atcc 19718                 |
| 107 | <a href="#">c2g7lA</a>  | Alignment | not modelled | 99.7 | 12 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> tetr-family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of putative transcription regulator sco7704 from2 streptomyces coelicor                                     |
| 108 | <a href="#">c3kkcB</a>  | Alignment | not modelled | 99.7 | 11 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> tetr family transcriptional regulator;<br><b>PDBTitle:</b> the crystal structure of tetr transcriptional regulator from2 streptococcus agalactiae 2603v                        |
| 109 | <a href="#">c2guhA</a>  | Alignment | not modelled | 99.7 | 21 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of the putative tetr-family transcriptional2 regulator from rhodococcus sp. rha1                   |
| 110 | <a href="#">c2hxoB</a>  | Alignment | not modelled | 99.7 | 13 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator;<br><b>PDBTitle:</b> structure of the transcriptional regulator sco7222, a tetr from2 streptomyces coelicolor                             |
| 111 | <a href="#">c3b6aC</a>  | Alignment | not modelled | 99.7 | 13 | <b>PDB header:</b> transcription<br><b>Chain:</b> C: <b>PDB Molecule:</b> actr protein;<br><b>PDBTitle:</b> crystal structure of the streptomyces coelicolor tetr2 family protein actr in complex with actinorhodin  |
| 112 | <a href="#">c2iu5A</a>  | Alignment | not modelled | 99.7 | 10 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> hth-type dhaklm operon transcriptional activator dhas;<br><b>PDBTitle:</b> dihydroxyacetone kinase operon activator dhas   |
| 113 | <a href="#">c3egqB</a>  | Alignment | not modelled | 99.7 | 12 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> tetr family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of a tetr-family transcriptional regulator (af_1817)2 from archaeoglobus fulgidus at 2.55 a resolution      |
| 114 | <a href="#">c2vprA</a>  | Alignment | not modelled | 99.7 | 11 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> tetracycline resistance repressor protein;<br><b>PDBTitle:</b> tet repressor class h in complex with 5a,6-2 anhydrotetracycline-mg   |
| 115 | <a href="#">c1bjzA</a>  | Alignment | not modelled | 99.7 | 16 | <b>PDB header:</b> transcription regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> tetracycline repressor;<br><b>PDBTitle:</b> tetracycline chelated mg2+-ion initiates helix unwinding for tet2 repressor induction   |
| 116 | <a href="#">c2qkoA</a>  | Alignment | not modelled | 99.7 | 12 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, tetr family protein;<br><b>PDBTitle:</b> crystal structure of transcriptional regulator rha06399 from2 rhodococcus sp. rha1                          |
| 117 | <a href="#">c2g7gA</a>  | Alignment | not modelled | 99.6 | 14 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> rha04620, putative transcriptional regulator;<br><b>PDBTitle:</b> the crystal structure of the putative transcriptional regulator2 rha04620 from rhodococcus sp. rha1                    |
| 118 | <a href="#">c2hxiA</a>  | Alignment | not modelled | 99.6 | 24 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator;<br><b>PDBTitle:</b> structural genomics, the crystal structure of a putative2 transcriptional regulator from streptomyces coelicolor a3(2)           |
| 119 | <a href="#">c2oerA</a>  | Alignment | not modelled | 99.6 | 11 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator;<br><b>PDBTitle:</b> probable transcriptional regulator from pseudomonas2 aeruginosa  |
| 120 | <a href="#">c2w53B</a>  | Alignment | not modelled | 99.6 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> repressor;<br><b>PDBTitle:</b> structure of smet, the repressor of the stenotrophomonas2 maltophilia multi drug efflux pump smedef.  |