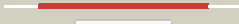
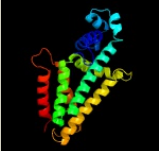


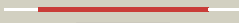



















Phyre2

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|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3295 (-) _3676063_3676728 |
| Date | Thu Aug 8 16:20:50 BST 2019 |
| Unique Job ID | 15491cee25366eef |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c4w97A_ |  Alignment |  | 99.9 | 16 | PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional repressor kstr2; PDBTitle: structure of ketosteroid transcriptional regulator kstr2 of2 mycobacterium tuberculosis |
| 2 | c3ccyA_ |  Alignment |  | 99.9 | 14 | PDB header: transcription regulator Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of a tetr-family transcriptional regulator from2 bordetella parapertussis 12822 |
| 3 | c3f1bA_ |  Alignment |  | 99.9 | 20 | PDB header: transcription regulator Chain: A: PDB Molecule: tetr-like transcriptional regulator; PDBTitle: the crystal structure of a tetr-like transcriptional regulator from2 rhodococcus sp. rha1. |
| 4 | c3himA_ |  Alignment |  | 99.9 | 18 | PDB header: transcription regulator Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: the crystal structure of a bacterial regulatory protein in the tetr2 family from rhodococcus rha1 to 2.2a |
| 5 | c2pbxB_ |  Alignment |  | 99.9 | 18 | PDB header: transcription Chain: B: PDB Molecule: hemagglutinin/protease regulatory protein; PDBTitle: vibrio cholerae hapr |
| 6 | c3lwiA_ |  Alignment |  | 99.9 | 14 | PDB header: transcription regulator Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of putative tetr-family transcriptional regulator2 (yp_752756.1) from syntrophomonas wolfei str. goettingen at 2.07 a3 resolution |
| 7 | c3e7qB_ |  Alignment |  | 99.9 | 16 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: the crystal structure of the putative transcriptional regulator from2 pseudomonas aeruginosa pao1 |
| 8 | c2qibA_ |  Alignment |  | 99.9 | 19 | PDB header: transcription Chain: A: PDB Molecule: tetr-family transcriptional regulator; PDBTitle: crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor |
| 9 | c3dcfB_ |  Alignment |  | 99.9 | 19 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator of the tetr/acrr family; PDBTitle: crystal structure of transcriptional regulator of the tetr/acrr family2 (yp_290855.1) from thermobifida fusca yx-er1 at 2.50 a resolution |
| 10 | c3vprA_ |  Alignment |  | 99.9 | 21 | PDB header: dna binding protein Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of a tetr family transcriptional regulator pfmr from2 thermus thermophilus hb8 |
| 11 | c2hyjA_ |  Alignment |  | 99.9 | 12 | PDB header: transcription Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: the crystal structure of a tetr-family transcriptional regulator from2 streptomyces coelicolor |

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|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c5gpcC_ | Alignment | | 99.9 | 15 | PDB header: transcription, dna binding protein/dna Chain: C: PDB Molecule: transcriptional regulator (tetr/acrr family); PDBTitle: structural analysis of fatty acid degradation regulator fadr from2 bacillus halodurans |
| 13 | c1vi0B_ | Alignment | | 99.9 | 15 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator |
| 14 | c4me9B_ | Alignment | | 99.9 | 14 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of a transcriptional regulator, tetr family2 (bce_2991) from bacillus cereus atcc 10987 at 2.50 a resolution |
| 15 | c2genA_ | Alignment | | 99.9 | 18 | PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: structural genomics, the crystal structure of a probable2 transcriptional regulator from pseudomonas aeruginosa pao1 |
| 16 | c3anpD_ | Alignment | | 99.9 | 17 | PDB header: transcription Chain: D: PDB Molecule: transcriptional repressor, tetr family; PDBTitle: crystal structure of thermus thermophilus fadr, a tetr family2 transcriptional repressor, in complex with lauroyl-coa. |
| 17 | c2fbqA_ | Alignment | | 99.9 | 15 | PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: the crystal structure of transcriptional regulator pa3006 |
| 18 | c3pasA_ | Alignment | | 99.9 | 14 | PDB header: transcription regulator Chain: A: PDB Molecule: tetr family transcription regulator; PDBTitle: crystal structure of a tetr family transcription regulator (maqu_1417)2 from marinobacter aquaeolei vt8 at 1.90 a resolution |
| 19 | c5k7fA_ | Alignment | | 99.9 | 15 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of apo aibr |
| 20 | c2rasB_ | Alignment | | 99.9 | 13 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of a putative tetr/acrr family transcriptional2 regulator (saro_0558) from novosphingobium aromaticivorans dsm at3 1.80 a resolution |
| 21 | c1u9nA_ | Alignment | not modelled | 99.9 | 17 | PDB header: dna binding protein Chain: A: PDB Molecule: transcriptional repressor ethr; PDBTitle: crystal structure of the transcriptional regulator ethr in2 a ligand bound conformation opens therapeutic perspectives3 against tuberculosis and leprosy |
| 22 | c2f07A_ | Alignment | not modelled | 99.9 | 11 | PDB header: transcription Chain: A: PDB Molecule: yvdt; PDBTitle: crystal structure of yvdt from bacillus subtilis |
| 23 | c2uxoB_ | Alignment | not modelled | 99.9 | 17 | PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional regulator ttgr; PDBTitle: ttgr in complex with tetracycline |
| 24 | c2g7sA_ | Alignment | not modelled | 99.9 | 12 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: the crystal structure of transcriptional regulator, tetr family, from2 agrobacterium tumefaciens |
| 25 | c5d19A_ | Alignment | not modelled | 99.9 | 15 | PDB header: transcription Chain: A: PDB Molecule: tetr family transcriptional regulator; PDBTitle: crystal structure of mycobacterium tuberculosis rv0302, form ii |
| 26 | c5ztcA_ | Alignment | not modelled | 99.9 | 12 | PDB header: transcription Chain: A: PDB Molecule: lmo2088 protein; PDBTitle: apo structure of tetr family transcription regulator lmo2088 of2 listeria monocytogenes egde |
| 27 | c3qbmA_ | Alignment | not modelled | 99.9 | 15 | PDB header: transcription regulator Chain: A: PDB Molecule: tetr transcriptional regulator; PDBTitle: crystal structure of a tetr transcriptional regulator (caur_2221) from2 chloroflexus aurantiacus j-10-fl at 1.80 a resolution |
| 28 | c3eupA_ | Alignment | not modelled | 99.9 | 10 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: the crystal structure of the transcriptional regulator, tetr |

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|----|-------------------------|-----------|--------------|------|--|
| | | | | | family2 from cytophaga hutchinsonii |
| 29 | c6azhA_ | Alignment | not modelled | 99.9 | 13 PDB header: transcription Chain: A: PDB Molecule: tetr family transcriptional regulator; PDBTitle: clostridium perfringens putative fatty acid metabolism regulator |
| 30 | c2ibdB_ | Alignment | not modelled | 99.9 | 16 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: possible transcriptional regulator; PDBTitle: crystal structure of probable transcriptional regulatory protein2 rha5900 |
| 31 | c5d1rA_ | Alignment | not modelled | 99.9 | 15 PDB header: transcription Chain: A: PDB Molecule: rv1816 transcriptional regulator; PDBTitle: crystal structure of mycobacterium tuberculosis rv1816 transcriptional2 regulator. |
| 32 | c2iaiA_ | Alignment | not modelled | 99.9 | 15 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative transcriptional regulator sco3833; PDBTitle: crystal structure of sco3833, a member of the tetr transcriptional2 regulator family from streptomyces coelicolor a3 |
| 33 | c1pb6D_ | Alignment | not modelled | 99.9 | 15 PDB header: transcription Chain: D: PDB Molecule: hypothetical transcriptional regulator ycdc; PDBTitle: crystal structure of hypothetical transcriptional regulator ycdc |
| 34 | c4ichA_ | Alignment | not modelled | 99.9 | 12 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a putative tetr family transcriptional regulator2 from saccharomonospora viridis dsm 43017 |
| 35 | c2qtqB_ | Alignment | not modelled | 99.9 | 12 PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of a predicted dna-binding transcriptional regulator2 (saro_1072) from novosphingobium aromaticivorans dsm at 1.85 a3 resolution |
| 36 | c2nx4A_ | Alignment | not modelled | 99.9 | 13 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: transcriptional regulator, tetr family protein; PDBTitle: the crystal structure of athe putative tetr-family transcriptional2 regulator rha06780 from rhodococcus sp. rha1. |
| 37 | c3on2C_ | Alignment | not modelled | 99.9 | 17 PDB header: structural genomics, unknown function Chain: C: PDB Molecule: probable transcriptional regulator; PDBTitle: structure of a protein with unknown function from rhodococcus sp. rha1 |
| 38 | c4cgrA_ | Alignment | not modelled | 99.9 | 18 PDB header: transcription Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: structure of regulator protein sco3201 from streptomyces coelicolor |
| 39 | c3bcqA_ | Alignment | not modelled | 99.9 | 15 PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator acrr; PDBTitle: conformational changes of the acrr regulator reveal a2 mechanism of induction |
| 40 | c5vl9D_ | Alignment | not modelled | 99.9 | 11 PDB header: transcription/dna Chain: D: PDB Molecule: regulatory protein tetr; PDBTitle: crystal structure of eilr in complex with eilo dna element |
| 41 | c3ppbB_ | Alignment | not modelled | 99.9 | 14 PDB header: transcription regulator Chain: B: PDB Molecule: putative tetr family transcription regulator; PDBTitle: crystal structure of a putative tetr family transcription regulator2 (shew_3104) from shewanella sp. pv-4 at 2.10 a resolution |
| 42 | c2raeA_ | Alignment | not modelled | 99.9 | 18 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, acrr family protein; PDBTitle: crystal structure of a tetr/acrr family transcriptional regulator from2 rhodococcus sp. rha1 |
| 43 | c3bhqB_ | Alignment | not modelled | 99.9 | 13 PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a putative tetr-family transcriptional regulator2 (mlr_4833) from mesorhizobium loti maff303099 at 1.54 a resolution |
| 44 | c3nrgA_ | Alignment | not modelled | 99.9 | 19 PDB header: transcription Chain: A: PDB Molecule: tetr family transcriptional regulator; PDBTitle: crystal structure of a tetr family transcriptional regulator2 (caur_2714) from chloroflexus aurantiacus j-10-fl at 2.56 a3 resolution |
| 45 | c3mn1A_ | Alignment | not modelled | 99.9 | 19 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulatory protein (probably tetr-family); PDBTitle: the crystal structure of kstr (rv3574) from mycobacterium tuberculosis2 h37rv |
| 46 | c3c07B_ | Alignment | not modelled | 99.9 | 20 PDB header: transcription regulator Chain: B: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of a tetr family transcriptional regulator from2 streptomyces coelicolor a3(2) |
| 47 | c3lsjA_ | Alignment | not modelled | 99.9 | 14 PDB header: transcription Chain: A: PDB Molecule: dest; PDBTitle: crystal structure of dest in complex with palmitoyl-coa |
| 48 | c5dajB_ | Alignment | not modelled | 99.8 | 16 PDB header: transcription regulator Chain: B: PDB Molecule: nald; PDBTitle: crystal structure of nald, the secondary repressor of mexab-oprm2 multidrug efflux pump in pseudomonas aeruginosa |
| 49 | c2zb9A_ | Alignment | not modelled | 99.8 | 15 PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of tetr family transcription regulator2 sco0332 |
| 50 | c4g12A_ | Alignment | not modelled | 99.8 | 20 PDB header: dna binding protein Chain: A: PDB Molecule: probable transcriptional regulatory protein (probably tetr- PDBTitle: crystal structure of putative tetr family transcriptional regulator,2 fad35r, from mycobacterium tuberculosis |
| 51 | c2hytA_ | Alignment | not modelled | 99.8 | 20 PDB header: transcription Chain: A: PDB Molecule: tetr-family transcriptional regulator; PDBTitle: crystal structure of a tetr-family transcriptional regulator (eca1819)2 from pectobacterium atrosepticum at 1.64 a resolution |

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|----|------------------------|-----------|--------------|------|----|---|
| 52 | c1rktA | Alignment | not modelled | 99.8 | 11 | PDB header: transcription Chain: A: PDB Molecule: protein yfir; PDBTitle: crystal structure of yfir, a putative transcriptional regulator from2 bacillus subtilis |
| 53 | c5mwrB | Alignment | not modelled | 99.8 | 11 | PDB header: transcription Chain: B: PDB Molecule: tetr family transcriptional regulator; PDBTitle: the fadr transcription regulator from sulfolobus acidocaldarius |
| 54 | c5ovyA | Alignment | not modelled | 99.8 | 19 | PDB header: dna binding protein Chain: A: PDB Molecule: putative transcriptional regulator, tetr family; PDBTitle: crystal structure of mab_4384 tetr |
| 55 | c3cjdB | Alignment | not modelled | 99.8 | 19 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of putative tetr transcriptional regulator2 (yp_510936.1) from jannaschia sp. ccs1 at 1.79 a resolution |
| 56 | c2oi8A | Alignment | not modelled | 99.8 | 17 | PDB header: transcription Chain: A: PDB Molecule: putative regulatory protein sco4313; PDBTitle: crystal structure of putative regulatory protein sco4313 |
| 57 | c3s5rA | Alignment | not modelled | 99.8 | 13 | PDB header: dna binding protein Chain: A: PDB Molecule: transcriptional regulator tetr family; PDBTitle: crystal structure of a putative transcriptional regulator of the tetr2 family (syn_02108) from syntrophus aciditrophicus at 2.60 a3 resolution |
| 58 | c3rh2A | Alignment | not modelled | 99.8 | 13 | PDB header: dna binding protein Chain: A: PDB Molecule: hypothetical tetr-like transcriptional regulator; PDBTitle: crystal structure of a tetr-like transcriptional regulator (sama_0099)2 from shewanella amazonensis sb2b at 2.42 a resolution |
| 59 | c3vuqD | Alignment | not modelled | 99.8 | 16 | PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (tetr/acrr family); PDBTitle: crystal structure of ttha0167, a transcriptional regulator, tetr/acrr2 family from thermus thermophilus hb8 |
| 60 | c6ayhA | Alignment | not modelled | 99.8 | 13 | PDB header: transcription Chain: A: PDB Molecule: tetr family transcriptional regulator; PDBTitle: salmonella enterica gusr |
| 61 | c3brua | Alignment | not modelled | 99.8 | 16 | PDB header: transcription Chain: A: PDB Molecule: regulatory protein, tetr family; PDBTitle: crystal structure of regulatory protein tetr from rhodobacter2 sphaeroides |
| 62 | c3g7rB | Alignment | not modelled | 99.8 | 15 | PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of sco4454, a tetr-family transcriptional regulator2 from streptomyces coelicolor |
| 63 | c1jumB | Alignment | not modelled | 99.8 | 12 | PDB header: transcription Chain: B: PDB Molecule: hypothetical transcriptional regulator in qaca 5' region; PDBTitle: crystal structure of the multidrug binding transcriptional repressor2 qacr bound to the natural drug berberine |
| 64 | c2wuiA | Alignment | not modelled | 99.8 | 12 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of mexz, a key repressor responsible for2 antibiotic resistance in pseudomonas aeruginosa. |
| 65 | c2g3bB | Alignment | not modelled | 99.8 | 19 | PDB header: transcription Chain: B: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of putative tetr-family transcriptional regulator2 from rhodococcus sp. |
| 66 | c3dewA | Alignment | not modelled | 99.8 | 15 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: the structure of a putative tetr family transcriptional regulator from2 geobacter sulfurreducens pca. |
| 67 | c3bjbE | Alignment | not modelled | 99.8 | 19 | PDB header: transcription regulator Chain: E: PDB Molecule: probable transcriptional regulator, tetr family protein; PDBTitle: crystal structure of a tetr transcriptional regulator from rhodococcus2 sp. rha1 |
| 68 | c3vibD | Alignment | not modelled | 99.8 | 14 | PDB header: dna binding protein Chain: D: PDB Molecule: mtrr; PDBTitle: structural basis for multidrug recognition and antimicrobial2 resistance by mtrr, an efflux pump regulator from neisseria3 gonorrhoeae |
| 69 | c2gfnA | Alignment | not modelled | 99.8 | 17 | PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator pksa related protein; PDBTitle: crystal structure of hth-type transcriptional regulator pksa related2 protein from rhodococcus sp. rha1 |
| 70 | c1zk8A | Alignment | not modelled | 99.8 | 14 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of transcriptional regulator from bacillus cereus2 atcc 14579 |
| 71 | c3nnrA | Alignment | not modelled | 99.8 | 9 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of a tetr-family transcriptional regulator2 (maqu_3571) from marinobacter aquaeolei vt8 at 2.49 a resolution |
| 72 | c3rd3B | Alignment | not modelled | 99.8 | 20 | PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulator; PDBTitle: structure of pseudomonas aeruginosa transcriptional regulator pa2196 |
| 73 | c4yzeD | Alignment | not modelled | 99.8 | 16 | PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional repressor nemr; PDBTitle: crystal structure of e.coli nemr reduced form |
| 74 | c6mj1A | Alignment | not modelled | 99.8 | 10 | PDB header: dna binding protein Chain: A: PDB Molecule: probable hth-type transcriptional regulator yttp; PDBTitle: crystal structure of refz (regulator of ftsz) from bacillus subtilis |
| 75 | c4gctA | Alianment | not modelled | 99.8 | 18 | PDB header: dna binding protein/dna Chain: A: PDB Molecule: nucleoid occlusion factor slma; |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | PDBTitle: structure of no factor protein-dna complex |
| 76 | c1zkgB_ | Alignment | not modelled | 99.8 | 19 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of transcriptional regulator, tetr family (tm1030)2 from thermotoga maritima at 2.30 a resolution |
| 77 | c3he0A_ | Alignment | not modelled | 99.8 | 20 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: the structure of a putative transcriptional regulator tetr family2 protein from vibrio parahaemolyticus. |
| 78 | c3qkxB_ | Alignment | not modelled | 99.8 | 14 | PDB header: transcription regulator Chain: B: PDB Molecule: uncharacterized hth-type transcriptional regulator hi_0893; PDBTitle: crystal structure of a tetr-family transcriptional regulator (hi0893)2 from haemophilus influenzae rd at 2.35 a resolution |
| 79 | c3f0cA_ | Alignment | not modelled | 99.8 | 14 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator from cytophaga2 hutchinsonii atcc 33406 |
| 80 | c2zcxA_ | Alignment | not modelled | 99.8 | 13 | PDB header: transcription Chain: A: PDB Molecule: tetr-family transcriptional regulator; PDBTitle: crystal structure of tetr family transcriptional regulator2 sco7815 |
| 81 | c3npiB_ | Alignment | not modelled | 99.8 | 12 | PDB header: gene regulation Chain: B: PDB Molecule: tetr family regulatory protein; PDBTitle: crystal structure of a tetr family regulatory protein (dip1788) from2 corynebacterium diphtheriae at 2.96 a resolution |
| 82 | c2of7A_ | Alignment | not modelled | 99.8 | 19 | PDB header: transcription regulator; Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: structural genomics, the crystal structure of a tetr-family2 transcriptional regulator from streptomyces coelicolor a3 |
| 83 | c2np5A_ | Alignment | not modelled | 99.8 | 18 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator (rha1_ro04179) from2 rhodococcus sp. rha1. |
| 84 | c5d1wD_ | Alignment | not modelled | 99.8 | 16 | PDB header: transcription Chain: D: PDB Molecule: rv3249c transcriptional regulator; PDBTitle: crystal structure of mycobacterium tuberculosis rv3249c2 transcriptional regulator. |
| 85 | c4za6A_ | Alignment | not modelled | 99.8 | 14 | PDB header: signaling protein Chain: A: PDB Molecule: tetr family transcriptional regulator; PDBTitle: structure of the r. erythropolis transcriptional repressor qsdr from2 tetr family |
| 86 | c3jsjC_ | Alignment | not modelled | 99.8 | 12 | PDB header: transcription regulator; Chain: C: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of a putative tetr-transcriptional regulator2 (sav143) from streptomyces avermitilis ma-4680 at 2.10 a resolution |
| 87 | c5e57B_ | Alignment | not modelled | 99.8 | 15 | PDB header: translation Chain: B: PDB Molecule: transcription regulator amtr; PDBTitle: crystal structure of mycobacterium smegmatis amtr |
| 88 | c3gziA_ | Alignment | not modelled | 99.8 | 20 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of a transcriptional regulator of the tetr family2 (shew_3567) from shewanella loihica pv-4 at 2.05 a resolution |
| 89 | c2hkuB_ | Alignment | not modelled | 99.8 | 17 | PDB header: transcription regulator Chain: B: PDB Molecule: a putative transcriptional regulator; PDBTitle: structural genomics, the crystal structure of a putative2 transcriptional regulator from rhodococcus sp. rha1 |
| 90 | c3vw0D_ | Alignment | not modelled | 99.8 | 14 | PDB header: transcription regulator Chain: D: PDB Molecule: putative regulatory protein; PDBTitle: crystal structure of the dequalinium-bound form of ramr2 (transcriptional regulator of tetr family) from salmonella3 typhimurium |
| 91 | c6g8hC_ | Alignment | not modelled | 99.8 | 19 | PDB header: transcription Chain: C: PDB Molecule: tetr/acrr family transcriptional regulator; PDBTitle: flavonoid-responsive regulator frra in complex with naringenin |
| 92 | c2qcoA_ | Alignment | not modelled | 99.8 | 13 | PDB header: transcription Chain: A: PDB Molecule: cmcr; PDBTitle: crystal structure of the transcriptional regulator cmcr from2 campylobacter jejuni |
| 93 | c1t33B_ | Alignment | not modelled | 99.8 | 18 | PDB header: transcription Chain: B: PDB Molecule: putative transcriptional repressor (tetr/acrr family); PDBTitle: structural genomics, the crystal structure of a putative2 transcriptional repressor (tetr/acrr family) from salmonella3 typhimurium lt2 |
| 94 | c3mvpA_ | Alignment | not modelled | 99.8 | 13 | PDB header: transcription regulator Chain: A: PDB Molecule: tetr/acrr transcriptional regulator; PDBTitle: the crystal structure of a tetr/acrr transcriptional regulator from2 streptococcus mutans to 1.85a |
| 95 | c4udsA_ | Alignment | not modelled | 99.8 | 13 | PDB header: transcription Chain: A: PDB Molecule: mbdr regulator; PDBTitle: crystal structure of mbdr regulator from azoarcus sp. cib |
| 96 | c3djpB_ | Alignment | not modelled | 99.8 | 11 | PDB header: dna binding protein Chain: B: PDB Molecule: transcription regulator, tetr family; PDBTitle: the crystal structure of a tetr transcription regulator2 from silicibacter pomeroyi dss |
| 97 | c3aqsD_ | Alignment | not modelled | 99.8 | 18 | PDB header: transcription regulator Chain: D: PDB Molecule: bacterial regulatory proteins, tetr family; PDBTitle: crystal structure of rolr (ncgl1110) without ligand |
| 98 | c1z0xA_ | Alignment | not modelled | 99.8 | 13 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of transcriptional regulator, tetr family from2 enterococcus faecalis v583 |
| 99 | c3ni7A_ | Alignment | not modelled | 99.8 | 15 | PDB header: transcription regulator Chain: A: PDB Molecule: bacterial regulatory proteins, tetr family; |

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|-----|------------------------|-----------|--------------|------|----|---|
| 99 | c3m7A | Alignment | not modelled | 99.8 | 15 | PDBTitle: crystal structure of the tetr transcriptional regulator from2 nitrosomonas europaea atcc 19718 PDB header: transcription |
| 100 | c2rekA | Alignment | not modelled | 99.8 | 15 | Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of tetr-family transcriptional regulator |
| 101 | c3c2bA | Alignment | not modelled | 99.8 | 13 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of tetr transcriptional regulator from agrobacterium2 tumefaciens |
| 102 | c5xs9B | Alignment | not modelled | 99.8 | 16 | PDB header: transcription Chain: B: PDB Molecule: tetr family transcriptional regulator; PDBTitle: crystal structure of mycobacterium smegmatis bioq |
| 103 | c4nn1A | Alignment | not modelled | 99.8 | 19 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator rv1219c of2 mycobacterium tuberculosis |
| 104 | c6ayiA | Alignment | not modelled | 99.8 | 13 | PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator uidr; PDBTitle: escherichia coli gusr |
| 105 | c3geuC | Alignment | not modelled | 99.8 | 13 | PDB header: cell adhesion Chain: C: PDB Molecule: intercellular adhesion protein r; PDBTitle: crystal structure of icar from staphylococcus aureus, a member of the2 tetracycline repressor protein family |
| 106 | c1ui6B | Alignment | not modelled | 99.8 | 14 | PDB header: antibiotic Chain: B: PDB Molecule: a-factor receptor homolog; PDBTitle: crystal structure of gamma-butyrolactone receptor (arpa-like protein) |
| 107 | c3colB | Alignment | not modelled | 99.8 | 14 | PDB header: transcription regulator Chain: B: PDB Molecule: putative transcription regulator; PDBTitle: crystal structure of putative transcription regulator from2 lactobacillus plantarum |
| 108 | c2id3A | Alignment | not modelled | 99.8 | 17 | PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator sco5951 from2 streptomyces coelicolor a3(2) |
| 109 | c2y31A | Alignment | not modelled | 99.8 | 14 | PDB header: transcription Chain: A: PDB Molecule: putative repressor simreg2; PDBTitle: simocyclinone c4 bound form of tetr-like repressor simr |
| 110 | c2dg8D | Alignment | not modelled | 99.8 | 15 | PDB header: gene regulation Chain: D: PDB Molecule: putative tetr-family transcriptional regulatory protein; PDBTitle: crystal structure of the putative transcripational regulator sco75182 from streptomyces coelicolor a3(2) |
| 111 | c2q24A | Alignment | not modelled | 99.8 | 18 | PDB header: transcription Chain: A: PDB Molecule: putative tetr family transcriptional regulator; PDBTitle: crystal structure of tetr transcriptional regulator sco0520 from2 streptomyces coelicolor |
| 112 | c5fg1A | Alignment | not modelled | 99.8 | 10 | PDB header: apoptosis Chain: A: PDB Molecule: nicr; PDBTitle: co-crystal structure of nicr2_hsp |
| 113 | c3b81A | Alignment | not modelled | 99.8 | 16 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, acrr family; PDBTitle: crystal structure of predicted dna-binding transcriptional regulator2 of tetr/acrr family (np_350189.1) from clostridium acetobutylicum at3 2.10 a resolution |
| 114 | c2fq4A | Alignment | not modelled | 99.8 | 16 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: the crystal structure of the transcriptional regulator (tetr family)2 from bacillus cereus |
| 115 | c3v6gA | Alignment | not modelled | 99.8 | 12 | PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulatory protein (probably deor- PDBTitle: crystal structure of transcriptional regulator |
| 116 | c5ydpC | Alignment | not modelled | 99.8 | 14 | PDB header: gene regulation Chain: C: PDB Molecule: tetr transcriptional regulatory protein; PDBTitle: crystal structure of tetr family repressor alkx from dietzia sp.2 strain dq12-45-1b implicated in biodegradation of n-alkanes |
| 117 | c2hxoB | Alignment | not modelled | 99.8 | 12 | PDB header: transcription Chain: B: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: structure of the transcriptional regulator sco7222, a tetr from2 streptomyces coelicolor |
| 118 | c2eh3A | Alignment | not modelled | 99.8 | 13 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of aq_1058, a transcriptional regulator (terr/acrr2 family) from aquifex aeolicus vf5 |
| 119 | c3g56A | Alignment | not modelled | 99.8 | 12 | PDB header: dna binding protein Chain: A: PDB Molecule: regulator of macrolide 2'-phosphotransferase i; PDBTitle: structure of the macrolide biosensor protein, mphr(a) |
| 120 | c4j13B | Alignment | not modelled | 99.8 | 17 | PDB header: transcription/dna Chain: B: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of ms6564-dna complex |