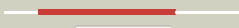




















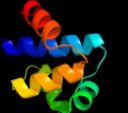


Phyre2

| | |
|---------------|-----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2745c (-) _3058203_3058541 |
| Date | Wed Aug 7 12:50:40 BST 2019 |
| Unique Job ID | 92dedf77930b53b5 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c1y9qA_ |  Alignment |  | 99.8 | 23 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, hth_3 family; PDBTitle: crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae |
| 2 | c5woqA_ |  Alignment |  | 99.8 | 80 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator clgr; PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis |
| 3 | c3f52A_ |  Alignment |  | 99.8 | 55 | PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum |
| 4 | c2bnoA_ |  Alignment |  | 99.7 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis. |
| 5 | c2ewtA_ |  Alignment |  | 99.7 | 24 | PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bldd |
| 6 | c3ivpD_ |  Alignment |  | 99.7 | 24 | PDB header: dna binding protein Chain: D: PDB Molecule: putative transposon-related dna-binding protein; PDBTitle: the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630. |
| 7 | d1y9qa1 |  Alignment |  | 99.7 | 22 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain |
| 8 | c3vk0B_ |  Alignment |  | 99.7 | 22 | PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhft from2 neisseria |
| 9 | d2b5aa1 |  Alignment |  | 99.7 | 28 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like |
| 10 | c3op9A_ |  Alignment |  | 99.7 | 15 | PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua |
| 11 | c3c1cC_ |  Alignment |  | 99.7 | 19 | PDB header: transcription regulator/dna Chain: C: PDB Molecule: regulatory protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.espl396i tetramer in complex with its natural 35 base-pair operator |

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|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c3lisB_ | Alignment | | 99.7 | 18 | PDB header: transcription Chain: B: PDB Molecule: csp231i c protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form) |
| 13 | d1rioa_ | Alignment | | 99.7 | 6 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors |
| 14 | c6b9rD_ | Alignment | | 99.7 | 20 | PDB header: oxidoreductase Chain: D: PDB Molecule: hydroxyethylphosphonate dioxygenase; PDBTitle: streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound |
| 15 | c2kpiA_ | Alignment | | 99.7 | 15 | PDB header: transcription regulator Chain: A: PDB Molecule: sos-response transcriptional repressor, lexa; PDBTitle: solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a |
| 16 | c3mifC_ | Alignment | | 99.7 | 17 | PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus. |
| 17 | c1b0nA_ | Alignment | | 99.7 | 29 | PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex |
| 18 | c6b9tH_ | Alignment | | 99.7 | 14 | PDB header: oxidoreductase Chain: H: PDB Molecule: methylphosphonate synthase; PDBTitle: crystal structure of mpns with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound |
| 19 | c5d4zF_ | Alignment | | 99.7 | 14 | PDB header: dna binding protein Chain: F: PDB Molecule: repressor; PDBTitle: crystal structure of repressor from salmonella-temperate phage |
| 20 | c3f6wE_ | Alignment | | 99.7 | 15 | PDB header: dna binding protein Chain: E: PDB Molecule: xre-family like protein; PDBTitle: xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000 |
| 21 | c2mezA_ | Alignment | not modelled | 99.7 | 18 | PDB header: rna binding protein Chain: A: PDB Molecule: multi-protein bridging factor (mbp-like); PDBTitle: flexible anchoring of archaeal mbf1 on ribosomes suggests role as2 recruitment factor |
| 22 | c3zhiA_ | Alignment | not modelled | 99.7 | 11 | PDB header: transcription Chain: A: PDB Molecule: ci; PDBTitle: n-terminal domain of the ci repressor from bacteriophage tp901-1 |
| 23 | c5jubA_ | Alignment | not modelled | 99.6 | 22 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of comr from s.thermophilus in complex with dna and2 its signalling peptide coms. |
| 24 | d1y7ya1 | Alignment | not modelled | 99.6 | 21 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like |
| 25 | d2r1jl1 | Alignment | not modelled | 99.6 | 27 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors |
| 26 | c4o8bA_ | Alignment | not modelled | 99.6 | 19 | PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of transcriptional regulator bswr |
| 27 | c2o38A_ | Alignment | not modelled | 99.6 | 11 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator |
| 28 | d2o38a1 | Alignment | not modelled | 99.6 | 11 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354 |
| | | | | | | PDB header: structural genomics, unknown function |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c3kxaD | Alignment | not modelled | 99.6 | 22 | Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae |
| 30 | d1adra | Alignment | not modelled | 99.6 | 25 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors |
| 31 | d1b0na2 | Alignment | not modelled | 99.6 | 29 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like |
| 32 | c2ebyA | Alignment | not modelled | 99.6 | 11 | PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli |
| 33 | d2ofya1 | Alignment | not modelled | 99.6 | 29 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like |
| 34 | d2icta1 | Alignment | not modelled | 99.6 | 13 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like |
| 35 | d1r69a | Alignment | not modelled | 99.6 | 15 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors |
| 36 | c3omtA | Alignment | not modelled | 99.6 | 17 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae. |
| 37 | c3b7hA | Alignment | not modelled | 99.6 | 19 | PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11 |
| 38 | c4mcxE | Alignment | not modelled | 99.6 | 18 | PDB header: toxin Chain: E: PDB Molecule: antidote protein; PDBTitle: p. vulgaris higba structure, crystal form 2 |
| 39 | c3eusB | Alignment | not modelled | 99.6 | 15 | PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi |
| 40 | d1x57a1 | Alignment | not modelled | 99.6 | 26 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like |
| 41 | d2croa | Alignment | not modelled | 99.6 | 21 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors |
| 42 | c3bs3A | Alignment | not modelled | 99.6 | 16 | PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis |
| 43 | d1sq8a | Alignment | not modelled | 99.6 | 21 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors |
| 44 | d1lmb3 | Alignment | not modelled | 99.6 | 6 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors |
| 45 | d1llib | Alignment | not modelled | 99.6 | 5 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors |
| 46 | c4pu4C | Alignment | not modelled | 99.6 | 17 | PDB header: toxin/antitoxin/dna Chain: C: PDB Molecule: toxin-antitoxin system antidote transcriptional repressor PDBTitle: shewanella oneidensis mr-1 toxin antitoxin system hipa, hipb and its2 operator dna complex (space group p21) |
| 47 | c3cecA | Alignment | not modelled | 99.6 | 13 | PDB header: transcription Chain: A: PDB Molecule: putative antidote protein of plasmid maintenance system; PDBTitle: crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution |
| 48 | c5fd4B | Alignment | not modelled | 99.6 | 28 | PDB header: transcription regulator Chain: B: PDB Molecule: comr; PDBTitle: crystal structure of comr from streptococcus suis |
| 49 | d1utxa | Alignment | not modelled | 99.6 | 24 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like |
| 50 | c2ef8A | Alignment | not modelled | 99.6 | 21 | PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is |
| 51 | c2jvIA | Alignment | not modelled | 99.6 | 22 | PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei |
| 52 | c3dnvB | Alignment | not modelled | 99.6 | 15 | PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein |
| 53 | d2a6ca1 | Alignment | not modelled | 99.6 | 22 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354 |
| 54 | c3pxpA | Alignment | not modelled | 99.6 | 18 | PDB header: transcription regulator Chain: A: PDB Molecule: helix-turn-helix domain protein; PDBTitle: crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution |
| 55 | c2trbA | Alignment | not modelled | 99.5 | 7 | PDB header: dna binding protein Chain: A: PDB Molecule: virulence-associated protein i; |

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|----|-------------------------|-----------|--------------|------|----|--|
| 55 | c3u6A | Alignment | not modelled | 99.5 | 7 | PDBTitle: structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii PDB header: dna binding protein |
| 56 | c4rykA | Alignment | not modelled | 99.5 | 29 | Chain: A: PDB Molecule: lmo0325 protein; PDBTitle: crystal structure of a putative transcriptional regulator from2 listeria monocytogenes egd-e |
| 57 | c4yv9C | Alignment | not modelled | 99.5 | 23 | PDB header: dna binding protein/inhibitor Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: x-ray crystal structure of streptococcus dysgalactiae shp pheromone2 receptor rgg2 |
| 58 | c6f8sA | Alignment | not modelled | 99.5 | 18 | PDB header: toxin Chain: A: PDB Molecule: xre family transcriptional regulator; PDBTitle: toxin-antitoxin complex grata |
| 59 | c2xcjB | Alignment | not modelled | 99.5 | 17 | PDB header: viral protein Chain: B: PDB Molecule: c protein; PDBTitle: crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2 |
| 60 | c4ghjA | Alignment | not modelled | 99.5 | 29 | PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator from2 vibrio vulnificus. |
| 61 | c5uk3J | Alignment | not modelled | 99.5 | 19 | PDB header: lyase Chain: J: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of cyanase from t. urticae |
| 62 | c3bdnB | Alignment | not modelled | 99.5 | 7 | PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor |
| 63 | c3qyxD | Alignment | not modelled | 99.5 | 20 | PDB header: transcription/dna Chain: D: PDB Molecule: esx-1 secretion-associated regulator espr; PDBTitle: crystal structure of mycobacterium tuberculosis espr in complex with a2 small dna fragment |
| 64 | c2grmB | Alignment | not modelled | 99.5 | 20 | PDB header: transcription Chain: B: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/icf10 complex |
| 65 | c4ybaA | Alignment | not modelled | 99.5 | 20 | PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein c; PDBTitle: the structure of the c.kpn2i controller protein |
| 66 | c2wusR | Alignment | not modelled | 99.5 | 19 | PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape protein rodz |
| 67 | c3t76A | Alignment | not modelled | 99.5 | 18 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii |
| 68 | c2qfcB | Alignment | not modelled | 99.5 | 23 | PDB header: transcription regulation Chain: B: PDB Molecule: plcr protein; PDBTitle: crystal structure of bacillus thuringiensis plcr complexed with papr |
| 69 | c2axzC | Alignment | not modelled | 99.4 | 20 | PDB header: transcription Chain: C: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/ccf10 complex |
| 70 | c3fymA | Alignment | not modelled | 99.4 | 19 | PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the 1a structure of ymfm, a putative dna-binding membrane2 protein from staphylococcus aureus |
| 71 | c4gqmA | Alignment | not modelled | 99.4 | 18 | PDB header: unknown function Chain: A: PDB Molecule: ct009; PDBTitle: crystal structure of a helix-turn-helix containing hypothetical2 protein (ct009) from chlamydia trachomatis in a sub-domain swap3 conformation |
| 72 | c2fjrB | Alignment | not modelled | 99.3 | 18 | PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186 |
| 73 | c5j9iH | Alignment | not modelled | 99.3 | 16 | PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain |
| 74 | c2ppxA | Alignment | not modelled | 99.2 | 21 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1735; PDBTitle: crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens |
| 75 | d2ppxA1 | Alignment | not modelled | 99.2 | 21 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like |
| 76 | c3fmyA | Alignment | not modelled | 99.2 | 14 | PDB header: dna binding protein Chain: A: PDB Molecule: hth-type transcriptional regulator mqsa PDBTitle: structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021) |
| 77 | c5d50I | Alignment | not modelled | 99.2 | 10 | PDB header: dna binding protein Chain: I: PDB Molecule: repressor; PDBTitle: crystal structure of rep-ant complex from salmonella-temperate phage |
| 78 | c5jaaB | Alignment | not modelled | 99.2 | 17 | PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 toxin-antitoxin complex |
| 79 | c6fkgC | Alignment | not modelled | 98.9 | 20 | PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex. |
| 80 | c3gn5B | Alignment | not modelled | 98.9 | 19 | PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021) |
| 81 | c3r1fO | Alignment | not modelled | 98.7 | 20 | PDB header: transcription Chain: O: PDB Molecule: esx-1 secretion-associated regulator espr; PDBTitle: crystal structure of a key regulator of virulence in |

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|-----|-------------------------|-----------|--------------|------|---|
| | | | | | mycobacterium2 tuberculosis |
| 82 | c2mqkA_ | Alignment | not modelled | 98.1 | 15 PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the mub aaa+ atpase |
| 83 | d1dwka1 | Alignment | not modelled | 97.8 | 10 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain |
| 84 | d1nera_ | Alignment | not modelled | 97.7 | 13 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors |
| 85 | c5u57B_ | Alignment | not modelled | 97.7 | 19 PDB header: oxidoreductase Chain: B: PDB Molecule: (s)-2-hydroxypropylphosphonic acid epoxidase; PDBTitle: psf4 in complex with fe2+ and (s)-2-hpp |
| 86 | c2iv1J_ | Alignment | not modelled | 97.7 | 10 PDB header: lyase Chain: J: PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase |
| 87 | c3bd1B_ | Alignment | not modelled | 97.0 | 18 PDB header: transcription Chain: B: PDB Molecule: cro protein; PDBTitle: structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1 |
| 88 | c5j2yA_ | Alignment | not modelled | 97.0 | 16 PDB header: gene regulation/dna Chain: A: PDB Molecule: regulatory protein; PDBTitle: molecular insight into the regulatory mechanism of the quorum-sensing2 repressor rsal in pseudomonas aeruginosa |
| 89 | c4la3B_ | Alignment | not modelled | 96.8 | 19 PDB header: lyase Chain: B: PDB Molecule: dimethylsulphoniopropionate (dmisp) lyase dddq; PDBTitle: crystal structure of dimethylsulphoniopropionate (dmisp) lyase dddq2 y131a in complex with dmisp |
| 90 | d1ic8a2 | Alignment | not modelled | 96.6 | 16 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain |
| 91 | d1lcda_ | Alignment | not modelled | 96.6 | 23 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator |
| 92 | d2bnma1 | Alignment | not modelled | 96.6 | 14 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like |
| 93 | d2bjca1 | Alignment | not modelled | 96.5 | 23 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator |
| 94 | d2hsqa1 | Alignment | not modelled | 96.5 | 18 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator |
| 95 | d1au7a2 | Alignment | not modelled | 96.4 | 17 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain |
| 96 | c2auwB_ | Alignment | not modelled | 96.4 | 11 PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718 |
| 97 | d1e3oc2 | Alignment | not modelled | 96.4 | 21 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain |
| 98 | c1efaa_ | Alignment | not modelled | 96.3 | 23 PDB header: transcription/dna Chain: A: PDB Molecule: lac repressor; PDBTitle: crystal structure of the lac repressor dimer bound to operator and the2 anti-inducer onpf |
| 99 | d1efaa1 | Alignment | not modelled | 96.3 | 22 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator |
| 100 | c2k9qB_ | Alignment | not modelled | 96.2 | 18 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of hth_xre family transcriptional2 regulator bt_p548217 from bacteroides thetaiotaomicron.3 northeast structural genomics consortium target btr244. |
| 101 | c2l8nA_ | Alignment | not modelled | 96.0 | 21 PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional repressor cytr; PDBTitle: nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna |
| 102 | d1qpza1 | Alignment | not modelled | 96.0 | 24 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator |
| 103 | c2lcva_ | Alignment | not modelled | 96.0 | 22 PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional repressor cytr; PDBTitle: structure of the cytidine repressor dna-binding domain; an alternate2 calculation |
| 104 | c1au7B_ | Alignment | not modelled | 95.8 | 28 PDB header: transcription/dna Chain: B: PDB Molecule: protein pit-1; PDBTitle: pit-1 mutant/dna complex |
| 105 | c1bdhA_ | Alignment | not modelled | 95.7 | 24 PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex |
| 106 | c3kxD_ | Alignment | not modelled | 95.7 | 29 PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi |
| 107 | c1lbgB_ | Alignment | not modelled | 95.7 | 23 PDB header: PDB COMPND: |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 108 | c3k2zA_ | Alignment | not modelled | 95.6 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: lexa repressor; PDBTitle: crystal structure of a lexa protein from thermotoga maritima |
| 109 | c3h5tA_ | Alignment | not modelled | 95.6 | 22 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum |
| 110 | c3l1pA_ | Alignment | not modelled | 95.6 | 21 | PDB header: transcription/dna Chain: A: PDB Molecule: pou domain, class 5, transcription factor 1; PDBTitle: pou protein:dna complex |
| 111 | c1ic8B_ | Alignment | not modelled | 95.6 | 17 | PDB header: transcription/dna Chain: B: PDB Molecule: hepatocyte nuclear factor 1-alpha; PDBTitle: hepatocyte nuclear factor 1a bound to dna : mody3 gene product |
| 112 | c5yszA_ | Alignment | not modelled | 95.6 | 30 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: transcriptional regulator celr-cellobiose complex |
| 113 | d1uxca_ | Alignment | not modelled | 95.5 | 21 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator |
| 114 | d1uxda_ | Alignment | not modelled | 95.5 | 25 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator |
| 115 | c1zvva_ | Alignment | not modelled | 95.3 | 18 | PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex |
| 116 | c2xsdC_ | Alignment | not modelled | 95.1 | 26 | PDB header: transcription/dna Chain: C: PDB Molecule: pou domain, class 3, transcription factor 1; PDBTitle: crystal structure of the dimeric oct-6 (pou3f1) pou domain2 bound to palindromic more dna |
| 117 | c3d1nK_ | Alignment | not modelled | 95.0 | 22 | PDB header: transcription regulator/dna Chain: K: PDB Molecule: pou domain, class 6, transcription factor 1; PDBTitle: structure of human brn-5 transcription factor in complex2 with corticotrophin-releasing hormone gene promoter |
| 118 | c3vwbA_ | Alignment | not modelled | 94.9 | 12 | PDB header: transcription/dna Chain: A: PDB Molecule: virulence regulon transcriptional activator virb; PDBTitle: crystal structure of virb core domain (se-met derivative) complexed2 with the cis-acting site (5-bru modifications) upstream ic5b promoter |
| 119 | c2h8rA_ | Alignment | not modelled | 94.6 | 17 | PDB header: transcription activator/dna Chain: A: PDB Molecule: hepatocyte nuclear factor 1-beta; PDBTitle: hepatocyte nuclear factor 1b bound to dna: mody5 gene2 product |
| 120 | d2awia1 | Alignment | not modelled | 94.6 | 22 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: PrgX N-terminal domain-like |