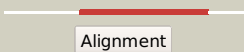

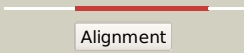



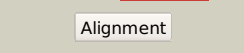



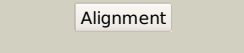

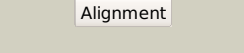



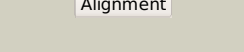

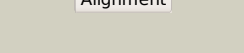

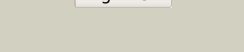



Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2528c_(mrr)_2851761_2852681 |
| Date | Wed Aug 7 12:50:16 BST 2019 |
| Unique Job ID | a3c6de974af2ab71 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c4oc8A_ |  Alignment |  | 100.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: restriction endonuclease aspbhi; PDBTitle: dna modification-dependent restriction endonuclease aspbhi |
| 2 | c4f0qC_ |  Alignment |  | 100.0 | 25 | PDB header: hydrolase Chain: C: PDB Molecule: restriction endonuclease; PDBTitle: mspji restriction endonuclease - p21 form |
| 3 | c4f0qA_ |  Alignment |  | 99.9 | 27 | PDB header: hydrolase Chain: A: PDB Molecule: restriction endonuclease; PDBTitle: mspji restriction endonuclease - p21 form |
| 4 | d1y88a2 |  Alignment |  | 99.9 | 20 | Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: MRR-like |
| 5 | c1y88A_ |  Alignment |  | 99.9 | 19 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1548; PDBTitle: crystal structure of protein of unknown function af1548 |
| 6 | c4xqkB_ |  Alignment |  | 97.2 | 26 | PDB header: hydrolase/dna Chain: B: PDB Molecule: llabiii; PDBTitle: atp-dependent type isp restriction-modification enzyme llabiii bound2 to dna |
| 7 | c3b73A_ |  Alignment |  | 96.7 | 21 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phih1 repressor-like protein; PDBTitle: crystal structure of the phih1 repressor-like protein from haloarcula2 marismortui |
| 8 | d1xmx_ |  Alignment |  | 96.6 | 17 | Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hypothetical protein VC1899 |
| 9 | d1ob8a_ |  Alignment |  | 96.1 | 11 | Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like |
| 10 | d1gefa_ |  Alignment |  | 95.9 | 19 | Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like |
| 11 | c3fovA_ |  Alignment |  | 95.3 | 19 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0102 protein rpa0323; PDBTitle: crystal structure of protein rpa0323 of unknown function from2 rhodopseudomonas palustris |

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|----|-------------------------|-----------|--------------|------|----|---|
| 12 | d1r7ja_ | Alignment | | 95.2 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Archaeal DNA-binding protein |
| 13 | d1uhma_ | Alignment | | 94.9 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5 |
| 14 | c2eo0A_ | Alignment | | 94.8 | 19 | PDB header: dna binding protein Chain: A: PDB Molecule: hypothetical protein st1444; PDBTitle: crystal structure of holliday junction resolvase st1444 |
| 15 | c5dymA_ | Alignment | | 94.6 | 16 | PDB header: dna binding protein Chain: A: PDB Molecule: padr-family transcriptional regulator; PDBTitle: crystal structure of a padr family transcription regulator from2 hypervirulent clostridium difficile r20291 - cdpadr_0991 to 1.893 angstrom resolution |
| 16 | c4esfA_ | Alignment | | 94.5 | 20 | PDB header: transcription Chain: A: PDB Molecule: padr-like transcriptional regulator; PDBTitle: crystal structure of padr-like transcriptional regulator (bce3449)2 from bacillus cereus strain atcc 10987 |
| 17 | c5flmE_ | Alignment | | 94.3 | 15 | PDB header: transcription Chain: E: PDB Molecule: dna-directed rna polymerases i, ii, and iii subunit rpabc1; PDBTitle: structure of transcribing mammalian rna polymerase ii |
| 18 | c6jyb_ | Alignment | | 94.2 | 18 | PDB header: transcription Chain: B: PDB Molecule: transcriptional repressor padr; PDBTitle: crystal structure of the padr-like transcriptional regulator bc17562 from bacillus cereus |
| 19 | c1f5tA_ | Alignment | | 94.2 | 22 | PDB header: transcription/dna Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence |
| 20 | c3f8fA_ | Alignment | | 94.1 | 13 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, padr-like family; PDBTitle: crystal structure of multidrug binding transcriptional regulator lmrr2 complexed with daunomycin |
| 21 | c5h20A_ | Alignment | not modelled | 94.0 | 24 | PDB header: transcription regulator Chain: A: PDB Molecule: putative padr-family transcriptional regulatory protein; PDBTitle: x-ray structure of padr-like transcription factor from bacteroid2 fragilis |
| 22 | c4esbA_ | Alignment | not modelled | 94.0 | 19 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, padr family; PDBTitle: crystal structure of padr-like transcriptional regulator (bc4206) from2 bacillus cereus strain atcc 14579 |
| 23 | c3hhhA_ | Alignment | not modelled | 94.0 | 15 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, padr family; PDBTitle: crystal structure of transcriptional regulator, a member of padr2 family, from enterococcus faecalis v583 |
| 24 | c1g3wA_ | Alignment | not modelled | 93.8 | 22 | PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr |
| 25 | c5zhcA_ | Alignment | not modelled | 93.6 | 25 | PDB header: dna binding protein Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of the padr-family transcriptional regulator rv34882 of mycobacterium tuberculosis h37rv |
| 26 | c4o6jA_ | Alignment | not modelled | 93.6 | 14 | PDB header: metal binding protein Chain: A: PDB Molecule: iron-dependent transcription repressor related protein; PDBTitle: crystal sturcture of t. acidophilum ider |
| 27 | c5x11G_ | Alignment | not modelled | 93.5 | 23 | PDB header: transcription/dna Chain: G: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of bacillus subtilis padr in complex with operator2 dna |
| 28 | c2it0A_ | Alignment | not modelled | 93.5 | 25 | PDB header: transcription/dna Chain: A: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of a two-domain ider-dna complex crystal2 form ii |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c3I09B_ | Alignment | not modelled | 93.5 | 17 | PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator2 (jann_22dec04_contig27_revised_gene3569) from jannaschia sp. ccs1 at3 2.81 a resolution |
| 30 | c3I7wA_ | Alignment | not modelled | 93.5 | 19 | PDB header: transcription Chain: A: PDB Molecule: putative uncharacterized protein smu.1704; PDBTitle: the crystal structure of smu.1704 from streptococcus mutans ua159 |
| 31 | c6faqA_ | Alignment | not modelled | 93.4 | 17 | PDB header: dna binding protein Chain: A: PDB Molecule: dna binding protein; PDBTitle: structure of h. salinarum rosr (vng0258) grown from kbr |
| 32 | c2dqlA_ | Alignment | not modelled | 93.2 | 16 | PDB header: circadian clock protein Chain: A: PDB Molecule: pex protein; PDBTitle: crystal structure of the circadian clock associated protein pex from2 anabaena |
| 33 | d1xmaa_ | Alignment | not modelled | 92.9 | 11 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PadR-like |
| 34 | c1xmaA_ | Alignment | not modelled | 92.9 | 11 | PDB header: transcription Chain: A: PDB Molecule: predicted transcriptional regulator; PDBTitle: structure of a transcriptional regulator from clostridium thermocellum2 cth-833 |
| 35 | c1fx7C_ | Alignment | not modelled | 92.9 | 23 | PDB header: signaling protein Chain: C: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of the iron-dependent regulator (ider) from2 mycobacterium tuberculosis |
| 36 | d1yg2a_ | Alignment | not modelled | 92.8 | 21 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PadR-like |
| 37 | c3I9fD_ | Alignment | not modelled | 92.2 | 19 | PDB header: transcription regulator Chain: D: PDB Molecule: putative uncharacterized protein smu.1604c; PDBTitle: the crystal structure of smu.1604c from streptococcus mutans ua159 |
| 38 | c5cviB_ | Alignment | not modelled | 92.1 | 16 | PDB header: transcription regulator Chain: B: PDB Molecule: slor; PDBTitle: structure of the manganese regulator slor |
| 39 | d1dzfa1 | Alignment | not modelled | 91.9 | 19 | Fold: Restriction endonuclease-like Superfamily: Eukaryotic RPB5 N-terminal domain Family: Eukaryotic RPB5 N-terminal domain |
| 40 | c2e1nA_ | Alignment | not modelled | 91.8 | 14 | PDB header: circadian clock protein Chain: A: PDB Molecule: pex; PDBTitle: crystal structure of the cyanobacterium circadian clock modifier pex |
| 41 | c5zqhA_ | Alignment | not modelled | 91.6 | 15 | PDB header: dna binding protein Chain: A: PDB Molecule: padr family transcriptional regulator; PDBTitle: crystal structure of streptococcus transcriptional regulator |
| 42 | d2esha1 | Alignment | not modelled | 91.4 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PadR-like |
| 43 | d1hsta_ | Alignment | not modelled | 91.2 | 10 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5 |
| 44 | d1ussa_ | Alignment | not modelled | 91.2 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5 |
| 45 | d1usta_ | Alignment | not modelled | 91.0 | 15 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5 |
| 46 | c2wj0B_ | Alignment | not modelled | 91.0 | 18 | PDB header: hydrolase/dna Chain: B: PDB Molecule: archaeal hjc; PDBTitle: crystal structures of holliday junction resolvases from2 archaeoglobus fulgidus bound to dna substrate |
| 47 | c2IsoA_ | Alignment | not modelled | 90.7 | 14 | PDB header: nuclear protein Chain: A: PDB Molecule: histone h1x; PDBTitle: solution nmr structure of the globular domain of human histone h1x,2 northeast structural genomics consortium (nesg) target hr7057a |
| 48 | c4a5mH_ | Alignment | not modelled | 90.6 | 21 | PDB header: transcription Chain: H: PDB Molecule: uncharacterized hth-type transcriptional regulator yybr; PDBTitle: redox regulator hyper in its oxidized form |
| 49 | c2h09A_ | Alignment | not modelled | 90.5 | 18 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator mntr; PDBTitle: crystal structure of diphtheria toxin repressor like protein2 from e. coli |
| 50 | c2rqpA_ | Alignment | not modelled | 90.2 | 12 | PDB header: gene regulation Chain: A: PDB Molecule: heterochromatin protein 1-binding protein 3; PDBTitle: the solution structure of heterochromatin protein 1-binding2 protein 74 histone h1 like domain |
| 51 | c4hqeB_ | Alignment | not modelled | 90.2 | 21 | PDB header: transcription/dna Chain: B: PDB Molecule: transcriptional regulator qsrr; PDBTitle: the crystal structure of qsrr-dna complex |
| 52 | c3elkA_ | Alignment | not modelled | 90.0 | 16 | PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator ta0346; PDBTitle: crystal structure of putative transcriptional regulator ta0346 from2 thermoplasma acidophilum |
| 53 | c5z7bB_ | Alignment | not modelled | 89.8 | 19 | PDB header: transcription Chain: B: PDB Molecule: padr family transcriptional regulator; PDBTitle: crystal structure of the vanr transcription factor in complex with2 vanillate PDB header: transcription |

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|----|-------------------------|-----------|--------------|------|----|--|
| 54 | c3df8A_ | Alignment | not modelled | 89.7 | 25 | Chain: A: PDB Molecule: possible hxlr family transcriptional factor; PDBTitle: the crystal structure of a possible hxlr family transcriptional factor2 from thermoplasma volcanium gss1 |
| 55 | d1hh1a_ | Alignment | not modelled | 88.5 | 21 | Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like |
| 56 | d1yqaa1 | Alignment | not modelled | 88.1 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5 |
| 57 | c3kfwX_ | Alignment | not modelled | 88.1 | 25 | PDB header: structural genomics, unknown function Chain: X: PDB Molecule: uncharacterized protein; PDBTitle: uncharacterized protein rv0674 from mycobacterium tuberculosis |
| 58 | d1ub9a_ | Alignment | not modelled | 87.6 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 59 | d2fswa1 | Alignment | not modelled | 86.9 | 20 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like |
| 60 | c3hruA_ | Alignment | not modelled | 86.3 | 16 | PDB header: transcription Chain: A: PDB Molecule: metalloregulator scar; PDBTitle: crystal structure of scar with bound zn2+ |
| 61 | d1z7ua1 | Alignment | not modelled | 86.2 | 22 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxlR-like |
| 62 | c5hs9A_ | Alignment | not modelled | 85.9 | 20 | PDB header: dna binding protein Chain: A: PDB Molecule: hth-type transcriptional regulator yodb; PDBTitle: crystal structure of the quinone-bound yodb from b. subtilis |
| 63 | c3f6oB_ | Alignment | not modelled | 85.3 | 15 | PDB header: transcription regulator Chain: B: PDB Molecule: probable transcriptional regulator, arsr family PDBTitle: crystal structure of arsr family transcriptional regulator,2 rha00566 |
| 64 | c1y1yE_ | Alignment | not modelled | 84.4 | 19 | PDB header: transferase/transcription/dna-rna hybrid Chain: E: PDB Molecule: dna-directed rna polymerases i, ii, and iii 27 PDBTitle: rna polymerase ii-tfiii-dna/rna complex |
| 65 | c4gcvD_ | Alignment | not modelled | 84.4 | 24 | PDB header: transcription Chain: D: PDB Molecule: putative transcription protein; PDBTitle: structure of a putative transcription factor (pa1374)from pseudomonas2 aeruginosa |
| 66 | d2fnaa1 | Alignment | not modelled | 83.6 | 17 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Helicase DNA-binding domain |
| 67 | c2ev5B_ | Alignment | not modelled | 83.1 | 17 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator mntr; PDBTitle: bacillus subtilis manganese transport regulator (mntr)2 bound to calcium |
| 68 | d2v7fa1 | Alignment | not modelled | 82.9 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rps19E-like |
| 69 | c3ri2B_ | Alignment | not modelled | 82.6 | 29 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, padr-like family; PDBTitle: crystal structure of padr family transcriptional regulator from2 eggerthella lenta dsm 2243 |
| 70 | c4hw0B_ | Alignment | not modelled | 82.5 | 17 | PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein sso10a-2; PDBTitle: crystal structure of sso10a-2, a dna-binding protein from sulfobolus2 solfataricus |
| 71 | d2hr3a1 | Alignment | not modelled | 81.9 | 20 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 72 | c2du9A_ | Alignment | not modelled | 81.7 | 17 | PDB header: transcription Chain: A: PDB Molecule: predicted transcriptional regulators; PDBTitle: crystal structure of the transcriptional factor from c.glutamicum |
| 73 | d1ixsb1 | Alignment | not modelled | 81.5 | 33 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Helicase DNA-binding domain |
| 74 | d1in4a1 | Alignment | not modelled | 80.7 | 37 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Helicase DNA-binding domain |
| 75 | c2oqgA_ | Alignment | not modelled | 80.4 | 18 | PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. rha1 |
| 76 | c5xyiT_ | Alignment | not modelled | 80.3 | 21 | PDB header: ribosome Chain: T: PDB Molecule: ribosomal protein s19e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome |
| 77 | d2d1ha1 | Alignment | not modelled | 80.0 | 24 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like |
| 78 | c3lmmA_ | Alignment | not modelled | 78.8 | 18 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the dip2311 protein from corynebacterium2 diphtheriae, northeast structural genomics consortium target cdr35 |
| 79 | c3h0gE_ | Alignment | not modelled | 78.7 | 22 | PDB header: transcription Chain: E: PDB Molecule: dna-directed rna polymerases i, ii, and iii subunit rpabc1; PDBTitle: rna polymerase ii from schizosaccharomyces pombe |
| | | | | | | PDB header: transcription |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 80 | c5aiqD_ | Alignment | not modelled | 78.5 | 20 | Chain: D: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of ligand-free nadr |
| 81 | c3j38T_ | Alignment | not modelled | 78.0 | 18 | PDB header: ribosome Chain: T: PDB Molecule: 40s ribosomal protein s19a; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins |
| 82 | c3zeyO_ | Alignment | not modelled | 77.8 | 26 | PDB header: ribosome Chain: O: PDB Molecule: ribosomal protein s19, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome |
| 83 | d2a61a1 | Alignment | not modelled | 76.8 | 22 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 84 | c5xxuT_ | Alignment | not modelled | 76.6 | 24 | PDB header: ribosome Chain: T: PDB Molecule: ribosomal protein es19; PDBTitle: small subunit of toxoplasma gondii ribosome |
| 85 | c3j3aT_ | Alignment | not modelled | 76.6 | 15 | PDB header: ribosome Chain: T: PDB Molecule: 40s ribosomal protein s19; PDBTitle: structure of the human 40s ribosomal proteins |
| 86 | c2nyxB_ | Alignment | not modelled | 76.5 | 22 | PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulatory protein, rv1404; PDBTitle: crystal structure of rv1404 from mycobacterium tuberculosis |
| 87 | c3iz6S_ | Alignment | not modelled | 75.7 | 24 | PDB header: ribosome Chain: S: PDB Molecule: 40s ribosomal protein s19 (s19e); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 88 | c6hz9N_ | Alignment | not modelled | 75.4 | 11 | PDB header: dna binding protein Chain: N: PDB Molecule: protein mcrc; PDBTitle: structure of mcrcb without dna binding domains (class 5) |
| 89 | c6j0eB_ | Alignment | not modelled | 74.9 | 20 | PDB header: transcription Chain: B: PDB Molecule: arsenic responsive repressor arsr; PDBTitle: structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression |
| 90 | d2f2ea1 | Alignment | not modelled | 74.5 | 24 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like |
| 91 | c3jyvT_ | Alignment | not modelled | 72.4 | 13 | PDB header: ribosome Chain: T: PDB Molecule: s19e protein; PDBTitle: structure of the 40s rna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution |
| 92 | c6az1X_ | Alignment | not modelled | 72.3 | 18 | PDB header: ribosome/antibiotic Chain: X: PDB Molecule: ribosomal protein s19e; PDBTitle: cryo-em structure of the small subunit of leishmania ribosome bound to2 paromomycin |
| 93 | c4zs8A_ | Alignment | not modelled | 70.4 | 20 | PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional repressor dasr; PDBTitle: crystal structure of ligand-free, full length dasr |
| 94 | c2lnbA_ | Alignment | not modelled | 70.1 | 18 | PDB header: immune system Chain: A: PDB Molecule: z-dna-binding protein 1; PDBTitle: solution nmr structure of n-terminal domain (6-74) of human zbp12 protein, northeast structural genomics consortium target hr8174a. |
| 95 | c2x4hA_ | Alignment | not modelled | 69.4 | 13 | PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfobolus solfataricus |
| 96 | c3u1dA_ | Alignment | not modelled | 69.4 | 21 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the structure of a protein with a gnr superfamily winged-helix-turn-2 helix domain from halomicrobium mukohataei. |
| 97 | d1ixrc1 | Alignment | not modelled | 69.1 | 40 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Helicase DNA-binding domain |
| 98 | c3f6vA_ | Alignment | not modelled | 69.1 | 16 | PDB header: transcription regulator Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: crystal structure of possible transcriptional regulator for arsenical2 resistance |
| 99 | c3boqB_ | Alignment | not modelled | 68.8 | 20 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi |
| 100 | c3edpB_ | Alignment | not modelled | 68.4 | 16 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lin2111 protein; PDBTitle: the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262 |
| 101 | d2p4wa1 | Alignment | not modelled | 67.5 | 17 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PF1790-like |
| 102 | d1ghca_ | Alignment | not modelled | 66.1 | 17 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5 |
| 103 | d3ctaa1 | Alignment | not modelled | 64.6 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 104 | d2etha1 | Alignment | not modelled | 63.8 | 20 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 105 | d2pw9a1 | Alignment | not modelled | 63.7 | 24 | Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: FdhD/NarQ |

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|-----|-------------------------|---|--------------|------|----|--|
| 106 | c2vldA |  Alignment | not modelled | 62.2 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: endonuclease nucs; PDBTitle: crystal structure of a repair endonuclease from pyrococcus abyssi |
| 107 | c4egzA |  Alignment | not modelled | 62.0 | 17 | PDB header: transcription/dna Chain: A: PDB Molecule: arabinose metabolism transcriptional repressor; PDBTitle: crystal structure of arar(dbd) in complex with operator orr3 |
| 108 | c5eriA |  Alignment | not modelled | 61.9 | 12 | PDB header: transcription Chain: A: PDB Molecule: marr family transcriptional regulator; PDBTitle: marr protein from peptoclostridium difficile da00132 |
| 109 | d2fbia1 |  Alignment | not modelled | 61.1 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 110 | c2ma3A |  Alignment | not modelled | 60.7 | 21 | PDB header: replication Chain: A: PDB Molecule: dna replication initiator (cdc21/cdc54); PDBTitle: nmr solution structure of the c-terminus of the minichromosome2 maintenance protein mcm from methanothermobacter thermoautotrophicus |
| 111 | c3eetA |  Alignment | not modelled | 60.7 | 11 | PDB header: transcription regulator Chain: A: PDB Molecule: putative gntr-family transcriptional regulator; PDBTitle: crystal structure of putative gntr-family transcriptional2 regulator |
| 112 | c2xznT |  Alignment | not modelled | 59.0 | 15 | PDB header: ribosome Chain: T: PDB Molecule: rps19e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2 |
| 113 | c3ctaA |  Alignment | not modelled | 59.0 | 24 | PDB header: transferase Chain: A: PDB Molecule: riboflavin kinase; PDBTitle: crystal structure of riboflavin kinase from thermoplasma acidophilum |
| 114 | c2zkzC |  Alignment | not modelled | 58.0 | 17 | PDB header: transcription Chain: C: PDB Molecule: transcriptional repressor pagr; PDBTitle: crystal structure of the transcriptional repressor pagr of bacillus2 anthracis |
| 115 | c2lkbB |  Alignment | not modelled | 57.5 | 19 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, arsr family; PDBTitle: solution structure of apo-nmtr |
| 116 | d2bv6a1 |  Alignment | not modelled | 56.5 | 27 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators |
| 117 | c3bpxB |  Alignment | not modelled | 56.0 | 13 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of marr |
| 118 | d1yyva1 |  Alignment | not modelled | 55.8 | 36 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: HxIR-like |
| 119 | c4pdeA |  Alignment | not modelled | 55.4 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: protein fdhd; PDBTitle: crystal structure of fdhd in complex with gdp |
| 120 | c3nrvC |  Alignment | not modelled | 55.3 | 13 | PDB header: transcription regulator Chain: C: PDB Molecule: putative transcriptional regulator (marr/emrr family); PDBTitle: crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1 |