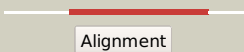
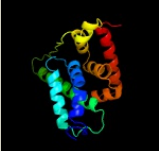
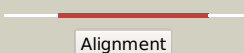

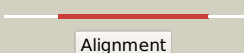

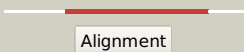
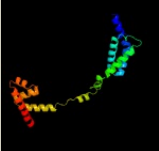
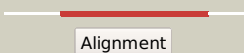

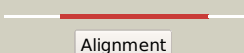

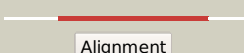





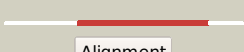

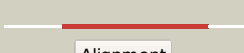



Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1221_(sigE)_1364419_1365192 |
| Date | Wed Jul 31 22:05:31 BST 2019 |
| Unique Job ID | 42ba54c1e61aacc1 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c5uxxC_ |  Alignment |  | 100.0 | 26 | PDB header: dna binding protein/unknown function Chain: C; PDB Molecule: rna polymerase sigma factor; PDBTitle: co-crystal structure of the sigma factor rpoe in complex with the2 anti-sigma factor nepr from bartonella quintana |
| 2 | c4cxfA_ |  Alignment |  | 100.0 | 30 | PDB header: transcription Chain: A; PDB Molecule: rna polymerase sigma factor cnrh; PDBTitle: structure of cnrh in complex with the cytosolic domain of cnry |
| 3 | c6in7B_ |  Alignment |  | 100.0 | 32 | PDB header: transcription Chain: B; PDB Molecule: rna polymerase sigma-h factor; PDBTitle: crystal structure of algu in complex with muca(cyto) |
| 4 | c6dvdF_ |  Alignment |  | 100.0 | 27 | PDB header: transferase/dna Chain: F; PDB Molecule: ecf rna polymerase sigma factor sigl; PDBTitle: crystal structure of mycobacterium tuberculosis transcription2 initiation complex(ecf sigma factor I) with 6 nt spacer and bromine3 labelled in position "-11 |
| 5 | c1or7A_ |  Alignment |  | 100.0 | 29 | PDB header: transcription Chain: A; PDB Molecule: rna polymerase sigma-e factor; PDBTitle: crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea |
| 6 | c5wurB_ |  Alignment |  | 100.0 | 37 | PDB header: metal binding protein Chain: B; PDB Molecule: ecf rna polymerase sigma factor sigw; PDBTitle: crystal structure of sigw in complex with its anti-sigma rsiw, an2 oxidized form |
| 7 | c5ipmF_ |  Alignment |  | 100.0 | 21 | PDB header: transcription, transferase/dna/rna Chain: F; PDB Molecule: rna polymerase sigma factor rpos; PDBTitle: sigmas-transcription initiation complex with 4-nt nascent rna |
| 8 | c5zx3F_ |  Alignment |  | 100.0 | 26 | PDB header: transcription Chain: F; PDB Molecule: ecf rna polymerase sigma factor sigh; PDBTitle: mycobacterium tuberculosis rna polymerase holoenzyme with ecf sigma2 factor sigma h |
| 9 | c3t0yA_ |  Alignment |  | 100.0 | 21 | PDB header: transcription regulator/protein binding Chain: A; PDB Molecule: response regulator; PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr |
| 10 | c5xe7A_ |  Alignment |  | 100.0 | 23 | PDB header: dna binding protein Chain: A; PDB Molecule: ecf rna polymerase sigma factor sigj; PDBTitle: crystal structure of mycobacterium tuberculosis extracytoplasmic2 function sigma factor sigj |
| 11 | c3vdoA_ |  Alignment |  | 100.0 | 27 | PDB header: dna binding protein/protein binding Chain: A; PDB Molecule: rna polymerase sigma factor sigk; PDBTitle: structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rska from mycobacterium3 tuberculosis |

| | | | | | | |
|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | c2q1zA_ | Alignment | | 100.0 | 23 | PDB header: transcription Chain: A: PDB Molecule: rpoe, ecf sige; PDBTitle: crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr |
| 13 | c6c03A_ | Alignment | | 100.0 | 31 | PDB header: transcription Chain: A: PDB Molecule: putative rna polymerase ecf-subfamily sigma factor; PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex |
| 14 | c2lfwA_ | Alignment | | 99.9 | 18 | PDB header: signaling protein Chain: A: PDB Molecule: phyr sigma-like domain; PDBTitle: nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1 |
| 15 | c1rp3G_ | Alignment | | 99.9 | 19 | PDB header: transcription Chain: G: PDB Molecule: rna polymerase sigma factor sigma-28 (flia); PDBTitle: cocrystal structure of the flagellar sigma/anti-sigma complex, sigma-2 28/flgm |
| 16 | c5tw1F_ | Alignment | | 99.9 | 19 | PDB header: transcription activator/transferase/dna Chain: F: PDB Molecule: rna polymerase sigma factor siga; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpA |
| 17 | c6c05F_ | Alignment | | 99.9 | 22 | PDB header: transcription Chain: F: PDB Molecule: rna polymerase sigma factor siga; PDBTitle: mycobacterium tuberculosis rnap holo/rbpA in relaxed state |
| 18 | c3mzyA_ | Alignment | | 99.9 | 22 | PDB header: rna binding protein Chain: A: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a |
| 19 | c3wodF_ | Alignment | | 99.9 | 19 | PDB header: transferase/transcription Chain: F: PDB Molecule: rna polymerase sigma factor; PDBTitle: rna polymerase-gp39 complex |
| 20 | c2a6eF_ | Alignment | | 99.8 | 22 | PDB header: transferase Chain: F: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: crystal structure of the t. thermophilus rna polymerase2 holoenzyme |
| 21 | c1l9uH_ | Alignment | not modelled | 99.8 | 19 | PDB header: transcription Chain: H: PDB Molecule: sigma factor siga; PDBTitle: thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution |
| 22 | d1or7a2 | Alignment | not modelled | 99.7 | 21 | Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors |
| 23 | c4iqcX_ | Alignment | not modelled | 99.7 | 22 | PDB header: transcription, transferase Chain: X: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: x-ray crystal structure of escherichia coli sigma70 holoenzyme |
| 24 | d1or7b2 | Alignment | not modelled | 99.6 | 26 | Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors |
| 25 | c2o7gA_ | Alignment | not modelled | 99.6 | 22 | PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the pribnow box recognition region of sigc from2 mycobacterium tuberculosis |
| 26 | c3iydF_ | Alignment | not modelled | 99.6 | 22 | PDB header: transcription/dna Chain: F: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: three-dimensional em structure of an intact activator-dependent2 transcription initiation complex |
| 27 | d1h3la_ | Alignment | not modelled | 99.6 | 32 | Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors |
| 28 | c3vepA_ | Alignment | not modelled | 99.6 | 32 | PDB header: membrane protein/transcription Chain: A: PDB Molecule: probable rna polymerase sigma-d factor; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda PDB header: transcription/membrane protein |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c3hugA | Alignment | not modelled | 99.5 | 32 | Chain: A: PDB Molecule: rna polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rslA2 in complex with -35 promoter binding domain of sigI |
| 30 | c3n0rA | Alignment | not modelled | 99.5 | 20 | PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr stress response regulator at 1.25 angstrom2 resolution |
| 31 | d1or7a1 | Alignment | not modelled | 99.5 | 37 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain |
| 32 | d1rp3a2 | Alignment | not modelled | 99.5 | 21 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain |
| 33 | c5fgmA | Alignment | not modelled | 99.4 | 47 | PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4 |
| 34 | c2o8xA | Alignment | not modelled | 99.4 | 34 | PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc |
| 35 | d1xsva | Alignment | not modelled | 99.3 | 24 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like |
| 36 | d1s7oa | Alignment | not modelled | 99.3 | 23 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like |
| 37 | d1smyf2 | Alignment | not modelled | 99.2 | 22 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain |
| 38 | d1ttya | Alignment | not modelled | 99.2 | 25 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain |
| 39 | d1rp3a3 | Alignment | not modelled | 99.1 | 19 | Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors |
| 40 | d1ku7a | Alignment | not modelled | 99.1 | 23 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain |
| 41 | d1ku3a | Alignment | not modelled | 99.0 | 23 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain |
| 42 | c4qicC | Alignment | not modelled | 98.9 | 18 | PDB header: signaling protein/dna binding protein Chain: C: PDB Molecule: sensory transduction regulatory protein, anti-anti-sigma PDBTitle: co-crystal structure of anti-anti-sigma factor phyr complexed with2 anti-sigma factor nepr from bartonella quintana |
| 43 | c5d4dP | Alignment | not modelled | 98.9 | 20 | PDB header: transcription/dna Chain: P: PDB Molecule: rna polymerase sigma factor siga; PDBTitle: crystal structure of thermus thermophilus product complex for2 transcription initiation with nad and ctp |
| 44 | c3t72o | Alignment | not modelled | 98.8 | 19 | PDB header: transcription/dna Chain: O: PDB Molecule: pho box dna (strand 1); PDBTitle: phob(e)-sigma70(4)-(rnap-beta-flap-tip-helix)-dna transcription2 activation sub-complex |
| 45 | d2p7vb1 | Alignment | not modelled | 98.8 | 22 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain |
| 46 | c1ku2A | Alignment | not modelled | 98.6 | 21 | PDB header: transcription Chain: A: PDB Molecule: sigma factor siga; PDBTitle: crystal structure of thermus aquaticus rna polymerase sigma2 subunit fragment containing regions 1.2 to 3.1 |
| 47 | d1yioa1 | Alignment | not modelled | 98.5 | 27 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 48 | c4x8kA | Alignment | not modelled | 98.5 | 22 | PDB header: transcription activator Chain: A: PDB Molecule: rna polymerase sigma factor siga; PDBTitle: mycobacterium tuberculosis rbpA-sid in complex with sigmaA domain 2 |
| 49 | c3qp5C | Alignment | not modelled | 98.3 | 16 | PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl) |
| 50 | c4ifuA | Alignment | not modelled | 98.2 | 16 | PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2 |
| 51 | c1x3uA | Alignment | not modelled | 98.2 | 21 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein fixj; PDBTitle: solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot |
| 52 | c3sztB | Alignment | not modelled | 98.2 | 26 | PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscR, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone |
| 53 | c2q0oA | Alignment | not modelled | 98.1 | 21 | PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing |
| | | | | | | PDB header: transcription/dna |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| 54 | c1h0mD_ | Alignment | not modelled | 98.1 | 25 | Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein trar bound2 to its autoinducer and to its target dna |
| 55 | c1zljE_ | Alignment | not modelled | 98.1 | 26 | PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain |
| 56 | d1a04a1 | Alignment | not modelled | 98.0 | 22 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 57 | d1ku2a2 | Alignment | not modelled | 98.0 | 18 | Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors |
| 58 | d1smf3 | Alignment | not modelled | 98.0 | 18 | Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors |
| 59 | d1siga_ | Alignment | not modelled | 97.9 | 14 | Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors |
| 60 | c5yixA_ | Alignment | not modelled | 97.9 | 20 | PDB header: dna binding protein Chain: A: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: caulobacter crescentus gcra sigma-interacting domain (sid) in complex2 with domain 2 of sigma 70 |
| 61 | c2rniA_ | Alignment | not modelled | 97.9 | 19 | PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain |
| 62 | c2krfB_ | Alignment | not modelled | 97.8 | 16 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a |
| 63 | c6jqsA_ | Alignment | not modelled | 97.8 | 28 | PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere |
| 64 | d1p4wa_ | Alignment | not modelled | 97.8 | 25 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 65 | c3c3wB_ | Alignment | not modelled | 97.8 | 25 | PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr |
| 66 | c5f64C_ | Alignment | not modelled | 97.8 | 20 | PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri |
| 67 | c5o8yG_ | Alignment | not modelled | 97.8 | 26 | PDB header: transcription Chain: G: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator. |
| 68 | d1fsea_ | Alignment | not modelled | 97.8 | 28 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 69 | d1l3la1 | Alignment | not modelled | 97.7 | 26 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 70 | c3cloC_ | Alignment | not modelled | 97.6 | 28 | PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution |
| 71 | c4yn8A_ | Alignment | not modelled | 97.6 | 20 | PDB header: dna binding protein Chain: A: PDB Molecule: response regulator chra; PDBTitle: crystal structure of response regulator chra in heme-sensing two2 component system |
| 72 | c3klnC_ | Alignment | not modelled | 97.6 | 27 | PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst |
| 73 | c4if4A_ | Alignment | not modelled | 97.6 | 20 | PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the magnesium and beryll fluoride-activated vvar2 from staphylococcus aureus |
| 74 | c4hyeB_ | Alignment | not modelled | 97.6 | 27 | PDB header: transcription activator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator spr1814 from streptococcus2 pneumoniae reveals unique interdomain contacts among narl family3 proteins |
| 75 | c5hevC_ | Alignment | not modelled | 97.5 | 28 | PDB header: transcription Chain: C: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the beryll fluoride-activated liar from2 enterococcus faecium |
| 76 | c1zn2A_ | Alignment | not modelled | 97.5 | 26 | PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styf |
| 77 | c1rnlA_ | Alignment | not modelled | 97.5 | 21 | PDB header: signal transduction protein Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narl; PDBTitle: the nitrate/nitrite response regulator protein narl from narl |
| 78 | c4go1A_ | Alignment | not modelled | 97.4 | 25 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli. |
| 79 | c2jpcA_ | Alignment | not modelled | 97.4 | 23 | PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | PDBTitle: ssrb dna binding protein |
| 80 | c2w48D_ | Alignment | not modelled | 97.4 | 22 | PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae |
| 81 | c5xt2C_ | Alignment | not modelled | 97.4 | 23 | PDB header: dna binding protein Chain: C: PDB Molecule: response regulator fixj; PDBTitle: crystal structures of full-length fixj from b. japonicum crystallized2 in space group p212121 |
| 82 | c6ideA_ | Alignment | not modelled | 97.3 | 16 | PDB header: transcription/dna Chain: A: PDB Molecule: transcriptional regulator luxr family; PDBTitle: crystal structure of the vibrio cholera vqma-ligand-dna complex2 provides molecular mechanisms for drug design |
| 83 | c1u78A_ | Alignment | not modelled | 96.7 | 15 | PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposable element tc3 transposase; PDBTitle: structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna |
| 84 | c6paxA_ | Alignment | not modelled | 96.4 | 26 | PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions |
| 85 | d1pdnc_ | Alignment | not modelled | 96.3 | 28 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain |
| 86 | c2cfxD_ | Alignment | not modelled | 95.4 | 16 | PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc |
| 87 | d2cfxa1 | Alignment | not modelled | 95.2 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain |
| 88 | d1k78a1 | Alignment | not modelled | 95.1 | 26 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain |
| 89 | c2w7nA_ | Alignment | not modelled | 95.0 | 17 | PDB header: transcription/dna Chain: A: PDB Molecule: trfb transcriptional repressor protein; PDBTitle: crystal structure of kora bound to operator dna: insight into2 repressor cooperation in rp4 gene regulation |
| 90 | c2dbbA_ | Alignment | not modelled | 95.0 | 20 | PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061 |
| 91 | d2d1ha1 | Alignment | not modelled | 94.9 | 12 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like |
| 92 | c2cg4B_ | Alignment | not modelled | 94.9 | 21 | PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc |
| 93 | d2cg4a1 | Alignment | not modelled | 94.9 | 23 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain |
| 94 | d1r1ua_ | Alignment | not modelled | 94.9 | 13 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators |
| 95 | c2vzbA_ | Alignment | not modelled | 94.6 | 23 | PDB header: dna-binding protein Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan |
| 96 | c3korD_ | Alignment | not modelled | 94.4 | 22 | PDB header: transcription Chain: D: PDB Molecule: possible trp repressor; PDBTitle: crystal structure of a putative trp repressor from staphylococcus2 aureus |
| 97 | c2lkpB_ | Alignment | not modelled | 94.3 | 13 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, arsr family; PDBTitle: solution structure of apo-nmtr |
| 98 | d2jn6a1 | Alignment | not modelled | 94.2 | 26 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like |
| 99 | d6paxa1 | Alignment | not modelled | 94.1 | 26 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain |
| 100 | c2m8eA_ | Alignment | not modelled | 94.1 | 19 | PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the pai subdomain of sleeping beauty transposase |
| 101 | c1r22B_ | Alignment | not modelled | 94.1 | 20 | PDB header: transcription repressor Chain: B: PDB Molecule: transcriptional repressor smtb; PDBTitle: crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form |
| 102 | c3frwF_ | Alignment | not modelled | 94.0 | 29 | PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative trp repressor protein; PDBTitle: crystal structure of putative trpr protein from ruminococcus obeum |
| 103 | c2e1cA_ | Alignment | not modelled | 94.0 | 21 | PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex |
| 104 | d1trra_ | Alignment | not modelled | 94.0 | 23 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR |
| 105 | c2l4aA_ | Alignment | not modelled | 93.9 | 18 | PDB header: dna binding protein Chain: A: PDB Molecule: leucine responsive regulatory protein; PDBTitle: nmr structure of the dna-binding domain of e.coli lrp |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|--|
| 106 | c2elhA_ | Alignment | not modelled | 93.9 | 20 | PDB header: dna binding protein Chain: A: PDB Molecule: cg11849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa |
| 107 | c4czdA_ | Alignment | not modelled | 93.8 | 23 | PDB header: lyase Chain: A: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway. |
| 108 | c4czdD_ | Alignment | not modelled | 93.8 | 18 | PDB header: lyase Chain: D: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway. |
| 109 | c2ia0A_ | Alignment | not modelled | 93.8 | 21 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hth-type transcriptional regulator pf0864; PDBTitle: transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864) |
| 110 | c2p6tH_ | Alignment | not modelled | 93.7 | 16 | PDB header: transcription Chain: H: PDB Molecule: transcriptional regulator, lrp/asnc family; PDBTitle: crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis |
| 111 | c4omzG_ | Alignment | not modelled | 93.6 | 7 | PDB header: transcription Chain: G: PDB Molecule: nlr; PDBTitle: crystal structure of nlr from sinorhizobium fredii |
| 112 | d1jhga_ | Alignment | not modelled | 93.6 | 20 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR |
| 113 | d1ilga1 | Alignment | not modelled | 93.6 | 20 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain |
| 114 | c2e7xA_ | Alignment | not modelled | 93.5 | 14 | PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand |
| 115 | c1ilgA_ | Alignment | not modelled | 93.4 | 19 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpa; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus |
| 116 | d2cyya1 | Alignment | not modelled | 93.3 | 21 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain |
| 117 | c5z7iC_ | Alignment | not modelled | 93.2 | 29 | PDB header: dna binding protein/dna Chain: C: PDB Molecule: cell cycle regulatory protein gcra; PDBTitle: caulobacter crescentus gcra dna-binding domain(dbd)in complex with2 unmethylated dsdna |
| 118 | c3i4pA_ | Alignment | not modelled | 93.2 | 13 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens |
| 119 | c6cmvA_ | Alignment | not modelled | 92.8 | 15 | PDB header: gene regulation Chain: A: PDB Molecule: transcriptional regulator lrs14-like protein; PDBTitle: crystal structure of archaeal biofilm regulator (abfr2) from2 sulfobolus acidocaldarius |
| 120 | d1r1ta_ | Alignment | not modelled | 92.8 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArSR-like transcriptional regulators |