# Phyre$^2$

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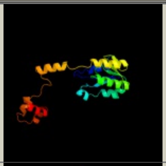
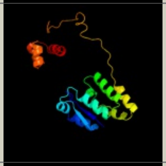
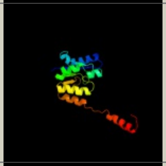
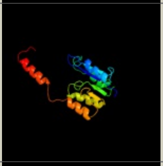
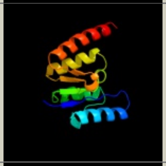
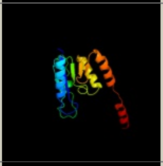
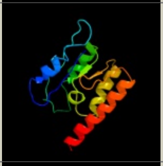
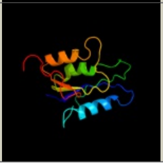
| Email | l.a.kelley@imperial.ac.uk |
| Description | P77607 |
| Date | Thu Jan 5 12:30:58 GMT 2012 |
| Unique Job ID | 1d3a40cb7c11de8a |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2gm4B_ | Alignment |  | 100.0 | 16 | **PDB header:**recombination, dna<br>**Chain:** B: **PDB Molecule:**transposon gamma-delta resolvase;<br>**PDBTitle:** an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna |
| 2 | c2r0qF_ | Alignment |  | 100.0 | 17 | **PDB header:**recombination/dna<br>**Chain:** F: **PDB Molecule:**putative transposon tn552 dna-invertase bin3;<br>**PDBTitle:** crystal structure of a serine recombinase- dna regulatory2 complex |
| 3 | d1gdta2 | Alignment |  | 99.9 | 15 | **Fold:**Resolvase-like<br>**Superfamily:**Resolvase-like<br>**Family:**gamma,delta resolvase, catalytic domain |
| 4 | d2gm4a2 | Alignment |  | 99.9 | 13 | **Fold:**Resolvase-like<br>**Superfamily:**Resolvase-like<br>**Family:**gamma,delta resolvase, catalytic domain |
| 5 | c3g13B_ | Alignment |  | 99.9 | 9 | **PDB header:**recombination<br>**Chain:** B: **PDB Molecule:**putative conjugative transposon recombinase;<br>**PDBTitle:** crystal structure of putative conjugative transposon recombinase from2 clostridium difficile |
| 6 | c3pkzK_ | Alignment |  | 99.8 | 16 | **PDB header:**recombination<br>**Chain:** K: **PDB Molecule:**recombinase sin;<br>**PDBTitle:** structural basis for catalytic activation of a serine recombinase |
| 7 | d2rsla_ | Alignment |  | 99.8 | 16 | **Fold:**Resolvase-like<br>**Superfamily:**Resolvase-like<br>**Family:**gamma,delta resolvase, catalytic domain |
| 8 | c3guvA_ | Alignment |  | 99.8 | 10 | **PDB header:**recombination<br>**Chain:** A: **PDB Molecule:**site-specific recombinase, resolvase family protein;<br>**PDBTitle:** crystal structure of a resolvase family site-specific recombinase from2 streptococcus pneumoniae |
| 9 | c3plox_ | Alignment |  | 99.8 | 13 | **PDB header:**recombination<br>**Chain:** X: **PDB Molecule:**dna-invertase;<br>**PDBTitle:** crystal structure of the fis-independent mutant of gin |
| 10 | c3bvpB_ | Alignment |  | 99.8 | 14 | **PDB header:**recombination<br>**Chain:** B: **PDB Molecule:**tp901-1 integrase;<br>**PDBTitle:** crystal structure of the n-terminal catalytic domain of tp901-12 integrase |
| 11 | d1hx7a_ | Alignment |  | 99.8 | 17 | **Fold:**Resolvase-like<br>**Superfamily:**Resolvase-like<br>**Family:**gamma,delta resolvase, catalytic domain |

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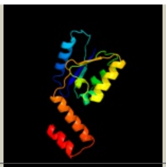
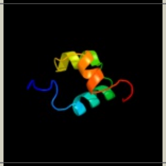
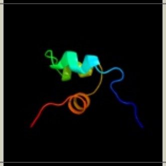
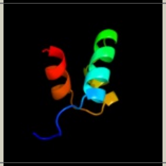
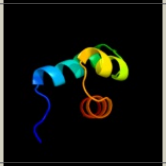
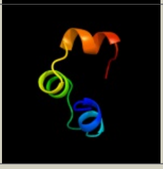
|---|---|---|---|---|---|---|
| 12 | c3lhfC_ | Alignment |  | 99.7 | 14 | **PDB header:**recombination<br>**Chain:** C: **PDB Molecule:**serine recombinase;<br>**PDBTitle:** the crystal structure of a serine recombinase from2 sulfolobus solfataricus to 2.3a |
| 13 | c3lhkA_ | Alignment |  | 99.7 | 11 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**putative dna binding protein mj0014;<br>**PDBTitle:** crystal structure of putative dna binding protein from2 methanocaldococcus jannaschii. |
| 14 | d1ijwc_ | Alignment |  | 97.4 | 24 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Recombinase DNA-binding domain |
| 15 | d1hcra_ | Alignment |  | 97.3 | 24 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Recombinase DNA-binding domain |
| 16 | c1u78A_ | Alignment |  | 97.0 | 16 | **PDB header:**dna binding protein/dna<br>**Chain:** A: **PDB Molecule:**transposable element tc3 transposase;<br>**PDBTitle:** structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna |
| 17 | d1pdnc_ | Alignment |  | 96.7 | 24 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Paired domain |
| 18 | c6paxA_ | Alignment |  | 96.6 | 24 | **PDB header:**gene regulation/dna<br>**Chain:** A: **PDB Molecule:**homeobox protein pax-6;<br>**PDBTitle:** crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions |
| 19 | d1k78a1 | Alignment |  | 96.3 | 26 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Paired domain |
| 20 | c3o60A_ | Alignment |  | 96.2 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**lin0861 protein;<br>**PDBTitle:** the crystal structure of lin0861 from listeria innocua to 2.8a |
| 21 | d2g7la1 | Alignment | not modelled | 96.2 | 15 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 22 | c3ljlB_ | Alignment | not modelled | 96.0 | 12 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**transcriptional regulator luxt;<br>**PDBTitle:** the crystal structure of the full-length transcriptional regulator2 luxt from vibrio parahaemolyticus rimd 2210633. |
| 23 | d2fq4a1 | Alignment | not modelled | 95.9 | 28 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 24 | c3sztB_ | Alignment | not modelled | 95.8 | 18 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**quorum-sensing control repressor;<br>**PDBTitle:** quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone |
| 25 | d2gena1 | Alignment | not modelled | 95.7 | 20 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 26 | d6paxa1 | Alignment | not modelled | 95.7 | 26 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Paired domain |
| 27 | d1zk8a1 | Alignment | not modelled | 95.7 | 21 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 28 | d1jt6a1 | Alignment | not modelled | 95.7 | 24 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 29 | d1t56a1 | Alignment | not modelled | 95.6 | 18 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like |

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| | | | | | | **Family:**Tetracyclin repressor-like, N-terminal domain |
| 30 | d2hyja1 | Alignment | not modelled | 95.6 | 32 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 31 | d1vi0a1 | Alignment | not modelled | 95.6 | 13 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 32 | d1rkta1 | Alignment | not modelled | 95.6 | 18 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 33 | d1ui5a1 | Alignment | not modelled | 95.6 | 16 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 34 | d2vkva1 | Alignment | not modelled | 95.6 | 26 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 35 | d1v7ba1 | Alignment | not modelled | 95.5 | 18 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 36 | d2iu5a1 | Alignment | not modelled | 95.5 | 12 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 37 | c3mvpA_ | Alignment | not modelled | 95.5 | 32 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**tetr/acrr transcriptional regulator;<br>**PDBTitle:** the crystal structure of a tetr/acrr transcriptional regulator from2 streptococcus mutans to 1.85a |
| 38 | c2iaiA_ | Alignment | not modelled | 95.5 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative transcriptional regulator sco3833;<br>**PDBTitle:** crystal structure of sco3833, a member of the tetr transcriptional2 regulator family from streptomyces coelicolor a3 |
| 39 | d2vkea1 | Alignment | not modelled | 95.5 | 32 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 40 | d2gfna1 | Alignment | not modelled | 95.5 | 12 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 41 | d2o7ta1 | Alignment | not modelled | 95.4 | 15 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 42 | c2pbxB_ | Alignment | not modelled | 95.4 | 28 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**hemagglutinin/protease regulatory protein;<br>**PDBTitle:** vibrio cholerae hapr |
| 43 | d2id6a1 | Alignment | not modelled | 95.4 | 24 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 44 | d2id3a1 | Alignment | not modelled | 95.3 | 26 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 45 | d2oi8a1 | Alignment | not modelled | 95.3 | 18 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 46 | d2fd5a1 | Alignment | not modelled | 95.3 | 8 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 47 | d2fbqa1 | Alignment | not modelled | 95.3 | 20 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 48 | d2d6ya1 | Alignment | not modelled | 95.2 | 15 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 49 | d2fx0a1 | Alignment | not modelled | 95.2 | 24 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 50 | c3e7qB_ | Alignment | not modelled | 95.2 | 17 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**transcriptional regulator;<br>**PDBTitle:** the crystal structure of the putative transcriptional regulator from2 pseudomonas aeruginosa pao1 |
| 51 | c3g7rB_ | Alignment | not modelled | 95.2 | 16 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**putative transcriptional regulator;<br>**PDBTitle:** crystal structure of sco4454, a tetr-family transcriptional2 regulator from streptomyces coelicolor |
| 52 | c3kkcB_ | Alignment | not modelled | 95.2 | 16 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**tetr family transcriptional regulator;<br>**PDBTitle:** the crystal structure of tetr transcriptional regulator from2 streptococcus agalactiae 2603v |
| 53 | d2g7ga1 | Alignment | not modelled | 95.2 | 21 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 54 | d3c07a1 | Alignment | not modelled | 95.2 | 15 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 55 | c2elhA_ | Alignment | not modelled | 95.2 | 17 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**cg11849-pa;<br>**PDBTitle:** solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa |
| 56 | d2i10a1 | Alignment | not modelled | 95.1 | 15 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like |

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| | | | | | | **Family:**Tetracyclin repressor-like, N-terminal domain |
| 57 | d2np5a1 | Alignment | not modelled | 95.1 | 24 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 58 | d1pb6a1 | Alignment | not modelled | 95.1 | 16 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 59 | d2g7sa1 | Alignment | not modelled | 95.1 | 24 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 60 | c2y31A_ | Alignment | not modelled | 95.0 | 8 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**putative repressor simreg2;<br>**PDBTitle:** simocyclinone c4 bound form of tetr-like repressor simr |
| 61 | d2g3ba1 | Alignment | not modelled | 95.0 | 18 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 62 | d2coba1 | Alignment | not modelled | 95.0 | 17 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Psq domain |
| 63 | c3nrgA_ | Alignment | not modelled | 94.9 | 8 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**tetr family transcriptional regulator;<br>**PDBTitle:** crystal structure of a tetr family transcriptional regulator2 (caur_2714) from chloroflexus aurantiacus j-10-fl at 2.56 a3 resolution |
| 64 | d1sgma1 | Alignment | not modelled | 94.9 | 12 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 65 | c2k27A_ | Alignment | not modelled | 94.9 | 24 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**paired box protein pax-8;<br>**PDBTitle:** solution structure of human pax8 paired box domain |
| 66 | d1nera_ | Alignment | not modelled | 94.9 | 12 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Phage repressors |
| 67 | d1gdta1 | Alignment | not modelled | 94.8 | 29 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Recombinase DNA-binding domain |
| 68 | d1z0xa1 | Alignment | not modelled | 94.7 | 16 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 69 | d1fsea_ | Alignment | not modelled | 94.6 | 34 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**C-terminal effector domain of the bipartite response regulators<br>**Family:**GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 70 | d1a04a1 | Alignment | not modelled | 94.6 | 38 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**C-terminal effector domain of the bipartite response regulators<br>**Family:**GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 71 | c2q0oA_ | Alignment | not modelled | 94.5 | 19 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar;<br>**PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing |
| 72 | c1h0mD_ | Alignment | not modelled | 94.4 | 15 | **PDB header:**transcription/dna<br>**Chain:** D: **PDB Molecule:**transcriptional activator protein trar;<br>**PDBTitle:** three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna |
| 73 | c1zljE_ | Alignment | not modelled | 94.4 | 24 | **PDB header:**transcription<br>**Chain:** E: **PDB Molecule:**dormancy survival regulator;<br>**PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain |
| 74 | d2hkua1 | Alignment | not modelled | 94.3 | 13 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 75 | c1r71B_ | Alignment | not modelled | 94.1 | 22 | **PDB header:**transcription/dna<br>**Chain:** B: **PDB Molecule:**transcriptional repressor protein korb;<br>**PDBTitle:** crystal structure of the dna binding domain of korb in2 complex with the operator dna |
| 76 | c3b7hA_ | Alignment | not modelled | 94.1 | 14 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**prophage lp1 protein 11;<br>**PDBTitle:** crystal structure of the prophage lp1 protein 11 |
| 77 | c3qp5C_ | Alignment | not modelled | 94.0 | 43 | **PDB header:**transcription<br>**Chain:** C: **PDB Molecule:**cvir transcriptional regulator;<br>**PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl) |
| 78 | c1x3uA_ | Alignment | not modelled | 94.0 | 32 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional regulatory protein fixj;<br>**PDBTitle:** solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot |
| 79 | c3frwF_ | Alignment | not modelled | 94.0 | 23 | **PDB header:**structural genomics, unknown function<br>**Chain:** F: **PDB Molecule:**putative trp repressor protein;<br>**PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum |
| 80 | c3t76A_ | Alignment | not modelled | 94.0 | 20 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulator vanug;<br>**PDBTitle:** crystal structure of transcriptional regulator vanug, form ii |
| 81 | d1t33a1 | Alignment | not modelled | 93.9 | 12 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 82 | d1biaa1 | Alignment | not modelled | 93.9 | 13 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Biotin repressor-like |

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|---|---|---|---|---|---|---|
| 83 | d1p4wa_ | Alignment | not modelled | 93.9 | 32 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**C-terminal effector domain of the bipartite response regulators<br>**Family:**GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 84 | d1r71a_ | Alignment | not modelled | 93.9 | 22 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**KorB DNA-binding domain-like<br>**Family:**KorB DNA-binding domain-like |
| 85 | c2jpcA_ | Alignment | not modelled | 93.8 | 38 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**ssrb;<br>**PDBTitle:** ssrb dna binding protein |
| 86 | c2krfB_ | Alignment | not modelled | 93.8 | 24 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma;<br>**PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a |
| 87 | d1yioa1 | Alignment | not modelled | 93.8 | 29 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**C-terminal effector domain of the bipartite response regulators<br>**Family:**GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 88 | d1l3la1 | Alignment | not modelled | 93.8 | 16 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**C-terminal effector domain of the bipartite response regulators<br>**Family:**GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 89 | d2jn6a1 | Alignment | not modelled | 93.7 | 27 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Cgl2762-like |
| 90 | c2rnjA_ | Alignment | not modelled | 93.7 | 32 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**response regulator protein vrar;<br>**PDBTitle:** nmr structure of the s. aureus vrar dna binding domain |
| 91 | d1xsva_ | Alignment | not modelled | 93.7 | 18 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**YlxM/p13-like |
| 92 | c3c3wB_ | Alignment | not modelled | 93.6 | 18 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr;<br>**PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr |
| 93 | d2cg4a1 | Alignment | not modelled | 93.6 | 22 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain |
| 94 | d2bjca1 | Alignment | not modelled | 93.6 | 27 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 95 | c3mzyA_ | Alignment | not modelled | 93.6 | 24 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**rna polymerase sigma-h factor;<br>**PDBTitle:** the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a |
| 96 | d1trra_ | Alignment | not modelled | 93.5 | 28 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**TrpR-like<br>**Family:**Trp repressor, TrpR |
| 97 | d1jhga_ | Alignment | not modelled | 93.4 | 31 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**TrpR-like<br>**Family:**Trp repressor, TrpR |
| 98 | c2l8nA_ | Alignment | not modelled | 93.4 | 35 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional repressor cytr;<br>**PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna |
| 99 | c3korD_ | Alignment | not modelled | 93.3 | 29 | **PDB header:**transcription<br>**Chain:** D: **PDB Molecule:**possible trp repressor;<br>**PDBTitle:** crystal structure of a putative trp repressor from staphylococcus2 aureus |
| 100 | d1b0na2 | Alignment | not modelled | 93.3 | 23 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**SinR domain-like |
| 101 | c3bs3A_ | Alignment | not modelled | 93.2 | 23 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**putative dna-binding protein;<br>**PDBTitle:** crystal structure of a putative dna-binding protein from bacteroides2 fragilis |
| 102 | d1lcda_ | Alignment | not modelled | 93.2 | 28 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 103 | c2lcvA_ | Alignment | not modelled | 93.0 | 35 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr;<br>**PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation |
| 104 | d1s7oa_ | Alignment | not modelled | 92.9 | 21 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**YlxM/p13-like |
| 105 | d1rp3a2 | Alignment | not modelled | 92.9 | 20 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors<br>**Family:**Sigma4 domain |
| 106 | c3trbA_ | Alignment | not modelled | 92.9 | 16 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**virulence-associated protein i;<br>**PDBTitle:** structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii |
| 107 | d1i1ga1 | Alignment | not modelled | 92.9 | 32 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain |
| 108 | d1vz0a1 | Alignment | not modelled | 92.8 | 32 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**KorB DNA-binding domain-like<br>**Family:**KorB DNA-binding domain-like |
| | | | | | | **Fold:**DNA/RNA-binding 3-helical bundle |

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| 109 | d1hlva1 | Alignment | not modelled | 92.8 | 23 | **Superfamily:**Homeodomain-like<br>**Family:**Centromere-binding |
| 110 | c2kpjA_ | Alignment | not modelled | 92.8 | 26 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**sos-response transcriptional repressor, lexa;<br>**PDBTitle:** solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a |
| 111 | d1uxda_ | Alignment | not modelled | 92.7 | 26 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 112 | c3cloC_ | Alignment | not modelled | 92.7 | 38 | **PDB header:**transcription regulator<br>**Chain:** C: **PDB Molecule:**transcriptional regulator;<br>**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 |
| 113 | d1y9qa1 | Alignment | not modelled | 92.7 | 11 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Probable transcriptional regulator VC1968, N-terminal domain |
| 114 | c2ebyA_ | Alignment | not modelled | 92.6 | 24 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ybaq;<br>**PDBTitle:** crystal structure of a hypothetical protein from e. coli |
| 115 | c3hosA_ | Alignment | not modelled | 92.6 | 14 | **PDB header:**transferase, dna binding protein/dna<br>**Chain:** A: **PDB Molecule:**transposable element mariner, complete cds;<br>**PDBTitle:** crystal structure of the mariner mos1 paired end complex with mg |
| 116 | d1qpza1 | Alignment | not modelled | 92.6 | 32 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 117 | c3hugA_ | Alignment | not modelled | 92.5 | 30 | **PDB header:**transcription/membrane protein<br>**Chain:** A: **PDB Molecule:**rna polymerase sigma factor;<br>**PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl |
| 118 | d1efaa1 | Alignment | not modelled | 92.4 | 27 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 119 | d1j5ya1 | Alignment | not modelled | 92.3 | 24 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Biotin repressor-like |
| 120 | c3fmyA_ | Alignment | not modelled | 92.2 | 20 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**hth-type transcriptional regulator mqsa<br>**PDBTitle:** structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021) |